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Tick-Borne Infections Council
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NEWSLETTER 2026, Volume 2

Quote: “There is a clear winner in the ongoing contest between humans and ticks. And it is not us.” Eisen, L.; Ticks and Tick-borne Diseases (2025); https://doi.org/10.1016/j.ttbdis.2026.102622

Highlights

- **Active surveillance for Heartland virus in North Carolina**
  Summary: This preprint details findings of HRTV in North Carolina, despite it only having been found in the state twice before.
- **Effect of housing floor type on tick survival**
  Summary: Tick survival varies by the type of flooring in the home, emphasizing the need to implement personal protective behaviors to prevent tick transportation into the home.
- ***Rickettsia* in ticks submitted by forestry workers**
  Summary: Forestry workers were asked to collect ticks during field surveys. From those ticks, the authors of this study found that many carried Rickettsia, indicating that forestry workers are at risk of tick-borne infections.
- **Nonspecific symptoms in Lyme disease patients in high-incidence areas in the United States**
  Summary: Patients who reported having Lyme disease were found to be more likely to experience various nonspecific symptoms like fatigue, pain, and cognitive difficulties.
- **Geographic variation in blacklegged tick-borne coinfections in the eastern United States**
  Summary: The pathogens associated with I. scapularis are becoming established across wider geographies, making co-circulation of these pathogens more common. The authors here investigate the geographic distribution and coinfection dynamics of I. scapularis-borne pathogens in the eastern United States.
- **Ecological dynamics of ticks, hosts, and pathogens in northeastern United States forests**
  Summary: Changes in mouse abundance affect nymph density, while larval feeding activity may be more influential in nymphal infection prevalence.
- **Perspectives on tick-borne disease prevention and research**
  Summary: This perspective piece from a key tick-borne disease researcher offers insights into tick-borne disease interventions and research in the United States.

- **Tick-borne pathogens in questing ticks, ticks on red deer, and ticks on horses in recreational areas in Poland**
  Summary: I. ricinus carries multiple tick-borne pathogens in northwestern Poland. They can be carried on red deer and horses, increasing the risk of exposure to these pathogens in recreational forests.
- **Perinatal transmission of *Borrelia burgdorferi***
  Summary: Existing evidence shows that Borrelia burgdorferi can be transmitted from mother to baby, making it important to understand how this transmission occurs and how to diagnose, prevent, and treat it.
- **Transfusion-related alpha-gal syndrome**
  Summary: The authors describe two patients with reactions consistent with transfusion-related alpha-gal syndrome.

TIC-NC Activities

In March, TIC-NC's scientific advisor and director Dr. Marcia E. Herman-Giddens presented to a Chapel Hill garden club about ticks and tick-borne diseases.

On March 18th, our vice president and treasurer Dr. Kim Brownley and director McGregor Bell participated in the UNC Total WellBeing Expo.

North Carolina

Active Surveillance for Heartland Virus in North Carolina: Clinical and Genomic Epidemiology

Background: Heartland virus (HRTV) is an emerging tick-borne virus capable of causing severe illness and death. The burden of disease is likely underestimated due to limited seroprevalence studies, lack of commercially available diagnostic tests, and an overlapping clinical syndrome with more commonly diagnosed bacterial diseases such as spotted fever group rickettsiosis or ehrlichiosis.

Methods: Active surveillance for Heartland virus disease was conducted at a large academic center from March to September 2024. Enrolled subjects included those who had testing sent for *Ehrlichia* polymerase chain reaction (PCR) along with fever and 2 of the 3 criteria: leukopenia, thrombocytopenia, and/or elevated liver function tests. Specimens with detectable RNA underwent whole genome sequencing and analysis.

Findings: Over 800 specimens were received with 53 individuals meeting enrollment criteria. Among these 53, two (3.8%) had detectable HRTV RNA in whole blood during the time of *Ehrlichia* PCR testing. The two cases had disparate clinical manifestations: one with mild disease which was identified in an outpatient setting, while a second case required intensive care unit-level support. Heartland virus genome sequences from the two cases were more similar to viruses from other states than they were to one another.

Interpretation: Despite only two prior reported cases of Heartland virus disease in North Carolina, we identified two individuals with acute HRTV viremia. Further surveillance for HRTV disease is necessary to understand the burden of disease and to facilitate further studies of virus pathogenesis and host responses.

Zychowski, D.L., et al.; preprint on *medRxiv* (2026); https://doi.org/10.64898/2026.02.27.26347100

Summary: This preprint details findings of HRTV in North Carolina, despite it only having been found in the state twice before.

