Original Paper

Human and Canine Tick-Borne Disease Surveillance in Oklahoma: One Health Ecological Triangulation Study

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Abstract

Background: Tick-borne diseases (TBDs) in the United States are increasing due to ecological and climate changes. However, national surveillance data are principally available only at aggregate state and federal levels, limiting granular analysis and constraining TBD diagnosis, prevention, and public health communication. From a One Health perspective, recognizing the shared environments of people and animals and integrating canine serological data with human surveillance can improve geographic risk assessment and reduce reporting bias. Oklahoma offers a useful case in point: several TBDs are endemic, the state contains significant vulnerable populations, and public health records date to 1928, providing a longitudinal record examinable at the county level.

Objective: With Oklahoma as a use case, we (1) identify geographic patterns and disparities in county-level human TBD reporting, (2) compare human TBD distribution with canine disease data to assess underreporting and geographic risk gaps, and (3) examine long-term disease trends and data inconsistencies across reporting periods.

Methods: A descriptive analytical ecological study using a One Health triangulation approach was conducted in which the units of analysis were counties (n=77) in the US state of Oklahoma. Data were summarized using 1990-forward human reporting histories, human county tables (2004-2007), and Companion Animal Parasite Council (CAPC) canine testing summaries (2012-2026). National Oceanic and Atmospheric Administration (NOAA) 1991-2020 Climate Normals were used to derive a Tick Season Risk Index summarizing county-level climatic suitability for tick activity. Primary outcomes included reported human cases, county-level human disease incidence rates (per 100,000 population), and canine positive tests, total tests, and percent-positive values.

Results: Trend, county burden, TBD incidence rate, and regional graphs illuminate variations that are not apparent in more aggregate state-level analyses. Central metro counties account for the largest number of tests performed and of reported human cases, while eastern, northeastern, and southeastern counties show stronger disproportionate burden signals. Several low-reporting western counties fall within a moderate Tick Season Risk Index range. This index is an exploratory 2-variable climatic screen, not a validated habitat suitability model; it cannot establish tick presence, habitat suitability, or the reasons for sparse case reporting, and no conclusion about surveillance gaps is drawn.

Conclusions: This study triangulates human, canine, and climatic data at the county level within a One Health framework, reporting a standardized index. Unlike prior studies, it addresses ehrlichiosis, spotted fever group rickettsiosis (SFR), and tularemia across nearly a century of public records, offering a replicable workflow that reveals discordance between human and canine surveillance. These findings support standardized reporting at the county level, integration of animal health data into human surveillance, and clinician awareness of TBD risks. Interpretation is limited by geolocation by residence rather than exposure and by canine serology that cannot distinguish *Ehrlichia* species pathogenic to humans.

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KEYWORDS

public health communication; One Health; tick-borne diseases; surveillance; canine

Introduction

Background

Tick-borne diseases (TBDs) are among the fastest-growing vector-borne public health threats in countries worldwide, driven by ecological disruption, land-use change, wildlife population shifts, and an increasingly warming climate. In the United States, ticks account for more than 75% of all vector-borne disease cases, and annual reports of tick-borne bacterial and protozoan diseases more than doubled between 2004 and 2016, surpassing 48,000 reported cases by the end of that period [1]. Despite this trajectory, the true burden is likely substantially underestimated. For example, the US Centers for Disease Control and Prevention (CDC) estimates that approximately 476,000 people are diagnosed and treated for Lyme disease (LD) each year in the United States, a figure that far exceeds the case counts captured by national surveillance, and similar reporting gaps affect other TBDs, including ehrlichiosis, Rocky Mountain spotted fever (RMSF), tularemia, and anaplasmosis [2,3]. Indeed, underreporting and misdiagnosis remain central and unresolved challenges in the surveillance system, attributable in part to the nonspecific symptom profiles of most TBDs and limited clinician familiarity outside established endemic regions [4].

The geographic range of vector tick species is actively expanding. The lone star tick (*Amblyomma americanum*) is the primary vector of ehrlichiosis, tularemia, Southern tick-associated rash illness (STARI), and Heartland virus infection and is associated with alpha-gal syndrome (AGS) in the United States. It has demonstrated ongoing northward and westward range expansion, a trend projected to accelerate under current and high-emissions climate scenarios [5-7]. Eisen and Eisen [8] documented substantial shifts in the geographic distribution of *Ixodes scapularis* over 5 decades, underscoring the need for continuously updated surveillance as vector ranges move beyond historically recognized endemic boundaries. In 2024, lone star ticks were found displacing blacklegged ticks in previously uninvaded northeastern habitats, with concurrent emergence of new human ehrlichiosis cases in those communities [9]. These dynamics underscore a core challenge: existing surveillance systems were largely designed for geographically stable, historically understood disease distributions and are poorly equipped to track pathogens in real time as vectors expand into new territory, underscoring the need for adaptive surveillance frameworks capable of tracking emerging tick-borne zoonoses as vector ranges shift [10].

Active surveillance in the United States relies on the CDC's National Notifiable Diseases Surveillance System (NNDSS), which gathers case reports submitted by health care providers and state health departments. However, except for LD and a limited number of years for selected other TBDs, the CDC provides access to case surveillance data only at the aggregate state and federal levels [11]. This restriction is a significant impediment to localized public health action. County-level TBD data, when made available at all by individual states, are provided inconsistently, with formats shifting from handwritten mortality logs to narrative reports to standardized electronic tables over the decades, making longitudinal or comparative analysis highly labor-intensive. Moreover, fragmented and often outdated national maps represent foundational barriers to effective risk communication, especially since national maps of tick distributions and associated pathogen prevalence are "often incomplete, outdated, or lacking entirely" [12]. The US Department of Health and Human Services (HHS) Tick-Borne Disease Working Group similarly confirms that data integration across surveillance systems and the lack of standardized county-level reporting remain among the highest-priority unmet needs in TBD surveillance and research [13].

