



NEWSLETTER 2025, Volume 4

Quotes: “Recent decades have seen a rise in the incidence of tick-borne diseases in the US, along with an increased number of pathogens transmitted by ticks, and geographic expansion of tick populations.” Rodino, K.G., et al.; *Journal of Clinical Microbiology* (2025); <https://doi.org/10.1128/jcm.00807-23>

New features:

- **We have created separate sections for tick and tick-borne disease news from North Carolina and the rest of the South.**

Highlights:

- **Updates to the CDC’s alpha gal syndrome website and tick removal instructions**
- **Expanding range of *Ixodes scapularis* and *Borrelia burgdorferi* in North Carolina**
- **Podcast episode about Lone Star Tick and Ehrlichiosis with Dr. Ron Falk, Dr. Ross Boyce, and Dr. Katherine Huffman-Falk**
- **Detection of *Rickettsia* and *Bartonella* in fleas and ticks collected from pet cats and dogs in Georgia**
- **Long-distance transport of ticks and tick-borne diseases by humans in Texas**
- **Impact of deer exclusion fencing on black-legged ticks**
- **Unique presentation of tularemia in pediatric patient**
- **Investigation of erythema migrans patients finds microbes in lesions**
- **Role of tick symbiotic organisms in tick-borne disease transmission**
- **Pill Clarity**

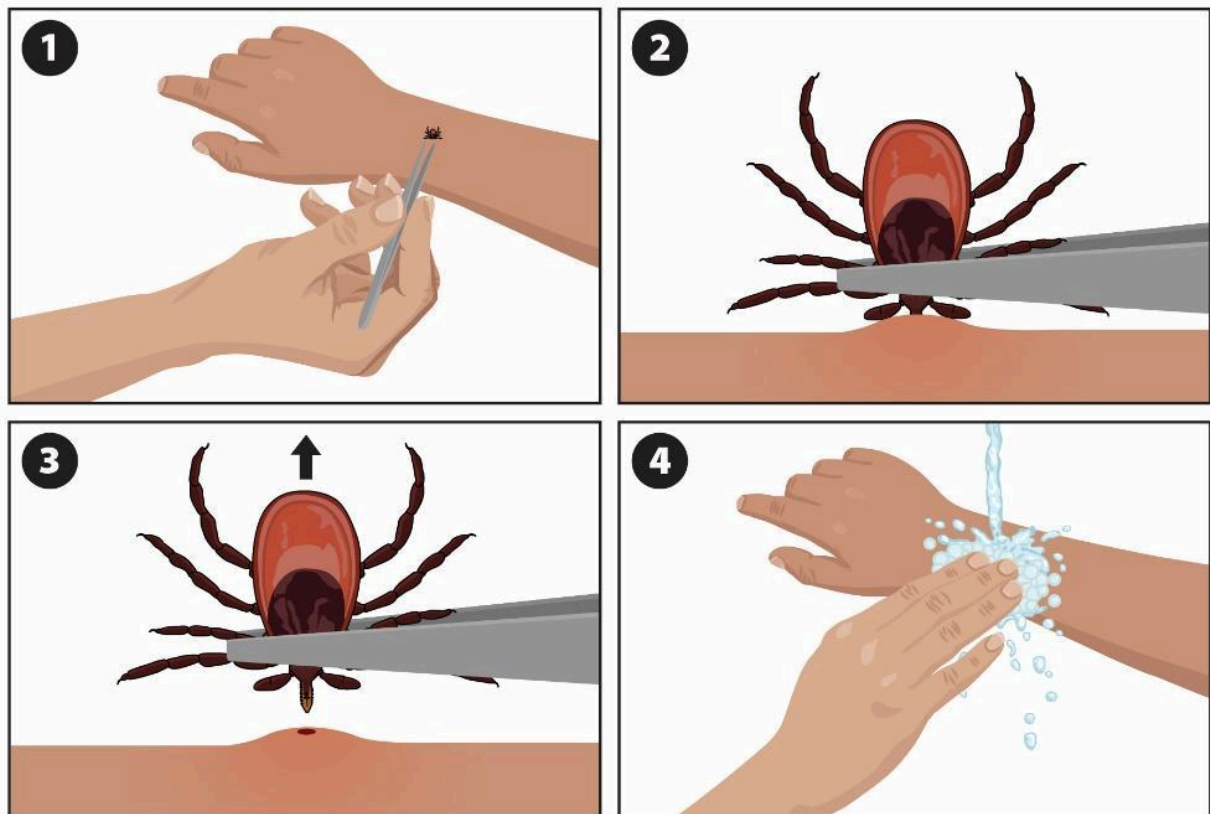
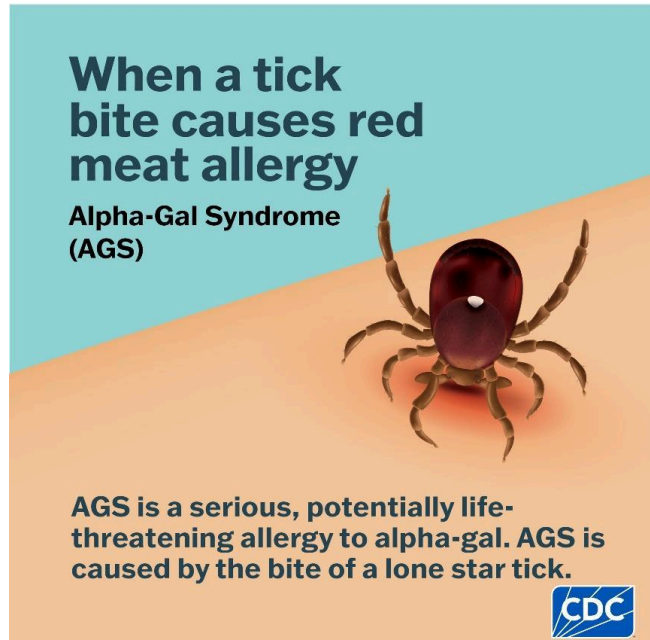
CDC Updates

Alpha Gal Syndrome Website

The CDC has updated their AGS website ([linked here](#)) to share the latest on what AGS is and how to prevent, diagnose, and manage it. Check out their newest figures and graphics [here](#).

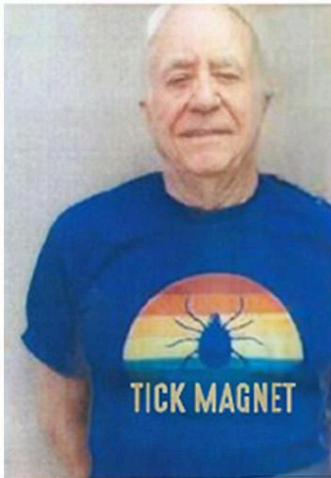
What to do after a tick bite

The CDC has update their steps to removing an attached tick with regular tweezers or fingers when fine-tipped tweezers are not available, including new photos to help guide tick removal. You can read their instructions [here](#).



TIC-NC Activities

On June 24th, Monte Westphal gave a presentation on ticks to an audience of over 50 people in Hendersonville, NC. He also distributed TIC-NC booklets to attendees.



Safely Enjoy the Outdoors: Let's talk Ticks!

Tuesday June 24, 7:00 PM
Village Hall

Join us as fellow resident and Blue Ridge Naturalist, Monte Westphal, talks all things, Tick's! He will teach us about the most common ticks, how to protect yourself from tick borne diseases, AND when you should seek medical attention after a tick bite.