The South

Effect of floor type on survival of *Amblyomma maculatum* and *Amblyomma americanum* (Acari: Ixodidae)

Exposure to ticks (Acari: Ixodidae) puts humans and their companion animals at risk of tick bites and potential pathogen transmission. Bites often occur when humans encounter ticks outdoors, but there may also be a risk in the home given the propensity of ticks to hitchhike on clothes and pets. We assessed survival of two tick species widely distributed across the southeastern

United States, *Amblyomma maculatum* Koch and A. americanum Linnaeus, on different types of flooring commonly found in residential homes. We placed ticks individually onto one of five different types of flooring (tile, wood, vinyl, short pile carpet, and long pile carpet; n = 180 total, 36 ticks per species per floor type). Ticks were contained in plastic cups fixed in place on each floor type to reduce movement and/or escape and promote tick contact with the flooring. Survival was assessed as a function of the interaction between species and floor type. We found that *A. maculatum* ticks survived for significantly longer periods of time than *A. americanum* (median survival/mean survival) on vinyl (22.5/25.4 vs. 11.5/10.4 d), wood (18.5/16.1 vs. 11.0/12.2 d), tile (21.0/20.4 vs. 6.5/7.33 d) and short pile carpet (20.0/20.8 vs. 10.5/10.8 d), but *A. americanum* lived longer overall on long pile carpet (13.0/10.4 vs. 13.0/14.9 d). Our findings help clarify expected tick survival following entry into the home, and how floor type can mediate in-home tick exposure. Furthermore, this work emphasizes the necessity of performing tick checks, wearing protective clothing, and applying appropriate acaricides to people and pets to prevent tick transportation into the home.

Sabet, A., et al.; *Journal of Vector Ecology* (2026); https://doi.org/10.52707/1081-1710-50.1-12

Summary: Tick survival varies by the type of flooring in the home, emphasizing the need to implement personal protective behaviors to prevent tick transportation into the home.

Beyond Rocky Mountain spotted fever: investigation of the presence and diversity of spotted fever *Rickettsia* species in ticks submitted from forestry workers

Ticks present a significant risk to people in the southern United States, particularly those who spend time outdoors, as ticks can transmit agents that cause various diseases. This study evaluated the risk of exposure to ticks positive for spotted fever group (SFG) *Rickettsia* species among forestry workers. From 2017 to 2021, forestry workers passively collected ticks during field surveys for the USDA Forest Service's Forest Inventory and Analysis program. We screened 1395 ticks for SFG-*Rickettsia*, including *Amblyomma americanum* (51.5% positive, N = 1,279), *A. maculatum* (40% positive, N = 10), and *Dermacentor variabilis* (22.6%, *N* = 106). The agent of Rocky Mountain spotted fever, R. *rickettsii*, was not detected; however, 7 different SFG *Rickettsia* species were identified. *Rickettsia amblyommatis* was the most common, present in 95.7% of A. *americanum* ticks. The pathogenic R. *parkeri* was rare, detected in 2 A. *americanum* nymphs and 2 A. *maculatum* males only. Several *Rickettsia* species, such as R. *montanensis, R. monacensis, Candidatus R. andeanae,* and *R. tamurae* subsp. buchneri, were identified in D. *variabilis*. Some of these species are suspected to be pathogenic. Rickettsia-positive ticks were detected year-round, with the highest prevalence in Tennessee and Kentucky, possibly due to larger sample submissions, which may have increased detection rates*. Dermacentor variabilis* were less likely to be *Rickettsia*-positive compared to *A. americanum.* Male ticks were less likely to carry *Rickettsia* than females and nymphs. The presence of Rickettsia-positive ticks found in this study poses a risk to forestry workers, emphasizing the importance of ongoing surveillance and education to prevent tick-borne infections.

Kobbekaduwa, V.C., et al.; *Journal of Medical Entomology* (2026); https://doi.org/10.1093/jme/tjaf177

Summary: Forestry workers were asked to collect ticks during field surveys. From those ticks, the authors of this study found that many carried Rickettsia, indicating that forestry workers are at risk of tick-borne infections.

National Section

Nonspecific Symptoms Attributable to Lyme Disease in High-Incidence Areas, United States, 2017-2021

For some patients who have Lyme disease (LD), nonspecific symptoms can persist after treatment and impair quality of life. Estimating the frequency and duration of such symptoms is challenging. Using commercial insurance claims data from 2017–2021 for enrollees residing in states where LD is common, we identified 24,503 case-patients with LD and matched them (1:5) with 122,095 control-patients with other diagnoses by demographics, medical service date, and inpatient/outpatient setting. We compared relative frequencies of diagnosis codes for pain, fatigue, and cognitive difficulties between case-patients and control-patients in the year after diagnosis. Those symptom codes occurred 5.0% more frequently among case-patients than among control-patients and comprised »11.0% of the total symptom codes among case-patients. Symptom code frequency among case-patients declined significantly in the 6–12 months after LD diagnosis and reached levels similar to control-patients by the end of the year, with the exception of fatigue.

Nawrocki, C.C., et al.; *Emerging Infectious Diseases (2025);* https://doi.org/10.3201/eid3114.250459

Summary: Patients who reported having Lyme disease were found to be more likely to experience various nonspecific symptoms like fatigue, pain, and cognitive difficulties.

Tularemia in New York, USA, 1993-2023

During 1993–2023, health officials in New York, USA, received reports of 30 tularemia cases. Of those, 43% were from Suffolk County, 69% were diagnosed during 2014–2023, and 1 person died. Tick surveillance detected *Francisella tularensis* in 1 pool of nymphs from Suffolk County, indicating localized risk.