The consequences of these kinds of surveillance gaps extend directly to public health communication and clinical practice. When localized data are unavailable, residents, clinicians, and public health agencies cannot accurately characterize disease risk in their communities. This is especially consequential in areas where TBD awareness is lower (eg, nonnortheastern US regions), and, for example, clinicians may not consider TBD diagnoses in the differential for febrile illness [4]. Triangulation of human-reported cases, canine serological data, and CDC records could significantly improve county-level surveillance resolution beyond what any single source provides, and research has called for broader consistency and application of integrated data approaches in TBD surveillance [6].

A One Health perspective, which recognizes the interdependence of human, animal, and environmental health across local, regional, and global scales [14], offers a substantively powerful lens through which to view these surveillance gaps. Canines (*Canis familiaris*) are well-established sentinels for human TBD risk: They share outdoor environments with humans, are exposed to the same tick vectors, and are tested for tick-borne infections at rates substantially exceeding those of humans [15]. Accordingly, expanded canine sentinel surveillance can be useful in the application of a range of zoonotic pathogens, including *Rickettsia* spp. and *Ehrlichia* spp. [16]. Moreover, canines are among the most commonly kept companion animals in US households, yielding a large, geographically distributed sentinel population for tick-borne pathogen exposure [17].

Oklahoma presents a particularly compelling use case for this approach. Several TBDs are endemic to the state, including tularemia, ehrlichiosis, RMSF, and Heartland virus infection, although not LD [18]. Tularemia cases in particular in Oklahoma, Arkansas, Kansas, and Missouri collectively account for approximately 50% of all nationally reported cases, with national tularemia incidence rising 56% from 2011 to 2022, with four-fifths of cases classified as probable, raising questions about diagnostic and reporting accuracy [19,20]. Note also that such issues are especially critical among various already vulnerable populations in the United States. For example, tularemia incidence among Indigenous American Indian or

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Alaska Native persons was approximately 5 times that of White persons nationwide, a disparity of acute relevance in Oklahoma, where almost half of the state land area comprises tribal territories and where poverty rates among native residents reach 19%-20%, well above the national average [19,21,22]. These populations face compounded vulnerability from both higher environmental exposure to tick vectors and reduced access to quality health care and timely diagnosis. In addition to elevated tick exposure, these native communities tend to have limited prior TBD knowledge, as is often the case among vulnerable populations, and tend to be underrepresented in TBD epidemiological observations and reporting [23].

A lack of standardization in TBD diagnostics and insufficient clinician education regarding regional endemic patterns are key drivers of both misdiagnosis and underreporting [4]. Clinically, ehrlichiosis and RMSF frequently present with overlapping flu-like symptoms, including fever, headache, myalgia, and thrombocytopenia, making differential diagnosis challenging without geographic context and a high index of suspicion [4,18,24]. Furthermore, some emerging conditions transmitted by the lone star tick, such as STARI, have no commercially available diagnostic tests, meaning patients may present with TBD-compatible symptoms, test negative for all notifiable diseases, and remain undiagnosed and untreated [25,26]. In states such as Oklahoma, where TBD prevention relies primarily on personal protective measures, the quality of public health communication directly determines whether residents and clinicians can take appropriate preventive and diagnostic action [27].

Objectives

The research objectives were to (1) identify geographic patterns and disparities in county-level human TBD reporting, (2) compare human and canine surveillance measures to characterize geographic concordance and discordance, and (3) describe long-term trends and inconsistencies across reporting periods.

Methods

Overview

Study Design and Setting

To address the identified intersecting gaps in surveillance resolution, data standardization, One Health data integration, and targeted public health communication, this study presents the US state of Oklahoma as a use case, using a descriptive analytical ecological design and a triangulation approach combining archival human TBD records with canine sentinel data at the county level [6]. That is, the unit of analysis was the county (n=77) in the US state of Oklahoma. Note that, other than LD, availability of TBD data is extremely limited at the county level, typically preventing exact year-to-year matches across reporting periods. The approach used here, reflecting a multimodal surveillance framework and the sentinel surveillance model [6,16], is designed to reveal geographic patterns in TBD burden that can remain invisible in standard aggregate national and state-level human surveillance and to identify specific gaps in public health communication that, if addressed, could meaningfully improve disease prevention, clinical diagnosis, and disease outcomes for all residents of the state. In STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) terms, this is a descriptive, retrospective ecological study: the unit of observation is the county rather than the individual, all data are secondary and aggregated, and no individual-level exposures or outcomes were analyzed. No hypothesis test was specified, and no inferential statistics were computed; findings are descriptive throughout.

Study Units, Variables, Data Sources, and Measurement

All 77 Oklahoma counties were included; there was no individual recruitment, sampling, matching, eligibility screening, or power calculation because the study used complete, publicly available aggregate county and state series for the periods described below. Primary variables were reported human cases, published human county incidence rates, canine positive and total tests, canine percent-positive values, and county climate normals.

The triangulation design integrated 4 complementary data streams: human TBD surveillance, CDC NNDSS county-level case counts together with Oklahoma State Department of Health (current and archival reports), canine serological data from the Companion Animal Parasite Council (CAPC), an environmental climate layer derived from the National Oceanic and Atmospheric Administration (NOAA), and historical archival records spanning 1928 onward. For the environmental layer, NOAA 1991-2020 30-year US Climate Normals were obtained for all 77 Oklahoma counties, and annual average temperature and annual average precipitation were extracted for each county. Each variable was rescaled to a 0-100 range, and the 2 were combined into a composite Tick Season Risk Index, weighting temperature at 55% and precipitation at 45%, to summarize each county's relative climatic suitability for *A americanum* questing activity [28,29].