North Carolina

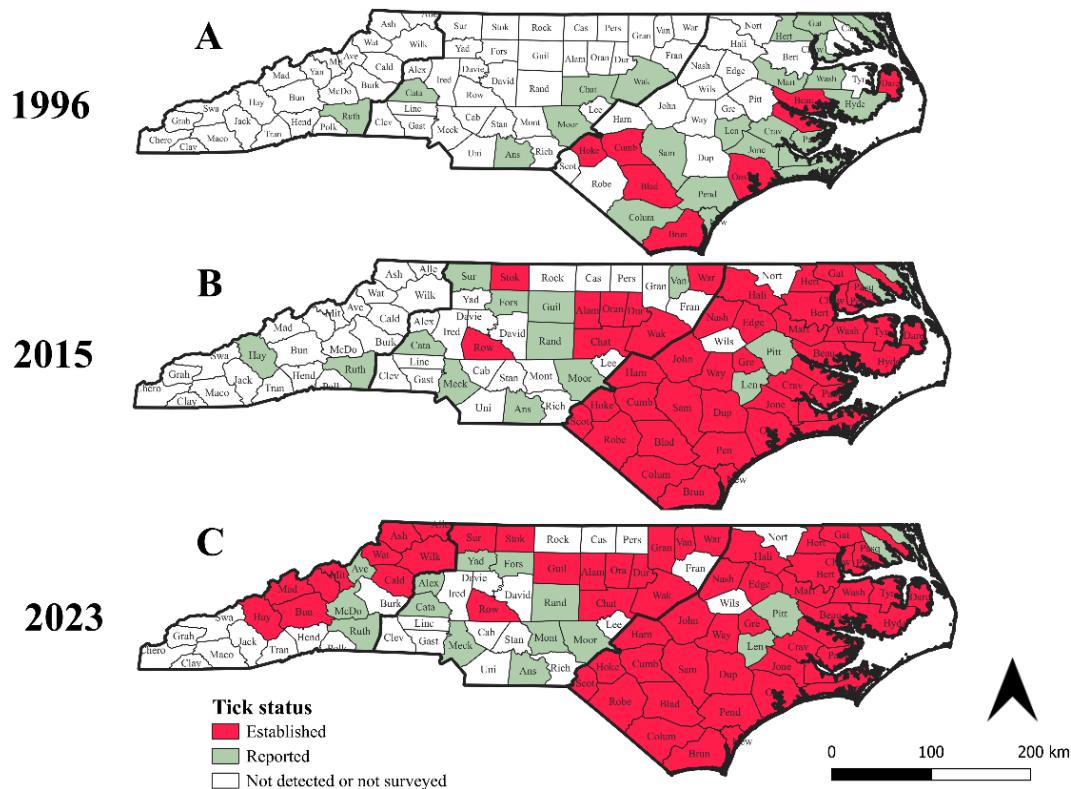
Expanding range of *Ixodes scapularis* Say (Acari: Ixodidae) and *Borrelia burgdorferi* infection in North Carolina counties, 2018-2023

North Carolina (NC) has been experiencing a recent surge in human Lyme disease (LD) cases. Understanding the distribution of tick-borne diseases necessitates understanding the distribution of the ticks that transmit their causative pathogens. Unfortunately, in NC, knowledge on tick distribution is outdated.

In this manuscript, we report the results of a state-wide entomologic survey conducted in 42 NC counties by flagging/dragging from spring 2018 to summer 2023. *Ixodes scapularis* nymphs and adults were screened for *Borrelia burgdorferi* (the causative agent of LD) and four other tick-borne bacterial pathogens (*Anaplasma phagocytophilum*, *B. mayonii*, *B. miyamotoi*, and *Babesia microti*) by the Centers for Disease Control and Prevention (CDC).

Consistent with current data on human LD cases incidence and distribution, results of this study indicated a range expansion of *I. scapularis* with higher tick densities and *B. burgdorferi* infection prevalence now occurring in the Blue Ridge Mountains province of western NC. Temporal analysis of *I. scapularis* presence data indicated that this shift is fairly recent (about 10 years).

Finally, in the Blue Ridge Mountains we detected a northeast-to-southwest gradient in *I. scapularis* tick and *B. burgdorferi* infection prevalence suggesting that this trend is driven by a spread of the northern clade *I. scapularis* ticks into NC from southwestern Virginia, along the Appalachian Mountains. Other pathogenic bacteria detected in *I. scapularis* ticks included *B. miyamotoi* and *A. phagocytophilum*, that were limited to the Blue Ridge Mountains. These results have important public health implications, including the need for enhanced tick surveillance, updated clinical awareness, and targeted public education in newly affected areas.



Reuben, A.G., et al.; *PLOS One* (2025); <https://doi.org/10.1371/journal.pone.0329511>

Summary: This study finds that the spatial range of *Ixodes scapularis* ticks and the pathogens they carry, including *Borrelia burgdorferi* (the causative agent of Lyme disease) has expanded in North Carolina.

Comparative evaluation of *Amblyomma americanum* and *Dermacentor variabilis* microbial agents and human disease case data in seven Piedmont counties of North Carolina, 2020-2023

Tick-borne pathogens pose an ongoing threat to human health in the southeastern United States, where tick and host abundances are high. In North Carolina, several medically important tick species are present, but in the Piedmont region, *Amblyomma americanum* is particularly

abundant and associated with multiple human pathogens, including *Rickettsia amblyommatis*, a hypothesized human pathogen.

In this study, we build on recent tick surveillance efforts across several North Carolina counties by screening *A. americanum* for *Ehrlichia ewingii*, *Ehrlichia chaffeensis*, and *R. amblyommatis* while also analyzing tick abundance, pathogen prevalence, and county-level human disease case data from the North Carolina Department of Health to assess potential correlations.

Our results reveal variation in pathogen prevalence across counties, with Chatham County consistently emerging as a high-risk area due to high tick abundance and elevated infection rates. However, we did not observe a strong correlation between tick abundance or pathogen prevalence and reported human disease cases at the county level. These findings highlight counties of elevated risk in a region experiencing an increasing burden of tick-borne disease and contribute to our understanding of ongoing public health trends.

Adams, D.R., et al.; *Journal of Vector Ecology* (2025); <https://doi.org/10.52707/1081-1710-50.2-120>

Summary: While there is variation in pathogen prevalence across the North Carolinian Piedmont counties, there is no strong correlation between tick abundance or pathogen prevalence and reported human cases at the county level.

Podcast: Lone Star Tick and Ehrlichiosis with Drs. Ross Boyce, Katherine Huffman-Falk, and Ronald Falk

Dr. Ron Falk speaks with Dr. Ross Boyce, an Associate Professor of Medicine and Epidemiology, and his wife who was recently bitten by the Lone Star Tick, retired nephrologist Dr. Katherine Huffman-Falk. Their conversation explores the patient's experience with ehrlichiosis, and the provider's approach to recognizing and treating the disease.

Eds. note: Although March to October is mentioned in the podcast as tick season in NC, ticks can be active all through the winter on warmer days, especially the black-legged tick. So, tick season in NC should be viewed as all year with the worst months being from March through October.

Check out this episode of *Chair's Corner with Dr. Ron Falk* [here](#).

The South

Detection of *Rickettsia* and *Bartonella* in fleas and ticks collected from pets at veterinary clinics in Georgia, United States

Many human infections are transmitted through contact with household pets. The purpose of this cross-sectional study was to determine the occurrence of ticks and fleas on pets (dogs and cats) in local veterinary clinics in Statesboro, Georgia. We screened ectoparasites

for *Rickettsia* and *Bartonella* and assessed owner knowledge and practices related to tick- and flea-borne diseases.

Ectoparasites were collected and identified using standard taxonomic keys, and their genomic DNA was extracted. Three TaqMan assays were used to test ectoparasites for flea-borne *Rickettsia* DNA. Nested PCR targeting riboflavin synthase encoding gene (*ribC*) was used to detect *Bartonella* species DNA. Restriction fragment length polymorphism analysis and sequencing were used to identify the microorganisms detected. Upon providing written consent, owners completed a self-administered questionnaire to provide information concerning their knowledge and practices about vector-borne diseases. Data from 27 pets were collected from 2 veterinary clinics during September to December 2014. A total of 58 ectoparasites including fleas (n = 51) and ticks (n = 7) were collected from 19 cats and dogs.