Gaber, D.T., et al.; Emerging Infectious Diseases (2026); https://doi.org/10.3201/eid3201.250854

Summary: The authors analyze historic tularemia cases in New York state.

Dermacentor occidentalis Ticks and Link to *Rickettsia lanei* Infections, California, USA

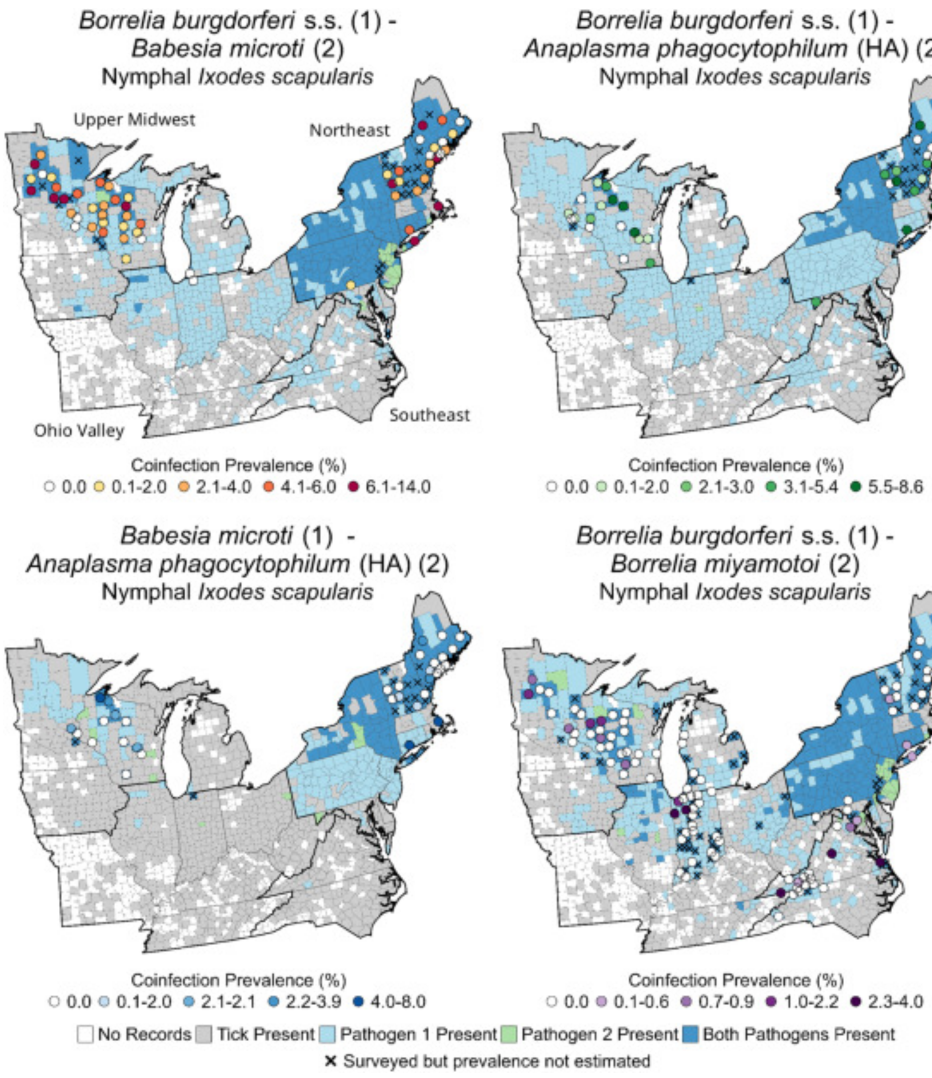
Rickettsia lanei is a newly recognized spotted fever group rickettsial species that causes severe Rocky Mountain spotted fever–like illness. We used genome sequencing, enabled by hybridization capture-based target enrichment, to establish *Dermacentor occidentalis* ticks as the likely source of a human infection with R. *lanei* in California, USA.

Probert, W.S., et al.; Emerging Infectious Diseases (2026); https://doi.org/10.3201/eid3201.251261

Summary: Authors used sequencing to detect *R. lanei* in *D*. occidentalis ticks, establishing them as the likely source of human infection.

Geographic variation in risk of blacklegged tick-borne coinfections in the eastern United States

Blacklegged tick *(Ixodes scapularis)*-associated diseases are increasing in incidence and geographic range in the United States. Pathogen range expansion may increase the risk of coinfections, which could complicate accurate diagnosis and treatment of tick-borne diseases.



