

Spatiotemporal patterns of Lyme disease in North Carolina: 2010–2020



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Summary

Background Lyme disease is the most common vector-borne disease in the United States with the majority of cases occurring in the Northeast, upper Midwest, and mid-Atlantic regions. While historically considered a low incidence state, North Carolina (NC) has reported an increasing number of cases over the past decade. Therefore, the aim of this study was to characterise the spatiotemporal evolution of Lyme disease in NC from 2010 to 2020.

Methods Confirmed and probable cases reported to the NC Division of Public Health without associated travel to high-transmission state were included in the analysis. The study period was divided into four sub-periods and data were aggregated by zip code of residence. The absolute change in incidence was mapped and spatial autocorrelation analyses were performed within each sub-period.

Findings We identified the largest absolute changes in incidence in zip codes located in northwestern NC along the Appalachian Mountains. The spatial distribution of cases became increasingly clustered over the study period (Moran's I of 0.012, $p = 0.127$ in 2010–2012 vs. 0.403, $p < 0.0001$ in 2019–2020). Identified clusters included 22 high-incidence zip codes in the 2019–2020 sub-period, largely overlapping with the same areas experiencing the greatest absolute changes in disease incidence.

Interpretation Lyme disease has rapidly emerged in northwestern NC with some zip codes reporting incidence rates similar to historically high incidence regions across the US Northeast, mid-Atlantic, and upper Midwest. Efforts are urgently needed to raise awareness among medical providers to prevent excess morbidity.

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Introduction

Lyme disease in the United States (US) is primarily caused by infection with *Borrelia burgdorferi* and transmitted to humans through the bite of *Ixodes scapularis* and *Ixodes pacificus* ticks. Early symptoms of Lyme disease including fever, headache, myalgia, and fatigue are non-specific.^{1,2} Approximately 75% of infected individuals develop erythema migrans (EM), a rash

often characterized by its distinct “bullseye” appearance.³ Untreated, a proportion of patients will progress to more severe manifestations including facial palsy (i.e., Bell's palsy), arthritis, and carditis. Treatment with tetracycline (e.g., doxycycline) and beta-lactam (e.g., amoxicillin, ceftriaxone) antibiotics remains the mainstay of therapy. Yet, even with early diagnosis and appropriate management, a proportion of patients will

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Research in context

Evidence before this study

We searched PubMed using search terms [(Lyme) OR (Borrelia)] AND [(North Carolina) OR (Virginia)] for any articles in any language published from database inception to January 8, 2024. The goal of the search was to identify relevant studies investigating the geographic expansion of Lyme disease into the southeastern United States. Our search identified 98 studies of which 45 were reviewed by title and abstract and determined to be relevant to the primary research question (Appendix, Table S1). The largest number of studies (17 of 45, 37.8%) examined the prevalence and the geographic distribution of the primary tick vector, *Ixodes scapularis*, and pathogen, *Borrelia burgdorferi*. There were also a number of relevant studies (12 of 45, 26.7%) documenting the seroprevalence of antibodies against *B. burgdorferi* in wildlife (e.g., deer, rodents) and companion animals (e.g., dogs). Notably, older studies—those generally conducted prior to 2004—tended to focus on the coastal areas of Virginia and North Carolina. There were fewer studies of human disease (16 of 45, 35.6%) with older studies primarily being case reports or case series of sporadic infections. More rigorous epidemiological analyses leveraging routine surveillance data, including studies exploring spatiotemporal changes and environmental correlates, were more frequent in the period after 2010. All of the epidemiological or spatiotemporal studies examined the southward expansion of Lyme disease transmission in Virginia, but not North Carolina. Overall, the literature documents the increasing prevalence of infected *I. scapularis* ticks and exposed animals in the western areas of these two states and particularly along the Appalachian Mountains. Genetic structure demonstrates these ticks are more similar to the northern origin *Ixodes* clade, suggesting

southward expansion from the Northeast and Mid-Atlantic regions rather than westward from the Coastal plains. Epidemiological studies show an increasing number of cases with spatial clustering in higher elevation areas of Virginia between 1998 and 2014.

Added value of this study

Our study, which is the first to investigate the spatiotemporal evolution of Lyme disease in North Carolina, highlights the continued geographic spread into the Southeastern United States. Specifically, we estimate that clusters of the zip codes in the northwestern part of the state now have incidence rates similar to those seen in traditional high transmission areas such as New England. Similarly, distinct clusters of disease emerged along the Blue Ridge Mountains. Notably, we observed that the leading edge of high-transmission zip codes moved approximately 100 miles south from the North Carolina–Virginia border during the period of analysis.