The cat flea, *Ctenocephalides felis* (n = 44), was the predominant flea species followed by *Pulex* sp. (n = 7). All ticks were *Ixodes scapularis*. Using PCR, RFLP, and sequencing, it was determined that the majority of cat fleas contained DNA of known human pathogens, including *Rickettsia asembonensis* (72.5%), *Rickettsia felis* (5.9%), *Bartonella henselae* (2%), and *Bartonella quintana* (7.8%). DNA of *B. quintana* was also detected in 2 *Pulex* sp. fleas and 2 ticks. Two animals had ectoparasites co-infected with *Rickettsia* and *Bartonella*.

Most owners (95.7%) knew that fleas can transmit animal disease agents, but they were less aware that fleas can spread diseases to humans, and only 12.5% of owners knew about cat scratch disease. Our data indicate that there is a risk of flea- and tick-borne zoonotic infections in households owning cats and dogs. Educational materials, vector-control preventive measures, and appropriate personal attitudes and practices are needed to ensure public health safety and wholesome interactions with pets.

Rajakaruna, R.S., et al.; *The Journal of Parasitology* (2025); <https://doi.org/10.1645/24-109>

Summary: This study found that many ticks and fleas could be found on domestic cats and dogs, and that they may be potential sources of infection for their owners.

Evidence for the long-distance transport of ticks and tick-borne pathogens by human travelers to Texas, USA

Background: The incidence of tick-borne diseases in the USA has surged in recent years, with >50 000 cases reported from an estimated half-million cases annually. While domestic vectors are well characterized, the role of human travel in transporting exotic ticks and pathogens remains poorly understood.

Methods: We analysed 4808 submissions of ticks removed from individuals to the Tick-Borne Disease Research Laboratory in Texas, USA, from 2004 to 2024. Tick species were identified phenotypically or through DNA-based sequencing, and pathogens (*Borrelia* spp., *Rickettsia* spp., *Ehrlichia* spp., *Anaplasma phagocytophilum* and *Babesia microti*) were detected using molecular assays. Submitter travel histories were cross-referenced with known tick geographic ranges to identify long-distance transport.

Results: We documented cases of intercontinental, international and domestic interstate transport of ticks by human travellers. Four *Ixodes ricinus* ticks—originating from Europe—were transported to Texas; one tick carried *Borrelia afzelii*, a Lyme disease pathogen not endemic to North America. Central and South American *Amblyomma* species were repeatedly imported, raising concerns for pathogen transmission and tick establishment. Domestic travellers also carried *Ixodes scapularis* ticks infected with *Borrelia burgdorferi* sensu stricto, *Babesia microti* and *A. phagocytophilum* from Lyme-endemic regions of the USA to Texas, along with non-native species *Ixodes pacificus*, *Dermacentor andersoni* and *Dermacentor occidentalis* from endemic areas in the western United States.

Conclusions: Long-distance transport of ticks by travellers represents an underrecognized pathway for the global spread of ticks and tick-borne pathogens. Clinicians should consider travel history in tick-borne illness diagnostics. Enhanced surveillance, public education and travel screening are critical to mitigating these risks.

Allen, M.S., et al.; *Journal of Travel Medicine* (2025); <https://doi.org/10.1093/jtm/taaf032>

Summary: Long-distance transport of ticks may facilitate the worldwide spread of ticks and their pathogens.

National Section

Diversity of Ticks and Rickettsiae in the Southwestern United States: Implications for Public Health

Background: Surveillance is important in addressing the significant public health concerns posed by tick-borne diseases. However, the southwestern U.S. presents particular challenges due to diverse tick fauna and varied ecologies.

Methods: From 2021 to 2022, we conducted a partner-based tick surveillance program in Arizona and California to assess the presence of *Rickettsia* spp. pathogens and species composition of tick vectors.

Results: A total of 913 ticks was collected, comprising in descending abundance *Rhipicephalus sanguineus*, *Dermacentor similis*, *Ixodes pacificus* (*I. pacificus*), *Argas* sp., *Otobius megnini*, and *Haemaphysalis leporispalustris*. Arizona submitted predominantly brown dog ticks (90.05% of all ticks from Arizona), while California showed greater tick species richness with five species identified. No *Rickettsia rickettsii* was detected, but a variety of other *Rickettsia* spp. was found in ticks from both Arizona and California and included *Rickettsia rhipicephali* (*R. rhipicephali*), *Rickettsia massiliae*, and *Rickettsia monacensis*-like rickettsial agents of *I. pacificus*, and two rickettsial organisms that were not identified to species: one *Rickettsia montanensis* or *Rickettsia raoultii*-like, and the other most similar to *Candidatus Rickettsia tarasevichiae* (*R. tarasevichiae*).

Conclusion: This research contributes to our understanding of tickborne diseases in the southwestern U.S., and emphasizes the need for targeted surveillance and intervention initiatives

in a region with complex relationships among ticks, hosts, and *Rickettsia* species. In particular, the finding of an apparently novel pairing of an unknown *Argas* sp. tick and *R. tarasevichiae*-like organism suggests that argasid species are an important target for future research. In addition, the results—both tick species submitted and resulting *Rickettsia* spp. identified—highlights the strengths and potential biases associated with a partner-based sampling method for tick surveillance.

Castillo, G.A., et al.; *Vector-Borne and Zoonotic Diseases* (2025); <https://doi.org/10.1089/vbz.2024.0102>

Summary: The southwestern US has historically been a challenging landscape for studying tick-borne diseases. This paper contributes to understanding of ticks and the diseases they carry in the region.

Tick infestation of birds in grasslands experiencing woody plant encroachment in the United States Great Plains

Woody plant encroachment is one of the largest threats to grasslands of the US Great Plains. Its spread, mainly due to fire suppression, affects entire ecosystems, including arthropod vectors, bird communities, and the ecology of vector-borne disease. Eastern redcedar (*Juniperus virginiana*), one of the primary encroaching species in this region, is known to increase abundance of pathogen-carrying tick species such as *Amblyomma americanum*; however, the role birds play in carrying ticks in association with eastern redcedar encroachment is unknown.

In areas of Oklahoma representing 3 stages of eastern redcedar encroachment, we mist-netted birds, sampled larval and nymphal ticks from them, and evaluated tick infestation of birds from May to October 2023. Of 140 birds sampled, 25.7% were infested with ticks, a higher prevalence of infestation than in most previous studies of birds in the United States. Notably, some birds were infested with *Ixodes scapularis*, which has rarely been found on wildlife other than reptiles in the southern US. There were no significant differences in prevalence or intensity of tick infestation in birds across differing levels of eastern redcedar encroachment, indicating that a high proportion of birds carry ticks in all encroachment stages.

This study provides the first evidence that birds contribute to the ecology of tick-borne disease systems in grasslands experiencing woody plant encroachment. Our results, which suggest birds are likely moving ticks into, out of, and among eastern redcedar-encroached grasslands of the US Great Plains, can help inform land management and public health efforts seeking to reduce disease risk.

Tucker, T.C., et al.; *Journal of Medical Entomology* (2025); <https://doi.org/10.1093/jme/tjaf072>

Summary: The findings from this paper show that birds contribute to tick-borne disease spread in grasslands experiencing woody plant encroachment in the United States.

The impact of deer exclusion fencing on host-seeking blacklegged ticks on suburban residential properties in southern New England

Recommendations to use deer-excluding fencing as a method to reduce blacklegged ticks (*Ixodes scapularis* Say) in residential settings are based primarily upon studies excluding deer from large areas (≥ 3.5 hectares), often in undeveloped woodland settings. Evidence is still needed on the efficacy of deer-excluding fences for tick management at smaller suburban residential properties common to tick-endemic areas of the northeastern United States.