To identify regions of coinfection risk across the eastern United States, we used a national database of tick-borne pathogen occurrence to identify areas of co-occurrence between four I. scapularis-borne human pathogens: *Anaplasma phagocytophilum* human-active variant *(Apha; anaplasmosis),* Babesia microti *(Bam; babesiosis),* Borrelia burgdorferi sensu stricto (Bbss; Lyme disease), and Borrelia miyamotoi *(Bmiya; hard tick relapsing fever).* Using testing data from 13,437 nymphs submitted to the United States Centers for Disease Control and Prevention from 2013 to 2024, we summarized the mean and variation in observed coinfection prevalence from site to regional scales. *Bbss-Bam, Bbss-Apha,* and *Bam-Apha* co-occurred primarily in the Northeast and Upper Midwest, whereas Bbss-Bmiya co-occurrence extended from those regions into the Ohio Valley and southern Appalachia. Within zones of co-occurrence, Bbss-Bam was the most prevalent coinfection, followed by *Bbss-Apha, Bam-Apha,* and *Bbss-Bmiya*. Except for Bbss-*Bmiya*, resampling simulations for all coinfections revealed coinfections form more often than expected by chance. This study is a first step in delineating acarological risk for I. scapularis-borne coinfections in the United States.

Grimaudo, A.T., et al.; *Ticks and Tick-Borne Diseases* (2026); https://doi.org/10.1016/j.ttbdis.2026.102610

Summary: The pathogens associated with *I. scapularis* are becoming established across wider geographies, making co-circulation of these pathogens more common. The authors here investigate the geographic distribution and coinfection dynamics of *I. scapularis-borne* pathogens in the eastern United States.

Pathogen and host associations of *Ixodes scapularis* (Acari: Ixodidae) in eastern Ohio 10 years post establishment

The blacklegged tick *(Ixodes scapularis)* is a primary vector of medical concern in the eastern United States, capable of infesting a wide range of hosts. The first established population in Ohio was detected on rural residential properties in Coshocton County and has since expanded across the state. To assess current conditions, these index sites were revisited, and questing ticks were collected between 2019 and 2021, with small mammals sampled in 2021. Ticks and host tissues were screened for *Borrelia burgdorferi* sensu lato, *Borrelia burgdorferi* sensu stricto, *Borrelia mayonii*, and *Anaplasma phagocytophilum.* A total of 654 questing blacklegged ticks and 106 small mammals representing eight species were sampled. White-footed mice *(Peromyscus leucopus)* and eastern chipmunks *(Tamias striatus)* were the most frequently infested hosts. Infection prevalence in ticks was 47.6% for B. burgdorferi sensu lato, 42.9% for B. burgdorferi sensu stricto, and 15.5% for A. *phagocytophilum*. Six of eight small mammal species tested positive, with infection prevalence of 60.4%, 19.8%, and 11.9% for the same pathogens, respectively. *Borrelia mayonii* was not detected. These infection prevalences are comparable to those reported in long-established Lyme-endemic regions in the northeastern and upper midwestern United States. Findings indicate that the enzootic Lyme disease cycle is now well established in parts of Ohio. Public health agencies should be aware of the increasing risk of tick-borne disease in the region, and these results support the importance of host-targeted interventions to reduce pathogen transmission and human disease risk.

Bai, N., et al.; *Journal of Medical Entomology* (2026); https://doi.org/10.1093/jme/tjaf169

Summary: The blacklegged tick *(I. scapularis)* first became established in Ohio about a decade ago, and findings from this study show that Lyme disease is now enzootic in many parts of the state.

Ecological dynamics of blacklegged ticks, vertebrate hosts, and associated zoonotic pathogens in northeastern forests

Specific host-tick interactions in temperate forest systems influence variation in density and infection prevalence of nymphal blacklegged tick *(Ixodes scapularis).* The density of infected nymphs (DIN), which is the product of nymphal infection prevalence (NIP) and density of questing nymphs (DON), influences the risk of human exposure to tick-borne pathogens. Questing nymphs (>2000) collected between 2014 and 2022 were screened for 16 zoonotic pathogens. More than a third (38.8%) of nymphs were infected with at least one pathogen, and *Borrelia burgdorferi* (the agent of Lyme disease) was detected in all six sampling locations and years. Pathogens included Babesia microti (NIP = 21.4%), Bo. Burgdorferi (19.3%), *Anaplasma phagocytophilum* (5.8%), Bo. miyamotoi (1.5%), Powassan virus (<0.01%), and two regionally emergent *Rickettsia* (10 nymphs sampled in 2016 and 2021). Rates of Ba. *microti* infection were high relative to prior work, and coinfection with Bo. *burgdorferi* increased during the study period. White-footed mouse (Peromyscus leucopus) and eastern chipmunk *(Tamias striatus)* are important zoonotic hosts in temperate forests. We evaluated how variation in host abundance and the number of larval ticks feeding per animal (larval burden) explained and predicted DIN, as well as DON and NIP independently. While both mouse abundance and mouse larval burden were positive predictors of DON in this study, their influence on NIP and DIN for commonly detected pathogens differed. Both mouse and chipmunk larval burden explained significant variation in *Bo. burgdorferi* DIN, and larval burden on mice specifically improved prediction when observed *Bo. burgdorferi* DIN was high. Chipmunk larval burden also predicted variance in *Bo. burgdorferi* NIP and also explained significant variation in *Ba. microti* DIN. While observed host-tick contact metrics improved predictive skill, underprediction was most evident when observed DIN or NIP was high. These results emphasize how tick-borne zoonoses depend on a distribution of larval meals across a community of hosts. For *Bo. burgdorferi* in particular, NIP may be stabilized by tick-feeding on a diverse host community. Thus, while large changes in mouse abundance may predict regional changes in DIN, local NIP in particular may be more responsive to shifts in larval feeding activity across the entire community of hosts.