Implications of all the available evidence

The rapid evolution of Lyme disease risk in North Carolina over the past decade poses a substantial threat to public health, especially as many of the most highly impacted areas also experience limited access to health services. Urgent efforts are needed to raise public awareness and educate medical providers in order to prevent excess morbidity. Furthermore, the continued southward expansion along the Blue Ridge Mountains from VA and now into NC suggest that public health programs in areas such as northern Georgia and the highlands of South Carolina should consider increased entomological and epidemiological surveillance.

experience persistent symptoms, known as post-treatment Lyme disease syndrome, which can adversely impact quality of life.^{4,6}

Lyme disease is the most common vector-borne disease in the US with more than 30,000 cases reported to the Centers for Disease Control and Prevention (CDC) each year.⁷ Lyme disease has been a nationally notifiable disease since 1991. Events are reported to state and local health departments and classified as confirmed, probable, or suspect cases in accordance with definitions established by the Council of State and Territorial Epidemiologists (CSTE).⁸ However, estimates using other data sources suggest that many more individuals are diagnosed and treated for the disease each year, reflecting substantial gaps in routine surveillance systems.⁹ Geographically, Lyme disease cases are most frequently reported in the northeast, upper Midwest, and mid-Atlantic regions.^{10,11} Case classification and reporting procedures vary based on the level of transmission. High-incidence jurisdictions, for example, are defined as those

with an average incidence of at least ten confirmed cases per 100,000 population for three consecutive years.⁸ Notably, estimates of transmission level are only made at the state or territory level, but not for sub-regions such as counties.

While historically classified as a low-incidence state, North Carolina (NC) (Fig. 1) has experienced an increase in the number of reported cases rising from 1.97 cases per 100,000 during the period 2012–2016 to 3.30 cases per 100,000 in 2019.¹² This change is likely attributable to the southward expansion of the tick vector and pathogen through southwestern Virginia (VA) along the southern Appalachian Mountain range, also known as the Blue Ridge Mountains.^{13,14} Notably, in 2019, a cluster of four confirmed cases among children at an outdoor wilderness camp was reported in Buncombe County near Asheville; the first cluster of Lyme disease with a common exposure in the state and the southernmost identified cluster in the US at the time.¹⁵

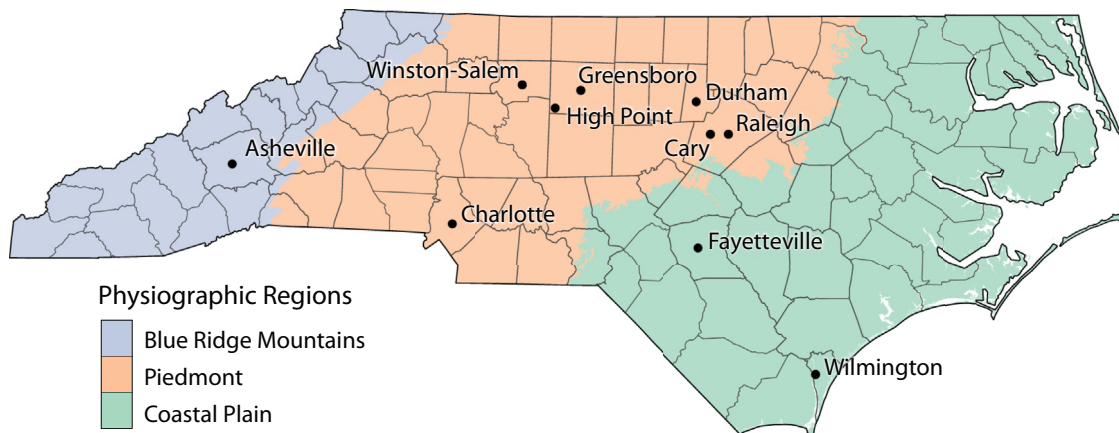


Fig. 1: Map of North Carolina showing three geographic regions and major metropolitan areas.

Therefore, we sought to quantify the changes in the incidence and spatial distribution of Lyme disease cases in NC from 2010 to 2020, leveraging data from the NC Electronic Disease Surveillance System (EDSS). We hypothesized that Lyme disease would demonstrate continued southward expansion along the Blue Ridge Mountains of western NC with the emergence of distinct spatial clusters during the period of 2016–2020. Such findings, especially at a high level of spatial resolution could inform prevention and control strategies in the affected areas, as surveys have shown that providers in low-incidence states have less experience with and knowledge of the diagnosis and management of Lyme disease.¹⁶

Methods

Data sources and geoprocessing

We obtained information regarding Lyme disease cases reported via NC EDSS between January 1, 2010 and December 31, 2020 from the NC Division of Public Health. Implemented in 2007, NC EDSS is a centralised web-based system for communicable disease surveillance that has been associated with improved case reporting.^{17–19} Cases were classified as confirmed, probable, or suspect according to the CSTE criteria active at the time of the report using the 2008, 2011, and 2017 case definitions (Table S2). Zip codes of cases were derived from the individual's reported address of residence. We utilised a shapefile with zip code polygons derived from the Esri database.²⁰ We spatially joined the 2020 census block centroid points ($N = 236,638$), the highest resolution data available from the US Census, to the zip code boundaries. To calculate the zip code population totals, we aggregated the block-level population data by zip code.

