TICNC

Tick-Borne Infections Council
of North Carolina, Inc.

NEWSLETTER 2023, Volume 2

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Quote: "The infrequency of reported *B. lonestari* infections despite the frequent isolation of the bacteria from host-seeking *A. americanum* ticks suggests that this species might have a lower pathogenic potential than other *Borrelia* spp. more often associated with human disease… Increasing availability of molecular diagnostics might enable *B. lonestari* to be identified as an emerging tickborne pathogen, particularly causing opportunistic infections among persons who are immunocompromised. Relapsing Fever Caused by Borrelia lonestari after Tick Bite in Alabama, USA." Vazquez G, et al. (See abstract below.)

Highlights…

- **STARI and Borrelia lonestari, a relapsing fever**
- **Borrelia garinii found in South Carolina**
- **Tick bite as a risk factor for alpha-gal**
- **Alpha-Gal:A Series of 5 Cases in Central North Carolina**
- **Prevalence and National Sensitization Patterns of Alpha-Gal IgE Among Military Personnel** ***Range 6% to 36%***
- **Bourbon virus in North Carolina**
- **Lyme Disease, China, 2005–2020**
- **Tick Control in a Connected World**
- **Rapid invasion of the Asian longhorned tick on Long Island, NY**
- **Japan-** ***longhorned ticks*** **increased with higher deer density**
- **Tick bite frequency, prevention practices and Lyme disease diagnoses among U.S. Hispanic survey respondents**
- **Perceived vulnerability for Lyme disease questionnaire**
- **Latest on the Lyme disease vaccine**
- **Lyme disease in Ashe County, NC**

- **A possible mild pathogen common in lone star ticks and others**
- **COVID-19 or Taking the COVID-19 Vaccine and a History of Lyme Disease**
- **Pfizer halts Lyme vaccine trial on Nantucket and Martha's Vineyard**
- **Bartonella spp. Infections Identified by Molecular Methods**

Vector-borne Working Group (VBWG) meeting dates for 2023: None announced.

Location:
Office of the Chief Medical Examiner Photo ID required.
4312 District Drive, Raleigh, NC 27607

Report from the State or Vectorborne Disease Work Group meeting
None: no meetings

Link to Notice to Medical Providers from the State Department of Public Health on Lyme Disease and Rickettsial Diseases: "Annual Update on Diagnosis and Surveillance for Tickborne Diseases"

The state has started issuing only one letter. Please see the homepage of our website to access. www.tic-nc.org.
To look at the (state) NCDHHS's tick data, go to epi.dph.ncdhhs.gov/cd/diseases/ticks.html

Case data for Lyme disease from the CDC for North Carolina

The CDC:
NC had 344 cases of reported Lyme disease in 2019.
NC had 264 cases of reported Lyme disease in 2020.
https://www.cdc.gov/lyme/datasurveillance/surveillance-data.html
Links to access Lyme and other tick-borne infections data from the CDC.
https://www.cdc.gov/lyme/datasurveillance/surveillance-data.html
Annual incidence. https://www.cdc.gov/lyme/datasurveillance/surveillance-data.html
https://wonder.cdc.gov/nndss/nndss_annual_tables_menu.asp
https://www.cdc.gov/lyme/datasurveillance/maps-recent.html
As of November 1, 2022, 2019 is the latest year for which there is Lyme disease data.
CDC: "More recent case counts are not publicly available at this time." (Accessed Nov 1, 2022.)

Where To Find CDC Case Definitions and their Statement that the Surveillance Case Definitions Are “not to be used as the sole criteria for establishing critical diagnosis”

Case Definition and Report Forms

The surveillance definition of Lyme disease was revised in January 2022.

See https://www.cste.org/resource/resmgr/ps/ps2021/21-ID-05_Lyme_Disease.pdf for the rationale behind the changes.

- ndc.services.cdc.gov/case-definitions/lyme-disease-2022/
- www.cdc.gov/lyme/resources/lymediseasecasereportform.pdf (for public health officials’ use)
- **Note from the CDC:** *The categorical labels used here to stratify laboratory evidence are intended to support the standardization of case classifications for public health surveillance. The categorical labels should not be used to interpret the utility or validity of any laboratory test methodology.* Accessed and copied Nov16, 2022 at https://ndc.services.cdc.gov/case-definitions/lyme-disease-2022/.

The surveillance definition of Rocky Mountain spotted fever/spotted fever rickettsiosis *was revised* in 2020.

- ndc.services.cdc.gov/case-definitions/spotted-fever-rickettsiosis-2020/

The Southeast Regional Center of Excellence in Vector-Borne Disease (SECVBD) will continue its vital work for another five years, thanks to renewed funding from the Centers for Disease Control and Prevention (CDC). Entomologist John Beier, Sc.D., a professor at the University of Miami Miller School of Medicine Department of Public Health Sciences, leads the Miller School’s SECVBD efforts in collaboration with the Miami-Dade County Mosquito Control Division.

Based at the University of Florida, the SECVBD was established in 2016, performing its initial work as the Zika epidemic reached the U.S. The center now includes an interdisciplinary team of researchers — from institutions including the Miller School, the University of South Carolina, University of North Carolina at Chapel Hill, Florida International University, Old Dominion University, and Ponce Health Sciences University in Puerto Rico — who work with leaders of state public health and mosquito and tick control agencies in the Southeast.

https://physician-news.umiamihealth.org/cdc-renews-funding-for-study-of-vector-borne-diseases/

State tick research and/or reports

The 2019 tick-borne disease surveillance summaries are now complete. You can view them at the bottom of the NC DHHS Epi Section Facts & Figures page, under Vector.

https://epi.dph.ncdhhs.gov/cd/vector/LymeSurveillanceSummary2020.pdf

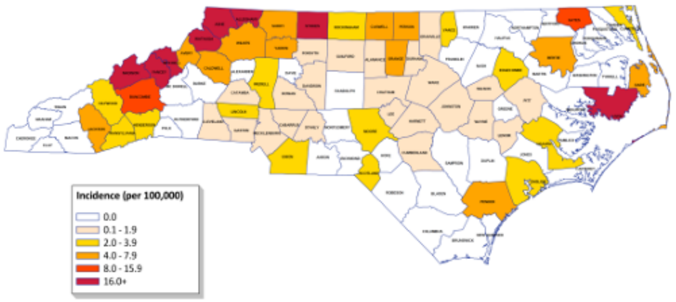
https://epi.dph.ncdhhs.gov/cd/vector/SpottedFeverGroupRickettsiosisSurveillanceSummary2020.pdf

Note: By the *former* CDC definition, six counties had confirmed cases of Lyme disease in two persons who had not traveled out of the county for 30 days after their tick exposure. **Therefore, these counties were endemic for Lyme disease by the former CDC definition: Wake, Guilford, Haywood, Alleghany, Buncombe, and Wilkes.** Counties with one case of locally acquired Lyme disease were: Cleveland (2008), Wilson (2009), Pitt (2009), Carteret (2009), Gates (2011), Perquimans (2011), Rowan (2013), Union (2013), Caldwell (2013), Franklin (2014), Stanley (2014), Duplin 2014.