LaDeau, S.L., et al.; *Ecosphere* (2025); https://doi.org/10.1002/ecs2.70508

Summary: Changes in mouse abundance affect nymph density, while larval feeding activity may be more influential in nymphal infection prevalence.

Why are the ticks winning, and what can we do about it?

Human illness associated with tick bites is on the rise in the United States. One root cause is that several human-biting tick species serving as pathogen vectors, including the blacklegged tick and the lone star tick, have expanded their geographic ranges in recent decades, with many areas in the U.S. now harboring multiple species of vector ticks. As currently used, personal tick bite prevention and environmental tick control have not succeeded in stemming the rising tide of humans being bitten by ticks. A national strategy to prevent and control vector-borne diseases provides a blueprint to solve the problem, but this will require sustained investments in tick bite prevention and tick control. Efforts are needed to: (i) stimulate industry engagement in development of novel technologies and products; (ii) intensify research to clarify the benefit of using different tick bite prevention and tick control methods, and clarify barriers to their adoption and use; (iii) establish publicly-funded local organizational structures to support individuals and communities in their efforts to prevent tick bites; and (iv) strengthen the workforce in public health, academia, and industry with expertise in ticks and tick-borne diseases. Solving the problem with ticks in the U.S. will be challenging but is worth pursuing because the alternative is for the public to accept that illness associated with tick bites now is simply a fact of life and that the problem is likely to get worse over time. This perspective paper includes “take home messages” and a conclusions section for an abbreviated read.

Eisen, L.; *Ticks and Tick-borne Diseases* (2026); https://doi.org/10.1016/j.ttbdis.2026.102622

Summary: This perspective piece from a key tick-borne disease researcher offers insights into tick-borne disease interventions and research in the United States.

Multi-County Tick Survey (Acari: Ixodidae) in Missouri USA, 2019 and 2021

Ongoing surveillance of tick populations is critical for informing the health of humans, livestock, and companion animals. From 2004 to 2019 in the USA and its territories, the National Notifiable Disease Surveillance System data show a 2.1-fold increase in all reportable notifiable tick-borne diseases (TBDs) in humans. Eight tick-borne zoonotic pathogens and 1 syndrome were described for the first time in the USA between 2004 and 2024. In Missouri, 33 counties were surveyed over a 2-year period (2019 and 2021). More than 3,811 ticks were collected during the study: 89.0% *Amblyomma americanum*, 10.9% *Dermacentor variabilis,* <0.1% *Amblyomma maculatum,* <0.1% *Haemaphysalis longicornus*, and <0.1% Ixodes spp. Significantly greater tick density was found in metropolitan areas as compared to rural counties ($P = 0.012$). Of the 2 level I ecoregions in Missouri, the Eastern Temperate Forest (ETF) had a significantly greater tick density ($P = 0.0045$). Even so, D. variabilis had significantly higher density in the Great Plains ecoregion than in ETF ($P = 0.031$). Ozark Highlands had the highest tick density of the 5 level III ecoregions surveyed (5.12 ticks/100 m2). A moderate, positive correlation between a county’s density of A. americanum nymphs and its quadrennial tick-borne disease rate was observed ($r = 0.68$, $P = 0.002$). Our study adds new data on established and reported tick populations for 13 counties and examines the relationships of tick density to TBDs and to area designation.

Norton P.J., et al.; *Journal of the American Mosquito Control Association* (2026); https://doi.org/10.2987/25-7276

Summary: This study offers new data on tick populations across Missouri.

International Section

First detection of one of the tick-borne lymphadenopathy (TIBOLA) etiological agent in ticks from a highly frequented sub-urban forest near Paris, France

In the context of global changes including climate, environmental and socio- economic modifications, the surveillance of tick populations in term of species distribution and harboured pathogens is an absolute necessity. With this aim in view, ticks were collected in May 2022 in an highly frequented suburban forest located near Paris, France. The objective was to identify tick species and tick-borne pathogens that may warrant long-term monitoring, as well as to assess added value of metatranscriptomic Next Generation Sequencing (mNGS) for the detection of known and possibly new pathogens in ticks. Both Dermacentor reticulatus and Ixodes ricinus were collected. In addition to expected pathogens detected in I. ricinus (i.e., *Anaplasma, Babesia,* and *Borrelia* species), we report the detection of *Rickettsia conorii subsp. raoultii,* a zoonotic bacterium never identified in the region before and transmitted by a tick species on the rise: D. *reticulatus*.

