Tick-Borne Infections Council
of North Carolina, Inc.

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NEWSLETTER 2025, Volume 2

Quotes: “The growth of interest in ticks and tick-borne diseases over the last 20 years has been striking, with an estimated 2.4 times as many publications as in the previous 20 years.”
Kahl, O., and Gray, J.S.; Ticks and Tick-Borne Diseases (2022); https://doi.org/10.1016/j.ttbdis.2022.102114

Highlights:

- **Eastern cottontails as TBD hosts in Virginia**
- **Defining the TBD infection risk among high-risk occupations in South Carolina**
- **Surveillance for Bourbon and Heartland Virus Infection in White-Tailed Deer and Feral Swine in Texas**
- **Completion of serological testing for spotted fevers and ehrlichiosis in North Carolina**
- **Estimating Ixodes scapularis density in the Eastern United States using climate and land cover data**
- **Tick populations and human disease risk along hiking trails in California after extreme weather events**
- **National surveillance of human ehrlichiosis in the United States**
- **Diversity of ticks and rickettsiae in the southwestern United States**
- **Lyme disease in Ukraine 2000-2023**
- **Lyme disease increases risk of gynecological conditions**

State Updates

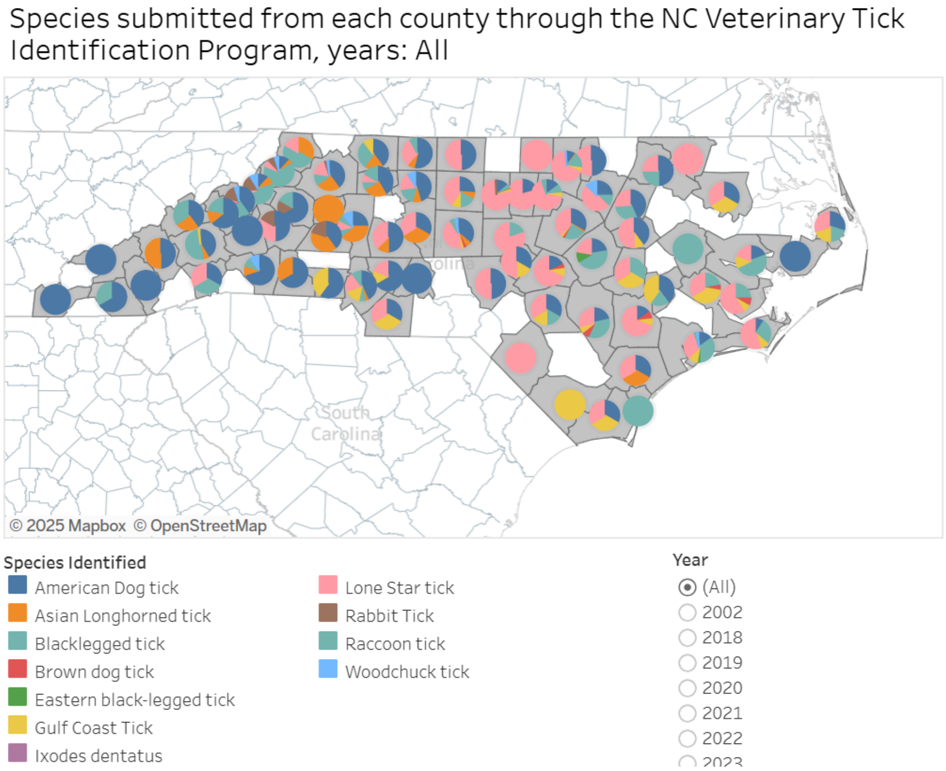
Tick-borne illness Surveillance Dashboard

In North Carolina, Public Health surveillance is conducted for the following tick-borne illnesses: anaplasmosis, ehrlichiosis, Lyme disease, and spotted fever illnesses including Rocky Mountain spotted fever.

The surveillance summary reports can be found here:

- Ehrlichiosis Surveillance Summary: 2023 **Updated: May 3, 2024** (PDF, 854KB)
- Spotted Fever Group Rickettsiosis Surveillance Summary: 2023 **Updated: May 3, 2024** (PDF, 834KB)
- Lyme Disease Surveillance Summary: 2023 **Updated: May 3, 2024** (PDF, 821KB)
- Tick Borne Disease Surveillance Summaries: 2022 **Updated: May 3, 2024** (PDF, 1.5MB)
- Tick Borne Disease Surveillance Summaries: 2021 (PDF, 2MB)
- Tick Borne Disease Surveillance Summaries: 2020 (PDF, 1.6MB)
- Tick Borne Disease Surveillance Summaries: 2019 (PDF, 1MB)

The NC Veterinary Tick Identification Program also has a map and dashboard showing the ticks submitted for identification and testing by county and tick species. Data are current through December 30, 2024.


Species submitted from each county through the NC Veterinary Tick Identification Program, years: All

TIC-NC Activities

On March 19, 2025 our scientific advisor, Dr. Marcia Herman-Giddens, gave a one hour presentation on Zoom to the Durham Garden Forum. The Forum is an independent, informal group in partnership with NC Cooperative Extension since 2009. Many of the current 170-plus members are Extension Master Gardeners. The questions from the participants were excellent.

Gardening & Ticks: Triangle Area

Durham Gardener's Forum

Marcia E. Herman-Giddens, PA, DrPH

UNC Gillings School of Global Public Health

North Carolina and the South

Eastern cottontails (*Sylvilagus floridanus*) as hosts for ticks infected with *Borrelia burgdorferi*, *Anaplasma phagocytophilum*, and Powassan virus in Virginia, USA

Tick-borne pathogen infections are an increasing occurrence globally, yet many aspects of pathogen maintenance and host-tick interactions remain poorly understood. Here, we consider the potential role of eastern cottontails (*Sylvilagus floridanus*) in the enzootic cycles of tick-borne pathogens of medical importance in Virginia. Over a 3-year period, ticks and blood were collected from rabbits acquired through passive surveillance in 21 counties in Virginia.