While recognizing that other environmental factors are also important in determining tick habitat suitability, climatic effects based principally on temperature and precipitation are used here as conventional exploratory indicators. The climate layer was used only to order counties by 2 county-average climate normals. It cannot establish tick presence or distinguish ecological absence from surveillance limitations. The selection of temperature and precipitation as the 2 input variables follows published species distribution modeling for *A americanum*, in which thermal and moisture variables are consistently identified as the dominant climatic correlates of the species' range. Ensemble modeling across the continental United States. identified temperature- and humidity-related variables, particularly average July vapor pressure, as the strongest determinants of climatically suitable habitat [30]; correlative ecological niche modeling retained annual precipitation, precipitation seasonality, mean diurnal temperature range, and maximum temperature of the warmest month as the most informative predictors of current and projected distribution [5]; and process-based modeling identifies accumulated degree-days as the limiting condition for population establishment at the northern range margin [31].

The 55%/45% weighting applied here, however, was not derived from a fitted species distribution model or from any published

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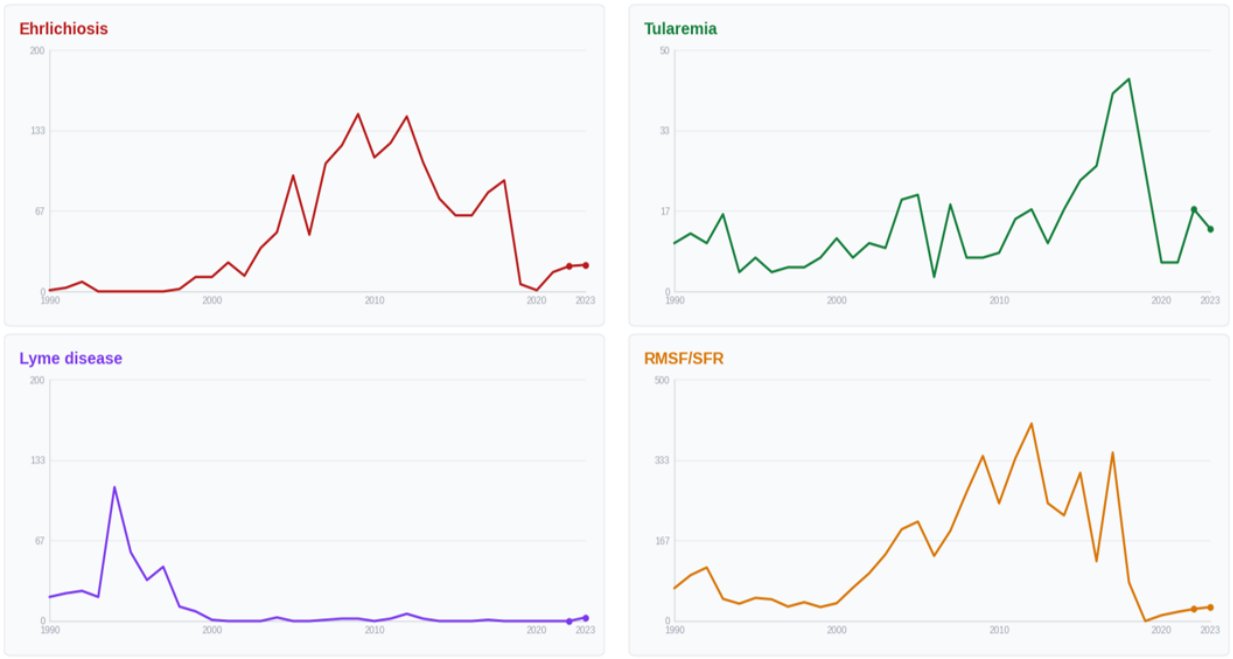
parameterization. It is a pragmatic, author-assigned approximation intended to give modest precedence to thermal conditions, consistent with the emphasis placed on temperature-related constraints in that literature [5,30,31], and it should be regarded as a transparent analytic convention rather than an empirically optimized weighting. Accordingly, the Tick Season Risk Index is used here solely as a coarse, relative screening layer for ordering counties along a climatic gradient. It is not a validated habitat suitability model; it was not calibrated or ground-truthed against active field sampling of host-seeking ticks, and no index value is proposed or implied as a threshold for *A americanum* establishment. Land cover, land use, host community composition, forest canopy and leaf-litter structure, and microclimate are likewise important determinants of local tick presence and abundance, and none were incorporated into the index [5,30,32,33]; counties classified here as climatically moderate may therefore still be unsuitable for *A americanum* for reasons the index cannot detect.

Variables and Methods

The descriptive analytic triangulation approach integrates county-level and statewide data streams to review TBD risk and surveillance gaps across the 77 Oklahoma counties. County-level results were displayed on standard Oklahoma county base maps [34], with county population taken into account when interpreting reported case incidence rates and low-population areas [35]. Canine serological data are available at the county level for multiple years from CAPC, constituting an important analytical resource for extending the geographic resolution of human TBD surveillance, especially in low-population and rural areas where human case counts are insufficient to signal endemic disease. Statewide TBD case counts were graphed from 1990 to 2023, parsed human incidence rates by county were summarized for 2004-2007, and CAPC canine testing summaries were summarized for 2012-2026; 2026 CAPC values should be interpreted as year-to-date. Tularemia is a secondary reportable TBD in Oklahoma and is attributable to both the lone star tick and the American dog tick (*Dermacentor variabilis*) [36]; it is therefore summarized alongside ehrlichiosis and RMSF/spotted fever group rickettsiosis (SFR), these being the 3 diseases available in the parsed 2004-2007 county tables. The county incidence rates were transcribed as printed in the 2004-2007 Oklahoma State Department of Health annual-summary county tables; the authors did not recalculate them. The source-table footnotes define each rate as reported cases divided by the relevant US Census Bureau county population and multiplied by 100,000. The 2004, 2005, and 2006 tables use the 2000 Census county population; the 2007 tables use the 2007 Census Bureau county population estimate [37-40].