Krupa, E.A., et al.; *PLOS Global Public Health* (2026); https://doi.org/10.1371/journal.pgph.0005705

Summary: Surveillance of tick populations near Paris, France found the presence of many known tick-borne diseases and also detected, for the first time, a bacterium responsible for TIBOLA.

Seroepidemiological survey to investigate *Rickettsia rickettsii* and *Rickettsia parkeri* in municipalities of the southeast Brazil

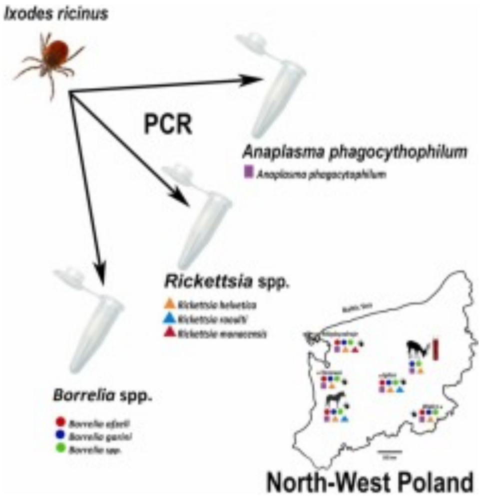
Spotted fever is a tick-borne rickettsiosis caused by several Rickettsia species—including *R. rickettsii, R. parkeri, and* others—with varying degrees of pathogenicity. Its nonspecific symptoms often lead to misdiagnosis such as dengue. This study investigated anti-*R. rickettsii* and *R. parkeri* antibodies in 152 patients with acute febrile illness who tested negative for dengue. Serological analysis using immunofluorescence assay found 29 reactive samples (19%) at a 1:64 dilution. Among them, 20.6% were male and 58.6% female, with an average age of 42.6 years. The average sample collection time totaled 14.6 days. Reactive samples included 13.1% for *R. rickettsii* and 5.9% for *R. parkeri.* These results suggest possible rickettsial infections in patients initially suspected of dengue.

Franco, M.B., et al.; *Revista Instituto Medicine Tropical São Paulo* (2026); https://doi.org/10.1590/S1678-9946202668001

Summary: *R. rickettsii* and *R. parkeri* were found in patients with acute febrile illness who were initially suspected to have dengue, highlighting the need to consider spotted fever even in non-endemic areas.

Occurrence of tick-borne pathogens in questing ticks, ticks from riding horses, and red deer blood in Western Pomerania, Poland

Ixodes ricinus is a widespread vector of numerous microorganisms pathogenic to humans and animals in Europe. The risk of exposure to tick-borne pathogens (TBPs) has increased in recent years due to climate change, the conversion of natural green areas to recreational areas, and growing human and animal populations, including pets. Using molecular methods, the prevalence, diversity, and co-occurrence of selected tick-borne microorganisms were assessed in questing *I. ricinus* collected from recreational areas (n = 409), in ticks feeding on horses (n = 135), and in blood samples from red deer (n = 42) in northwestern Poland. In ticks, *Borrelia afzelii* (15 %), B. *garinii* (14 %), other *Borrelia* spp. (25.2 %), *Anaplasma phagocytophilum* (4.6 %), *Rickettsia helvetica* (11 %), *R. raoultii (*0.5 %) and *R. monacensis* (0.3 %) were identified. In deer blood samples, *B. garinii* (2.4 %), *Borrelia* spp. (4.8 %), *A. phagocytophilum* (9.5 %) and *R. helvetica* (4.8 %) were detected. Dual co-detection were observed, including *B. afzelii* and *Borrelia* spp. (8.3 %), *Rickettsia* spp. and *Borrelia* spp. (2.4 %), *Anaplasma* spp. and *Borrelia* spp. (0.9 %), in questing ticks, in ticks collected from horses, and in the deer blood samples. One triple pathogen co-detection (*Borrelia* spp., *A. phagocytophilum*, and *R. helvetica;* 0.2 %) was identified in questing ticks, and two quadruple pathogen combinations involving A. *phagocytophilum* or *R. helvetica* with different *Borrelia* spp. were detected in deer blood (0.3 %) and ticks feeding on horses (0.6 %), respectively.These findings highlight a substantial risk of exposure to multiple TBPs in forested recreational areas and underscore the potential for the simultaneous acquisition of at least two pathogens.



Rymaszewska, A., et al.; *Veterinary Microbiology* (2026); https://doi.org/10.1016/j.vetmic.2026.110932

Summary: *I. ricinus* carries multiple tick-borne pathogens in northwestern Poland. They can be carried on red deer and horses, increasing the risk of exposure to these pathogens in recreational forests.