Seven hundred seventy ticks were collected from 90 of the 121 rabbits examined in this study. Tick species collected from the rabbits included *Haemaphysalis leporispalustris, Haemaphysalis longicornis, Amblyomma americanum, Dermacentor variabilis*, and *Ixodes* spp. Ticks identified as *Ixodes* spp. and *H. leporispalustris* were tested in pools for *Borrelia burgdorferi, Borrelia miyamotoi, Anaplasma phagocytophilum*, and Powassan virus (POWV). *Borrelia burgdorferi* and *A. phagocytophilum* were detected in several *Ixodes* spp. pools yielding a pooled infection rate of 4.6% and 3.7%, respectively. These bacterial pathogens along with POWV were detected in pools of *H. leporispalustris* yielding pooled infection rates of 0.2%, 0.2%, and 0.5%, respectively. In addition, 3 rabbits were found to have neutralizing antibodies against POWV indicating exposure to this tick-borne flavivirus. We describe the presence of infected ticks (including juvenile ticks that could bite humans as adults) utilizing rabbits as hosts, as well as evidence of POWV infection (1.75% seroprevalence) in rabbit sera. These results provide useful information about the role of rabbits as hosts to infected ticks, though cannot ascertain their role in the maintenance or the transfer of pathogens from the rabbits to naïve ticks. Future studies are warranted to explore any additional roles these and other lagomorphs may be playing in the enzootic cycle of tick-borne pathogens.

Schiff, P., et al.; *Journal of Medical Entomology* (2025); https://doi.org/10.1093/jme/tjaf009

Summary: This study collected ticks and blood from rabbits across Virginia over a three-year period and found that ticks do use rabbits as hosts, with evidence of POWV infection in a small portion of the rabbits, showing that rabbits can play a role in the life cycle of ticks and their pathogens.

Defining the tick-borne disease occupational risk among 4 high-risk vocations in South Carolina

Tick-borne diseases account for 75% of all vector-borne disease cases in the United States of America. The increase in incidence has been linked with increased exposure among outdoor workers, thus becoming occupational hazards. This brief study aimed to identify the potential occupational exposures among 4 vocational groups in South Carolina (SC) using a knowledge, attitudes, and practices questionnaire survey. A total of 176 individuals responded to the survey, across SC State Parks, SC Department of Natural Resources, SC Forestry Commission, and SC animal shelter and veterinary office employees. Veterinary-related employees had the lowest exposure risk, while forestry employees were the group with highest risk. The findings yielded discrepancies in perceived risk and preventive measures adopted; identifying a potential opportunity to develop an education and training program tailored to outdoor worker populations to maintain low tick bite exposures.

Gual-Gonzalez, L., Abiodun, T., and Nolan, M.S.; *Journal of Medical Entomology* (2025); https://doi.org/10.1093/jme/tjaf020

Summary: This study found differences in knowledge and preventive measures taken against tick-borne diseases among four occupations considered high-risk for TBDs.

Surveillance for Serological Evidence of Bourbon and Heartland Virus Infection in White-Tailed Deer and Feral Swine in Texas

Background: The tick-borne pathogens, Bourbon virus (BRBV) and Heartland virus (HRTV) are the cause of febrile illnesses that may progress to severe and fatal diseases.

Materials and Methods: As a preliminary effort to determine if these viruses were enzootic in Texas, ticks and blood samples were collected from feral swine (*Sus scrofa*) and white-tailed deer (*Odocoileus virginianus*) (WTD) killed by gunning as part of an abatement program during 2019–2021 in Travis County, Texas. Ticks were collected from these animals by hand and blood samples were obtained by cardiac puncture using 22-gauge needles and 5 mL syringes. Information was recorded for each animal, including date, sex, and location. The species of ticks were identified morphologically using a taxonomic key, and serum samples were tested for neutralizing antibodies to BRBV and HRTV.

Results: A total of 83 *Ixodes scapularis* and 58 *Amblyomma americanum* ticks were collected from feral swine, and 196 *I. scapularis* and 11 *Dermacentor albipictus* from WTD. Although *A. americanum*, the implicated vector of both viruses was collected from feral swine, neutralizing antibody was not detected to BRBV, but 12% (9/75) had antibody to HRTV as evidence of a previous infection. Of the serum samples obtained from WTD, all were negative for BRBV neutralizing antibody, but 6.6%% (5/75) were positive for HRTV antibody.

Conclusion: These preliminary results indicated that HRTV was enzootic in Travis County, Texas and further studies are warranted to determine the specific tick vectors and the possible role of WTD and feral swine in the maintenance and transmission cycle of this virus.

Valdez, K., et al.; *Vector-Borne and Zoonotic Diseases* (2025); https://doi.org/10.1089/vbz.2024.0107

Summary: Heartland virus was found to be enzootic in Travis County, TX. More work is needed to better understand the ecology of this disease.

Completion of paired serological testing algorithms for spotted fever rickettsiosis and ehrlichiosis, North Carolina: 2017-2020

Background :*Ehrlichia and Rickettsia* are tick-borne pathogens capable of causing severe disease. Paired serological testing, involving both acute and convalescent samples, remains the primary method of diagnostic confirmation and source of surveillance data. Yet few patients complete recommended testing algorithms.

Methods: We examined the demographic, clinical, and geographic factors associated with obtainment of convalescent samples for patients with suspected ehrlichiosis and spotted fever rickettsiosis using results from a large academic center in North Carolina between 2017 and 2020.

