Tick-Borne Infections Council
of North Carolina, Inc.

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NEWSLETTER 2025, Volume 1

Quotes: “Tick-borne disease (TBD) incidences are rising globally, highlighting the need for effective prevention strategies that consider the ecological context of disease transmission.”
Martins, P.M., Mahon, M., and Rohr, J.; *Authorea* (preprint; 2024); DOI: 10.22541/au.173080302.22539768/v1

Highlights:

- **North Carolina surveillance dashboard and updates**
- **Heartland Virus Infection in Elderly Patient Initially Suspected of Having Ehrlichiosis, North Carolina, USA**
- **Transfusion related babesiosis in a non-endemic region (Western New York)**
- **Identifying the geographic leading edge of Lyme disease in the United States with internet searches: A spatiotemporal analysis of Google Health Trends data**
- **Spatial and temporal distribution of Ixodes scapularis and tick-borne pathogens across the northeastern United States**
- **Minor Hosts Have a Major Impact on the Enzootic Transmission of Borrelia burgdorferi**
- **Contrasting pathogen prevalence between tick and dog populations at Chornobyl**
- **mRNA Vaccines Against Tick-borne Diseases**

State Updates

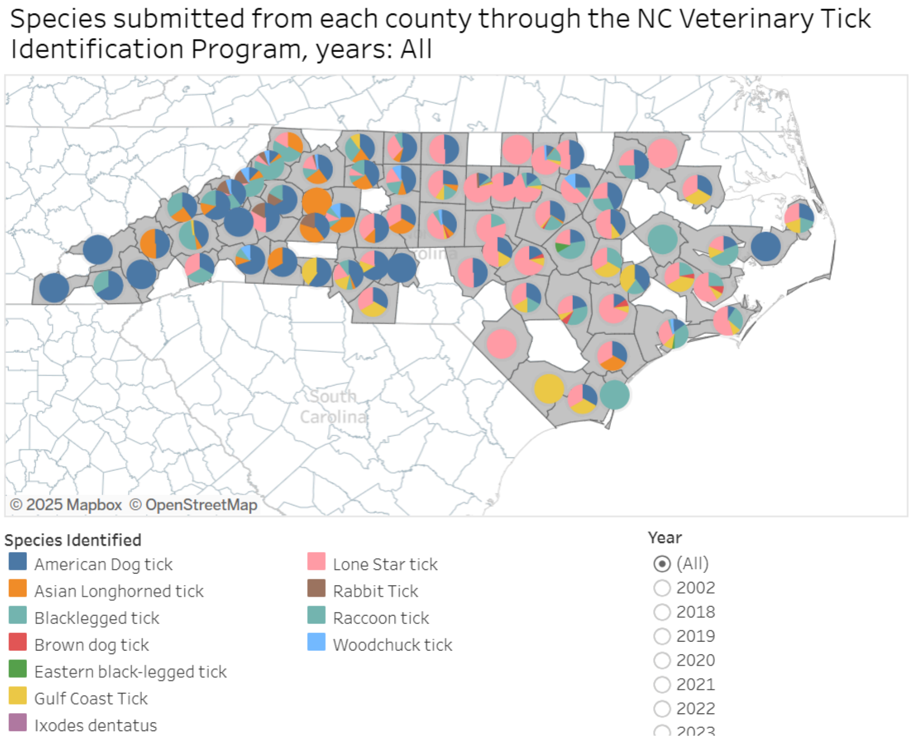
Tick-borne illness Surveillance Dashboard

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:

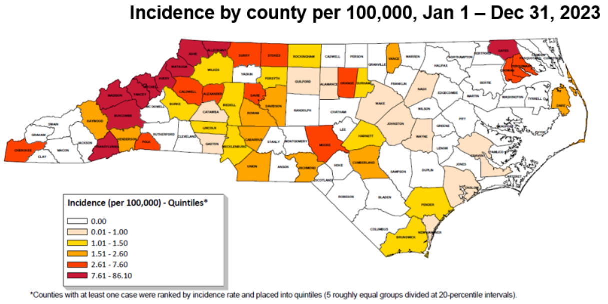
- Ehrlichiosis Surveillance Summary: 2023 **Updated: May 3, 2024** (PDF, 854KB)
- Spotted Fever Group Rickettsiosis Surveillance Summary: 2023 **Updated: May 3, 2024** (PDF, 834KB)
- Lyme Disease Surveillance Summary: 2023 **Updated: May 3, 2024** (PDF, 821KB)
- Tick Borne Disease Surveillance Summaries: 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. As of January 23rd:

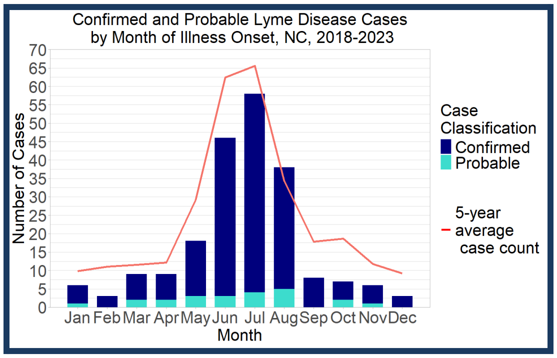

Species submitted from each county through the NC Veterinary Tick Identification Program, years: All

NCDHHS Updates for the North Carolina Mosquito and Vector Control Association

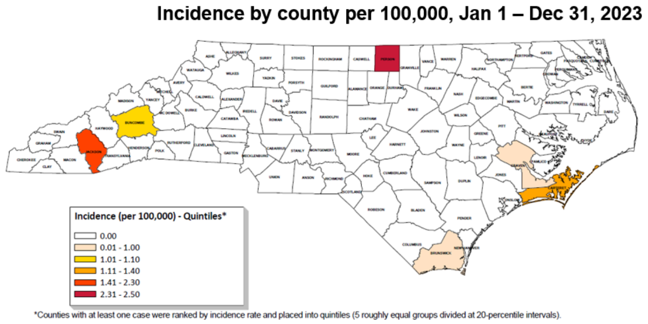
Lyme disease:


Incidence by county per 100,000, Jan 1 – Dec 31, 2023

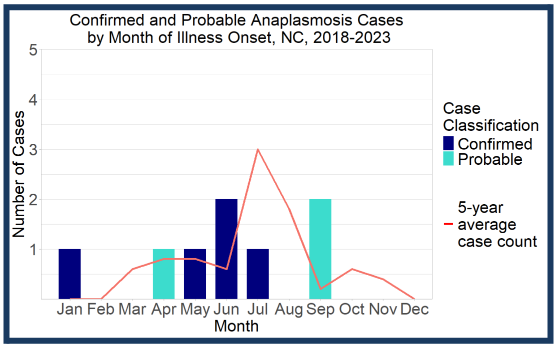
*Counties with at least one case were ranked by incidence rate and placed into quintiles (5 roughly equal groups divided at 20-percentile intervals).


Confirmed and Probable Lyme Disease Cases by Month of Illness Onset, NC, 2018-2023

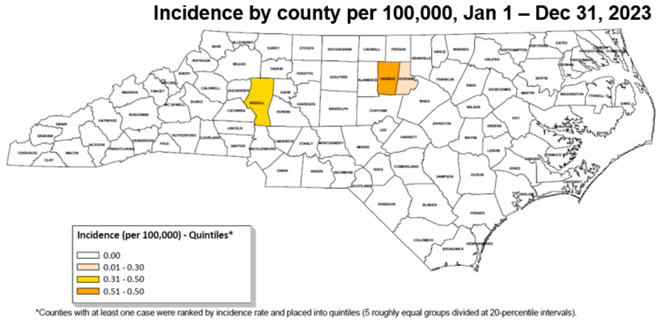
Anaplasmosis:


Incidence by county per 100,000, Jan 1 – Dec 31, 2023

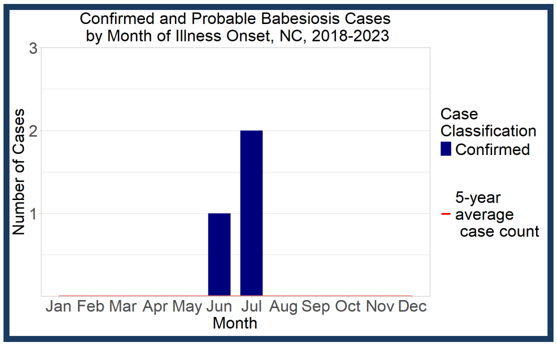
*Counties with at least one case were ranked by incidence rate and placed into quintiles (5 roughly equal groups divided at 20-percentile intervals).


Confirmed and Probable Anaplasmosis Cases by Month of Illness Onset, NC, 2018-2023

Babesiosis:

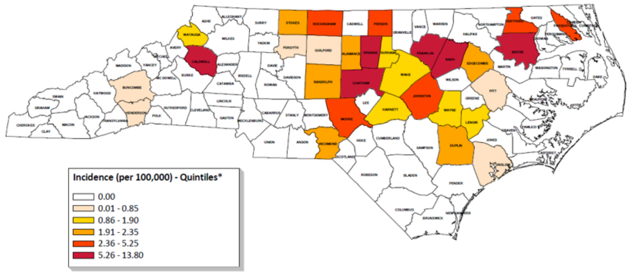

Incidence by county per 100,000, Jan 1 – Dec 31, 2023

*Counties with at least one case were ranked by incidence rate and placed into quintiles (5 roughly equal groups divided at 20-percentile intervals).

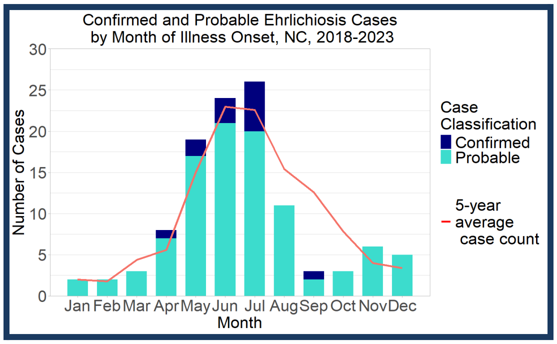

Confirmed and Probable Babesiosis Cases by Month of Illness Onset, NC, 2018-2023

Ehrlichiosis:

Incidence by county per 100,000, Jan 1 – Dec 31, 2023 (*E. chaffeensis*)

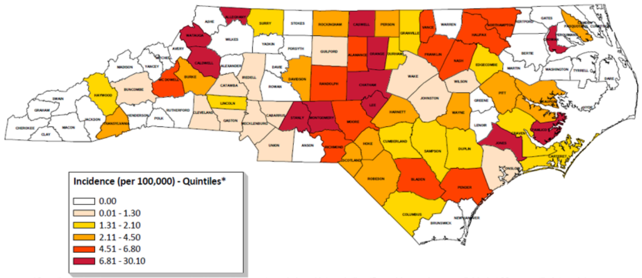


*Counties with at least one case were ranked by incidence rate and placed into quintiles (5 roughly equal groups divided at 20-percentile intervals).

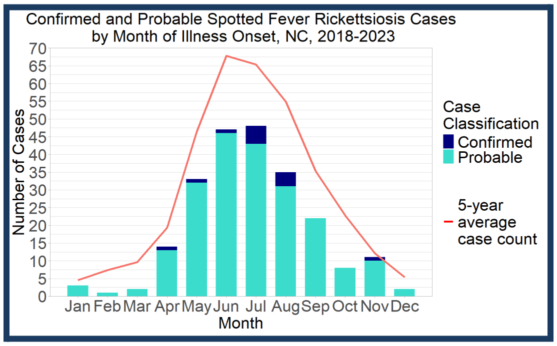


Spotted fever rickettsiosis:

Incidence by county per 100,000, Jan 1 – Dec 31, 2023

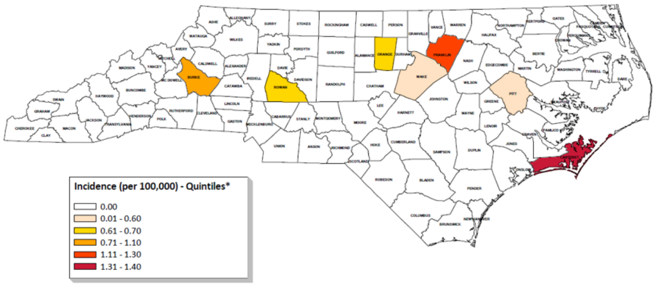


*Counties with at least one case were ranked by incidence rate and placed into quintiles (5 roughly equal groups divided at 20-percentile intervals).