Distribution of tick-borne microorganisms in human-biting ticks in France collected through a Citizen-science program

Ticks occupy diverse habitats, increasing the risk of human exposure. Assessing the public health threat posed by ticks requires rigorous monitoring of their distribution and of the prevalence of tick-borne pathogens. In France since 2017, the citizen science program CiTIQUE monitors human tick bites through multiple complementary approaches. Citizens can report bites and submit biting ticks to a national tick bank for research and surveillance. This study aimed to investigate human exposure to tick-borne microorganisms including pathogens across France, using ticks submitted through the CiTIQUE program. In total, 2009 ticks were selected from the CiTIQUE tick bank, identified, and screened for microorganisms using a real-time microfluidic PCR method. Most bites involved *Ixodes ricinus* nymphs except in Mediterranean regions where *Dermacentor* and *Rhipicephalus* ticks were more common. Twenty-six microorganisms were detected, eighteen of which are potentially pathogenic to humans. These pathogens were widely distributed across the country. Borrelia spp. were the most frequently detected pathogens with spatial variation among regions. *Anaplasma phagocytophilum* infection rates varied from region to region. *Neoehrlichia mikurensis* was found in seven out of twelve French regions. Rickettsia species diversity was highest in the southeast, associated with a greater diversity of vectors. Five percent of ticks were infected with more than one pathogen. Although spatial heterogeneity was observed, no region was free of infected ticks. This study demonstrates the power of citizen science for nationwide surveillance of tick-borne pathogens, providing a large-scale overview of pathogen diversity and distribution across France from crowdsourced tick data.

Durand, J., et al.; *Ticks and Tick-borne Diseases* (2026); https://doi.org/10.1016/j.ttbdis.2026.102612

Summary: Citizen science is a valuable tool for surveillance of tick-borne pathogens.

Molecular Section

Perinatal transmission of *Borrelia burgdorferi:* advancing scientific and clinical understanding of Lyme disease in pregnancy

Perinatal transmission of *Borrelia burgdorferi* sensu lato (Bb), the spirochetal agent of Lyme disease, is an issue of public health importance and research significance. This alternate mode of transmission and the potential risk of adverse pregnancy outcomes were communicated within public health spheres following the first suspected case in 1985. Subsequent studies in reservoir and non-reservoir animal hosts, in addition to case reports of perinatal morbidity and mortality in humans brought further attention to the field. Decades later, however, the incidence and epidemiologic impact of perinatal transmission of Bb, as well as the clinical spectrum and potential long-term health sequelae of gestationally exposed children, remain understudied and poorly defined. In June 2022, a Banbury Conference on Perinatal Transmission of Lyme disease was convened at Cold Spring Harbor Laboratory in New York. This manuscript conveys conference findings and research recommendations to advance scientific and clinical understanding of this important issue.

Faber, S., et al.; *Frontiers in Medicine* (2026); https://doi.org/10.3389/fmed.2026.1794120

Summary: Existing evidence shows that *Borrelia burgdorferi* can be transmitted from mother to baby, making it important to understand how this transmission occurs and how to diagnose, prevent, and treat it.

Combination antibiotic therapy is required to eliminate *Bartonella henselae* in multiple microenvironments

Bartonella are gram-negative, facultative intracellular bacteria. Infection by *Bartonella* manifests as different clinical syndromes collectively known as bartonellosis. The well-known diseases caused by these bacteria are cat scratch disease (*Bartonella henselae),* trench fever (*Bartonella quintana)* and Carrion's disease *(Bartonella bacilliformis).* Excluding *B. bacilliformis*, which is evolutionarily more distinct than the other species, *Bartonella* infections result in self-limiting disease that is often undiagnosed and untreated. However, individuals with compromised immune systems or other undefined conditions may experience clinical manifestations, which can become life-threatening and need to be treated with effective antibiotics. To date, there is no standard treatment course for these infections, and many doctors prescribe antibiotics based on limited case studies. Within the host, *Bartonella* can grow extracellularly, intracellularly, and in biofilms. To determine an effective antibiotic strategy, it is important to understand *Bartonella* susceptibility in each of these growth conditions. We hypothesized that combination antibiotic treatments are required to effectively eliminate *Bartonella henselae* growth, particularly in biofilm and intracellular environments. Our previous work has shown that *B. henselae* treatment with single antibiotics in different media, as well as in DH82 canine macrophages, was ineffective in eliminating bacteria. We expanded this work with different antibiotics supported by case reports, as well as double and triple combinations. The following antibiotics were tested: doxycycline, gentamicin, azithromycin, azlocillin, rifampin, and clarithromycin. We found that while monotherapy may inhibit growth extracellularly, it is ineffective when used against intracellular bacteria or pre-existing biofilms. Gentamicin in combination with either rifampin or azlocillin significantly reduced bacterial growth in multiple microenvironments. The effectiveness of combination therapy supports the notion that *Bartonella* species utilize host cells and biofilms as antibiotic evasion strategies.

Olsen, E.L. and Embers, M.E.; *Frontiers in Microbiology* (2026); https://doi.org/10.3389/fmicb.2026.1726180

Summary: *Bartonella henselae* is capable of surviving many different types of antibiotic treatment, and multiple antibiotics are needed to treat infections as a result of the evasion strategies that *Bartonella* species utilize.