Results: Over 4400 patients underwent serological testing of an acute sample for *Rickettsia* (N = 4224) and *Ehrlichia* (N = 2339); however, only 15.0% (662/4,415) had testing performed on a convalescent sample. Over the study period, the proportion of convalescent testing completed increased from 4% to 23% for *Ehrlichia*, 7% to 11% for *Rickettsia*, and 12%

to 28% for both. A reactive test on the acute sample, undergoing testing for both pathogens, and proximity to a health facility were significantly associated with obtainment and testing of a convalescent sample. The presence of a reactive acute titer for *Ehrlichia* and *Rickettsia* had 8.3 (95% CI: 6.3, 10.9) and 8.2 (95% CI: 6.5, 10.3) times the probability of obtainment of a convalescent sample compared to non-reactive results, respectively.

Conclusion: Our findings suggest that clinicians' knowledge of tick-borne disease testing practices, in addition to patient distance to health facilities, contribute to poor performance of testing completion. Moreover, these results highlight the need for more investment in public health surveillance and ultimately, assays that are not dependent on convalescent testing.

Liao, H., et al.; *Clinical Infectious Diseases* (2025); https://doi.org/10.1093/cid/ciaf176

Summary: This study found that clinician and patient factors were both involved in the poor completion of testing. More surveillance and non-convalescent assays are needed.

Investigating Anaplasma and Borrelia Rates in North Central West Virginia Ticks

Ixodid (Acari: Ixodidae) ticks are widespread, diverse, and known as carriers of several important diseases. Lyme borreliosis is the most common tick-borne illness reported in West Virginia with more than 100 cases per 100,000 WV residents. Anaplasmosis is a bacterial infection caused by *Anaplasma phagocytophilum* which can also be carried by *Ixodes scapularis* ticks. In humans, Anaplasmosis may mimic other common infections, but can develop severe complications if left untreated. Anaplasma may also infect household pets such as cats and dogs. Anecdotal reports of Anaplasmosis in animals have increased dramatically in the last few years. The WV Office of Epidemiology and Prevention Services Vector Borne Disease reports that human cases of anaplasmosis tripled from 2022 to 2023. *Ixodes* ticks previously tested for *Borrelia* were retested for *Anaplasma* using real-time PCR analysis. Our data show a 2% *Borrelia* infection rate across 899 tested ticks. In addition, we detected a 17% *Anaplasma* infection rate in 388 tested ticks, with one instance of coinfection. These data suggest that there may be a higher incidence of *Anaplasma* infection than *Borrelia* in the same sample population of ticks. Through this research we will continue to track the changing rates of tick infection in order to better communicate vector-borne disease risks to the local community.

Scronce, M.C., et al.; *West Virginia Academy of Science* 99th Annual Meeting Abstracts (2025); https://doi.org/10.55632/pwvas.v97i2.1201

Summary: This abstract discusses the patterns of Anaplasma and Borrelia in West Virginia, supporting the continuing surveillance of vector-borne diseases in the state.

National Section

A new spotted fever group *Rickettsia* genotype in *Haemaphysalis leporispalustris* from Maine, USA

Spotted fever group (SFG) rickettsioses are increasingly recognized worldwide as threats to public health. *Rickettsia rickettsii, Rickettsia parkeri*, and *Rickettsia rickettsii* subspecies *californica* cause spotted fever rickettsioses, including Rocky Mountain spotted fever. These disease agents are transmitted to humans by various tick vectors in the United States. There is growing concern that other tick species, such as *Haemaphysalis leporispalustris*, may also transmit new and potentially unrecognized SFG rickettsial pathogens. In this study, we found that 6.1 % of 296 questing *H. leporispalustris* ticks (21 larvae, 260 nymphs, 9 males, and 6 females) collected from 38 towns across nine counties in Maine, USA, were positive for *Rickettsia* spp. Further multilocus sequence typing and phylogenetic analysis revealed that this is a new *Rickettsia* genotype (*Rickettsia* sp. ME2023) belonging to the SFG group and close to *Candidatus* Rickettsia lanei. Tick vectors and rickettsial species associated with SFG rickettsioses in New England warrant further investigation. Additionally, the role of *H. leporispalustris* in pathogen enzootic cycles and transmission requires further study.

Xu, G., et al.; *Ticks and Tick-borne Diseases* (2025); https://doi.org/10.1016/j.ttbdis.2025.102465