We measured *I. scapularis* abundance at 16 fenced and 16 unfenced properties in Fairfield County, Connecticut, Westchester County, New York, and Washington County, Rhode Island. Overall, adult and nymphal *I. scapularis* encounter rates (ticks per sampling meter) were slightly higher on unfenced properties compared to within fenced properties, but differences were not significant ($P > 0.05$).

Among fenced properties alone, tick encounter rates were significantly higher in areas immediately outside of fences compared with inside of fences for nymphs ($P = 0.005$), but not for adults ($P > 0.05$). Prevalence of tick pathogen infection with *Borrelia burgdorferi* sensu stricto, *Borrelia miyamotoi*, *Babesia microti*, *Babesia odocoilei*, or *Anaplasma phagocytophilum* did not differ significantly between fenced and unfenced properties ($P > 0.05$). Irrespective of fencing, adult tick abundance was higher at properties with stonewalls, dense herbaceous ecotone vegetation, and an absence of bird feeders. Nymphal tick encounter rates were associated with stonewalls, an absence of bird feeders, and presence of dense herbaceous understory vegetation. Household survey data revealed that deer were observed within some fenced areas. Our findings do not provide strong evidence that deer-excluding fences at properties smaller than 3.5 hectares suppress blacklegged ticks.

Conally, N.P., et al.; *Journal of Medical Entomology* (2025); <https://doi.org/10.1093/jme/tjaf070>

Summary: Deer exclusion fencing does not appear to suppress black-legged tick populations at properties smaller than 3.5 hectares, particularly because there are other features that may support tick populations and deer can still be found within fenced areas.

Tularemia: A Unique Presentation for a Rare Disease

This report highlights an uncommon presentation of tularemia in a high-risk pediatric patient to increase awareness and broaden the differential diagnosis among clinicians. A previously healthy eight-year-old female presented to the emergency department multiple times within two weeks with nonspecific flu-like symptoms, worsening purulent conjunctival injection, fever, and left-sided facial swelling. She was initially diagnosed with several conditions, including corneal abrasion, preseptal cellulitis, and dacryocystitis, and was treated with antibiotics without symptom resolution. Upon admission, the patient showed signs of a severe infectious process with febrile illness, leukocytosis, and orbital involvement. A detailed history revealed high-risk exposures, including tick bites and animal contact. Tularemia testing was positive, and the patient was treated with a prolonged course of gentamicin, resulting in complete resolution of symptoms. Tularemia, caused by *Francisella tularensis*, can present with various symptoms and is often difficult to diagnose without high clinical suspicion. The case emphasizes the importance

of considering rare diseases such as tularemia in endemic regions, especially when initial treatments fail.

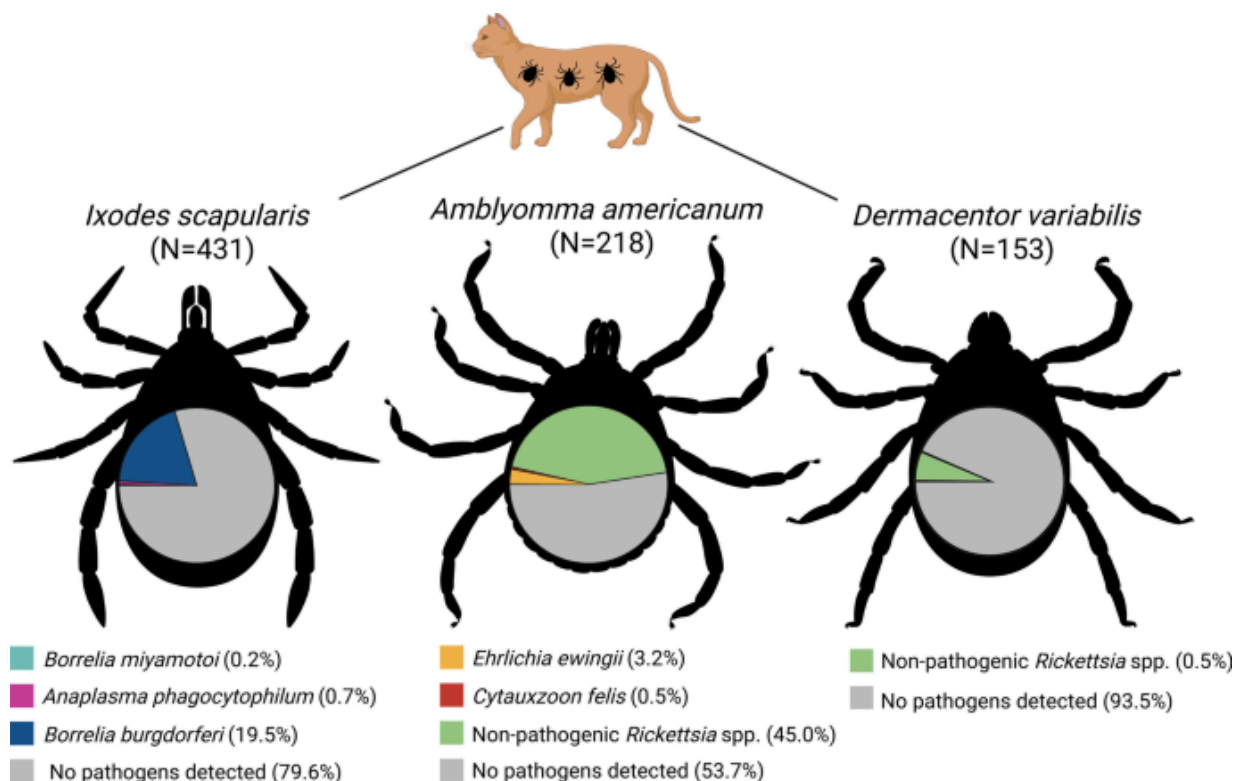
Allison, J., et al.; *Cureus* (2025); <https://doi.org/10.7759/cureus.84503>

Summary: This report describes an unusual presentation of tularemia in a pediatric patient and highlights the need to consider rare diseases in their endemic areas.

Detection of pathogens within Ixodid ticks collected from domestic cats across the USA

Background: Ixodid ticks and tick-borne diseases continue to be an emerging health concern in the USA. Companion animals dwell in close proximity with people; therefore, it is important to understand how they might contribute to the maintenance of tick-borne pathogens, especially zoonoses, in the peri-domestic environment. Domestic cats are often overlooked in epidemiological investigations of tick-borne infections compared with their canine counterparts.

Methods: The purpose of this study was to investigate the potential exposure of domestic cats to tick-borne pathogens by molecularly testing adult Ixodid ticks collected from cats that were presented for veterinary care. A total of 802 ticks collected from 512 individual cats were tested by conventional polymerase chain reaction (PCR). Ticks were morphologically identified as *Ixodes scapularis* ($n = 431$), *Amblyomma americanum* ($n = 218$), and *Dermacentor variabilis* ($n = 153$).



Results: The most prevalent pathogen detected was *Borrelia burgdorferi* s.s., detected in 19.5% of *I. scapularis*. *Ehrlichia ewingii* was detected in 3.2% of *A. americanum*. *Anaplasma phagocytophilum* was detected in 0.7% of *I. scapularis*. *Cytauxzoon felis* was detected in 0.5% of *A. americanum*. *Borrelia miyamotoi* was detected in 0.2% of *I. scapularis*. Submitting clinics were contacted to gather additional information on cats infested by pathogen-infected ticks. This information did not yield a meaningful relationship between potential pathogen exposure and development of clinical signs around the time of tick collection.