Travel history

We reviewed any travel history preceding the reported illness that was documented in the case report. The date of earliest illness identification was defined as the

earliest date among (i) date of symptom onset, (ii) date of laboratory testing, (iii) date of diagnosis by a health-care provider, or (iv) date of report, depending on the information available. To account for the fact that symptom onset date was not available for every case, the relevant travel history definition was set between three and 60 days, which extended the known incubation period an additional 30 days. The travel history was subsequently defined as (i) travel history to a CSTE-defined high incidence state in the US, (ii) travel to a CSTE-defined low incidence state or country (low-incidence area), (iii) no relevant travel history, or (iv) unknown travel history. Cases with relevant travel history to a high-incidence area or with a reported tick bite acquired during out-of-state travel in a low incidence area were excluded from the spatial analysis in order to limit the dataset to infections likely to have occurred in NC.

Analysis

To examine and compare temporal trends, the study period was divided into four sub-periods: 2010–2012, 2013–2015, 2016–2018, and 2019–2020. Only confirmed and probable cases meeting the previously defined travel history requirements were included in the primary spatial analysis. Zip code level incidence was mapped for each of the four sub-periods. We applied the CSTE threshold of ≥ 10 confirmed cases per 100,000 population to classify incidence in each zip code, but also reported the incidence of confirmed and probable cases consistent with publicly-available CDC surveillance data. The absolute change in incidence between 2010–2012 and 2019–2020 was also calculated and mapped to identify the geographic areas with the largest increases over the study period.

Global spatial autocorrelation analysis was performed using zip code level incidence to determine whether there was a random, dispersed, or clustered distribution of Lyme disease cases for each of the four sub-periods using Moran's I .²¹ The neighbour definition used for Moran's I was the Queen case definition, which identifies neighbours as zip codes that share a common

edge or common vertex.²² Local spatial autocorrelation was also conducted for zip code level incidence using the Local Indicator of Spatial Association (LISA).²³ LISA identifies spatial clusters of high and low incidence (i.e., high incidence in a zip code and high incidence in neighbouring zip codes and vice versa) in addition to high and low outliers, which are zip codes with a high incidence and neighbours with a low incidence and vice versa. We performed two sensitivity analyses including one utilising only confirmed cases and a second incorporating suspect cases to estimate how case classification affected spatial patterns identified in the primary analysis. All analyses were performed using R (Version 4.1.0) and specifically the tmap package to produce maps and the spdep package to conduct the spatial analysis.²⁴

Ethical considerations

The study was approved by the institutional review board of the University of North Carolina at Chapel Hill (IRB 20-3502). As a limited data set under CFR 45, Part 164.514 (e), written informed consent or waiver of HIPAA authorization was not required.

Role of the funding source

The funders of the study had no role in study design, data collection, data analysis, data interpretation, or writing of the report.

Results

There were 3234 cases of Lyme disease reported in NC EDSS between 2010 and 2020, including 529/3234 (16.4%) confirmed cases, 1738/3234 (53.7%) probable cases, and 967/3234 (29.9%) suspect cases (Table 1). The median age of reported cases was 41 years (interquartile range [IQR] 24–57) with females comprising slightly more than half of reported cases (1802/3234, 55.7%). A total of 88/529 (16.6%) confirmed cases and 128/1738 (7.4%) probable cases were determined to have a relevant travel history and were subsequently excluded from the subsequent analysis. Notably, 949/967 (98.1%) suspect cases, which are not routinely investigated, did not have available information on travel history. A total of 2053 cases were eligible for the analysis across all of the sub-periods.

The annual number of cases increased over the study period (Fig. 2). From 2010 to 2012, the mean statewide incidence was 1.2 cases per 100,000, while the mean incidence in zip codes reporting at least one case, representing approximately 20% of zip codes, was substantially higher at 4.5 cases per 100,000 (Table 2). Spatially, cases were scattered throughout the state during this sub-period (Fig. 2A). The mean statewide incidence doubled in the 2013–2015 sub-period with an average incidence of 2.5 cases per 100,000. Cases remained scattered throughout the state, but there were 107 more zip codes