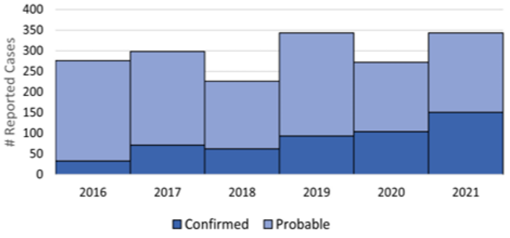
State tick research and/or reports

The 2021 tick-borne disease surveillance summaries are now complete. You can view them at the bottom of the NC DHHS Epi Section Facts & Figures page, under Vector epi.dph.ncdhhs.gov/cd/lyme/LymeSurveillanceSummary2021.pdf

Confirmed and Probable Incidence of Lyme Disease Cases by County of Residence, NC, 2021

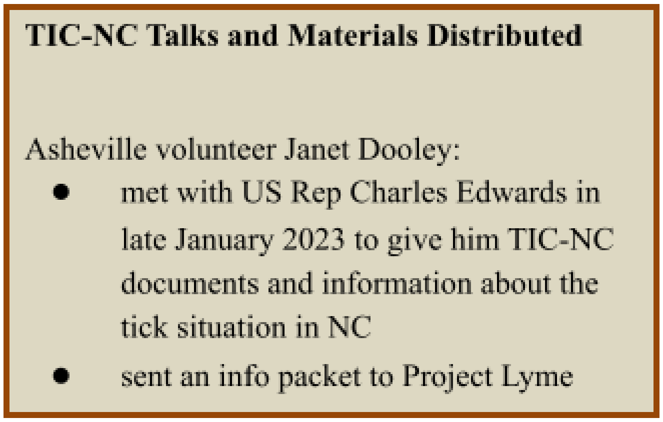


Confirmed and Probable Cases of Lyme Disease by Year, NC, 2016-2021; n= 1758



Note: Map is for 2021 only.

TIC-NC Activities



TIC-NC Talks and Materials Distributed

Asheville volunteer Janet Dooley:

- met with US Rep Charles Edwards in late January 2023 to give him TIC-NC documents and information about the tick situation in NC
- sent an info packet to Project Lyme

North Carolina and the South

More proof of Lyme disease in Ashe County, NC

Investigation of a Symptomatic Tick Bite Patient Confirms Borrelia burgdorferi in Ixodes scapularis and White-Footed Mice in Ashe County, North Carolina

In June 2021, a traveler to Ashe County, North Carolina, was bitten by an Ixodes scapularis tick. The patient experienced axillary lymphadenopathy and an erythematous rash near the bite site. We confirmed Borrelia burgdorferi sensu stricto through PCR testing and DNA sequencing in the attached tick and later from mice trapped inside the cabin where the patient stayed. Clark & Herman-Giddens. VECTOR-BORNE AND ZOONOTIC DISEASES, doi: 10.1089/vbz.2022.0042. Open access.

More evidence about what is called STARI

Relapsing Fever Caused by Borrelia lonestari after Tick Bite in Alabama, USA

We report an immunocompromised patient in Alabama, USA, 75 years of age, with relapsing fevers and pancytopenia who had spirochetemia after a tick bite. We identified Borrelia lonestari by using PCR, sequencing, and phylogenetic analysis. Increasing clinical availability of molecular diagnostics might identify B. lonestari as an emerging tickborne pathogen.

The first reported human case of *B. lonestari* infection was identified in an elderly patient with an erythema migrans-like rash that developed after an *A. americanum* tick bite; PCR identified *B. lonestari* in both a skin biopsy and the removed tick (*8*). In contrast, the patient we report had a longer illness and a pattern of relapsing fevers, absence of erythema migrans, and a possible Jarisch–Herxheimer reaction after initiation of antimicrobial therapy. *B. lonestari* has not been previously reported to cause tickborne relapsing fever, but this manifestation is not unexpected given the close homology to *B. miyamotoi*, the cause of hard tick relapsing fever (9). The patient's immunocompromised condition from CD20 monoclonal antibody therapy might also have affected the patient's clinical manifestations.

The infrequency of reported *B. lonestari* infections despite the frequent isolation of the bacteria from host-seeking *A. americanum* ticks suggests that this species might have a lower pathogenic potential than other *Borrelia* spp. more often associated with human disease. However, this assumption is hindered by the difficult isolation of *B. lonestari* through classic laboratory methods, including culturing (2,10). This case and associated sequence analysis highlight the clinical utility of molecular diagnostics for patients with suspected tickborne diseases. Increasing availability of molecular diagnostics might enable *B. lonestari* to be identified as an emerging tickborne pathogen, particularly causing opportunistic infections among persons who are immunocompromised. Vazquez G, et al. *Emerging Infectious Diseases*, *29*(2), 441-444. https://doi.org/10.3201/eid2902.221281.

Phylogenetic tree showing the genetic differences between the Lyme disease group of Borrelia spp. and the relapsing fever group

Figure. Phylogenetic analysis of bacterial sequence derived from patient's blood (gray shading) in study of relapsing fever caused by Borrelia lonestari after tick bite in Alabama, USA.

Phylogenetic tree was constructed from representative V1/V2 regions of 16S rRNA gene sequences from different Borrelia spp. known to cause Lyme disease or relapsing fever. GenBank accession numbers are indicated after the species names. The bacterial sequence from the patient sample formed a high-confidence clade with B. lonestari sequences and was most closely related to B. miyamotoi. Nodes with >95% confidence bootstrap values are labeled with black circles, and branch tips are labeled with gray triangles.

Borrelia garinii found in South Carolina

Genomic Confirmation of Borrelia garinii, United States

Lyme disease is a multisystem disorder primarily caused by Borrelia burgdorferi sensu lato. However, B. garinii, which has been identified on islands off the coast of Newfoundland and Labrador, Canada, is a cause of Lyme disease in Eurasia. We report isolation and whole-genome nucleotide sequencing of a B. garinii isolate from a cotton mouse (Peromyscus gossypinus) in South Carolina, USA. We identified a second B. garinii isolate from the same repository. Phylogenetic analysis does not associate these isolates with the previously described isolates of B. garinii from Canada.