Conclusions: This study is the largest survey for pathogens within Ixodid ticks collected from domestic cats in the USA and the only survey in which retrospective clinical information was retrieved. While the effect of many tick-borne pathogens on feline health remains unclear, this study demonstrates that cats infested with ticks are at risk for pathogen exposure and may be a source for harboring pathogen-infected ticks in and around the home.

Smith, R.C., et al.; *Parasites & Vectors* (2025); <https://doi.org/10.1186/s13071-025-06902-z>

Summary: This study provides unique and foundational insights into the pathogens carried by Ixodid ticks associated with domestic cats. It also shows that cats infected with ticks may be at risk for pathogen exposure and could be a reservoir for tick-borne pathogens.

Update on North American tick-borne diseases and how to diagnose them

Recent decades have seen a rise in the incidence of tick-borne diseases in the US, along with an increased number of pathogens transmitted by ticks, and geographic expansion of tick populations. A variety of laboratory testing methodologies are available for the diagnosis of tick-borne diseases, including serology, microscopy, and molecular-based methods. The preferred approach varies by the specific disease, locally available test options, and the stage of illness at patient presentation. This mini-review focuses on updates in our understanding of the epidemiology of tick-borne diseases in the US and advances in the field of laboratory diagnostics.

Rodino, K.G., et al.; *Journal of Clinical Microbiology* (2025); <https://doi.org/10.1128/jcm.00807-23>

Summary: This review summarizes the epidemiology, diagnostics, and clinical characteristics of major tick-borne diseases in the United States.

Spatial distribution and clustering of medically important tick species in Illinois: Implications for tick-borne disease risk

The geographic range of medically significant tick species has expanded across the United States, with Illinois experiencing increased tick populations and incidence of tick-borne diseases (TBDs) in recent decades.

This study investigated the spatial distribution of three tick species: *Amblyomma americanum* (lone star tick), *Dermacentor variabilis* (American dog tick), and *Ixodes scapularis* (blacklegged tick) in Illinois, using data collected through active surveillance from 2018 to 2022. A total of 476 records of 1414 ticks were analyzed. Spatial analytical techniques,

including species distribution mapping, Inverse Distance Weighted (IDW) interpolation, Hot Spot (Getis-Ord Gi*), and Cluster and Outlier (Anselin Local Moran's I) analyses, were applied to identify distribution patterns and statistically significant local clusters.

The species distribution mapping results revealed distinct geographic patterns: *A. americanum* was most prevalent in southern, *D. variabilis* in central and southern, and *I. scapularis* in central and northeastern Illinois regions, respectively. With agreement between Hot Spot and Cluster-outlier analysis, counties with significantly high tick prevalence were identified, including 10 counties for *A. americanum* in southern Illinois, four counties for *D. variabilis* in central and southern Illinois, and seven counties for *I. scapularis* in central and northeastern Illinois.

The study results correspond with incidence of TBDs reported to the Illinois Department of Public Health (IDPH), including ehrlichiosis, Rocky Mountain spotted fever, Lyme disease, and anaplasmosis. These findings provide insights into the geographic variability of tick distributions, emphasizing the importance of targeted public health strategies and tick control efforts to mitigate the burden of TBDs in Illinois.

Hussain A., et al.; *Ticks and Tick-borne Diseases* (2025); <https://doi.org/10.1016/j.ttbdis.2025.102533>

Summary: This paper shows the spatial distribution of three tick species in Illinois, which may inform targeted public health strategies and tick control efforts.

International Section

Influence of forest structural complexity on small mammal body condition and its impact on tick burden and pathogen prevalence

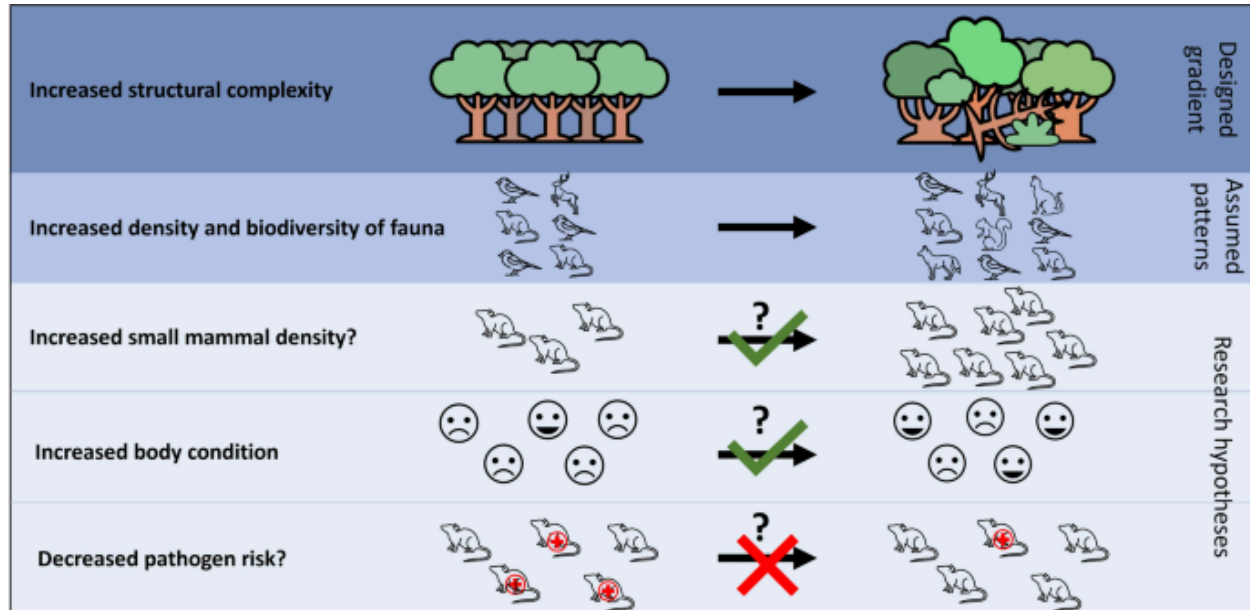
Background: More and more forest management focuses on increasing structural complexity to improve environmental conditions for biodiversity and forest functioning. However, it remains uncertain whether animal populations also benefit from increased forest structure. Small mammals are key reservoirs for zoonotic diseases, so understanding how forest structure changes their condition and how this, in turn, affects infection dynamics is critical for animal and human health.

Methods: This study examined relationships between forest structural complexity, individual body condition (scaled mass index (SMI) and telomere length), pathogen prevalence, and tick load in bank voles and wood mice across 19 forest plots in northern Belgium, representing a gradient of structural complexity.

Results: Results showed that higher forest complexity, especially with more dead wood and a well-developed herb layer, increased small mammal abundance. Density varied by tree species, with highest abundances in oak and lowest in poplar forests. In addition, body condition improved with structural complexity; SMI increased with woody layer complexity in wood mice and with dead wood availability in bank voles. No clear relationship between telomere length

and forest complexity was observed. The relationship between body condition and pathogen prevalence was species- and pathogen-specific. Small mammals in better body condition were more likely to host *Borrelia burgdorferi* (causing Lyme disease), particularly in complex forests, indicating a higher infection risk with increasing structural complexity.

Conclusions: Forest management practices that aim to enhance forest structure and biodiversity may thus inadvertently increase zoonotic disease risk and should take these findings in consideration to minimize the risk for human health.



Vanroy, T., et al.; *Parasites & Vector* (2025); <https://doi.org/10.1186/s13071-025-06874-0>

Summary: The relationship between forest structural complexity (e.g., dead wood, developed herb layers) and tick/pathogen prevalence is complicated. Forest management practices that aim to enhance forest structure and biodiversity may accidentally be increasing the risk of zoonotic diseases.