| | Confirmed (N = 529) | Probable (N = 1738) | Suspect (N = 967) | Overall (N = 3234) |
|----------------------------------|---------------------|---------------------|-------------------|--------------------|
| Sex | | | | |
| Female | 232 (43.9%) | 984 (56.6%) | 586 (60.6%) | 1802 (55.7%) |
| Male | 295 (55.8%) | 752 (43.3%) | 375 (38.8%) | 1422 (44%) |
| Unknown | 2 (0.4%) | 2 (0.1%) | 6 (0.6%) | 10 (0.3%) |
| Age (Years) | | | | |
| Median (IQR) | 39 (14–58) | 41 (25–57) | 43 (27–56) | 41 (24–57) |
| Unknown | 0 (0%) | 1 (0.1%) | 1 (0.1%) | 2 (0.1%) |
| Race | | | | |
| White | 347 (65.6%) | 871 (50.1%) | 125 (12.9%) | 1343 (41.5%) |
| Black or African American | 8 (1.5%) | 74 (4.3%) | 15 (1.6%) | 97 (3%) |
| Asian | 4 (0.8%) | 9 (0.5%) | 1 (0.1%) | 14 (0.4%) |
| American Indian or Alaska Native | 0 (0%) | 4 (0.2%) | 2 (0.2%) | 6 (0.2%) |
| Multiple | 1 (0.2%) | 1 (0.1%) | 0 (0%) | 2 (0.1%) |
| Other | 3 (0.6%) | 16 (0.9%) | 4 (0.4%) | 23 (0.7%) |
| Unknown | 166 (31.4%) | 763 (43.9%) | 820 (84.8%) | 1749 (54.1%) |
| Ethnicity | | | | |
| Hispanic | 11 (2.1%) | 34 (2.0%) | 6 (0.6%) | 51 (1.6%) |
| Non-Hispanic | 303 (57.3%) | 797 (45.9%) | 121 (12.5%) | 1221 (37.8%) |
| Unknown | 215 (40.6%) | 907 (52.2%) | 820 (86.9%) | 1962 (60.7%) |
| Travel History | | | | |
| Travel to high incidence area | 88 (16.6%) | 128 (7.4%) | 0 (0%) | 216 (6.7%) |
| Travel to low incidence area | 16 (3%) | 46 (2.6%) | 0 (0%) | 62 (1.9%) |
| None reported | 286 (54.1%) | 945 (54.4%) | 18 (1.9%) | 1249 (38.6%) |
| Unknown | 139 (26.3%) | 619 (35.6%) | 949 (98.1%) | 1707 (52.8%) |

Table 1: Demographic characteristics and travel history of reported cases of Lyme disease by case classification.

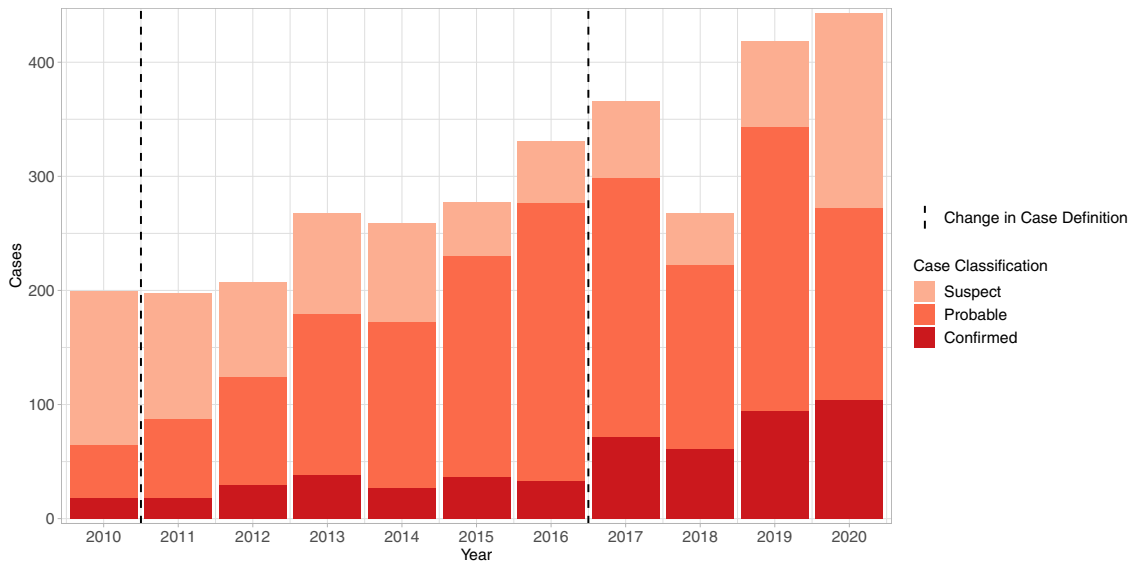


Fig. 2: Lyme disease cases reported to the NC Division of Public Health, 2010 to 2020. Cases are stratified by case classification (i.e., confirmed, probable, and suspect) with case definition changes shown by dotted line.