Alpha-Gal Section

The α-Gal Epitope (Galα1-3Galβ1-4GlcNAc) as Therapeutic Agent in Cancer Immunotherapy, Vaccine Effectiveness Amplification and Injured Tissue Regeneration

The α-gal epitope is synthesized in non-primate mammals and New-World monkeys by the glycosylation enzyme α1,3galactosyltransferase (α1,3GT), encoded by the *GGTA1* gene. Ancestral Old-World monkeys and apes synthesizing α-gal epitopes underwent extinction 20–30 million years ago. Their mutated offspring, with the inactivated *GGTA1* gene, survived and produced the natural anti-Gal antibody, specifically binding α-gal epitopes. Anti-Gal protected the surviving offspring from lethal viruses presenting α-gal epitopes, which killed α-gal-synthesizing parental primates. Anti-Gal constitutes ~1% of human immunoglobulins and is also produced in Old-World monkeys and apes. α-Gal epitopes can serve as therapeutic agents in several clinical disciplines: 1. *Cancer immunotherapy:* Engineering cancer cells to express α-gal epitopes results in anti-Gal binding to these cells and localized activation of the complement system that kills these cancer cells and recruits the antigen-presenting cells (APCs) dendritic cells and macrophages. Anti-Gal bound to cancer cells targets them for robust uptake by APCs, which process internalized tumor antigens (TAs) and transport them to lymph nodes for activation of cytotoxic T-cells. These T-cells kill TA-presenting metastatic tumor cells. Clinical trials demonstrated that such engineering is achieved by intra-tumoral injection of α-gal glycolipids, the use of recombinant α1,3GT, or the use of oncolytic viruses containing the *GGTA1* gene. 2. *Viral vaccines:* Inactivated whole-virus vaccines presenting α-gal epitopes bind anti-Gal, which targets them for extensive uptake by APCs, thereby increasing their immunogenicity by ~100-fold. 3. *Injured-tissue regeneratio*n: Anti-Gal binding to α-gal-presenting nanoparticles administered to wounds, into the post-myocardial infarction (MI) injured myocardium and into injured spinal cord, activates the complement system that recruits pro-regenerative macrophages, which orchestrate regeneration by recruiting stem cells and the secretion of pro-regenerative cytokines. All these findings suggest that α-gal/anti-Gal antibody interaction can serve as a novel therapeutic approach, applicable to various clinical settings.

Galili, U.; *International Journal of Molecular Sciences (*2026); https://doi.org/10.3390/ijms27062737

Summary: Alpha-gal epitopes may be useful for multiple clinical therapies, but consideration must be taken to prevent reactions in patients with alpha-gal syndrome.

Isolated Gastrointestinal Alpha-gal Meat Allergy Is a Cause for Gastrointestinal Distress Without Anaphylaxis

Allergy and oncology journals have primarily published research on alpha-gal allergy, and it has not been described previously in the GI literature. We describe patients with the allergy who presented with isolated GI symptoms.

Croglio, M.P., et al.; *Gastroenterology* (2021); https://doi.org/10.1053/j.gastro.2021.01.218

Summary: Some patients with alpha-gal syndrome develop GI symptoms without the more traditional manifestations of food allergy, likes hives or anaphylaxis.

Transfusion-related alpha-gal syndrome: Two new cases expanding the demographic and geographic spectrum, and evidence of a diagnostic gap in allergic transfusion reaction evaluation

Background: Transfusion-related alpha-gal syndrome (TRAGS) has recently been proposed as a cause of allergic transfusion reactions (ATRs) in which alpha-gal-specific IgE in sensitized group O (or potentially group A) recipients reacts with epitopes on group B or AB plasma-containing components. Fewer than 10 cases have been reported, all from the Northeast and mid-Atlantic United States, and alpha-gal–specific ATR evaluation practices are unstudied.

Study Design and Methods: Two patients with ATRs consistent with TRAGS at a large academic medical center in Nashville, Tennessee are reported alongside a 5-year retrospective cohort analysis of group O and A recipients experiencing ATRs following transfusion of group B or AB plasma-containing products. Alpha-gal IgE testing, AGS diagnosis documentation, and documented consideration of IgA deficiency were assessed for each qualifying reaction.

Results: Both index patients had pre-existing AGS diagnoses unrecognized at component selection; one was a 42-year-old female and the second an 83-year-old male. Among 50 qualifying ATRs in 44 patients, including 13 severe or anaphylactic reactions, alpha-gal IgE testing was not performed for any event, and no patient had a documented AGS diagnosis. IgA deficiency was considered in eight patients (18%), yielding no diagnoses.

Conclusion: TRAGS occurs in the tick-endemic southeastern United States across a broader demographic range than previously recognized. IgA deficiency, present in <0.3% of the population, was considered in 18% of qualifying patients while alpha-gal sensitization, affecting 20%-30% in this region, was investigated in none. Integration of AGS history into pre-transfusion risk assessment and ATR evaluation protocols is warranted.

Foster, M., et al.; *Transfusion* (2026); https://doi.org/10.1111/trf.70196

Summary: The authors describe two patients with reactions consistent with transfusion-related alpha-gal syndrome.

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