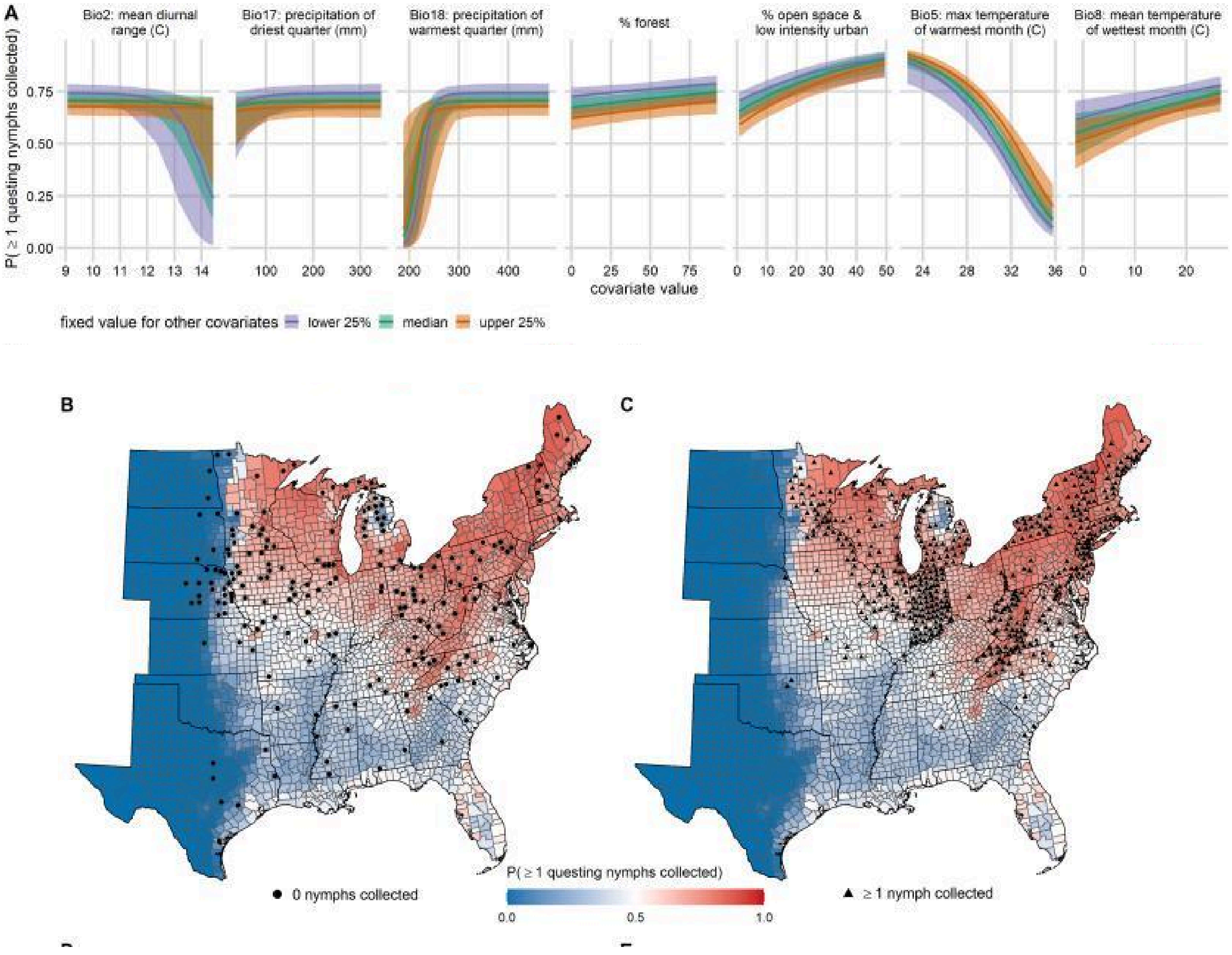
Summary: This paper describes a new *Rickettsia* genotype in the spotted fever group in Maine, warranting further study.

Estimating the density of questing *Ixodes scapularis* nymphs in the eastern United States using climate and land cover data

Tick-borne diseases pose a persistent and increasing threat to public health. In the United States, the majority of human infections are caused by pathogens spread by the blacklegged tick, *Ixodes scapularis*. Most infections are reported during the summer months, when nymphal ticks are active in states in the Northeast and Upper Midwest. The density of questing *I. scapularis* nymphs (DON) provides an estimate for the risk of human encounters with nymphs, but it is a resource intensive metric to obtain from field sampling. Thus, DON estimates are limited in the US national tick surveillance database, the ArboNET Tick Module. We estimated DON across all counties in the eastern US using a zero-inflated negative binomial model utilizing tick surveillance data reported to ArboNET (2004–2023) as well as climate and land cover data. The model estimated generally low DON across the southeastern US and Great Plains states with higher estimates in the Upper Midwest and Northeast regions. We assigned counties to relative acarological encounter risk categories based on estimated DON: zero or lower quartile DON estimates were scored as low risk, whereas inter- and upper-quartile DON estimates were scored as moderate-high risk. Counties with moderate-high DON reported from field sampling were accurately categorized by the model as moderate-high encounter risk (99 % sensitivity). However, 80 % of sampled counties reporting low DON were classified as moderate-high risk (20 % specificity). These misclassified counties were typically situated in recently colonized areas in the Northeast and Upper Midwest and likely indicated areas potentially suitable for tick population expansion. Our model yielded a very high negative predictive value (96 %) indicating the model did very well estimating low relative encounter risk in counties where no or few nymphs were collected, and a fair positive predictive value (60 %) indicated that densities may not have reached an expected peak in some locations, particularly in the Northeast, Upper Midwest, and northern states in the Southeast. Further tick surveillance is needed to evaluate and to refine these predictions. The resulting maps are useful for estimating relative risk of nymphal encounters across the eastern US where field data are sparse and may aid in efforts aimed at promoting the use of personal protective measures in communities that are at risk for nymphal tick encounters.

Holcomb, K.M., Foster, E., and Eisen, R.J.; *Ticks and Tick-borne Diseases* (2025);
https://doi.org/10.1016/j.ttbdis.2025.102446

Summary: Combining climate, land cover, and tick nymph data, this paper creates that model that estimates nymph density across the United States based on their climatic and land cover characteristics.