reporting cases,—a 66% relative increase—than in the previous sub-period (Table 3, Fig. 2B). The mean incidence continued to increase from 2016 to 2018, with the incidence in counties reporting at least one case rising from 6.6 to 11.6 cases per 100,000. Zip codes in the northwestern part of the state—specifically in Ashe, Alleghany, and Surry counties—appeared to have a number of zip codes that in our sensitivity analysis limited only to confirmed cases would meet thresholds for high incidence areas, defined as ≥ 10 confirmed cases per 100,000 (Figure S1). In the most recent period, which overlaps with the onset of the COVID-19 pandemic, the incidence across the state was modestly decreased at 2.8 cases per 100,000. However, the incidence in counties reporting at least one case continued to rise, reaching 21.1 cases per 100,000. Similar to the 2016–2018 sub-period, zip codes in the northwestern part of the state had higher incidence with an expansion of high-incidence zip codes into Watauga, Mitchell, Yancey, and Buncombe counties (Fig. 2D, Figure S4). During this same two-year period, incidence in the larger Blue Ridge

Mountains region reached 15.9 cases per 100,000 (Table 3). When assessing absolute changes in zip-code level incidence from the initial to final sub-period, the greatest magnitude increases were found in the north-western parts of the state (Fig. 3, Fig. 4).

During the 2010–2012 sub-period, there was no clustering pattern of cases as demonstrated by a Moran’s I of 0.012 ($p = 0.13$) (Table S3). A few clusters were identified in the Coastal Plains region, specifically in Pasquotank and Perquimans counties during this sub-period (Fig. 5A). Cases continued to exhibit a random spatial distribution during the 2013–2015 sub-period (Moran’s I: 0.029, $p = 0.06$), when high and low clusters appeared throughout the Piedmont region (Fig. 5B). In 2016–2018, however, there was moderate clustering of cases, with the emergence of a large cluster of high observations incorporating 12 contiguous zip codes primarily centered in Ashe County in the northwest-ernmost region of NC (Moran’s I: 0.123, $p < 0.0001$)

| Period | Cases | Zip codes with >1 case (n, %) | Incidence in all zip codes ^a | Incidence in zip codes reporting ≥ 1 case ^a |
|-----------|-------|-------------------------------|---|---|
| 2010–2012 | 246 | 161 (21.2) | 1.2 | 4.5 |
| 2013–2015 | 519 | 268 (35.3) | 2.5 | 6.6 |
| 2016–2018 | 712 | 326 (42.9) | 3.5 | 11.5 |
| 2019–2020 | 576 | 234 (30.8) | 2.8 | 21.1 |

^aPopulation estimates derived from 2020 census data.

Table 2: Mean annual incidence (cases per 100,000) of confirmed and probable Lyme disease in North Carolina.

| Area | Cases | Population | Incidence (per 100,000) |
|--------------------------|-------|------------|-------------------------|
| Geographic Region | | | |
| Blue Ridge Mountains | 258 | 813,134 | 15.9 |
| Piedmont | 216 | 6,791,607 | 1.6 |
| Coastal Plain | 87 | 2,789,207 | 1.6 |
| Clusters | | | |
| Northwest | 103 | 53,052 | 97.1 |
| West | 59 | 34,874 | 84.6 |

Table 3: Mean annual incidence of confirmed and probable Lyme disease in geographic regions and contiguous clusters, 2019–2020.