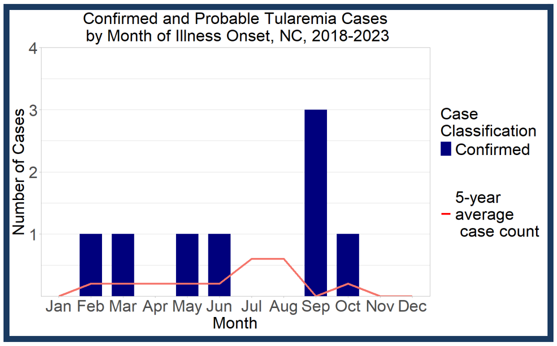


Tularemia:

Incidence by county per 100,000, Jan 1 – Dec 31, 2023

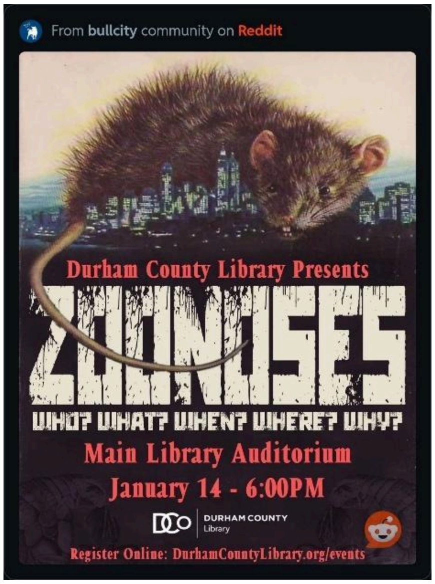


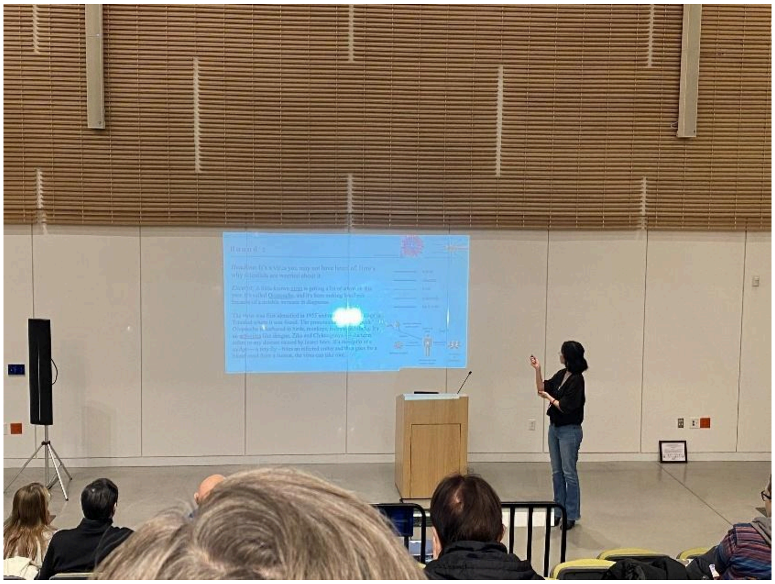
*Counties with at least one case were ranked by incidence rate and placed into quintiles (5 roughly equal groups divided at 20-percentile intervals).



TIC-NC Activities

January 2025: On January 14, 2025, TIC-NC board member Melody Xiao, MHS, gave a talk at the Durham Main County Library on zoonotic disease in North Carolina as part of the library's "Who, What, When, Where, Why?" series bringing science to the general public.





North Carolina and the South

Heartland Virus Infection in Elderly Patient Initially Suspected of Having Ehrlichiosis, North Carolina, USA

Ehrlichia chaffeensis and *E. ewingii* are tickborne intracellular bacteria that cause human ehrlichiosis (*1*). In the United States, ehrlichiosis occurs primarily in south-central, southeastern, and mid-Atlantic states. In 2019, nearly half of *E. chaffeensis* ehrlichiosis cases occurred in 4 US states: Arkansas, Missouri, New York, and North Carolina (*2*). Heartland virus (HRTV), another tickborne pathogen, is an emerging zoonotic virus and has been reported in 14 states, including North Carolina, since its initial discovery in 2009 in Missouri. (*3*). We report a case of HRTV infection in a patient in North Carolina who was initially suspected of having ehrlichiosis.
Barbarin, A.M., et al.; *Emerging Infectious Diseases* (2024); https://doi.org/10.3201/eid3012.240646

Summary: This case report describes a patient in North Carolina who was initially diagnosed with *Ehrlichia chaffeensis* then diagnosed with Heartland virus and *Ehrlichia ewingii*, both of which were also found in the ticks at the patient's residence.

National Section

Reservoir host community and vector density predict human tick-borne diseases across the eastern United States

Tick-borne disease (TBD) incidences are rising globally, highlighting the need for effective prevention strategies that consider the ecological context of disease transmission. We analyzed the relationship between human prevalence of four TBDs in the eastern U.S. and various ecological and climatic factors. Babesiosis showed a negative relationship with mean annual temperature, while ehrlichiosis exhibited no significant associations. Anaplasmosis prevalence was positively linked to nymphal tick densities, with competent host abundance mediating the relationship between prevalence and small mammal richness. Lyme disease prevalence correlated positively with densities of ticks, infected ticks, deer, and reservoir hosts, while negatively correlating with precipitation, temperature, and small mammal richness. We expand on the dilution effect in Lyme disease by linking reservoir hosts, tick density, and human cases at broader scales. Our findings suggest that TBD intervention efficacy may vary based on tick and host dynamics, underscoring the importance of ecological context in designing effective strategies.