For the comparative index (Figure 1 [41]), the human component was the mean of the 12 printed county incidence-rate values for 3 diseases—ehrlichiosis, RMSF/SFR, and tularemia—across 4 years (2004-2007). All 12 values were available for each county, and printed zeros were retained. The canine component was pooled positive tests divided by pooled total tests, multiplied by 100, across canine LD, anaplasmosis, and ehrlichiosis observations from 2012 to 2026; 2026 values were year-to-date. The comparative index was calculated for counties with a positive pooled canine testing denominator (n=59). The remaining 18 counties were classified as having no canine data and were not assigned a value. Within the 59 eligible counties, each component was converted to an average-rank percentile score, and the 2 scores were averaged with equal weight. Map classes were defined by empirical quintiles of the resulting index.

Figure 1. Statewide annual reported human tick-borne disease cases in Oklahoma, 1990-2023. Small multiples show ehrlichiosis, tularemia, Lyme disease, and RMSF/SFR. Values are the annual OSDH history-table counts used in the analysis. Source: Oklahoma State Department of Health, Number of Reported Cases of Communicable Diseases, Oklahoma, 1990-2024. OSDH: Oklahoma State Department of Health; RMSF: Rocky Mountain spotted fever; SFR: spotted fever group rickettsiosis.



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Regarding the human component, we have the following equation:

$$H_c = \frac{1}{12}\sum_{d\in D_H}\sum_{y\in Y_H} IR_{c,d,y}$$

For the canine component, we have the following equation:

$$C_c = 100\frac{\sum_{k\in D_C}\sum_{t\in Y_C} Pos_{c,k,t}}{\sum_{k\in D_C}\sum_{t\in Y_C} Tot_{c,k,t}}$$

For percentile transformation, we have the following equation:

$$P_{j,c} = 100\frac{R_{j,c}-1}{\mathrm{n}-1}, \mathrm{j}\in\{H,C\}, \mathrm{n}=59$$

Regarding the comparative index, we have the following equation:

$$I_c = \frac{P_{H,c}+P_{C,c}}{2}$$

Here, DH and YH denote the sets of diseases and years included in the human component, and DC and YC denote the sets of diseases and years included in the canine component, where DH = {ehrlichiosis, RMSF/SFR, tularemia}, YH = {2004, 2005, 2006, 2007}, DC = {LD, anaplasmosis, ehrlichiosis}, and YC = {2012, …, 2026}. IRc,d,y is the printed human incidence rate per 100,000 population for county c, disease d, and year y. Posc,k,t and Totc,k,t are the canine-positive and total tests for county c, disease k, and year t. Rj,c is the average rank of component j among the 59 eligible counties, with tied values assigned the mean of their ranks. Pj,c is the percentile score, and Ic is the equally weighted comparative index.

Descriptive annual means, sample SDs, and ranges were calculated from 34 statewide annual observations per disease (1990-2023). No inferential tests were performed.

Bias and Missing Data

Potential biases include passive case ascertainment, changing case definitions and reporting formats, veterinary access and testing practices, noncontemporaneous human and canine periods, geolocation by residence or testing location rather than exposure, and canine assays that do not distinguish *Ehrlichia* species. Suppressed or unavailable human values were treated as missing rather than 0; no missing value was imputed. Counties with no CAPC canine records or 0 total canine tests were excluded from the comparative index rather than assigned 0% positivity, and pooled canine percent-positive values based on small test denominators are less stable than those from counties with larger testing volumes.

Variation in Oklahoma's public health TBD reporting formats across decades (also exemplifying national inconsistencies) is shown in Textbox 1. This research required manual extraction of data from heterogeneous archival formats spanning nearly a century. The table shows the variability in reporting format, geographic resolution, and case definition across all primary data sources used in this study.

Textbox 1. Evolution of public health tick-borne disease (TBD) data reporting formats, Oklahoma State Department of Health, and US Centers for Disease Control and Prevention (CDC), selected periods 1928-2022. Missing data in any period does not indicate 0 cases.

- 1928: handwritten archival mortality report; first recorded tularemia death. Data manually extracted.
- 1940s-1960s: printed narrative reports with mortality counts embedded in paragraph text; no standardized format.
- 1970s: shift from mortality to case reporting. Reports begin including county-level breakdowns in some years; formats vary by year.
- 1980s-1990s: periodic graph and table formats are introduced; demographic breakdowns (ie, age and sex) appear in some but not all reports. Case counts for Rocky Mountain spotted fever (RMSF), ehrlichiosis, and tularemia appear at endemic levels.
- 2000s-2010s: annual state-level case reports only; county-level data rarely provided. Format shifts between narrative, tabular, and mapped presentations. Some files are in nonreadable formats requiring manual data entry.
- 2016-2022: CDC provides aggregate 4-year county-level datasets for selected TBDs (ehrlichiosis 2016-2019 and 2019-2022; tularemia 2016-2019 and 2019-2022). No county-level data for individual years. The Companion Animal Parasite Council (CAPC) provides annual county-level canine data.

Ethical Considerations

This study is exempt in accordance with HHS' Revised Common Rule, 45 CFR 46.102(e)(1), and uses only publicly available, aggregate data with no identifiable private information [42,43]. Informed consent is excluded and defined as not applicable under 45 CFR 46.102(l)(2). No individual was recruited, contacted, enrolled, or identified, and no compensation was provided. We confirm that the materials contain no images of identifiable individuals.