Investigation of erythema migrans patients identifies *Borrelia* species and *Neoehrlichia mikurensis* with implications for clinical assessment

Emerging tick-borne infections pose public health challenges and may complicate treatment decisions. The EMBio study, a multicenter observational study, aims to describe erythema migrans (EM), an early localized manifestation of *Borrelia burgdorferi sensu lato* (s.l.) infection, and investigate the occurrence of tick-borne co-infections among patients presenting with this skin lesion. Additionally, the study seeks to determine relations between EM morphology, other clinical manifestations, specific pathogens, and disease prognosis.

Clinical characteristics, skin biopsies, and blood samples were analyzed from 26 patients to assess co-infections, quantity, *Borrelia* species, and spirochete load. *Borrelia* DNA was detected

in 88% of EM skin lesions, with *Borrelia afzelii* as the predominant species. Two cases of co-infections were identified, one involving two *Borrelia* species and one involving *Borrelia afzelii* and the intracellular bacterium *Neoehrlichia mikurensis*. Notably, homogeneous EM lesions harbored significantly higher spirochete quantities in the central zone compared to annular lesions, suggesting that lesion morphology reflects local bacterial density.

This supports the value of molecular diagnostics in detecting mixed infections and supports morphology-guided biopsy strategies in the clinical assessment of cutaneous infections. This study contributes to a better understanding of co-infection dynamics and may improve diagnostic accuracy and patient management in endemic settings.

Cronhjort, S., et al.; *Scientific Reports* (2025); <https://doi.org/10.1038/s41598-025-07291-0>

Summary: Ongoing studies of erythema migrans – a hallmark early manifestation of *Borrelia burgdorferi sensu lato* infection, or Lyme disease – have found *Borrelia* species and *Neoehrlichia mikurensis* in the skin lesions.

Tick-Borne Infectious Diseases in China, 2003–2023

Tick-borne diseases (TBDs) pose a substantial threat to global public health, including China. This article systematically reviews the epidemiology of TBDs in Chinese mainland between 2003 and 2023. We retrieved and analyzed the incidence and distribution of notable bacterial, viral, and parasitic TBDs in China, and discussed their clinical characteristics, diagnostic approaches, and vectors. Severe fever with thrombocytopenia syndrome is the leading TBD in China, with cases rapidly increasing since its first report in 2009, and a high case fatality rate of 5%–33% in patients with severe disease. Other TBDs reported in China include spotted fever group rickettsiosis, human granulocytic anaplasmosis, Lyme borreliosis, babesiosis, and tick-borne encephalitis. Infections with emerging tick-borne pathogens, such as Yezo virus and Beiji nairovirus, have appeared very recently. Although evidence of human infection with Crimean-Congo hemorrhagic fever virus, *Francisella tularensis*, and *Bartonella* is currently unavailable, continuous monitoring of these pathogens remains necessary. This study enhances our understanding of TBDs, provides guidance for public health decision-making regarding important bacterial, viral, and parasitic TBDs, and offers new opportunities for TBD research in China.

Zhu, Y., et al.; *China CDC Weekly* (2025); <https://weekly.chinacdc.cn/en/article/doi/10.46234/ccdcw2025.150>

Summary: There is a large diversity and wide distribution of tick species in China, leading tick-borne diseases to become a significant threat to public health.

Ticks jump in a warmer world: Global distribution shifts of main pathogenic ticks are associated with future climate change

In recent decades, the threats of ticks and tick-borne diseases (TBDs) have increased extensively with environmental change, urbanization, and rapidly changing interactions between humans and animals. However, the large-scale distribution of tick and TBD risks, as well as their relationship with environmental change, remains inadequately unclear.

Here, we first proposed a “tick-pathogen-habitat-human” model to project the global potential distribution of main pathogenic ticks using a total of 70,714 occurrence records. Meanwhile, the effects of ecological factors and socio-economic factors driving the distribution pattern were evaluated. Based on this, the risk distribution of TBDs was projected by large-scale “tick-pathogen-disease” analysis. Furthermore, the distribution shifts of tick suitability were projected under different shared socio-economic pathways in the future.

Our findings demonstrate that warm temperate countries (e.g., the United States, China and European countries) in the Northern Hemisphere represent significant high-risk regions for ticks and TBDs. Specifically, solar radiation of January emerges as the main decisive factor determining the risk distribution pattern. Future shifts of tick suitability showed decrease trend under low greenhouse gas emission scenarios but increase trend under high scenarios. These suitability shifts were significantly correlated with future temperature (9 species) and precipitation (19 species) related factors. Collectively, in this study we first shaped the global risk distribution of main ticks and TBDs as well as tick suitability shifts correlated with future global climate change, which will provide helpful references for disease prevention and administration. The methods proposed here will also shed light on other emerging and recurrent zoonotic diseases (e.g., COVID-19, monkeypox) in the future.

Cao, B., et al.; *Journal of Environmental Management* (2025); <https://doi.org/10.1016/j.jenvman.2025.124129>

Summary: Both the spatial distributions and vector suitability of ticks shift with future climate change under various climate scenario projections.

Molecular Section

Molecular detection of a canine respiratory pathogen, *Mycoplasma cynos*, in the lone star tick *Amblyomma americanum* (Acari: Ixodidae)

Mycoplasma cynos (Rosendal 1973, Mycoplasmatales, *Mycoplasmataceae*) is a significant bacterial pathogen within the Canine Infectious Respiratory Disease Complex (CIRD), causing substantial morbidity worldwide in pet and kennel dog populations. While its role as both a primary and secondary pathogen in respiratory disease is established, the epidemiology and potential for vector-borne transmission of *M. cynos* remains understudied.

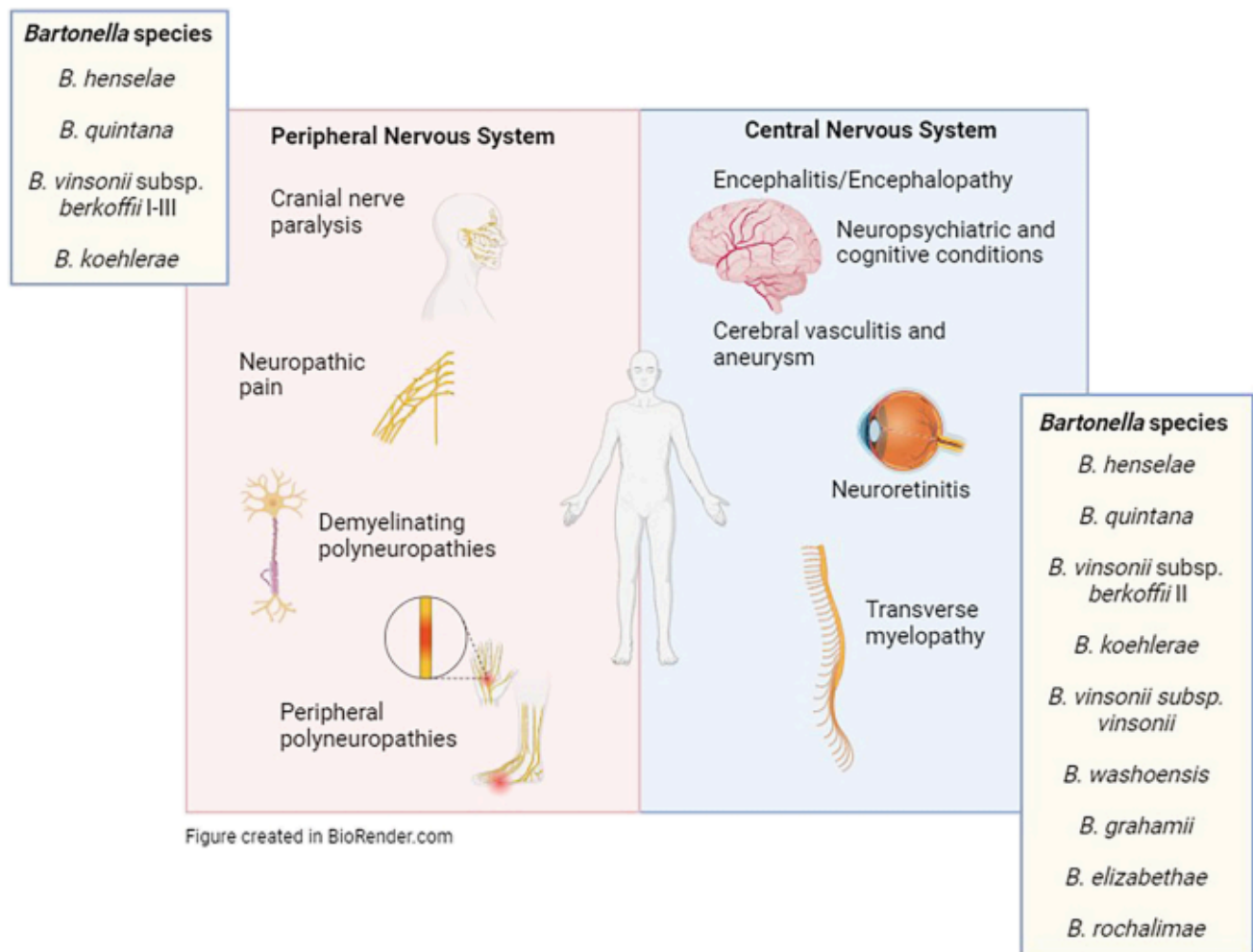
Here, we describe an identified association of *M. cynos* with a lone star tick, *Amblyomma americanum* L., collected in New Jersey, USA, using a next-generation metabarcoding approach. Sequence identity and phylogenetic analysis confirmed its provenance as a canine-derived *M. cynos* strain, and to our knowledge, represents the first identification of this pathogen in ticks. These findings suggest a potential tick-mediated epidemiological link between canine hosts and the environment, underlining the need for further studies on tick-borne transmission dynamics and their role in the broader ecology of canine and wildlife respiratory pathogens.