Martins, P.M., Mahon, M., and Rohr, J.; *Authorea* (preprint; 2024); DOI: 10.22541/au.173080302.22539768/v1

Summary: The paper analyzes the relationship between anaplasmosis, babesiosis, ehrlichiosis, and Lyme disease prevalence and various ecological and climatic factors in the eastern United States. Such factors include temperature, tick density, small mammal richness, and precipitation.

Transfusion related babesiosis in a non-endemic region (Western New York)

Babesiosis, an emerging tick-borne zoonosis caused by parasites of the genus Babesia, is typically transmitted via the black-legged tick. Occasionally, *Babesia* can also be transmitted through red blood cell transfusion. In this report, we present a case of babesiosis resulting from a red blood cell transfusion in an area where the pathogen is not endemic. The patient presented with a high-grade fever and hemolytic anemia. This case underscores the critical importance of recognizing Babesia as a cause of hemolysis and emphasizes the necessity of implementing universal screening of blood products for Babesia. Enhanced vigilance in blood safety protocols is imperative to prevent transfusion-associated babesiosis.

Aladeen, J. et al.; *Oxford Medical Case Reports* (2024); https://doi.org/10.1093/omcr/omae133

Summary: This case report describes a case of babesiosis resulting from a blood transfusion, emphasizing the need for *Babesia* screening of blood products.

Identifying the geographic leading edge of Lyme disease in the United States with internet searches: A spatiotemporal analysis of Google Health Trends data

Background

The geographic footprint of Lyme disease is expanding in the United States, which calls for novel methods to identify emerging endemic areas. The ubiquity of internet use coupled with the dominance of Google's search engine makes Google user search data a compelling data source for epidemiological research.

Objective

We evaluated the potential of Google Health Trends to track spatiotemporal patterns in Lyme disease and identify the leading edge of disease risk in the United States.

Materials and methods

We analyzed internet search rates for Lyme disease-related queries at the designated market area (DMA) level (n = 206) for the 2011–2019 and 2020–2021 (COVID-19 pandemic) periods. We used maps and other exploratory methods to characterize changes in search behavior. To assess statistical correlation between searches and Lyme disease cases reported to Centers for Disease Control and Prevention (CDC) between 2011 and 2019, we performed a longitudinal ecological analysis with modified Poisson generalized estimating equation regression models.

Results

Mapping DMA-level changes in "Lyme disease" search rates revealed an expanding area of higher rates occurring along the edges of the northeastern focus of Lyme disease. Bivariate maps comparing search rates and CDC-reported incidence rates also showed a stronger than expected signal from Google Health Trends in some high-risk adjacent states such as Michigan, **North Carolina**, and Ohio, which may be further indication of a geographic leading edge of Lyme disease that is not fully apparent from routine surveillance. Searches for "Lyme disease" were a significant predictor of CDC-reported disease incidence. Each 100-unit increase in the search rate was significantly associated with a 10% increase in incidence rates (RR = 1.10, 95% CI: 1.07, 1.12) after adjusting for environmental covariates of Lyme disease identified in the literature.

Conclusion

Google Health Trends data may help track the expansion of Lyme disease and inform the public and health care providers about emerging risks in their areas.

Wychgram, C., et al.; *PLOS One* (2024); https://doi.org/10.1371/journal.pone.0312277

Summary: Google Health Trends data may be a useful tool in tracking the expansion of Lyme disease and giving health professionals a heads up that Lyme is emerging in their area.

Spatial and temporal distribution of *Ixodes scapularis* and tick-borne pathogens across the northeastern United States

Background

The incidence of tick-borne diseases is increasing across the USA, with cases concentrated in the northeastern and midwestern regions of the country. *Ixodes scapularis* is one of the most important tick-borne disease vectors and has spread throughout the northeastern USA over the past four decades, with established populations in all states of the region.

Methods

To better understand the rapid expansion of *I. scapularis* and the pathogens they transmit, we aggregated and analyzed *I. scapularis* abundance and pathogen prevalence data from across the northeastern USA, including the states of Connecticut, Maine, New Hampshire, New York and Vermont, from 1989 to 2021. Maine was the only state to collect data during the entire time period, with the other states collecting data during a subset of this time period starting in 2008 or later. We harmonized *I. scapularis* abundance by county and tick season, where the nymph season is defined as May to September and the adult season is October to December, and calculated *I. scapularis* pathogen infection prevalence as the percentage of ticks that tested positive for *Anaplasma phagocytophilum*, *Babesia microti*, *Borrelia burgdorferi*, and *Borrelia miyamotoi*. We then explored temporal trends in *I. scapularis* abundance and pathogen prevalence data using linear models.

Results

The resulting dataset is one of the most spatially and temporally comprehensive records of tick abundance and pathogen prevalence in the USA. Using linear models, we found small or insignificant changes in the abundance of nymphs and adults over time; however, *A. phagocytophilum*, *B. microti* and *B. burgdorferi* prevalence in both nymphs and adults has increased over time. For the period 2017–2021, the statewide average prevalence of *B. burgdorferi* ranged from 19% to 25% in *I. scapularis* nymphs and from to 49% to 54% in *I. scapularis* adults. The statewide average prevalence of all other pathogens in *I. scapularis* for 2017–2021, including *A. phagocytophilum* (4–6% for nymphs, 4–9% for adults), *B. microti* (4–8% for nymphs, 2–13% for adults) and *B. miyamotoi* (1–2% for nymphs, 1–2% for adults), was considerably less.