Results

Outcome Data and Main Results

All 77 counties were represented in county-level displays; the comparative index (Figure 1) was computable for 59 counties, and the 18 counties without a usable canine denominator are shown as "no canine data." Availability varied by source and period (Textbox 1). Across the 2 aggregated CDC reporting periods, reported human case totals fell for every disease examined: ehrlichiosis from 243 (2016-2019) to 44 (2019-2022),

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RMSF/SFR from 553 to 56, tularemia from 136 to 55, anaplasmosis from 10 to 2, and LD from 1 to 0 (Table 1). Statewide annual counts show ehrlichiosis and RMSF/SFR peaking in the 2000s and early 2010s and declining sharply after 2019, while tularemia fluctuates without a sustained trend (Figure 2). Across 1990-2023 (34 annual observations per disease), mean annual reported counts were 47.2 for ehrlichiosis (SD 48.6; range 0-147), 13.5 for tularemia (SD 9.6; range 3-44), 11.1 for LD (SD 22.6; range 0-111), and 135.7 for RMSF/SFR (SD 117.2; range 0-409). Canine testing over 2012-2026 returned a far larger number of positive results than the human system recorded cases over any comparable period, with 5189 canine ehrlichiosis positives, 253 anaplasmosis positives, and 114 LD positives in 2019 alone (Table 1). Counties in the eastern, northeastern, and southeastern regions of the state (including Latimer, Pittsburg, Haskell, Adair, Cherokee, Sequoyah, Mayes, and McIntosh) reflect elevated human county average incidence rates for ehrlichiosis, RMSF/SFR, and tularemia (2004-2007; Figure 1) coinciding with high CAPC canine percent-positivity for LD, anaplasmosis, and ehrlichiosis (2012-2026; Multimedia Appendix 1). Ranked by number of reported human cases, the leading counties are concentrated in the central metropolitan area, whereas ranking the same counties by incidence rate shifts the leaders to the sparsely populated east and southeast (Multimedia Appendices 2 and 3), a regional contrast that persists when counties are aggregated to a region (Figure 3A). The canine data show the same divergence between count and proportion: positive-test totals are highest in the most populous counties, while percent-positive values are highest in eastern and southeastern counties (Figure 3B; Multimedia Appendices 1 and 4).

County-aggregated Tick Season Risk Index values derived from NOAA 1991-2020 Climate Normals were highest in the southeastern and northeastern regions (index approximately 67-77/100), intermediate in the central region (approximately 60/100), and lowest in the western (southwestern and northwestern) regions, where values nonetheless remained within a moderate range (approximately 45-53/100). While not verified against field collection of host-seeking ticks, these values represent relative climatic ordering among Oklahoma counties rather than absolute or validated measures of habitat suitability (Multimedia Appendix 5).

Table 1. Reported human cases and canine positive tests for selected tick-borne diseases by disease and reporting period, Oklahoma, United States. Human case data from CDC[a] NNDSS[b] county-level datasets (4-year aggregated periods); canine positive-test data from CAPC[c] serological testing records (single-year counts, 2019). Human data are aggregated across 2 four-year periods (2016-2019 and 2019-2022), which overlap in 2019; canine values are single-year positive-test counts for 2019[d].

Disease	Principal vector	Pathogen	Reported surveillance values		
			Human, 2016-2019	Human, 2019-2022	Canine, 2019
Lyme disease	Blacklegged tick (*Ixodes scapularis*)	*Borrelia burgdorferi*	1	0	114
RMSF[e]	American dog tick (*Dermacentor variabilis*)[f]	*Rickettsia rickettsii*	553	56	—[g]
Anaplasmosis	Blacklegged tick (*I scapularis*)	*Anaplasma phagocytophilum*	10	2	253
Ehrlichiosis	Lone star tick (*Amblyomma americanum*)	*Ehrlichia chaffeensis* [h]	243	44	5189
Tularemia	Lone star tick (*A americanum*) and American dog tick (*D variabilis*)	*Francisella tularensis*	136	55	—

[a]CDC: US Centers for Disease Control and Prevention.

[b]NNDSS: National Notifiable Diseases Surveillance System.

[c]CAPC: Companion Animal Parasite Council.

[d]This table lists the principal vector and pathogen for each disease as commonly reported in surveillance and is not exhaustive. Reported human anaplasmosis counts are small and are presented as reported; *Anaplasma phagocytophilum* is transmitted by *Ixodes scapularis*, which is not established across most of Oklahoma [8,18], and no published epidemiologic investigation has established that reported Oklahoma human anaplasmosis cases were locally acquired. These counts are therefore not interpreted here as evidence of local human transmission.

[e]RMSF: Rocky Mountain spotted fever.

[f]For Rocky Mountain spotted fever, in addition to the American dog tick (*D variabilis*), the brown dog tick (*Rhipicephalus sanguineus*) transmits *R rickettsii* in parts of the southern and southwestern United States and along the US-Mexico border [44,45].

[g]An em dash (—) indicates no available canine data for that disease (Companion Animal Parasite Council canine serology covers Lyme disease, anaplasmosis, and ehrlichiosis).

hEhrlichiosis in humans and canines is caused by several Ehrlichia species beyond E chaffeensis, including Ehrlichia ewingii and Ehrlichia muris eauclairensis in humans, and Ehrlichia canis (transmitted by Rhipicephalus sanguineus and D variabilis) and E ewingii in canines [46,47]. The CDC's NNDSS human ehrlichiosis category combines E chaffeensis, E ewingii, and undetermined ehrlichiosis or anaplasmosis, as used in this study.