MLST analyses of both isolates and whole-genome sequencing of SCCH-7 showed that these isolates are not closely related to *B. garinii* strains from Canada; however, they are closely related to a subset of Eurasian isolates. How and when *B. garinii* arrived in South Carolina remains unknown. There were no reported Lyme disease outbreaks in the southeastern United States in humans at the time the strains were deposited in the repository or during the subsequent 2 decades. This finding minimizes the urgency for an immediate new search for *B. garinii* in this region. Nonetheless, clinical vigilance for *B. garinii* in humans in this region seems warranted.
Rudenko N, et al. *Emerging Infectious Diseases*, *29*(1), 64-69. https://doi.org/10.3201/eid2901.220930. Open access.

Tick bite as a risk factor for alpha-gal specific IgE antibodies and development of alpha-gal syndrome

The disaccharide galactose-α-1,3-galactose (alpha-gal) is expressed in mammals other than humans, apes, and old-world monkeys. In humans, elevated immunoglobulin-E (IgE) antibodies specific for alpha-gal can result in allergic hypersensitivity known as alpha-gal syndrome (AGS). Case reports and series suggest that tick bites can induce alpha-gal specific IgE antibodies.
We conducted a case-control study comparing AGS patients from a North Carolina allergy clinic with controls who were patients at a nearby internal medicine clinic. Cases and controls were administered a questionnaire to obtain information about demographics, home environment, outdoor activities, and recollection of tick bite. Serum samples taken at the time of enrollment were tested for total IgE, alpha-gal sIgE, and antibodies to other tickborne pathogens.

AGS patients were more likely to recall finding a tick on themselves (OR=11.20, 95% CI 4.97-25.15), live near wooded forest (OR=2.27, 95% CI 0.92-5.55), and spend 17 or more hours per week outdoors in wooded areas (OR=5.58, 95% CI 2.56-12.19). AGS patients were also more likely to report 4 or more tick bites (OR=33.05, 95% CI 9.92-155.12) and reactions at the site of tick bites (OR=7.93, 95% CI 3.74-16.80). Elevated alpha-gal sIgE was also observed in 33% of controls and was also associated with tick exposure in the controls (OR=4.25, 95% CI 2.21-8.18).

The results define tick bite as a risk factor for AGS and elevated alpha-gal sIgE. Kersh GJ, et al. Annals of Allergy. Asthma & Immunology, https://doi.org/10.1016/j.anai.2022.11.021. *Open access.*

Alpha-Gal Syndrome in the Infectious Diseases Clinic: A Series of 5 Cases in Central North Carolina

Alpha-gal syndrome (AGS) is a recently described allergy to galactose-α-1,3-galactose, an oligosaccharide present in mammalian meat. AGS can present with angioedema, urticaria, and anaphylaxis arising 3–6 hours after ingestion, although symptoms such as gastrointestinal distress, fatigue, and arthralgias are also reported. Because AGS appears to be associated with tick bites, patients may present to infectious diseases (ID) clinics for evaluation.

We documented a series of 5 patients referred to the University of North Carolina ID Clinic between 2020 and 2022 for various tick-borne infections that were found to have symptoms and laboratory testing consistent with AGS. Patients were subsequently referred to the Allergy and Immunology Clinic.

Patients were referred to the ID Clinic for persistent symptoms following positive tick-borne disease testing or presumed tick-borne infection. All patients had an elevated alpha-gal immunoglobulin E and clinical presentation consistent with AGS. Common symptoms included episodic gastrointestinal distress (eg, cramping, nausea, diarrhea), fatigue, arthralgias, and subjective cognitive impairment, but a notable absence of severe anaphylaxis. Four patients were seen by at least 1 nonallergy specialist prior to referral to ID. Patients reported substantial improvement in their symptoms following dietary restriction.

ID physicians should be aware of AGS as a cause of persistent, nonspecific symptoms following a tick exposure or tick-borne illness. Further research is needed to determine the prevalence of alpha-gal sensitization and AGS following tick-borne bites. Boyce, RM et al. *Open Forum Infectious Diseases*, doi.org/10.1093/ofid/ofac663.

See link to recent radio/media coverage on Cummins' and UNC research: https://www.npr.org/sections/health-shots/2023/04/02/1166431106/ticks-ick-the-latest-science-on-the-red-meat-allergy-caused-by-some-tick-bites.

Prevalence and National Sensitization Patterns of Alpha-Gal IgE Among Military Personnel *Range 6% to 36%*

IgE antibodies to the oligosaccharide galactose-alpha-1,3-galactose (alpha-gal) are causally-related to a syndrome of mammalian meat allergy that is linked to tick bites and is common in parts of the southeastern USA. There has been limited surveillance of alpha-gal sensitization nationally and in the military population.

Here we surveyed baseline alpha-gal IgE prevalence in serum samples from 3000 service members who presented to one of 10 military bases in the central/eastern USA. Serum was collected from 2002-2007 at the time personnel presented to the base and was bio-banked in the Department of Defense Serum Repository. Alpha-gal IgE was assayed by ImmunoCAP (cut-off 0.1 kU/L) and related to home of record at time of enlistment.

Of the cohort, 2456 subjects were male (81.9%) and median age was 19 years (IQR18-22). Home of record spanned all 50 states, with a median of 36 recruits per state (range 3-261). Overall prevalence of alpha-gal IgE was 6.0%. Focusing on the 35 states with at least 20 personnel, the highest prevalence rates were in Arkansas (36%), Oklahoma (35%) and Missouri (29%). States with intermediate prevalence included Kentucky (14%), Mississippi (13%), North Carolina (12%), Tennessee (10%), Alabama (10%), Minnesota (9%) and Virginia (7%). There were no cases from Utah, West Virginia, Colorado or Michigan and less than 2% in Wisconsin, Massachusetts, Washington, Illinois and New York.

Baseline prevalence of alpha-gal IgE among military personnel was 6.0%. There were significant regional differences, with an overall pattern consistent with the known range of the lone star tick (*Amblyomma americanum*). Wilson J, et al. Journal of Allergy and Clinical Immunology, doi.org/10.1016/j.jaci.2022.12.299

South Carolina RMSF in a 72-year-old woman with no known tick exposure

An Unsuspected Case of Rocky Mountain Spotted Fever: A Lesson to Keep a Broad Differential