Conclusions

Our efforts revealed the complications of creating a comprehensive dataset of tick abundance and pathogen prevalence across time and space due to variations in tick collection and pathogen testing methods. Although tick abundance has not changed along the more southern latitudes in our study over this time period, and only gradually changed in the more northern latitudes of our study, human risk for exposure to tick-borne pathogens has increased due to increased pathogen prevalence in *I. scapularis*. This dataset can be used in future studies of *I. scapularis* and pathogen prevalence across the northeastern USA and to evaluate models of *I. scapularis* ecology and population dynamics.

Price, L.E., et al.; *Parasites & Vectors* (2024); https://doi.org/10.1186/s13071-024-06518-9

Summary: The research team created a dataset of tick abundance and pathogen prevalence across time and space in the United States, which can be used to further study *Ixodes scapularis* ecology and populations.

Perspectives from federal and state public health departments on their participation in and the utility of *Ixodes scapularis* (Acari: Ixodidae) and *Ixodes pacificus* tick and tick-borne pathogen surveillance in the United States

In response to notable increases in tick-associated illnesses in the United States, recent public health policies encouraged multi-sector collaborative approaches to preventing vector-borne diseases. Primary prevention strategies focus on educating the public about risks for tick-borne diseases and encouraging adoption of personal protection strategies. Accurate descriptions of when and where people are at risk for tick-borne diseases aid in the optimization of prevention messaging. Tick and tick-borne pathogen data can be used to fill gaps in epidemiological surveillance. However, the utility of acarological data is limited by their completeness. National maps showing the distribution of medically important tick species and the pathogens they carry are often incomplete or non-existent. Recent policies encourage accelerated efforts to monitor changes in the distribution and abundance of medically important ticks and the presence and prevalence of human pathogens that they carry, and to provide actionable, evidence-based information to the public, health care providers and public health policy makers. In 2018, the Centers for Disease Control and Prevention initiated a national tick surveillance program focused on *Ixodes* ticks. The national program coordinated and expanded upon existing efforts led by public health departments and academic institutions. Here, we describe experiences of state public health departments engaged in *Ixodes* tick surveillance, including information on why they initiated *Ixodes* surveillance programs, programmatic objectives, and strategies for maintaining tick surveillance programs. We share experiences and challenges in interpreting or communicating tick surveillance data to stakeholders and explore how the acarological data are used to complement epidemiological data.

Eisen, R.J., et al.; *Journal of Medical Entomology* (2024); https://doi.org/10.1093/jme/tjae149

Summary: This paper shares the experiences and challenges of federal and state public health departments related to tick-borne pathogen surveillance.

Tick Utilization of Eastern Redcedar Encroached Areas at the Individual Tree Scale in Oklahoma

The Great Plains region is experiencing a biome-level conversion as grasslands are being rapidly encroached by eastern redcedar (*Juniperus virginiana* L.; ERC) which, in turn, causes abiotic and biotic changes throughout the region. These changes brought about by ERC encroachment are providing habitat for ticks and mosquitoes that increase the risk for vector-borne diseases. This study evaluated the influence of ERC on the abundance of ticks at the tree level by matching CO2 traps under individual ERC trees with traps in nearby grass patches at seven sites across central and western Oklahoma. From 3,654 ticks collected, significantly more adult and nymphal *Amblyomma americanum* (L.) and adult *Dermacentor variabilis* (Say) were collected under the individual ERC trees compared to the adjacent grass patches. Along with growing evidence that larger-scale ERC encroachment increases the abundance of ticks, this finding suggests that even single ERC trees within an encroached area provide sufficient habitat for *A. americanum* and *D. variabilis*. This study also contributes novel information about the fine-scale effects of this invasive encroaching tree species on the ecology of vector-borne disease systems.

Horton, O., et al.; *Southwestern Entomologist* (2024); https://doi.org/10.3958/059.049.0421

Summary: This study describes how eastern redcedar encroachment into grasslands affects the ecology of ticks in the same area.

Minor Hosts Have a Major Impact on the Enzootic Transmission of *Borrelia burgdorferi*

In the northeast United States, subadult deer ticks feeding on white-footed mice are thought to drive the force of transmission of *Borrelia burgdorferi* (*B. burgdorferi*), the agent of Lyme disease. However, control measures targeting mice have produced inconsistent results, suggesting that other animals are significant contributors to enzootic transmission. Such contributions have previously been difficult to quantify. We used a retrotransposon-based host blood meal assay to measure the relative contribution of hosts to enzootic *B. burgdorferi* transmission at two insular sites in Massachusetts. Over 6 years, we identified mice and deer as the most common larval hosts at our Nantucket Island site. Infected nymphal ticks were derived mainly from mice (35%) and shrews (31%), despite shrews having fed only 12% of larvae. Deer were identified in 19% of the infected nymphs, despite their known reservoir incompetence. Shrews were consistently the most important host in our Martha's Vineyard site and were identified as the source of 41% of nymphs overall and 39% of the infected nymphs. Sciurids were variable contributors, feeding from 4% to 42% of the larval ticks each year, and contributed no infected nymphs in 2020 and as many as 83% in 2023. We conclude that host contributions to feeding larval ticks change over time and within sites and that shrews may be more influential than mice at some sites. Shrews, sciurids, and even deer may contribute to *B. burgdorferi* maintenance. Hosts that apparently feed a minor proportion of ticks can have a major impact on the force of *B. burgdorferi* transmission.

Goethert, H., et al.; *The American Journal of Tropical Medicine and Hygiene* (2024); https://doi.org/10.4269/ajtmh.24-0283

Summary: The authors of this study investigated the relative contribution of various hosts to *B. burgdorferi* transmission on Nantucket Island and found that shrews, sciurids (animals in the squirrel family), and deer are more important hosts than previously expected, and mice were not the most influential hosts.

Regional Variability of Spotted Fever Group *Rickettsia* Genospecies: Insights from Eight Regions in Russia

Introduction: In recent years, there has been growing interest in tick-borne infections, particularly tick-borne rickettsioses (TBRs). Assessing the genospecies composition and regional distribution of spotted fever group rickettsiae (SFGR) is crucial for optimizing risk-based surveillance of TBR. However, the genospecies diversity of SFGR populations in the Russian Federation remains understudied. To address this, we studied ticks collected from vegetation, humans, and animals in eight regions of Russia to identify the SFGR genospecies, which may have significance for human morbidity.