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Figure 2. Oklahoma county comparative tick-borne disease surveillance signal. For each county, the human component is the mean of 12 printed incidence-rate values (3 diseases × 4 years, 2004-2007); the canine component is pooled positive tests divided by pooled total tests across 3 diseases and 2012-2026. Each component was converted to an average-rank percentile across the 59 counties with canine testing data, and the 2 percentile ranks were averaged with equal weight; the 18 counties without a usable canine denominator are shown as “no canine data” and were excluded from ranking and quintile classification. Classes are quintiles; numbers identify the 5 highest-index counties; heavy boundaries and labels show analytical regions; 2026 is year-to-date. Darker shading denotes a stronger combined surveillance signal, not a higher number of cases or tests. Sources: Oklahoma State Department of Health annual-summary county tables (2004-2007) and Companion Animal Parasite Council canine testing summaries (2012-2026).

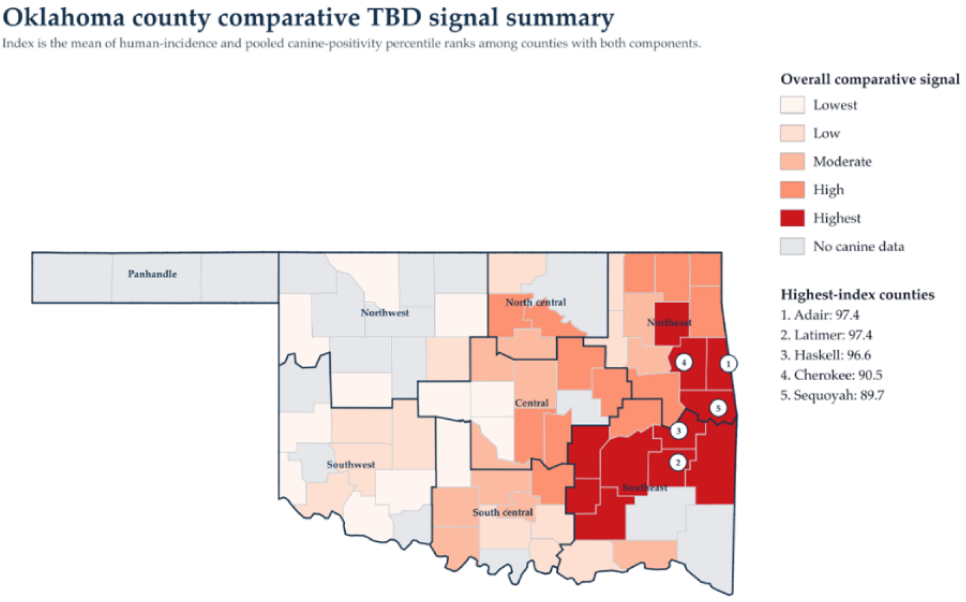
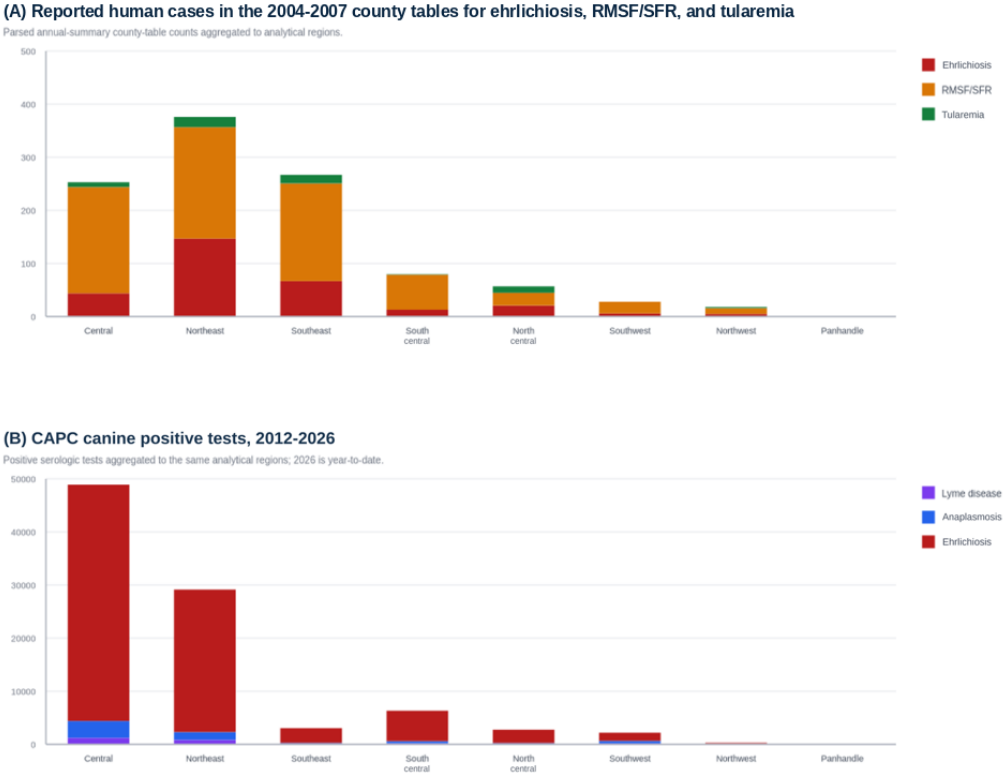


Figure 3. Human and canine surveillance results by Oklahoma analytical region. (A) Reported human cases in the 2004-2007 county tables for ehrlichiosis, RMSF/SFR, and tularemia. (B) Canine positive tests from CAPC for LD, anaplasmosis, and ehrlichiosis, 2012-2026; 2026 values are year-to-date. Panels use different scales and periods and are shown together for geographic comparison, not direct numerical equivalence. Human case counts and canine positive-test counts are complementary surveillance signals and are not directly comparable incidence estimates. CAPC: Companion Animal Parasite Council; LD: Lyme disease; RMSF: Rocky Mountain spotted fever; SFR: spotted fever group rickettsiosis.