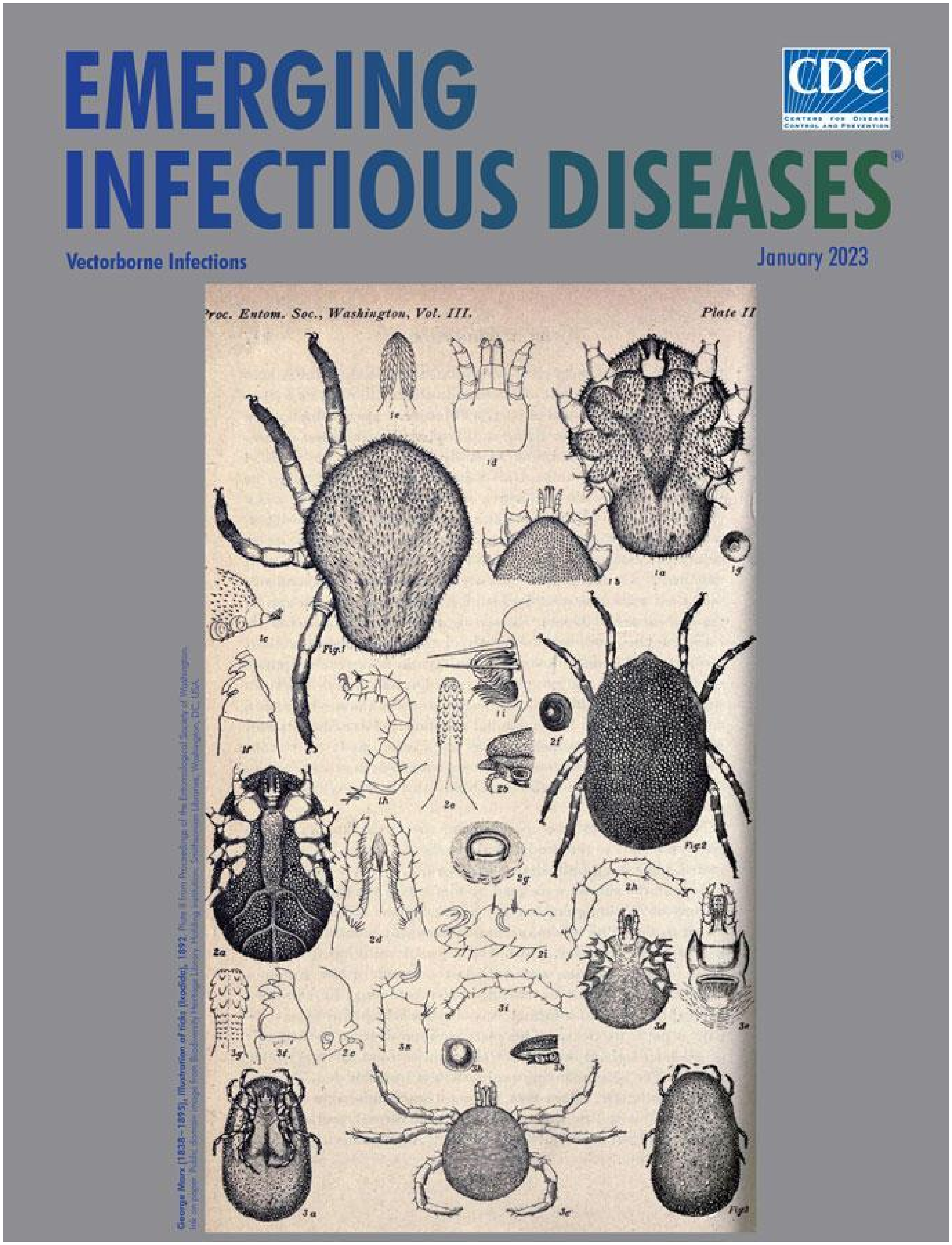
Rocky Mountain spotted fever (RMSF), a tick-borne illness, can cause serious illness or death even in a healthy individual. Unfortunately, this illness can be difficult to diagnose as symptoms are nonspecific and oftentimes mimic benign viral illnesses. Delayed diagnosis can be detrimental as the timing of antibiotic administration is critical to prevent associated morbidity and mortality. A careful travel and social history can sometimes provide clues to make the diagnosis. Being aware of lesser-known objective findings such as hyponatremia, neurologic derangements, transaminitis, and thrombocytopenia may help raise suspicion for the disease. This is a case of a 72-year-old woman who presented with nonspecific symptoms and hyponatremia without known tick exposure. She was eventually diagnosed with RMSF. The timing of her presentation corresponded with a surge in COVID-19 infections throughout her area of residence, which further complicated her presentation and contributed to a delayed diagnosis.

This case of RMSF illustrates a classic example of how this disease, which often mimics common viral illnesses, can easily be overlooked. The typical presenting triad for RMSF consists of fever, headache, and rash. Atypical presentations are commonly seen, however, and may complicate diagnosis. Up to 15% of patients do not develop a rash, and only 49% of people have a rash in the first 3 days of symptom onset.[2] The rash, when present, typically starts on the ankles and wrists, spreads to the trunk, and involves the palms and soles with sparing of the face. Our patient's rash was subtle and a bit delayed in onset. Her rash also spread in the opposite manner as the classic rash, making diagnosis less obvious. Quiroga M & Petz C. *Journal of Investigative Medicine High Impact Case Reports*. 2022;10. doi:10.1177/23247096221145014.

Comprehensive Review of Emergence and Virology of Tickborne Bourbon Virus in the United States.

The emergence of SARS-CoV-2 and the worldwide COVID-19 pandemic triggered considerable attention to the emergence and evolution of novel human pathogens. Bourbon virus (BRBV) was first discovered in 2014 in Bourbon County, Kansas, USA. Since its initial discovery, several cases of BRBV infection in humans have been identified in Kansas, Oklahoma, and Missouri. BRBV is classified within the Thogotovirus genus; these negative-strand RNA viruses appear to be transmitted by ticks, and much of their biology remains unknown. In this review, we describe the emergence, virology, geographic range and ecology, and human disease caused by BRBV and discuss potential treatments for active BRBV infections. This virus and other emerging viral pathogens remain key public health concerns and require continued surveillance and study to mitigate human exposure and disease.

Serologic testing was performed on a wide array of common mammal and avian fauna found near the sites of confirmed human cases in Missouri and at a distant site in **North Carolina** (still within the range of *A. americanum* ticks); numerous mammals were seropositive for BRBV, including domestic dogs, eastern cottontail rabbits, horses, raccoons, and white-tailed deer. Roe MK et al. *Emerging Infectious Diseases*, *29*(1), 1-7. https://doi.org/10.3201/eid2901.212295.



Breedlove, B. (2023). Up Close with Ticks. *Emerging Infectious Diseases*, *29*(1), 229-230. https://doi.org/10.3201/eid2901.ac2901.

Perioperative implications of patients with alpha gal allergies

Alpha gal syndrome is IgE mediated response to mammalian products. Alpha gal syndrome has been identified worldwide. Symptoms of alpha gal syndrome can be as severe as anaphylaxis. Many surgical products and drugs contain mammalian products. Prevention of exposure in the perioperative space can mitigate risk. Mazier M, et al. Journal of Clinical Anesthesia, doi.org/10.1016/j.jclinane.2023.111056.