Materials and Methods: From 2020 to 2024, we collected 2,431 ticks from eight regions of Russia, representing Western Siberia (Altai Krai), North Caucasus (Karachay-Cherkessia), Southern Russia (Astrakhan Oblast), the Volga region (Samara Oblast), Central Russia (Moscow, Tula Oblast, Oryol Oblast), and Central Europe (Kaliningrad Oblast). We utilized commercial qPCR kits for SFGR screening and identified genospecies by Sanger sequencing partial genes for citrate synthase (*gltA*) and outer-membrane protein A (*ompA*), comparing the results with the GenBank database.

Results: Our findings revealed six distinct genospecies of SFGR across the eight regions of Russia; however, the diversity of these genospecies varied by region. The highest diversity (five genospecies: *R. raoultii*, *R. slovaca*, *R. helvetica*, *R. monacensis*, and *R. aeschlimannii*) was found in North Caucasus in ticks from three genera. In Western Siberia, we detected three genospecies—*R. sibirica*, *R. raoultii*, and *R. helvetica*—in two genera of ticks. In the Volga region, the genospecies *R. slovaca* and *R. raoultii* were found in *Dermacentor* ticks, while in Southern Russia, *R. raoultii* and *R. aeschlimannii* were identified in two different genera of ticks. Central Russia (three regions) and Europe showed a similar pattern, with *R. raoultii* in *Dermacentor* and *R. helvetica* in *Ixodes*.

Conclusions: Our study highlights significant regional variations in SFGR genospecies diversity in Russia, underscoring the necessity for ongoing research and monitoring for public health.

Rakov, A.V., Chekanova, T.A., and Petremgvdlishvili, K.; *MDPI* (2024); https://sciforum.net/paper/view/21314

Summary: This study found six distinct genospecies of Spotted Fever Group *Rickettsia* in Russia, with varying diversity by region. More research is needed to understand the diversity in Spotted Fever Group *Rickettsia*.

Contrasting pathogen prevalence between tick and dog populations at Chornobyl

Background: The 1986 disaster at the Chornobyl Nuclear Power Plant released massive amounts of radioactive material into the local environment. In addition to radiation, remediation efforts and abandonment of military-industrial complexes contributed to contamination with heavy metals, organics, pesticides and other toxic chemicals. Numerous studies have evaluated the effects of this contamination on the local ecology. However, few studies have reported the effect of this contamination on vector-borne pathogens and their hosts. In this manuscript, we characterize tick-borne pathogen presence at two sample locations within the Chornobyl Exclusion Zone, one at the Nuclear Power Plant (NPP) and another 16 km away in Chornobyl City (CC).

Methods: Ticks and whole-blood samples were collected from free-breeding dogs captured at the NPP and CC. Endpoint PCR and quantitative PCR were used to identify tick species and to assess the presence of specific tick-borne pathogens, including Anaplasma phagocytophilum, Borrelia burgdorferi sensu lato, Babesia spp., Bartonella spp., Francisella tularensis and general Anaplasmataceae. A droplet digital PCR assay was developed for Babesia canis and A. phagocytophilum to evaluate their presence in dogs from the two populations. Pathogen prevalences between the two sample populations were compared by calculating Z-scores.

Results: Ticks were identified as Ixodes ricinus (n = 102) and Dermacentor reticulatus (n = 4). Overall, 56.9% of I. ricinus ticks were positive for at least one pathogen. A significantly higher prevalence of A. phagocytophilum and B. burgdorferi was found in ticks at the NPP (44.0% and 42.0%, respectively) compared to CC (23.1% and 19.2%, respectively). Babesia spp. (including B. canis and B. caballi) were detected in 8.8% ticks at similar proportions for both populations. Interestingly, we found a significantly lower level of A. phagocytophilum in dogs at the NPP (1.8%) than in dogs at CC (11.7%). In total, 24.3% of dogs were positive for B. canis, evenly distributed across the two populations.

Conclusions: The results of this study show contrasting pathogen prevalence in both ticks and dogs at the NPP and CC, which may reflect the differential exposures at the two locations. This work adds an important new component to our understanding of the consequences of prolonged exposure to environmental contamination on the wildlife and ecology within the Chornobyl Exclusion Zone.

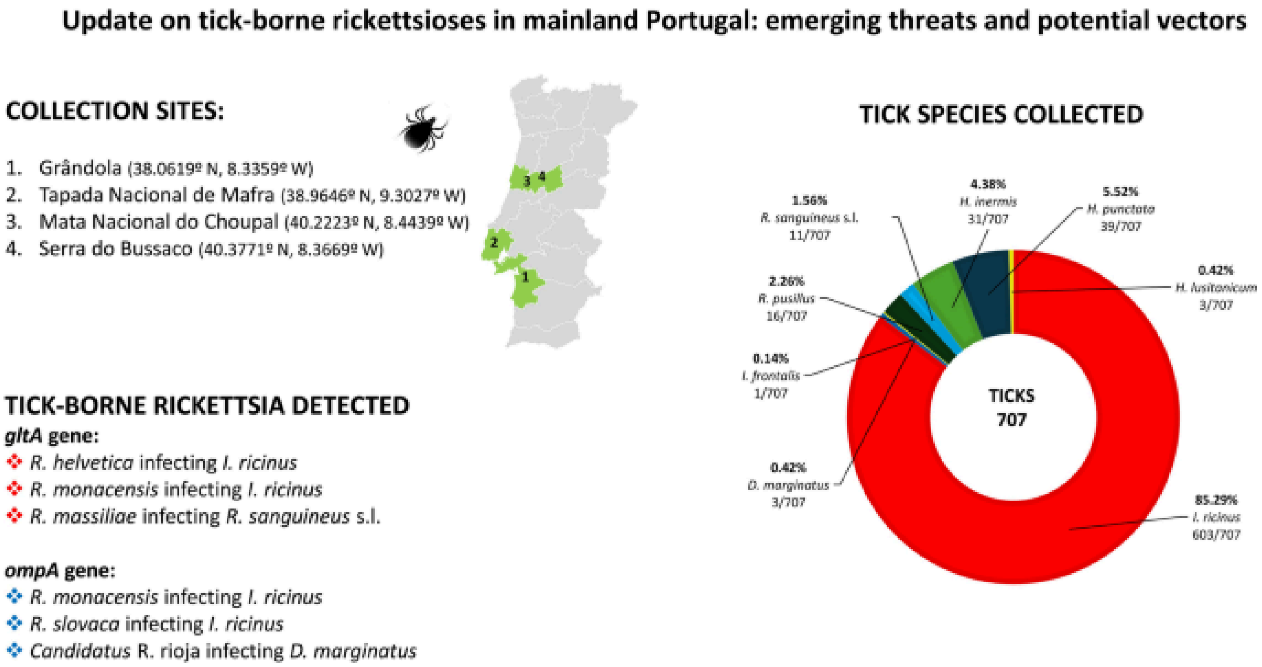
Dillon, M.N., et al.; *Parasites & Vectors* (2024); https://doi.org/10.1186/s13071-024-06563-4