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Human and Canine Case Comparisons

Table 1 presents a summary reference of selected TBDs in Oklahoma. The statewide findings show the largest reported human ehrlichiosis values in the 2000s-2010s and lower reported values after 2019. County-level results identify Tulsa, Oklahoma, Pittsburgh, LeFlore, and Pottawatomie counties as the counties with the highest number of reported human cases in the parsed 2004-2007 tables, while CAPC canine ehrlichiosis percent-positive is highest in Haskell, Cherokee, Sequoyah, Mayes, and McIntosh among counties with at least 500 total tests. The county graphs show the highest number of canine positive tests in Oklahoma, Tulsa, Cleveland, Rogers, and Washington counties, while canine percent-positive values were highest in eastern, northeastern, and southeastern counties. Average human county incidence rates for the 3 diseases available in the parsed 2004-2007 county tables (ehrlichiosis, RMSF/SFR, and tularemia) were highest in Latimer, Pushmataha, Pittsburg, Haskell, and Adair counties.

Discussion

Principal Findings

Viewed through a One Health lens, this study used a descriptive analytic triangulation approach to examine county-level human and canine TBD data in Oklahoma across nearly a century of archival public health records, with three stated objectives: (1) to identify geographic patterns and disparities in human TBD reporting at the county level, (2) to compare human TBD distribution with canine disease data to assess potential underreporting and geographic risk gaps, and (3) to present historical TBD data to illustrate long-term disease trends and data inconsistencies. Across all 3 objectives, findings were consistent and mutually reinforcing. Geographic patterns in human ehrlichiosis and tularemia were highly localized, concentrated primarily in central and northeastern counties, and differed substantially from the broader spatial distribution suggested by canine ehrlichiosis data, which extended into low-density southwestern counties where 0 human cases were recorded. Historical tularemia data revealed dramatic and largely unexplained variation in case counts across decades, illustrating the instability and inconsistency that characterize passive TBD surveillance. Taken together, the findings identify geographic discordance between the human and canine surveillance systems that warrants targeted epidemiologic and entomological follow-up [6,16].

The marked geographic discordance between human and canine ehrlichiosis distributions in this study is consistent with the national literature on TBD underreporting and the limitations of passive surveillance. Passive surveillance systems such as the CDC NNDSS are known to substantially undercount true TBD incidence, as case reports depend on patients seeking care, clinicians ordering appropriate tests, and laboratories reporting confirmed results, a chain of events that is less likely to occur in rural, low-density areas with limited health care access [1,4]. Even in areas with well-established ehrlichiosis burden, the use of confirmatory molecular testing (polymerase chain reaction [PCR]) has been minimal, with fewer than 1% of tested samples undergoing PCR-based confirmation, underscoring how testing gaps perpetuate surveillance blind spots [48].

Nationwide, *Ehrlichia ewingii* ehrlichiosis, one of the species included in this study's combined ehrlichiosis counts, was found to be expanding geographically between 2013 and 2021, with clinician education identified as a critical unmet need for improving diagnosis [49]. In Oklahoma, the absence of human cases in western counties stands in stark contrast to robust canine positivity in those same areas, a pattern that aligns with the well-established role of canines as early sentinels for tick-borne pathogen exposure in communities where human testing rates are insufficient [16,44]. This interpretation must nonetheless be tempered by the recognition that both human and canine cases are assigned to county of residence rather than county of exposure, so some of the discordance between human and canine distributions may reflect where people and canines live rather than where they encountered infected ticks.

Canine CAPC records provide a signal that is complementary to, rather than equivalent to, human surveillance, in that they capture the number of canine tests performed and the percentage positive rather than confirmed human cases. Two features of these data constrain how far that signal can be carried. First, neither the human nor the canine datasets record travel or exposure history, and both are geolocated by residence or testing location rather than by site of exposure. Second, canine ehrlichiosis serology does not distinguish among *Ehrlichia* species, so an unknown share of canine positivity may represent *Ehrlichia canis*, which is not a recognized human pathogen and is transmitted by dog ticks that do not vector the human-pathogenic species. Canine positivity is therefore best read as evidence of tick exposure and *Ehrlichia* circulation in the canine population, and only indirectly as a marker of human ehrlichiosis risk. Multimodal spatial analysis has demonstrated that canine serological data substantially improved county-level TBD risk assessment beyond what human case reports alone could provide, directly supporting the approach taken here [6].

The integration of county-level climate data as a fourth layer supplies only coarse context: a moderate score means that county-average temperature and precipitation fall near the middle of the Oklahoma distribution. It does not establish *A americanum* presence, habitat suitability, or the reason for sparse human reports. Land use, land cover, host availability, microclimate, and range-expansion timing were not measured [5,30,32,33].

Because the comparative index standardizes a human incidence-rate summary and a canine percent-positive summary, it identifies counties where the 2 surveillance measures rank relatively high. It does not estimate disease burden, individual risk, or local exposure, and a high number of cases or tests need not correspond to a high standardized signal.

Several low-population western counties register weak combined signals, but these data cannot distinguish low transmission from limited ascertainment. The human (2004-2007) and canine (2012-2026) periods are noncontemporaneous, so range expansion between periods could also contribute to discordance. Targeted entomological sampling and exposure-based

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epidemiologic investigation are required before attributing the pattern to ecology or surveillance.