The tick-borne cat infection

***Cytauxzoon felis*: An Overview**
Cytauxzoon felis is a tick-transmitted, obligate, hemoprotozoal, piroplasmid pathogen of felids and the causative agent of cytauxzoonosis. It has a complex life cycle which includes a tick as its definitive host and a felid as its intermediate host. Since its first description in 1976, C. felis infections of felids have been reported in several southeastern and south-central U.S. states, overlapping with the ranges of its two known biological vectors, Amblyomma americanum (Lone star tick) and Dermacentor variabilis (American dog tick).

Infected felids demonstrate disease as either an acute, often-fatal, infection, or a subclinical carrier infection. To develop effective *C. felis* transmission control strategies, the incidence of acute cytauxzoonosis, patient risk factors, the role of domestic cat carriers, and ecological variabilities need to be investigated further. Of equal importance is communicating these strategies for high-risk cat populations, including recommending year-round use of an acaricide product for all cats that spend any time outdoors.

More studies are needed to further identify factors affecting *C. felis* and other *Cytauxzoon* spp. infection, transmission, disease progression, and treatment options and outcomes within the U.S. and globally. Here we provide an overview of *C. felis* highlighting its lifecycle within its definitive host, transmission to its intermediate host, symptoms and signs providing evidence of transmission, definitive diagnosis, current treatment and prevention strategies, and future considerations regarding this condition. Wikander YM, Reif KE. *Pathogens* 2023, *12*(1), 133. doi.org/10.3390/pathogens12010133.

Tick bite frequency, prevention practices and Lyme disease diagnoses among U.S. Hispanic survey respondents

Tick bite prevention practices, knowledge of Lyme disease (LD) symptoms and transmission, and patterns of LD diagnoses among Hispanic persons have been reported but not comprehensively evaluated. In 2014, CDC examined questions from a prospective nationwide survey of U.S. Hispanic adults conducted via the Offerwise QueOpinas panel regarding ticks and LD. From October to November, a total of 2,649 surveys were released and 1,006 completed surveys returned.

Overall, 44% of respondents reported routinely practising at least one form of personal protection against tick bites, and wearing repellent was the most commonly reported method (29%).

Approximately 6% of respondents reported a tick bite for either themselves or someone in their household during the previous 12 months. An individual or household diagnosis of LD in the previous year was reported by 2% of respondents, with the highest proportion of diagnoses reported by respondents from high LD incidence states.

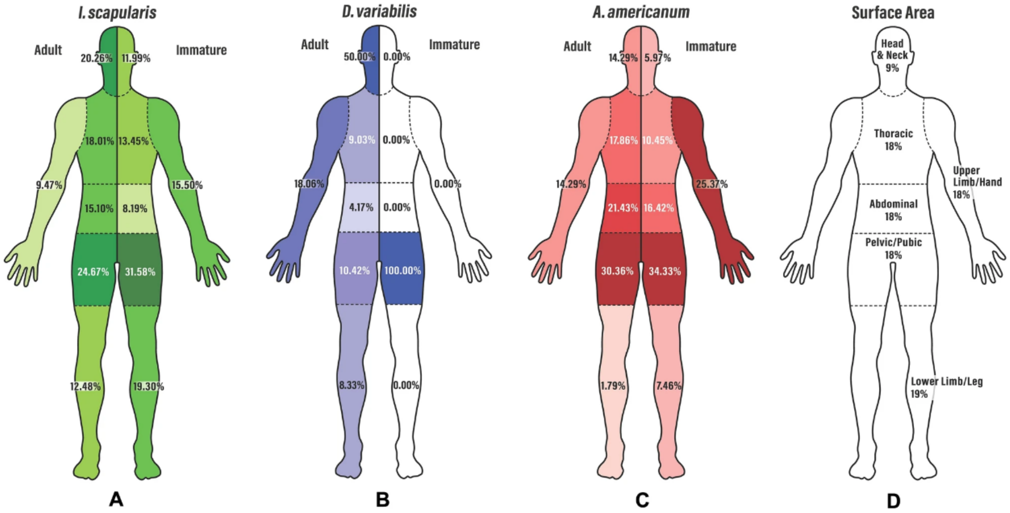
The annual incidence of healthcare provider-diagnosed LD in the survey population was higher than national surveillance estimates for reported LD among U.S. Hispanic persons during 2000–2013. As annual incidence of LD continues to increase, it is important to ensure equitable access to information about LD, including disease transmission, manifestations, and prevention recommendations. Results from this survey can help inform public health outreach focused on effective tick bite prevention methods and early recognition of LD. Beck A, et al. Zoonoses and Public Health, doi.org/10.1111/zph.12864.

National Section

Human attachment site preferences of ticks parasitizing in New York.

Ticks transmit several arthropod-borne pathogens in New York State. The primary human-biting ticks in this region are *Ixodes scapularis*, *Amblyomma americanum*, and *Dermacentor variabilis*. Body regions where tick bites human vary depending on the tick species and life stage, and clothing worn by the host. A community tick submission system was used to acquire information about bite-site location prior to pathogen testing to understand species and life stage-specific body-segment preferences.

These data resulted in the identification of species-specific preferences for location, with *D. variabilis* preferentially biting the head and neck and *A. americanum* preferring the thighs, groin, and abdomen. *Ixodes scapularis* was found across the body, although it showed a significant life stage difference with adults preferring the head, midsection, and groin, while nymphs/larvae preferred the extremities. Infection with *Borrelia burgdorferi* resulted in a significant change in attachment site. This provides an assessment of which body region ticks of the most common species in New York are likely to be found. Hart CS, et al. *Sci Rep* **12**, 20897 (2022). https://doi.org/10.1038/s41598-022-25486-7.



A representation of the body segment distribution of (**A**) *I. scapularis*, (**B**) *D. variabilis*, and (**C**) *A. americanum*. These are divided into adult and nymph/larval ticks for each species. These are compared to the corresponding average predicted surface area of each bodily segment (**D**). Statistically significant changes in distribution were observed compared to the assumption of equal distribution over the body, with *D. variabilis* strongly preferring the head and neck and *A. americanum* preferring the groin/pelvic/thigh area, with *I. scapularis* showing a more somewhat even distribution. Figures were generated with assistance from Sabra Snyder.

Ohio Public Health

The Ohio Department of Health (ODH) Zoonotic Disease Program, in partnership with ODH Laboratory, local public health partners, and sanitary district partners, conducts statewide vectorborne disease surveillance which includes monitoring for human and veterinary cases. https://odh.ohio.gov/know-our-programs/zoonotic-disease-program/news/vectorborne-disease-update
For a good article on ticks and safety see:
https://www.farmanddairy.com/top-stories/how-to-assess-your-risk-for-illness-after-removing-a-tick/748127.html.

Rapid invasion and expansion of the Asian longhorned tick (*Haemaphysalis longicornis*) into a new area on Long Island, New York, USA.