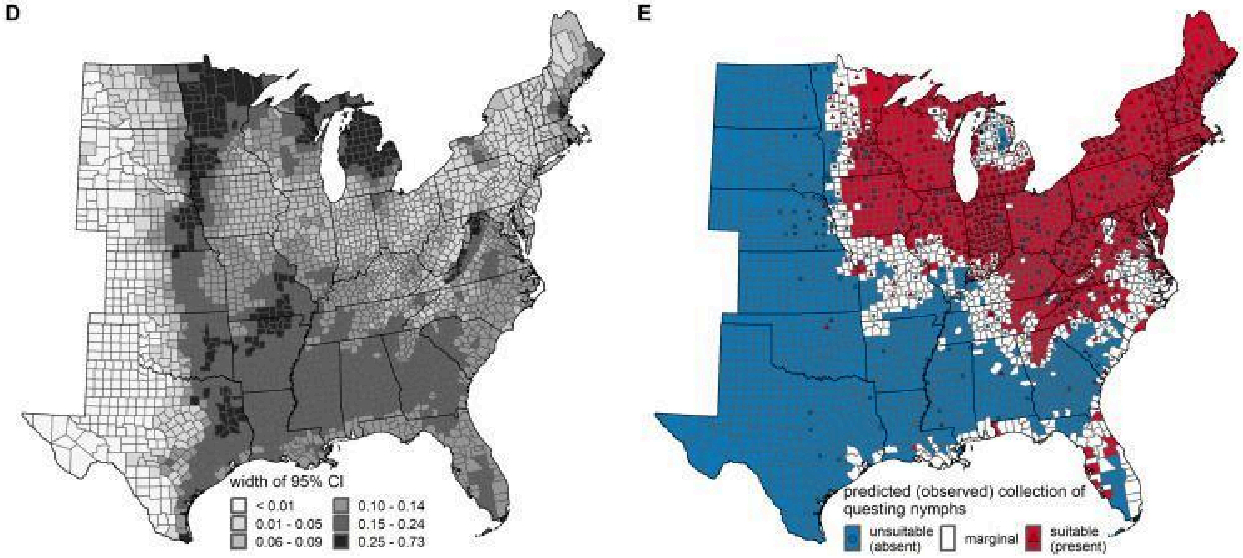


Figure 3 from paper. Predicted probability of collecting at least one questing *I. scapularis* nymph per 1000m^2.

Companion animal veterinary personnel have occupational risk for tularemia and One Health role for tularemia prevention in Kansas

Objective: To learn the knowledge, attitudes, and practices of veterinarians and technicians in Kansas regarding the occupational risk of tularemia, personal protection, patient diagnosis and management, zoonotic risk communication, and public health reporting.

Methods: Kansas veterinarians and technicians serving cats and dogs completed an online survey between June and September 2024.

Results: The survey was completed by 109 veterinarians and 19 technicians. Forty-three percent (47 of 109) of veterinarians reported diagnosing tularemia in cats and 13% (14 of 109) in dogs. Seven percent (8 of 109) of veterinarians reported having had tularemia. When performing procedures with a high risk of exposure, such as lancing abscesses in tularemia suspects, glove use was 100% but additional personal protective equipment was inconsistent, including eye protection (81 of 116 [70%]) and surgical face mask (69 of 116 [59%]). Antibody titer and PCR were common diagnostics, but 42% (26 of 62) of veterinarians reported never submitting a confirmatory test, with owner finances being the primary hurdle. Veterinarians and technicians have inconsistent knowledge about reporting regulations, but 91% (58 of 64) discuss tularemia's public health risk with pet owners.

Conclusions: Veterinarians are not only diagnosing tularemia in their patients but also contracting the disease themselves. Education should be targeted toward diagnostics, protection, and reporting.

Clinical Relevance: Veterinary personnel play an essential One Health role in the prevention and control of tularemia in Kansas through environmental tick and wildlife management, diagnosis and treatment of sick pets, and education about transmission and protection precautions for people. Designating tularemia as reportable in animals would allow determination of disease trends and more rapid public health follow-up.

KuKanich, K.S., Mulcahy, E.R., and Petro E.M.; *Journal of the American Veterinary Medical Association* (February 2025); https://doi.org/10.2460/javma.24.11.0725

Summary: Veterinarians and veterinary technicians in Kansas were surveyed to learn about their knowledge, attitudes, and current practices surrounding tularemia, a bacterial tick-borne disease. The study found that veterinary personnel are knowledgeable about tularemia but are less knowledgeable about reporting requirements, and PPE is not consistently used.

Local tick populations and human disease risk along popular hiking trails in northern California after multiple weather extremes

This field study describes the abundance of ticks and the prevalence of tick-borne pathogens in two hiking areas, Stebbins Cold Canyon (SCC) and Skyline Wilderness Park (SKY), in northern California. These areas have experienced extreme weather events, including wildfire, drought, and heavy rainfall, which have changed the environment. Questing ticks were collected over nine months, identified to species, and screened for tick-borne pathogens using qPCR. Four hundred and fifty-nine ticks were collected, including 54 adults from SCC and 405 from SKY, consisting of 279 (68.9%) larvae, 2 (0.5%) nymphs, and 124 (30.6%) adults. At SCC, Ixodes pacificus and Dermacentor occidentalis accounted for 92.6% (50/54) and 7.4% (4/54), respectively. At SKY, I. pacificus (16.8%, 68/405), D. occidentalis (12.3%, 50/405), D. similis (0.7%, 3/405), and D. albipictus (70.4%, 285/405) were collected. Overall, the prevalence of tick-borne pathogens was low in the collected ticks. Borrelia burgdorferi sl (0.8%, 1/121) and Rickettsia rhipicephali (1.7%, 2/121) were found at SKY. Rickettsia tillamookensis was identified at SCC and SKY with a prevalence of 3.7% (2/54) and 1.7% (2/121), respectively. Babesia duncani was identified in 3.7% (2/54) and 1.2% (5/405) of ticks at SCC and SKY, respectively. These findings suggest that multiple tick species can withstand extreme weather events, providing further data regarding the effects of weather extremes and climate change on tick populations and pathogen prevalence. This study is one of the first to report B. duncani in I. pacificus ticks in California, particularly in Solano County.

Kretsch-York, C.M., et al.; *Journal of Vector Ecology* (2025); https://doi.org/10.52707/1081-1710-50.1-69

Summary: This paper describes the tick population and presence of human tick-borne pathogens in Northern California following a variety of weather events, like drought, wildfire, and rainfall. It finds that multiple California tick species can withstand weather events, but there is low pathogen prevalence.

National Surveillance of Human Ehrlichiosis Caused by *Ehrlichia ewingii*, United States, 2013-2021

Human ehrlichiosis is a potentially fatal tickborne disease caused by 3 species: *Ehrlichia chaffeensis*, *E. ewingii*, and *E. muris eauclairensis*. In the United States, 234 confirmed cases of *E. ewingii* ehrlichiosis were reported to the Centers for Disease Control and Prevention through the National Notifiable Diseases Surveillance System during 2013–2021; average annual incidence was 0.08 cases/1 million population. *E. ewingii* ehrlichiosis was reported more commonly among older, White, non-Hispanic, and male patients. Incidence and case counts generally increased yearly, except for 2020 and 2021. The highest number of cases were reported from Missouri and Arkansas. We report the geographic expansion of *E. ewingii* ehrlichiosis and the continued public health challenge of clarifying clinical manifestations of this infection. Clinician education will be essential to implement molecular assays to properly diagnose *E. ewingii* infection in patients and gain a better understanding of the epidemiology of this emerging disease.