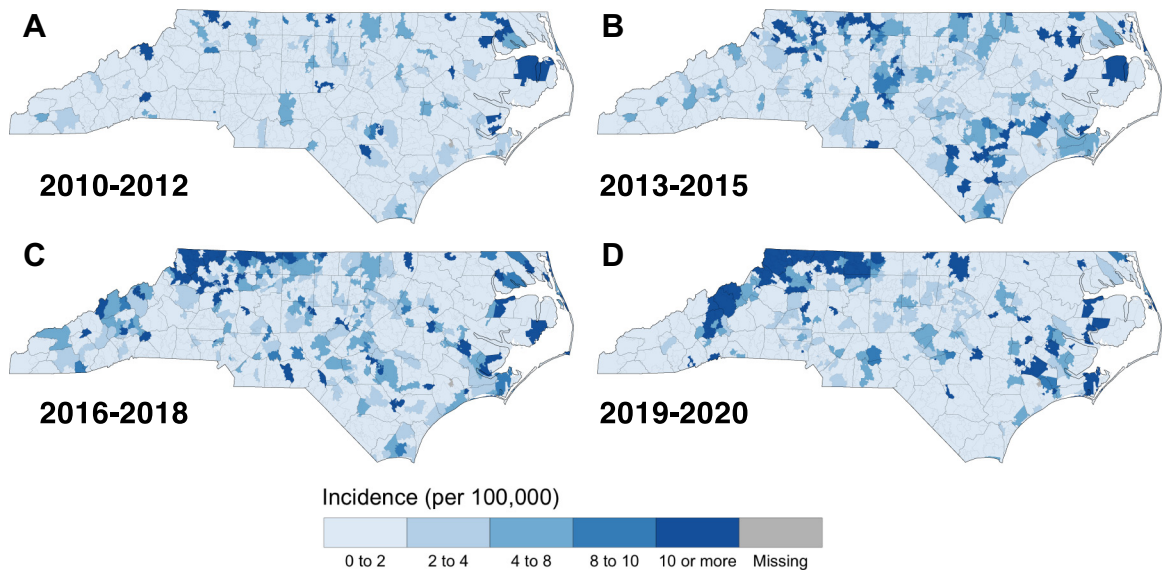


Fig. 3: Zip code level incidence of confirmed and probable cases of Lyme disease for each sub-period.

(Fig. 5C). In the 2019–2020 period, we observed strong clustering of cases, with a Moran’s I of 0.403 ($p < 0.0001$). Notably, two large clusters of high zip codes (22 zip codes total) were identified including an enlarged cluster centred in Ashe County along with a new cluster further to the southwest encompassing much of Mitchell and Yancey Counties (Fig. 5D). These clusters identified in the last sub-period largely overlapped with high incidence zip codes and zip codes with the highest absolute change in incidence in 2019–2020. The mean annual incidence in these clusters was 97.1 and 84.6 cases per 100,000 for the northwesternmost and western clusters, respectively (Table 3).

In the sensitivity analyses we found similar trends and patterns (Figures S1–S4) with an emergence of high incidence clusters in northwestern NC. Clustering patterns were similar to the primary analyses in the latter two periods when using only confirmed cases, but, in contrast with the primary analysis, Moran’s I results were statistically significant across all sub-periods when also considering suspect cases (Tables S4 and S5). Furthermore, there are an increased number of clusters in the analyses, primarily in the Coastal Plain region, when including suspect cases, but these are scattered and without a clear pattern of coalescence.

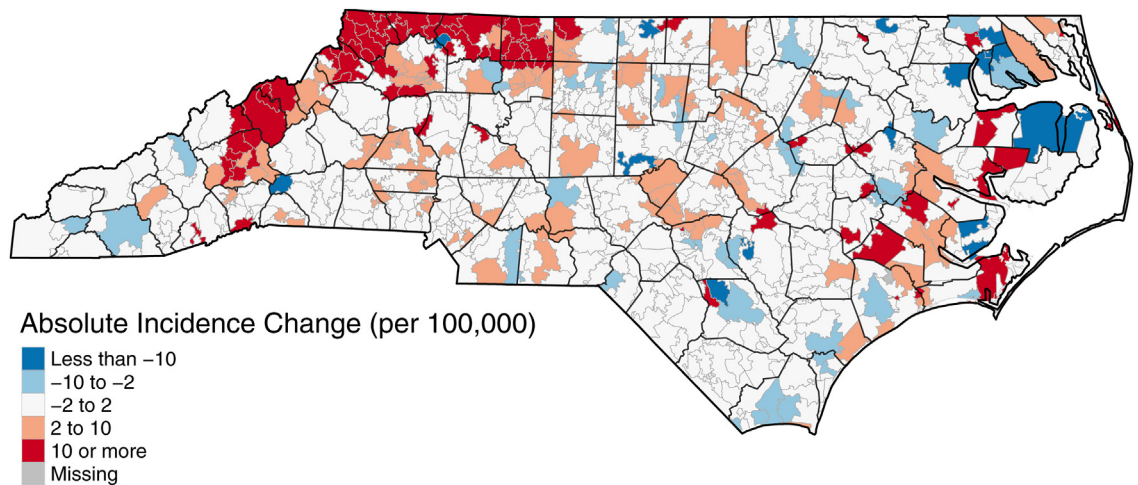


Fig. 4: Absolute change in the incidence of reported confirmed and probable cases of Lyme disease between the first (2010–2012) and most recent (2019–2020) sub-periods.