Since its discovery in the United States in 2017, the Asian longhorned tick (*Haemaphysalis longicornis*) has been detected in most eastern states between Rhode Island and Georgia. Long Island, east of New York City, a recognized high-risk area for tick-borne diseases, is geographically close to New Jersey and New York sites where *H. longicornis* was originally found.

However, extensive tick surveys conducted in 2018 did not identify *H. longicornis* on Long Island. In stark contrast, our 2022 tick survey suggests that *H. longicornis* has rapidly invaded and expanded in multiple surveying sites on Long Island (12 out of 17 sites). Overall, the relative abundance of *H. longicornis* was similar to that of lone star ticks, *Amblyomma americanum*, a previously recognized tick species abundantly present on Long Island.

Interestingly, our survey suggests that *H. longicornis* has expanded within the Appalachian forest ecological zone of Long Island's north shore compared to the Pine Barrens located on the south shore of Long Island. The rapid invasion and expansion of *H. longicornis* into an insular environment are different from the historical invasion and expansion of two native tick species, *Ixodes scapularis* (blacklegged tick or deer tick) and *A. americanum*, in Long Island. The implications of *H. longicornis* transmitting or introducing tick-borne pathogens of public health importance remain unknown. Benach JL, et al. Ticks and Tick-borne Diseases, https://doi.org/10.1016/j.ttbdis.

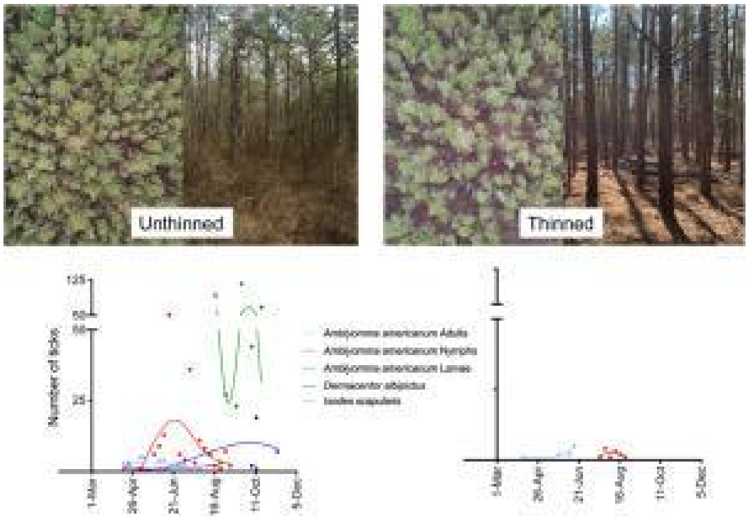
Tick abundance and diversity are substantially lower in thinned vs. unthinned forests in the New Jersey Pinelands National Reserve, USA

Forest thinning is a management tool used in the New Jersey Pinelands and elsewhere to improve forest health and resilience, mitigate wildfire risk, and manage for wildlife. Forest thinning leads to warmer drier microclimates, which have been shown in both field and laboratory studies to reduce tick survival and reproduction.

To directly assess the effects of forest thinning on the abundance and diversity of ticks and on the prevalence of tick-borne human pathogens, we sampled ticks weekly from March to November 2021 at three replicated pairs of thinned and unthinned forest sites composed primarily of pitch-pine, shortleaf pine, and various oak species. We characterized microclimate in the understory and forest floor at each sampling plot by deploying multiple data loggers to monitor temperature and relative humidity throughout the study period.

As expected, we found that thinned plots were significantly drier and warmer than unthinned plots. We also found that average questing tick abundance was 92% lower in thinned as compared with unthinned plots. Of the three main tick species collected in unthinned plots (*Amblyomma americanum, Ixodes scapularis*, and *Dermacentor albipictus*) only *A. americanum* and a single *I. scapularis* were collected in thinned plots. Prevalence of *Ehrlichia* species in *A. americanum* did not differ between treatments, and the sole *I. scapularis* collected in a thinned plot was infected with *Borrelia burgdorferi* sensu lato.

However, the significant and much lower tick abundance in thinned plots indicates a lower risk of human-tick encounters. Our results add to the growing evidence that landscape and forest management can reduce local tick abundance, thereby reducing tick-borne disease risk. Washkwich J et al. Ticks and Tick-borne Diseases, doi.org/10.1016/j.ttbdis.2022.102106.



Bourbon Virus Transmission, New York, USA

In July 2019, Bourbon virus RNA was detected in an *Amblyomma americanum* tick removed from a resident of Long Island, New York, USA. Tick infection and white-tailed deer *(Odocoileus virginianus)* serosurvey results demonstrate active transmission in New York, especially Suffolk County, emphasizing a need for surveillance anywhere A. *americanum* ticks are reported…. the tick was also positive for *Ehrlichia ewingii* bacteria. Dupuis AP, et al. Emerging Infectious Diseases, 29(1), 145-148. https://doi.org/10.3201/eid2901.220283.

Perceived vulnerability for Lyme disease questionnaire: A social science tool for understanding tick-borne disease attitudes

- Perceived vulnerability scale is novel in case of Lyme and vector-borne diseases.
- Perceived vulnerability is encompassed by susceptibility and emotional discomfort.
- Perceptions of susceptibility correlate with self-efficacy and motivation.
- Emotional discomfort towards ticks has a strong relationship with preventative behaviors.

While an overwhelming majority of research on human dimensions of ticks focuses on risk perceptions and engaging in preventative behavior, this study highlights the psychological validity of perceived vulnerability as a construct in this context and establishes a need for further exploration of its relationship with Lyme disease. With emotional discomfort being found to have a strong psychological influence on people's intent to engage in preventative behaviors, future studies as well as outreach messaging should bring this construct more to the center stage and parse out the full role that fear, disgust, and discomfort play in facilitating perceptions of ticks. Olechnowicz C, et al. Ticks and Tick-borne Diseases, doi.org/10.1016/j.ttbdis.2023.102120.

Prevalence of *Borrelia burgdorferi* and diversity of its outer surface protein C (*ospC*) alleles in blacklegged ticks (*Ixodes scapularis*) in Delaware

Characterizing the diversity of genes associated with virulence and transmission of a pathogen across the pathogen's distribution can inform our understanding of host infection risk. *Borrelia burgdorferi* is a vector-borne bacterium that causes Lyme disease in humans and is common in the United States. The outer surface protein C (*ospC*) gene of *B. burgdorferi* exhibits substantial genetic variation across the pathogen's distribution and plays a critical role in virulence and transmission in vertebrate hosts. In fact, *B. burgdorferi* infections that disseminate across host tissues in humans are associated with only a subset of *ospC* alleles.