Moustafa, M.A.M., et al.; *Journal of Medical Entomology* (2025); <https://doi.org/10.1093/jme/tjaf062>

Summary: This study presents the first known identification of *Mycoplasma cynos*, a bacterial pathogen causing respiratory diseases in dogs, in ticks.

Neurobartonellosis: emerging from obscurity!

Background: *Bartonella* species are fastidious, intracellular bacteria responsible for an expanding array of human pathologies. Most are considered to be transmitted by direct inoculation with infected bodily fluids from a mammalian reservoir species or vector-transmitted through a variety of arthropod species and their excrement. However, there are mounting reports of infection in the absence of documented animal or vector contact. A variety of *Bartonella* species have been documented in conditions affecting both the peripheral and central nervous systems. More common conditions, including neuroretinitis, are often associated with *Bartonella henselae*. However, *Bartonella quintana*, the agent of trench fever, as well as emerging pathogens related to rodent reservoir species, *B. grahamii* and *B. elizabethae*, have also been documented. Encephalitis and encephalopathy, also most often associated with *B. henselae*, have been reported with *B. quintana*, *B. washoensis* (ground squirrels) and *B. vinsonii subsp. vinsonii* (voles) infections. *Bartonella* infections have also been associated with



peripheral neuropathies, such as cranial nerve paresis and neuropathic pain, including infection with less commonly encountered species such as *Bartonella koehlerae*. Recently, molecular diagnostic testing revealed that DNA from *Bartonella* spp. was found to be more prevalent in blood of patients with neuropsychiatric disorders such as schizophrenia and psychoses compared to healthy controls.

Methods: A systematic literature search was conducted on PubMed, Google Scholar and Web of Science. Search terms included *Bartonella* and specific neurological conditions and focused on peer-reviewed case reports published after 2012 pursuant to a prior review, with limited exceptions for conditions not previously covered. Published diagnostic testing, serology, molecular testing or pathology were necessary for inclusion, except for one case, which had clinical and epidemiological evidence consistent with diagnosis along with follow-up.

Results: Neurobartonellosis included neuralgic amyotrophy, complex regional pain syndrome, chronic inflammatory demyelinating polyneuropathy, cranial nerve paralysis, Guillain-Barré syndrome, peripheral vasculitic polyneuropathy, acute transverse myelopathy, neuroretinitis, encephalitis/encephalopathy, cerebral vasculitis/aneurysm, and neuropsychiatric conditions.

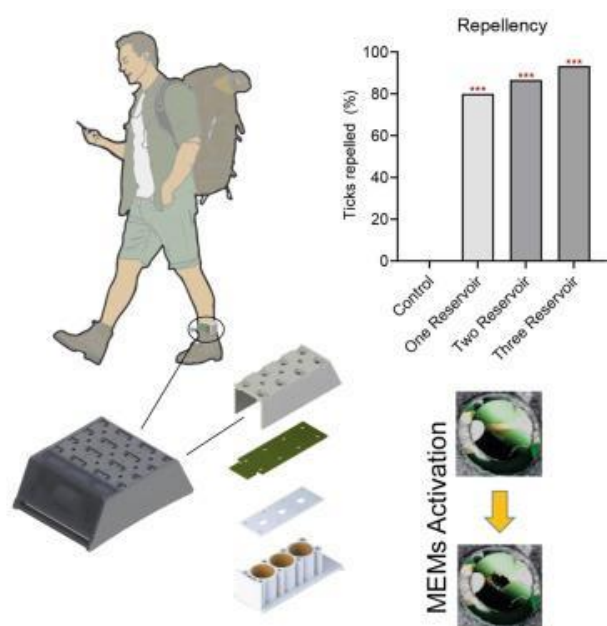
Conclusions: The breadth of reported symptoms and clinical syndromes associated with an increasing number of *Bartonella* species continues to expand. Increased clinical awareness of this important zoonotic pathogen is necessary to advance One Health among the medical and veterinary communities.

Bush, J.C., et al.; *Parasites & Vectors* (2024); <https://doi.org/10.1186/s13071-024-06491-3>

Summary: While neurobartonellosis is becoming better understood, there is still a substantial need for research that addresses their pathogenesis, diagnostics, and treatment regimens.

A wearable wireless controlled-release device as the next-generation personal protection against vector-borne diseases

To address compliance issues with topical and spatial treatments and to improve protection against vectors, we present a wearable wireless device that integrates micro-electro-mechanical systems (MEMS) and electronics with advanced spatial repellents (SRs) as the next generation of personal protection. This platform, named the adaptive barrier controlled release device (AB-CRD), features Bluetooth connectivity and digital controls for the storage and selective release of SRs from multiple sealed reservoirs. Repellent release is initiated by discharging a capacitor to break a sealing membrane, allowing controlled diffusion. The AB-CRD was demonstrated in an *in vitro* assay against *Dermacentor variabilis* (American dog



tick) as a proof of concept. Experimental results showed that dose escalation of a transfluthrin-based formulation produced increasing repellency, with mean values of 78%, 83%, and 88% for one, two, and three reservoirs, respectively. The AB-CRD represents a novel controlled-release platform for personal protection against vector bites, offering an efficient and adaptable solution.

D'hers, S., et al.; *Cell Reports Physical Science* (2025); <https://doi.org/10.1016/j.xcrp.2025.102693>

Summary: The research team presents a wearable wireless anti-vector device that may be more efficient, adaptable, and consistent than topical or spatial interventions.

Correlation between COVID-19 severity and previous exposure of patients to *Borrelia* spp.