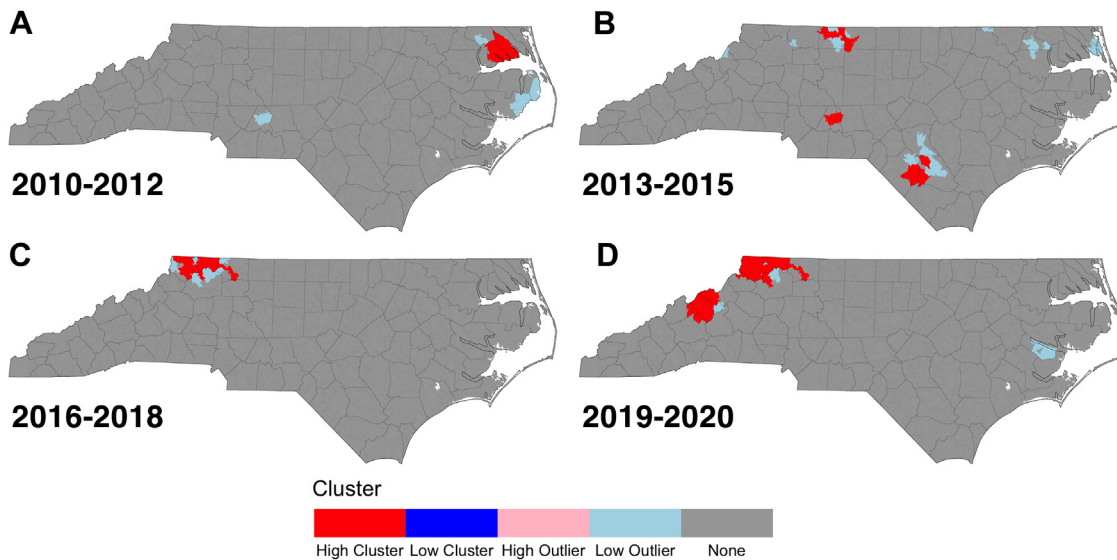


Fig. 5: Clusters identified through local spatial autocorrelation using reported confirmed and probable cases of Lyme disease for each sub-period.

Discussion

Our analysis of the epidemiology and spatiotemporal evolution of Lyme disease in NC from 2010 to 2020 demonstrates substantial and focal increases in incidence throughout the decade with clusters of disease emerging in the northwestern part of the state. While the state level incidence rate remains relatively low in NC, incidence within the high transmission clusters is comparable to that reported in consistently high incidence states such as Pennsylvania and New Jersey. Over the same period, we observed the leading edge of high-incidence zip codes and clusters move approximately 80–100 miles in a southwestward direction along the Blue Ridge Mountains. Given the relatively short time-frame over which these changes occurred, dedicated efforts and resources are needed to equip affected communities, especially medical providers who may not have experience with the diagnosis and management of Lyme disease, to respond to the evolving risk. Our findings, which build on similar southward expansion seen throughout VA in the prior decade,¹³ also suggest that see continued spread along neighbouring areas with similar ecology—potentially west into Tennessee and south into Georgia and South Carolina—may occur in the coming years. Medical professionals and public health practitioners in these neighbouring areas should be aware of the trends reported herein, especially when evaluating patients with consistent symptoms and relevant regional travel histories.

In prior decades, the strongest evidence for increased risk of Lyme disease in NC came from entomological studies that documented the presence of *I. scapularis* and *B. burgdorferi* exposed wildlife along the coastal plains of eastern VA and NC.^{25–27} These studies would

suggest that any southward expansion would take place through this region. While we did identify transient, relatively isolated clusters in the Coastal Plains region during the first two sub-periods of our study, these findings like reflect low numbers of cases in zip codes with relatively small populations. In contrast, we observed stable and contiguous clusters occurring in the western part of the state over the latter two sub-periods. The total population within these clusters approaches 90,000 residents, which suggests that small population sizes are unlikely to be contributing to spurious findings. Instead, these clusters offer evidence of distinct and lasting changes in disease incidence from the surrounding areas.

In contrast, the identification of *I. scapularis* ticks in northwestern NC is a more recent phenomenon.¹⁰ Perhaps as prelude to our findings, previous studies have identified similar southward expansion through western VA during the previous decade (1998–2014).¹³ There is genetic evidence that *I. scapularis* ticks in this region are more closely related to the northern clade, which exhibits more aggressive questing behaviours, than the southern clade.^{28,29} This finding suggests that the southward expansion of the tick vector and pathogen from the Northeast and mid-Atlantic regions is responsible for the observed changes in disease incidence, rather than a westward expansion from the Coastal plains. Unfortunately, formal tick and pathogen surveillance did not begin in western NC until 2018. However, data from northwestern counties conducted in 2019 demonstrate establishment of *I. scapularis* ticks infected with *B. burgdorferi*.³⁰