Adams, S.N., et al.; *Emerging Infectious Diseases* (2025); https://doi.org/10.3201/eid3102.240279

Summary: This paper describes the trends of human ehrlichiosis in the United States from 2013-2021.

Two Human Cases of Fatal Meningoencephalitis Associated with Potosi and Lone Star Virus Infections, United States, 2020-2023

We used clinical metagenomic next-generation sequencing of cerebrospinal fluid to investigate bunyavirus infections in 2 immunocompromised patients in the United States who had fatal meningoencephalitis. Potosi virus has been isolated from mosquito vectors and Lone Star virus from tick vectors. These findings highlight the power of metagenomic next-generation sequencing in broad-based, agnostic detection of emerging viral infections that test negative using conventional targeted diagnostic methods.

Chiu, C.Y., et al.; *Emerging Infectious Diseases* (2025); https://doi.org/10.3201/eid3102.240831

Summary: Metagenomic next-generation sequencing was used to identify bunyavirus infections in two immunocompromised patients in the United States. This method can be used for the detection of emerging viral infections that otherwise do not show up through conventional diagnostic methods.

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: This study used partner-based sampling to assess the presence of *Rickettsia* spp. pathogens and their tick vectors in the southwestern US.

Time From Onset to Diagnosis of Alpha-Gal Syndrome

Alpha-gal syndrome (AGS) is an emerging, tick-borne allergy to the galactose-α-1,3-galactose (alpha-gal) carbohydrate, estimated to impact up to 450 000 individuals in the US.[1] This molecule is found in mammalian meat, mammal-derived products, and certain pharmaceuticals. In the US, the distribution of AGS cases closely resembles the distribution of the lone star tick, *Amblyomma americanum*. Symptoms present 2 to 8 hours after consuming a product containing alpha-gal and can be life-threatening. A 2022 survey found that 42% of health care practitioners in the US had never heard of AGS and an additional 35% were “not too confident” in their ability to diagnose and manage the condition. Challenges in receiving timely care can reveal disparities among various patient populations eventually diagnosed. We analyzed a group of patients with AGS seeking care at an allergy clinic in North Carolina for factors that may have influenced their ability to receive a timely and accurate diagnosis. A comparison with a previous AGS cohort from the same allergy clinic was performed to understand diagnosis trends over time.

Maki, C.K., et al.; *JAMA Network Open* (2025); https://jamanetwork.com/journals/jamanetworkopen/fullarticle/2831189#google_vignette

Summary: This research letter finds that time between first symptom onset and confirmed alpha-gal syndrome diagnosis has shortened, and that there are disparities involved in access to care for alpha-gal.

Methods of active surveillance for hard ticks and associated tick-borne pathogens of public health importance in the contiguous United States: a comprehensive systematic review

Tick-borne diseases in humans and animals have increased prevalence across the United States. To understand risk factors underlying tick-borne diseases it is useful to conduct regular surveillance and monitoring of ticks and the pathogens they carry, in a sustained and effective manner. Using the Preferred Reporting Items for Systematic Reviews and Meta-Analysis guidelines, this study aims to summarize the previously used methods for active surveillance of ticks and tick-borne pathogens, identify the existing knowledge gaps in ongoing surveillance, and highlight and guide the mechanisms required to inform those gaps for more effective and sustainable future surveillance efforts. After screening 2,500 unique studies between 1944 and 2018, we found 646 articles that performed active surveillance of hard ticks and/or their associated tick-borne pathogens of public health importance within the United States. An additional 103 articles were included for the 2019 to 2023 period. Active surveillance has been performed in ~42% of the counties (1944 to 2018) and ~23% of the counties (2019 to 2023) within the contiguous US, and states with the most coverage are in the Northeast, Upper Midwest, and along the West coast. The most reported tick was *Ixodes scapularis* (195 studies) and most commonly reported pathogen was *Borrelia burgdorferi* (143 studies). Overall, surveillance efforts have increased and become more diversified, and methods of tick and tick-borne pathogens testing have undergone changes, but those efforts are mainly concentrated in focal regions of a county. Future surveillance efforts should follow Centers for Disease Control and Prevention guidelines and target areas of United States with scarce reports of active surveillance and build collaborations and resources to increase surveillance.

Chakraborty, S., et al.; *Journal of Medical Entomology* (2025); https://doi.org/10.1093/jme/tjaf031

Summary: This systematic analysis found that surveillance efforts for TBDs have increased and methods have changed, but these efforts are largely geographically clustered and more comprehensive efforts are needed.

International Section

Tick-borne pathogens in ticks removed from humans in Northern Italy, 2018-2023

The rising prevalence and transmission of tick-borne pathogens (TBPs) represent a significant public health issue all over the world, including in Italy.

The region of Lombardy, in Northern Italy, is particularly endemic for TBPs. While evidence indicates a high exposure risk to infected ticks, there is a lack of data on ticks collected from humans.