Predictors for the risk of severe COVID-19 are crucial for patient care and control of the disease. Other infectious diseases as potential comorbidities in SARS-CoV-2 infection are still poorly understood. Here we identify association between the course of COVID-19 and Lyme disease (borreliosis), caused by *Borrelia burgdorferi* transmitted to humans by ticks. Exposure to *Borrelia* was identified by multi-antigenic (19 antigens) serological testing of patients: severe COVID-19 (hospitalized), asymptomatic to mild COVID-19 (home treated or not aware of being infected), and not infected with SARS-CoV-2. Increased levels of *Borrelia*-specific IgGs strongly correlated with COVID-19 severity and risk of hospitalization. This suggests that a history of tick bites and related infections may contribute to the risks in COVID-19. Though mechanisms of this link is not clear yet, screening for antibodies targeting *Borrelia* may help accurately assess the odds of hospitalization for SARS-CoV-2 infected patients, supporting efforts for efficient control of COVID-19.

Szewczyk-Dabrowska, A., et al.; *Scientific Reports* (2025); <https://doi.org/10.1038/s41598-022-20202-x>

Summary: This older study shows that prior exposure to *Borrelia* was associated with increased COVID-19 severity and risk of hospitalization.

Roles of Tick Symbiotic Microorganisms in Pathogen Transmission

Ticks have garnered significant research interest owing to their ability to vector pathogens into humans and animals. The intricate symbiotic associations between ticks and tick microbiota substantially influence developmental processes, reproductive success, and potential to serve as vectors for tick-transmitted diseases. This paper reviews the epidemiology of diseases transmitted by ticks and delves into the composition and function of tick endosymbionts in transmission and infection. This review also highlights the role of tick immunity in maintaining gut homeostasis. Finally, tick symbiont-pathogen interactions and potential strategies for controlling tick-borne diseases by leveraging symbiotic relationships are discussed.

Chang, X., et al.; *Zoonoses* (2025); DOI: 10.15212/ZOONOSSES-2024-0067

Summary: The symbiotic relationship between ticks and their microbiota influences tick-borne disease uptake and transmission.

Alpha-Gal Section

Pill Clarity (official website: pillclarity.org)

Alpha-gal syndrome has emerging relevance in cardiovascular medicine, given that patients may become sensitized to products containing alpha-gal. Thus, it is important for patients and clinicians to know what ingredients are contained in the medications they take.

Pill Clarity (visit the website for more information: pillclarity.org) is one resource increasing transparency in medications. This database contains information on ingredients found in commonly used medications, with pharmacist support for any questions that remain unanswered. Pill Clarity supports patients who have alpha-gal syndrome, have gluten or lactose allergies, are vegan, have religious preferences (halal, kosher, etc.), are environmentally conscious, or are animal welfare-minded.

Shah, S.A.; American College of Cardiology's *Cardiology Magazine* (2025);

<https://www.acc.org/Latest-in-Cardiology/Articles/2025/07/01/01/Feature-The-Overlooked-Cardiac-Implications-of-Alpha-Gal-Syndrome>

Alpha-Gal on the Rise: The Alarming Growth of Alpha-Gal Syndrome in High-Risk Regions

Background: Mammalian meat allergy (MMA), increasingly linked to delayed hypersensitivity reactions such as alpha-gal syndrome, is a growing public health concern. This study evaluates the incidence, prevalence, and incidence rate of MMA in a large, diverse population of over 114 million individuals across two time periods (2015-2020 and 2021-2025), with stratification by age, sex, race, and ethnicity.

Methods: Using longitudinal electronic health record data, we calculated incidence proportion, prevalence, and incidence rate (cases per person-day) for MMA diagnoses. Analyses were stratified by demographic factors and compared across time windows. Predictive modeling was used to estimate future trends in high-risk populations.

Results: MMA increased dramatically across all demographics. Overall incidence proportion rose by over 5,500%, with the most substantial increases observed in individuals over 40 years old. Age-stratified analysis within racial groups revealed particularly sharp increases among Black (9,530%) and Hispanic (7,678%) adults over 40. Females experienced a steeper rise in incidence rate (11,169%) than males (7,426%). Predictive modeling projects continued growth through 2030, with incidence proportions in Black and Hispanic populations expected to increase by 57% and 72%, respectively.

Conclusion: MMA is emerging as a rapidly increasing diagnosis, particularly among middle-aged and older adults in racially diverse populations. These findings highlight the need for targeted public health efforts, including clinician education, adult-focused screening, and prevention strategies - especially in communities with rising allergy rates. Enhanced awareness

and early identification are critical to mitigating the rising burden of this potentially life-threatening allergic condition.

Ross, M., et al.; *Cureus* (2025); <https://doi.org/10.7759/cureus.88415>

Summary: Analysis of longitudinal electronic health data combined with predictive modeling show that the incidence of mammalian meat allergy associated with alpha-gal has been and will continue to be on the rise, particularly in already high-risk groups such as Black and Hispanic adults over 40 years.

Association between tick-bite history and safety of gelatin-containing vaccines: Analysis of a large database of the United States

Alpha-gal syndrome (AGS) is an allergic reaction caused by sensitization to alpha-gal, a sugar molecule in gelatin-containing vaccines. Tick bites can induce alpha-gal IgE sensitization, as ticks inject alpha-gal through their saliva. However, there is no real-world data on the anaphylaxis rates associated with gelatin-containing vaccines in patients with tick bite history.

We utilized TriNetX, a research network database, to analyze data in November 2024. The history of tick bites (i.e., the presence of a tick-bite history) was categorized into three groups: ehrlichiosis, tularemia, and bites from nonvenomous arthropods. Vaccines were classified into two categories: (1) gelatin-containing vaccines (live intranasal influenza [FluMist], varicella, measles/mumps/rubella [MMR], oral typhoid, rabies [RabAvert], and yellow fever vaccines [YF-VAX]) and (2) gelatin-free vaccines.

Anaphylactic episodes were identified in patients with a history of tick bites who developed anaphylaxis within one day following vaccination. The anaphylaxis rates after receiving gelatin-containing vaccines were 0.06 %, 0.7 %, and 0.2 % in patients with ehrlichiosis, tularemia, and nonvenomous arthropod bites, respectively. In contrast, the anaphylaxis rates after receiving gelatin-free vaccines were 0.04 %, 0.0 %, and 0.1 % in patients with ehrlichiosis, tularemia, and nonvenomous arthropod bites, respectively. Among the gelatin-containing vaccines, live intranasal influenza and varicella vaccines posed a higher rate of anaphylaxis compared to other gelatin-containing vaccines. While tick bites are associated with AGS, a history of tick bites is not a contraindication for most gelatin-containing vaccines, including MMR, oral typhoid, rabies, and yellow fever vaccines. Further investigations are warranted to evaluate the safety of intranasal influenza and varicella vaccines in this population.

Chiu, C.Y., et al.; *Ticks and Tick-borne Diseases* (2025); <https://doi.org/10.1016/j.ttbdis.2025.102532>

Summary: A history of tick bites does not appear to influence the safety of gelatin-containing vaccines.

Opinion: Ecologists and entomologists wanted! An open invitation to alpha-gal syndrome research

In this Opinion, the authors investigated peer-reviewed publications on alpha-gal syndrome (AGS), also known as red meat allergy, since its first description in the literature in 2009 to

October 2024 to understand academic discipline and geographic affiliation of associated authors. We raise the issue of disproportionate contribution between medical disciplines and ecology/entomology disciplines and emphasize the positive future impacts of increased collaboration between the fields to address current gaps in our fundamental knowledge of this unique tick-borne disease.

Barnett, K.M., et al.; *Ticks and Tick-Borne Diseases* (2025); <https://doi.org/10.1016/j.ttbdis.2025.102538>

Summary: Research on alpha-gal syndrome is conducted disproportionately by those in medical professionals, but to generate fundamental knowledge on the disease, more input from ecologists and entomologists is required.



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