Summary: Ticks and dogs located at the Nuclear Power Plant at Chornobyl (Chernobyl) have different levels of pathogen carriage than those in Chornobyl City. This contributes to our understanding of prolonged exposure of ticks, dogs, and pathogens to environmental contamination at the Chornobyl Exclusion Zone.

Regional Variability of Spotted Fever Group *Rickettsia* Genospecies: Insights from Eight Regions in Russia

The present study highlights the necessity for ongoing surveillance to map and monitor both questing and feeding ticks, along with their vertebrate hosts. Effective control strategies are of utmost importance to mitigate the escalating threat of TBR. Additionally, the present study provides valuable epidemiological insights into TBR in Portugal, including the identification of *R. slovaca* infecting *I. ricinus* - an unconventional tick-pathogen relationship - and the first report of Candidatus R. rioja infecting D. marginatus in Portugal. In conclusion, this study contributes with valuable data regarding epidemiological results on ticks and TBR circulating in Portugal, emphasizing the importance of proactive measures to address this emerging public health challenge.

Moerbeck, L., et al.; *Parasites & Vectors* (2024); https://doi.org/10.1186/s13071-024-06627-5



Update on tick-borne rickettsioses in mainland Portugal: emerging threats and potential vectors

COLLECTION SITES:

1. Grândola (38.0619º N, 8.3359º W)
2. Tapada Nacional de Mafra (38.9646º N, 9.3027º W)
3. Mata Nacional do Choupal (40.2223º N, 8.4439º W)
4. Serra do Bussaco (40.3771º N, 8.3669º W)

TICK-BORNE RICKETTSIA DETECTED

***gltA* gene:**

- *R. helvetica* infecting *I. ricinus*
- *R. monacensis* infecting *I. ricinus*
- *R. massiliae* infecting *R. sanguineus* s.l.

***ompA* gene:**

- *R. monacensis* infecting *I. ricinus*
- *R. slovaca* infecting *I. ricinus*
- *Candidatus* R. rioja infecting *D. marginatus*

Summary: This study summarizes tick collection in Portugal, as well as associated pathogens.

Molecular Section

Transovarial transmission of *Rickettsia* spp., *Francisella*-like endosymbionts, and *Spiroplasma* spp. in *Dermacentor reticulatus* ticks

Research on the transovarial transmission of pathogens whose reservoirs and vectors are ticks has led to an understanding of the mechanisms related to the circulation and persistence of selected microorganisms in natural foci. The primary aim of this study was to investigate the possibility of transovarial transmission of *Rickettsia* spp. in *Dermacentor reticulatus* ticks, and the influence of *Francisella*-like endosymbionts (FLEs) and *Spiroplasma* spp. on the efficiency of the egg-laying process and transmission of selected pathogens.

In total, 16,600 eggs were obtained under laboratory conditions from 55 females, with an average of 346 eggs per female. Adults, eggs, and hatched larvae were tested using polymerase chain reaction (PCR) for the presence of *Rickettsia* and endosymbionts.

DNA fragments of *Rickettsia* spp. were found in females (56.4 %) and in pools of eggs (72.9 %) and larvae (62.4 %). FLEs and *Spiroplasma* endosymbionts were confirmed in females (80 % and 14.5 %, respectively), pools of eggs (81.6 % and 26.1 %, respectively), and larvae (82.7 % and 46.2 %, respectively). Transovarial transmission was confirmed in *Rickettsia raoultii*, FLEs, and *Spiroplasma ixodetis*. No correlation was observed between the occurrence of individual endosymbionts and the efficiency of egg laying and transovarial transmission in *Rickettsia* spp.

In conclusion, transovarial transmission of *Rickettsia* spp., FLEs and *Spiroplasma* spp. in *D. reticulatus* plays an important role in their persistence and circulation in the environment. However, further research is required on this topic.

Kloc, A. et al.; *Ticks and Tick-borne Diseases* (2024); https://doi.org/10.1016/j.ttbdis.2024.102421

Summary: This study found that certain tick-borne pathogens can be passed from the mother tick to her eggs. This may play an important role in maintaining these pathogens in the environment.

mRNA Vaccines Against Tick-borne Diseases

Vector-borne diseases that account for more than 700 000 deaths annually are carried by arthropods that spread viruses, bacteria, and parasites. Effective vaccines are needed for most of the diseases spread by mosquitoes, ticks, sandflies, and other vectors. Since pathogens that live in arthropods for part of their life cycle adapt to different conditions and often do not rely upon a single virulence effector for pathogenesis, it is harder to develop vaccines with long-lasting protection. The increasing cost of development, clinical trials, and deployment are additional obstacles to the generation of effective protective measures. This can be partially solved by mRNA vaccines that can be produced on a large scale, in quick turnover time, and in a cost-efficient manner. Modified mRNA vaccines, combined with lipid nanoparticles or another strong adjuvant, can help induce the immune system to develop an effective memory response. Furthermore, this vaccine platform allows multiple antigens to be targeted simultaneously. Recent discoveries in mRNA vaccines against tick-borne diseases also shift the paradigm from developing therapies that neutralize pathogens to those that target the vector. Among tick-borne diseases, three mRNA vaccines – two targeting Powassan virus or Crimean–Congo hemorrhagic fever and a third multiantigen mRNA vaccine that specifically targets *Ixodes scapularis* ticks to prevent Lyme disease, are being developed. In this chapter, we will discuss the recent advances in mRNA-based vaccines against tick-borne diseases.