Therefore, a long-term surveillance programme was implemented from 2018 to 2023 to identify selected pathogens in ticks retrieved from humans. The presence of *Rickettsia* spp., *Borrelia* *burgdorferi* sensu lato complex*, Francisella* spp*., Coxiella burnetii* and tick-borne encephalitis virus was evaluated. A total of 2,453 ticks were collected and most belonged to the species *Ixodes ricinus* (93.5 %; n = 2,293). Additionally, *Ixodes* spp. (n = 35), *Ixodes hexagonus* (n = 7), *Rhipicephalus sanguineus* (sensu lato) species complex (n = 16), *Dermacentor* spp. (n = 5), *Dermacentor reticulatus* (n = 7) and *Dermacentor marginatum* (n= 1) were identified. The nymph stage was the prevalent life stage at retrieval (n = 1,778), followed by adults (n = 443) and larvae (n = 134). Overall, 18.7 % (459/2,453) of ticks were infected with at least one pathogen and co-infections were found in 6.3 % (29/459) of the positive ticks. In the examined sample, the frequency of infection in adult ticks (90/443; 20.3 %) was higher than that observed in nymphs (335/1778; 18.8 %). The most frequently detected pathogens were *Borrelia burgdorferi* s.l. (10.1 %) and *Rickettsia* spp. (10 %). Interestingly, *Francisella tularensis* and *Coxiella burnetii* were found to be of low prevalence, suggesting a lower exposure of humans to these diseases, despite still posing a serious threat to human health due to their pathogenicity. This study raises awareness about the potential risk of tick-borne diseases in Northern Italy.

Olivieri, E., et al.; *Acta Tropica* (2025); https://doi.org/10.1016/j.actatropica.2025.107582

Summary: This study describes the results of a long-term tick-borne disease surveillance program in Italy. Roughly 18.7% of ticks were infected with at least one pathogen, indicating that there is risk of tick-borne disease infection for humans in Northern Italy.

First European record of *Rickettsia bellii* in *Amblyomma rotundatum* from *Rhinella marina* imported to Poland

This study reports on the first documented case of *Amblyomma rotundatum* ticks, a species typically found in the Americas, parasitising an imported toad in Poland. A total of 12 ticks were collected from a single *Rhinella marina* toad. These ticks were identified as female specimens of *A. rotundatum* using an examination of morphological characteristics and a molecular analysis. Polymerase chain reaction testing revealed that 75.0% (9/12) of these females were positive for *Rickettsia* spp. Sequencing of positive samples confirmed the presence of *R. bellii.* However, no DNA evidence of *Borrelia* spp. and *Anaplasma* spp. was detected in the tested ticks. Nevertheless, given the limited number of tick specimens collected from a single host, further research is required to elucidate the pathogen profile of a tick species. This finding represents the second European report of *A. rotundatum* associated with exported animals, underscoring the importance of vigilance in monitoring the potential spread of ticks and tick-borne pathogens through the global wildlife trade.

Dyczko, D., et al.; *Experimental and Applied Acarology* (2025); https://doi.org/10.1007/s10493-025-01007-9

Summary: This paper details the first known import of *R. marina* into Poland, touching on the larger issues of invasive species and the pathogens they carry.

Lyme disease in Ukraine in 2000-2023

Background: Lyme disease (LD) is the most common tick-borne zoonotic infection in Europe and North America, caused by Borrelia spp., primarily transmitted through the bite of infected Ixodes ticks. The disease has become a significant public health concern in Ukraine, with the number of reported cases steadily increasing since the initiation of official registration in 2000. Despite this trend, the epidemiological characteristics of LD in Ukraine, particularly its geographic distribution and the influence of socio-political events on its prevalence, remain underexplored.

Objective: This study aimed to investigate the incidence of LD in Ukraine from 2000 to 2023.

Material and methods: The study utilized official statistical data of registered LM cases in Ukraine from the Ministry of Health of Ukraine and relevant literature sources.

Results: Over the 23-year period (2000-2023), a total of 45,371 cases of Lyme disease (LD) were recorded in Ukraine, with an annual average of 1,890 ± 1,662 cases. A significant increase was observed in 2015, with an additional rise in 2022, both likely linked to socio-political events such as the reorganization of health services and the war-related population displacement. The highest incidence was recorded in 2023, at 14.08 cases per 100,000 population. Geographic analysis revealed that Kyiv and the Kyiv region had the highest incidence rates, with urban areas being disproportionately affected. Notably, 83.2% of the cases were recorded among urban residents, reflecting a clear urban-rural disparity.

Conclusions: The incidence of Lyme disease in Ukraine has significantly increased over the past 23 years, particularly in urban areas. The peaks in 2015 and 2022 suggest potential links to socio-political disruptions, such as changes in health services and population displacement due to the war. These findings underscore the need for improved public health strategies, with a particular focus on managing LD in urban settings, and addressing the urban-rural disparity in case distribution.

Zolotukhin, O., et al.; *Przeglad Epidemiologiczny* (2025); https://doi.org/10.32394/pe/195666

Summary: This study describes the dynamics of Lyme disease in Ukraine between 2000 and 2023, finding that the incidence has risen significantly.

Molecular Section

Lyme disease increases risk for multiple gynecological conditions

Lyme disease (LD) is an illness caused by the spirochete Borrelia burgdorferi (B. burgdorferi). Borrelia is known to disseminate through organs, including the skin, joints, spinal cord, bladder, and heart, leading to Lyme arthritis, neuroborreliosis, and Lyme carditis. While previous studies have investigated the impact of LD on pregnancy in both mice and humans and have found the presence of B. burgdorferi in the uterus of mice, we studied the impact of LD on the non-pregnant female reproductive tract. We use a mouse model for LD and find an ongoing and severe infection of the reproductive tract of female mice, which persists up to 15-months post-inoculation. This infection results in uterine glandular cysts and endometrial hyperplasia as well as vaginal epithelial thickening, polymorphonuclear and mononuclear cell epithelial infiltration, and epithelial desquamation into the vaginal lumen. Strikingly, we find that age has an impact on the extent of gynecologic pathology such that aged female mice (1-year old) that are reproductively senescent have more gynecologic pathology with infection compared to young mice (15-weeks old) when infected for the same length of time. Using large-scale electronic healthcare record data, we report that LD additionally results in increased infection-associated risk of menorrhagia (1.5-fold), miscarriage (1.62-fold), uterine fibroids (1.42-fold), and endometriosis (1.93-fold). Underreporting of gynecological outcomes is pervasive throughout many different infectious diseases, and LD-associated gynecological pathologies may have been similarly underappreciated in the field. This work suggests that further study of the female reproductive tract and the effects of B. burgdorferi infection therein will help clarify and expand the knowledge of myriad LD outcomes.