Delaware has a high incidence of Lyme disease, but the diversity of *ospC* in *B. burgdorferi* in the state has not been evaluated. We used PCR to amplify *ospC* in *B. burgdorferi*-infected blacklegged ticks (*Ixodes scapularis*) in sites statewide and used short-read sequencing to identify *ospC* alleles. *B. burgdorferi* prevalence in blacklegged ticks varied across sites, but not significantly so. We identified 15 previously characterized *ospC* alleles accounting for nearly all of the expected diversity of alleles across the sites as estimated using the Chao1 index.

Nearly 40% of sequenced infections (23/58) had more than one *ospC* allele present suggesting mixed strain infections and the relative frequencies of alleles in single infections were positively correlated with their relative frequencies in mixed infections. Turnover of *ospC* alleles was positively related to distance between sites with closer sites having more similar allele compositions than more distant sites. This suggests a degree of *B. burgdorferi* dispersal limitation or habitat specialization. *OspC* alleles known to cause disseminated infections in humans were found at the highest frequencies across sites, corresponding to Delaware's high incidence of Lyme disease. Shifflet A, et al. Ticks and Tickborne Diseases. doi.org/10.1016/j.ttbdis.2023.102139.

Consequences of Contracting COVID-19 or Taking the COVID-19 Vaccine for Individuals with a History of Lyme Disease

Individuals with Lyme disease can be very symptomatic. This survey compares the burden of illness for individuals with a history of Lyme disease (HLD) with individuals with a HLD who have either contracted COVID-19 or who have taken the COVID-19 vaccine. The findings describe the relative symptom burden among these three groups using a cross-sectional descriptive survey investigating the burden of Lyme disease in a pandemic. The survey includes the General Symptom Questionnaire-30 (GSQ-30), a brief self-report scale designed to assess the symptom burden in Lyme disease (LD).

The results of this survey show that the overall burden of illness among individuals with HLD is not significantly different after contracting COVID-19 or after COVID-19 vaccination. A new survey will be needed to better understand why one in five individuals with a HLD reported long COVID after contracting COVID-19. These results should help clinicians and their patients to discuss the consequences of contracting a COVID-19 infection or being vaccinated against COVID-19. Cameron DJ & McWhinney SR. *Antibiotics* 2023, *12*(3), 493; https://doi.org/10.3390/antibiotics12030493.

Pfizer halts Lyme vaccine trial on Nantucket and Martha's Vineyard, citing violations

By Rasheek Tabassum Mujib, Cape Cod Times, February 24, 2023.

Pharmaceutical giant Pfizer last weekend abruptly halted a Lyme disease vaccine trial on Nantucket and Martha's Vineyard, citing violations of "good clinical practice" by Care Access, the Boston research group running the trials.

The trial, developed by Pfizer in partnership with the French company Valneva, started last summer in 50 Lyme-endemic communities. Both Nantucket and Martha's Vineyard have high rates of tick-borne diseases and were selected as sites.

According to a Feb. 17 statement from Pfizer, "good clinical practice" is an international ethical and scientific quality standard for clinical trials.

"Once Pfizer learned of potential violations of GCP, it conducted a thorough review of the operations and data collection at the clinical trial sites run by the third party and followed standard operating safeguards to determine the correct course of action," reads the statement. https://www.yahoo.com/entertainment/pfizer-halts-lyme-vaccine-trial-092614784.html.

Bartonella spp. Infections Identified by Molecular Methods, United States

Bartonella spp. are fastidious, gram-negative intracellular bacteria that are transmitted to humans by insect vectors. The genus includes 12 species associated with human infection: *B. henselae*, *B. quintana*, *B. bacilliformis*, *B. elizabethae*, *B. vinsonii*, *B. koehlerae*, *B. clarridgieae*, *B. alsatica*, *B. doshiae*, *B. grahamii*, *B. rattimassiliensis*, and *B. tribocorum* (*1*,*2*). Bartonellosis cases are not nationally notifiable in the United States, limiting knowledge of disease epidemiology.

Molecular methods can enable rapid identification of *Bartonella* spp. infections, which are difficult to diagnose by using culture or serology. We analyzed clinical test results of PCR that targeted bacterial 16S rRNA hypervariable V1–V2 regions only or in parallel with PCR of *Bartonella*-specific *ribC* gene. We identified 430 clinical specimens infected with *Bartonella* spp. from 420 patients in the United States. Median patient age was 37 (range 1–79) years; 62% were male. We identified B. *henselae* in 77%, B. *quintana* in 13%, B. *clarridgeiae* in 1%, B. *vinsonii* in 1%, and B. *washoensis* in 1% of specimens. B. *quintana* was detected in 83% of cardiac specimens; B. *henselae* was detected in 34% of lymph node specimens. We detected novel or uncommon *Bartonella* spp. in 9 patients. Molecular diagnostic testing can identify *Bartonella* spp. infections, including uncommon and undescribed species, and might be particularly useful for patients who have culture-negative endocarditis or lymphadenitis.
McCormick DW, et al. Emerging Infectious Diseases, 29(3), 467-476. https://doi.org/10.3201/eid2903.221223.

International Section

Abundance of *the longhorned tick* increased with higher Deer Impact Score, which represents relative deer density

The relationship between *Haemaphysalis longicornis* and sika deer abundance on Tsushima Islands, Japan

Tick-borne diseases such as Severe Fever with Thrombocytopenia Syndrome (SFTS) are of concern as new issues in public health and conservation medicine. The SFTS virus especially is a fatal infection for feline animals…
Here, we report our investigation of the tick fauna on Tsushima Islands and its comparison with the abundance of Tsushima sika deer (*Cervus nippon pulchellus*). The flagging method was used at five collection sites on Tsushima islands in May 2022. We collected 131 ticks of three species, *Haemaphysalis longicornis* (127 individuals), *H. formosensis* (3) and *Amblyomma testudinarium* (1), among which *H. longicornis* was the dominant species. The abundance of *H. longicornis* increased with increased Deer Impact Score, which represents relative deer density based on five deer signs (bark stripping on *Cryptomeria japonica* or *Chamaecyparis obtusa* trees, browsing marks on the understory vegetation, deer fecal pellets, deer tracks, and deer trails). This study indicated that deer abundance may be an important factor in determining *H. longicornis* abundance. Notably, *H. longicornis* is known to serve as vector for several tick-borne pathogens, including SFTS virus. The relationships between ticks and wildlife hosts are expected to provide essential information from the perspectives of vector control, disease risk prediction,

and conservation of rare species. Suzuki KK, et al. Zoosymposia, https://doi.org/10.11646/zoosymposia.22.1.90.