Arora, G. and Fikrig, E.; *Trends in mRNA Vaccine Research* (2024); https://doi.org/10.1002/9783527838394.ch10

Summary: This book chapter discusses the utility of mRNA vaccines for tick-borne diseases, considering existing challenges to vaccination against TBDs.

Examining Infant and Child Neurodevelopmental Outcomes After Lyme Disease During Pregnancy

Lyme disease is the most common vector-borne disease in the United States. Recent environmental and socioecological changes have led to an increased incidence of Lyme and other tick-borne diseases, which enhances the urgency of identifying and mitigating adverse outcomes of Lyme disease exposure. Lyme disease during pregnancy, especially when untreated, may lead to adverse pregnancy and neonatal outcomes; however, long-term child outcomes following utero exposure to Lyme disease have not yet been systematically assessed. This concise review describes the current state of knowledge of Lyme disease as a congenital infection and the potential effects of in utero exposure to Lyme disease infection on the neurodevelopment of infants and children. We highlight the importance of distinguishing between acute Lyme disease and a chronic condition termed Post-Treatment Lyme Disease Syndrome, as the impacts of both conditions on the developing fetus and subsequent child development may differ. The importance of placental pathology for patients with acute or chronic symptoms of Lyme disease in pregnancy is explored. Future research aiming to understand and protect neurodevelopment after antenatal Lyme disease must carefully collect potentially confounding variables such as symptomatology and treatment, use clear and standard case definitions, and follow children into school-age and beyond.

Williams, M.E., et al.; *Pathogens* (2024); https://doi.org/10.3390/pathogens13121029

Summary: This review discusses the impact of utero exposure to Lyme disease and encourages further research into neurodevelopment after antenatal Lyme disease.

Genetic and Immunological Insights into Tick-Bite Hypersensitivity and Alpha-Gal Syndrome: A Case Study Approach

Tick-bite hypersensitivity encompasses a range of clinical manifestations, from localized allergic reactions to systemic conditions like alpha-gal syndrome (AGS), an IgE-mediated allergy to galactose-α-1,3-galactose (α-Gal). This study investigated the clinical, molecular, immunological, and genetic features of two hypersensitivity cases. Two cases were analyzed: a 30-year-old woman with fixed drug reaction (FDR)-like hypersensitivity and a 10-year-old girl with AGS exhibiting borderline α-Gal-specific IgE. Diagnostic methods included allergen-specific IgE quantification, HLA genotyping, histopathological examination, and the molecular detection of tick-borne pathogens using microfluidic PCR. Case I demonstrated histopathological features of chronic lymphocytic inflammation and eosinophilic infiltrates, with HLA-B13 and DRB113 alleles indicating genetic susceptibility to hypersensitivity, while histological findings suggested a localized FDR-like reaction. Case II exhibited borderline α-Gal-specific IgE, resolving completely with a mammalian-free diet. The presence of HLA-DRB101 and DQB1*05 in the second patient indicated a genetic predisposition to AGS and other atopic conditions. No infectious etiology was identified in either case. These findings emphasize the heterogeneity of tick-related hypersensitivity and the importance of HLA genotypes in susceptibility. Comprehensive molecular, immunological, and genetic profiling offers valuable insights into the mechanisms of hypersensitivity, supporting personalized approaches for the diagnosis and management of tick-induced allergic conditions.

Banovic, P., et al.; *International Journal of Molecular Sciences* (2025); https://doi.org/10.3390/ijms26020680

Summary: This study found that there is a variety of mechanisms that lead to the development of alpha-gal syndrome. Given that people with tick bite hypersensitivities do not have the same underlying causes of alpha-gal, diagnosis and management of tick-induced allergic conditions should be personalized.

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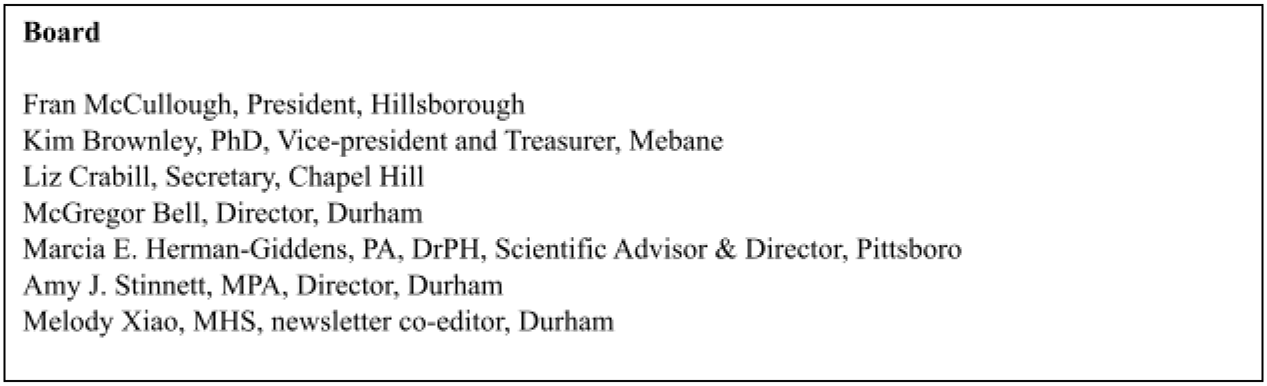

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