Hansen Colburn, P.S., et al.; *medRxiv* (preprint, 2025); https://doi.org/10.1101/2025.03.03.25323258

Summary: The impact of Lyme disease on the female reproductive tract and gynecological pathologies has thus far been understudied. This study found that Lyme results in an increase in many gynecological pathologies like menorrhagia, miscarriage, uterine fibroids, and endometriosis.

Bartonella henselae, Babesia odocoilei and *Babesia divergens*-like MO-1 infection in the brain of a child with seizures, mycotoxin exposure and suspected Rasmussen's encephalitis

Background: In conjunction with more sensitive culture and molecular diagnostic testing modalities, simultaneous or sequential infection with more than 1 vector borne zoonotic pathogen is being increasingly documented in human patients. On a frequent basis, many people are exposed to apparently healthy, but infected, domestic and wild animals, the arthropod vectors with which these animals have co-evolved, and the bacterial, protozoal and other pathogens for which various animals are reservoirs. Unsuspected zoonotic transmission by scratch, bite, or vector exposures can result in chronic, indolent, or potentially life-threatening infections.

Methods: In December 2016, at 2 years of age, a male child residing in Ontario, Canada received facial scratches from a feral cat. In August 2018, seizures began 8 days after the child developed a focal, suspected insect bite rash. In June 2019, potential mold toxicity in the child's bedroom was assessed by fungal culture and urinary mycotoxin assays. Beginning in January 2022, *Bartonella* spp. serology (indirect fluorescent antibody assays), polymerase chain reaction (PCR) amplification, DNA sequencing, and enrichment blood and brain cultures were used on a research basis to assess *Bartonella* spp. bloodstream and central nervous system (brain biopsy) infection. In 2024, using recently developed PCR and DNA sequencing targets, *Babesia* species infection was retrospectively assessed due to the rash observed in 2018.

Results: Although there was historical cat and suspected tick exposures, serological testing for *Bartonella henselae* and *Borrelia burgdorferi* were repeatedly negative. Sequential neurodiagnostic testing partially supported a diagnosis of Rasmussen's encephalitis. Astrogliosis was the only brain biopsy histopathological abnormality. *Bartonella henselae* DNA was amplified and sequenced from enrichment cultures of brain tissue. Retrospectively, *Babesia odocoilei* and *Babesia divergens*-like MO-1 infections were confirmed by amplification and sequencing of DNA extracted from enrichment blood cultures processed in January 2022, from blood and brain tissue cultures in June 2022, and blood in January and June 2023.

Conclusions: Infection with *B. henselae*, *B. odocoilei*, and *B. divergens*-like MO-1, complicated by mycotoxin exposure, created a complex clinical scenario for this child, his parents, and his doctors.

Breitschwerdt, E.B., et al.; *Journal of Central Nervous System Disease* (2025); https://doi.org/10.1177/11795735251322456

Summary: This case report details a complex clinical situation for a child involving co-infection by *Babesia* spp.

The epidemiology and clinical manifestations of anaplasmosis in humans: a systematic review of case reports

Anaplasmosis, caused by *Anaplasma phagocytophilum*, is an emerging tick-borne disease affecting humans and animals with a broad spectrum of clinical manifestations. This systematic review and analysis aimed to synthesise the epidemiology, clinical features, diagnostic methods, and treatment outcomes of anaplasmosis, emphasising enhanced surveillance and management strategies. The systematic review encompassed 73 cases from various geographic regions, revealing fever as the predominant symptom, alongside myalgia, headache, chills, and arthralgia. Molecular testing, particularly PCR, emerged as the primary diagnostic tool, aiding in identifying *Anaplasma* species. Co-infections are uncommonly described in the cases analysed, showing borreliosis and viral infections, underscoring the complexity of disease presentation. Doxycycline monotherapy demonstrated high efficacy, with a low mortality rate, while alternative antimicrobial options and combination therapy were considered in specific scenarios. This study contributes to understanding anaplasmosis's global burden and highlights the importance of continued research and collaborative efforts to mitigate its impact on public health.

Acosta-España, J.D., et al.; *Journal of Infection and Public Health* (2025); https://doi.org/10.1016/j.jiph.2025.102765

Summary: This review gives an overview of current knowledge of anaplasmosis.

Pre-clinical strategies and emerging technologies driving advances in the alpha-gal syndrome

Alpha-gal syndrome (AGS) is a unique allergic condition triggered by IgE antibody production against the mammalian oligosaccharide galactose-α-1,3-galactose (α-gal). The syndrome, acquired by bites from multiple tick species, leads to delayed allergic reactions after consuming mammalian-derived products containing α-gal, including red meat, dairy, and select medications.

AGS is especially prevalent in regions with high tick exposure and has become a global public health concern, with rising cases across continents. Despite growing research, including recent findings suggesting that asymptomatic α-gal sensitization may contribute to coronary artery disease, the precise immune mechanisms—particularly B cell-mediated IgE production following tick bites—remain poorly understood. Additionally, the tick saliva components that trigger sensitization and the role of the skin-gut axis in food allergy development are knowledge gaps. AGS research has benefited from animal models like mice, zebrafish, and pigs, which replicate key syndrome features, though have limitations. Humanized mouse models and human organoid systems now offer promising tools for investigating AGS pathogenesis and testing potential therapies. This review explores current pre-clinical methodologies, challenges, and the future of AGS research, emphasizing innovative models that may bridge knowledge gaps and advance therapeutic development.

Erickson, L.D., et al.; *Allergology International* (2025); https://doi.org/10.1016/j.alit.2025.03.004

Summary: This review summarizes clinical and molecular knowledge about alpha-gal syndrome.

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TIC-NC is grateful for the financial contributions of Insect Shield International, LLC.

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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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