Systematic Review and Meta-analysis of Lyme Disease Data and Seropositivity for *Borrelia burgdorferi*, China, 2005–2020

Since its initial identification in 1986, Lyme disease has been clinically diagnosed in 29 provinces in China; however, national incidence data are lacking. To summarize Lyme disease seropositivity data among persons across China, we conducted a systematic literature review of Chinese- and English-language journal articles published during 2005–2020. According to 72 estimates that measured IgG by using a diagnostic enzyme-linked assay (EIA) alone, the seropositivity point prevalence with a fixed-effects model was 9.1%. A more conservative 2-tier testing approach of EIA plus a confirmatory Western immunoblot (16 estimates) yielded seropositivity 1.8%.

Seropositivity by EIA for high-risk exposure populations was 10.0% and for low-risk exposure populations was 4.5%; seropositivity was highest in the northeastern and western provinces. Our analysis confirms Lyme disease prevalence, measured by seropositivity, in many Chinese provinces and populations at risk. This information can be used to focus prevention measures in provinces where seropositivity is high. Stark J, et al. *Emerging Infectious Diseases*, *28*(12), doi.org/10.3201/eid2812.212612.

Figure 3. Forest plot illustrating seropositivity estimates for *Borrelia burgdorferi*, by province, China, 2005–2020. The red horizontal line indicates the summary estimate based on the primary analysis; error bars indicate 95%...

Tick Control in a Connected World: Challenges, Solutions, and Public Policy from a United States Border Perspective

Ticks are able to transmit the highest number of pathogen species of any blood-feeding arthropod and represent a growing threat to public health and agricultural systems worldwide. While there are numerous and varied causes and effects of changes to tick-borne disease (re)emergence, three primary challenges to tick control were identified in this review from a U.S. borders perspective. (1) Climate change is implicated in current and future alterations to geographic ranges and population densities of tick species, pathogens they can transmit, and their host and reservoir species, as highlighted by *Ixodes scapularis* and its expansion across southern Canada. (2) Modern technological advances have created an increasingly interconnected world, contributing to an increase in invasive tick species introductions through the increased speed and frequency of trade and travel. The introduction of the invasive *Haemaphysalis longicornis* in the eastern U.S. exemplifies the challenges with control in a highly interconnected world. (3) Lastly, while not a new challenge, differences in disease surveillance, control, and management strategies in bordering countries remains a critical challenge in managing ticks and tick-borne diseases. International inter-agency collaborations along the U.S.–Mexico border have been critical in control and mitigation of cattle fever ticks (*Rhipicephalus* spp.) and highlight the need for continued collaboration and research into integrated tick management strategies. These case studies were used to identify challenges and opportunities for tick control and mitigation efforts through a One Health framework. Tiffin HS, et al. *Trop. Med. Infect. Dis.* **2022**, *7*(11), 388; https://doi.org/10.3390/tropicalmed7110388.

Infection with Neoehrlichia mikurensis promotes the development of malignant B-cell lymphomas

The tick-borne pathogen Neoehrlichia (N.) mikurensis is implicated in persistent infection of the vascular endothelium. B cells are crucial for the host defence to this infection. Chronic stimulation of B cells may result in B-cell transformation and lymphoma. Five patients with malignant B-cell lymphoma and concomitant N. mikurensis infection were investigated regarding clinical picture, lymphoma subtype, B-cell lymphoma immunophenotype and IGHV (variable region of the immunoglobulin heavy) gene repertoire. Three of the five patients improved markedly and ceased lymphoma treatment after doxycycline treatment to eliminate N. mikurensis. Sequencing the B-cell lymphoma IGHV genes revealed preferred usage of the IGHV1 (IGHV1-2, and -69) and IGHV3 (IGHV3-15, -21, -23) families. In conclusion, N. mikurensis infection may drive the development of malignant B-cell lymphomas. Eradication of the pathogen appears to induce remission with apparent curing of the lymphoma in some cases. Wennerås C, et al. Br J Haematol, doi:10.1111/bjh.18652.

“Candidatus Neoehrlichia mikurensis” (Ca. N. mikurensis) is a tick-borne bacterial pathogen that can cause disease particularly among immune compromised persons. It is now called neoehrlichiosis. Symptoms include fever, migrating pain, and vascular/thromboembolic complications. The bacterium was named after its discovery in ticks and rodents on the Japanese island of Mikura.

Seven tick species and 6 genera of pathogens on these chimpanzees

Survey of ticks and tick-borne pathogens in wild chimpanzee habitat in Western Uganda

A total of 470 ticks were collected, which led to the identification of seven tick species: *Haemaphysalis parmata* (68.77%), *Amblyomma tholloni* (20.70%), *Ixodes rasus* sensu lato (7.37%), *Rhipicephalus dux* (1.40%), *Haemaphysalis punctaleachi* (0.70%), *Ixodes muniensis* (0.70%) and *Amblyomma paulopunctatum* (0.35%). The presence of ticks, irrespective of species, was influenced by temperature and type of vegetation but not by relative humidity. Molecular detection revealed the presence of at least six genera of tick-borne pathogens (*Babesia*, *Theileria*, *Borrelia*, *Cryptoplasma*, *Ehrlichia* and *Rickettsia*). The Afrotopical tick *Amblyomma tholloni* found in one chimpanzee nest was infected by *Rickettsia* sp. Lacroux et al. *Parasites & Vectors*, Vol 16, Article number: 22 (2023).

A possible mild pathogen common in lone star ticks and others

Rickettsia amblyommatis in Ticks: A Review of Distribution, Pathogenicity, and Diversity

Figure 1. World map displaying the distribution of *Rickettsia amblyommatis*-infected ticks. Map created using **www.mapchart.net** (accessed on 27 January 2023).

Rickettsia amblyommatis is a potentially pathogenic species of *Rickettsia* within the spotted fever group vectored by ticks. While many studies have been published on this species, there is debate over its pathogenicity and the inhibitory role it plays in diagnosing illnesses caused by other spotted fever group *Rickettsia* species. Many publications have recorded the high infection prevalence of *R. amblyommatis* in tick populations at a global scale.

While this species is rather ubiquitous, questions remain over the epidemiological importance of this possible human pathogen. With tick-borne diseases on the rise, understanding the exact role that *R. amblyommatis* plays as a pathogen and inhibitor of infection relative to other tick-borne pathogens will help public health efforts. The goal of this review was to compile the known literature on *R. amblyommatis*, review what we know about its geographic distribution, tick vectors, and pathogenicity, assess relatedness between various international strains from ticks by phylogenetic analysis and draw conclusions regarding future research needed. Richardson EA, et al. *Microorganisms* 2023, *11*(2), 493; doi.org/10.3390/microorganisms11020493. Open access.

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Tick-Borne Infections Council of North Carolina is a non-profit 501(c)3 organization formed to improve the recognition, treatment, control, and understanding of tick-borne diseases in North Carolina. We are all-volunteer and appreciate donations.

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