There are multiple ecological, climatic, and physical factors that may be driving the shifts in host, vector, and

pathogen distributions.^{26,31,32} *Ixodes* ticks are typically found in humid environments with mild temperature, leaf-litter, and forest cover.³³ As temperatures rise with global climate change, tick populations may migrate towards higher elevations with cooler temperatures, as has been reported with *I. ricinus* in Europe.³⁴ Associations with elevation and vegetation were observed as Lyme disease expanded southward through VA.³⁵ Existing north-south topographic corridors in the southern Appalachian Mountains may also play a key role in the movement of *I. scapularis*. In particular, the New River, the second largest river in NC has been identified as a potential corridor for deer to transport ticks and pathogens.³⁶ While urban expansion along the Northeastern I-95 corridor has been correlated with increasing Lyme disease incidence, we assess risk is likely to be associated with wildlife-settlement interfaces in northwestern NC.³⁷ Altered land use and vegetation patterns may influence Lyme transmission and expansion, potentially through the impact on white-tailed deer populations, which serve as an important host of *I. scapularis* ticks.³⁸ With multiple, potentially interacting factors, further research is needed to understand the drivers of Lyme disease emergence in northwestern NC, which currently sits at the leading edge of southern transmission.

Limitations

Our study has a number of strengths, including analysis of a dataset covering more than a decade of cases and the use of zip codes to provide a relatively fine scale description of Lyme disease distribution. Yet, there are also important limitations. First, there were changes in the case definitions throughout the study period that may have impacted the number of reported cases throughout the study period. Fortunately, the changes were modest and therefore unlikely to have resulted in large changes in reporting. Another limitation is that a travel history was not documented for all cases. Even when present, our classification of travel history was limited by the completeness and detail of the provider's notes. However, the extent of missing information on travel history did not vary significantly across counties, suggesting that there was no differential effect of non-reporting on spatial patterns. Another limitation is in using the incubation period to establish the inclusion criteria for the analysis. In low incidence areas for Lyme disease, there may be delays in diagnosis or difficulty in identifying symptoms of early disease. Cases in these areas may have an incubation period based on disseminated Lyme disease symptoms, which could overestimate the incubation period. As a result, these cases may be inaccurately included in the spatial analysis as having locally acquired disease. Additionally, case locations were reported based on zip code of residence, which may not be representative of the location of tick exposure, perhaps due to in-state travel. In regard to disease incidence, estimates in the latter sub-period may

have been impacted by the COVID-19 pandemic due to changes in care seeking (e.g., less testing) and decreased case investigations. We also made direct—albeit informal—comparisons between the incidence of Lyme disease in zip codes in NC versus state-level data in the historically high-incidence northeastern region. These comparisons are intended to highlight both the intensity and spatial heterogeneity of Lyme transmission in NC, ideally to provide support for enhanced surveillance and prevention efforts, but should not be interpreted as evidence of statistical equivalence.

Conclusions

In summary, our analysis demonstrates that Lyme disease has emerged in northwestern NC over the past decade with some areas reporting incidence rates similar to those observed in Northeastern states. The rapid evolution of disease risk poses a substantial threat to public health. Interventions targeting these high transmission areas—many of which are classified as health professional shortage areas—are urgently needed to prevent excess morbidity.³⁹ In addition to targeted communication campaigns emphasising prevention strategies (e.g., permethrin-treated clothing among outdoor workers, use of topical repellents), specific efforts are needed to educate medical providers regarding the diagnosis and management of Lyme disease. While NC may not be considered a high-transmission state—largely because such classifications are made at the state level—providers in the western part of the state should be educated about and encouraged to utilise post-exposure prophylaxis consistent with existing clinical guidelines that acknowledge within state heterogeneity in transmission intensity.^{40,41} In addition, the continued southward expansion along the Blue Ridge Mountains from VA and now into NC suggest that public health programs in areas such as northern Georgia and the highlands of South Carolina should consider increased entomological and epidemiological surveillance.⁴²

Contributors

Study conception and design: NVM, PLD, AGH, RMB. Funding: RMB. Study implementation: NVM, ABM, DAG, CW, PLD, RMB. Data analysis: NVM, AGH, SWS, PLD, RMB. First draft of manuscript: NVM, ABM, DAG, RMB. Revisions: All. Raw Data: Mokashi, Williams, Boyce. Verified data Mokashi, Delamater, Boyce.

Final Responsibility: Boyce.

Data sharing statement

Deidentified individual data that supports the results will be shared beginning 9–36 months following publication provided the investigator who proposes to use the data has approval from an Institutional Review Board (IRB), Independent Ethics Committee (IEC), or Research Ethics Board (REB), as applicable, and executes a data use/sharing agreement with UNC.

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Declaration of interests

All authors have completed the ICMJE uniform disclosure form and declare: no financial relationships with any organizations that might have an interest in the submitted work in the previous three years except that noted in the funding section; no other relationships or activities that could appear to have influenced the submitted work.

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Appendix A. Supplementary data

Supplementary data related to this article can be found at <https://doi.org/10.1016/j.lana.2024.100792>.

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