The sharp decline in human ehrlichiosis case counts between the 2 CDC reporting periods observed in this study may reflect changes in case definition [49], testing practices, the COVID-19 pandemic's disruption of routine health care visits, or some combination thereof, rather than a true reduction in disease burden, a distinction with significant implications for how these trends are communicated to clinicians and the public. Several factors have been identified as plausible explanations for the observed decline in reported ehrlichiosis and tularemia cases between the 2016-2019 and 2019-2022 periods. Most prominently, the later reporting period encompasses the COVID-19 pandemic (2020-2021), which had well-documented effects on both health care–seeking behavior and disease surveillance nationwide. Emergency department visits for tick bites decreased substantially in 2020 relative to 2017-2019, and the number of LD tests performed fell by approximately 25%, concluding that TBD case reporting in 2020 was likely artificially reduced by pandemic-associated changes in health care–seeking behavior despite ongoing or even increased tick exposure [50].

Critically, the CDC's own national surveillance analysis of *E ewingii* ehrlichiosis explicitly noted that, although cases increased overall across 2013-2021, the number of reported cases decreased in 2020 and 2021 compared with previous years, an effect attributed to the COVID-19 pandemic and observed across other TBDs as well [49]. Pandemic-related delays in the diagnosis and treatment of SFR and ehrlichiosis in the southeastern United States also affected not only whether cases were reported but also how promptly they were diagnosed [51]. Given that the 2019-2022 CDC dataset used in this study includes 2 full pandemic years, the steep declines observed for both ehrlichiosis and tularemia in Oklahoma are likely attributable in substantial part to pandemic-related surveillance artifacts rather than to a true reduction in disease transmission.

Another possibility raised is whether improved public health messaging may have positively influenced the use of TBD prevention measures among Oklahoma residents, thereby contributing to fewer infections. The evidence on this point is suggestive but inconclusive. Personal protective measures (including use of US Environmental Protection Agency [EPA]–registered repellents, permethrin-treated clothing, and postexposure tick checks) are effective at reducing tick bites when used consistently, and community survey research indicates that individuals who have previously seen TBD information from their health department report higher use of repellents and tick checks than those who have not [52,53]. However, owing to cross-sectional study designs, it cannot be determined whether educational efforts are driving protective behaviors or whether individuals with higher perceived risk are simply more likely to seek out such information [53].

No Oklahoma-specific data are available to confirm that prevention messaging measurably reduced TBD incidence, and the magnitude and abruptness of the observed declines, concentrated in the pandemic years, are more consistent with surveillance disruption than with gradual behavioral shifts. While enhanced prevention messaging remains a worthwhile public health goal and may contribute to long-term risk reduction, the available evidence does not support attributing the observed case declines primarily to improved prevention behavior. This ambiguity reinforces a central argument of this study: without consistent, granular surveillance data, it is not possible to distinguish a genuine reduction in disease from an artifact of reporting, which in turn limits the ability to evaluate the effect of public health interventions.

Historical tularemia data in Oklahoma reveal a pattern of substantial unexplained variation in case counts across decades. National tularemia surveillance reporting covering 2011-2022 indicates an increase of 56% over that period, although four-fifths of cases were classified as probable rather than confirmed, raising important questions about the accuracy of diagnostic classification and testing practices [19]. While national tularemia surveillance data have confirmed Oklahoma's status as a high-burden state [54], reliance on probable case classifications introduces significant uncertainty into surveillance trends and may partly explain the wide variation in Oklahoma's historical case counts. Changes in surveillance case definition criteria over the time frame examined represent another plausible, and largely unquantifiable, source of this variation. Case definitions for nationwide notifiable TBDs have been revised repeatedly; for tularemia, the disease was removed from the national notifiable list in 1994 and reinstated in 2000 with a revised case definition that introduced a probable case category, and the ehrlichiosis and spotted fever rickettsiosis definitions have likewise been restructured on several occasions to reflect changes in laboratory methods and recognized etiologic agents [11,19,49]. Because the historical Oklahoma records analyzed here span decades before standardized national case definitions existed, and because each revision alters which illnesses are counted, some of the apparent decade-to-decade variation in tularemia case counts may reflect changes in what constituted a reportable case rather than true changes in disease occurrence.

Still, enhanced surveillance and recognition of localized ecological factors, including tick density and land use, as key drivers of case clustering suggest that Oklahoma's tularemia variation may reflect shifting environmental conditions as much as changes in surveillance capacity [55]. The observation that single-year tularemia mortality counts in earlier decades approached the total case counts seen across recent 4-year surveillance periods is particularly striking and likely reflects some combination of higher historical case fatality rates before modern antibiotic availability, changes in case ascertainment over time, and reduced environmental exposure or improved clinical management in more recent years [19]. More research using longitudinal ecological and entomological data is needed to disentangle these competing explanations.

However, the interpretation of tularemia case variation requires caution. Tularemia is unique among the TBDs examined in this study in having multiple nontick transmission routes. *Francisella tularensis* can infect humans not only through the bite of infected ticks (in Oklahoma, principally the American dog tick, *D variabilis*, and the lone star tick, *A americanum*) and deer flies, but also through ingestion of contaminated food or water,

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inhalation of infectious aerosols, and direct contact with infected animal tissues, for example, through cuts sustained while butchering an infected rabbit or other lagomorph [19,36,56]. Aerosol transmission has also been documented during agricultural and landscaping activities when machinery such as a tractor or lawnmower passes over an infected animal carcass [36,57]. Consequently, the geographic and temporal pattern of reported tularemia cases cannot be assumed to reflect tick vector distribution or density alone; variation may equally be influenced by hunting and trapping activity, rabbit and rodent population dynamics, agricultural practices, drinking water sources, and the relative frequency of each exposure route in a given county and year [19,56].

This multiplicity of transmission pathways is an important consideration for the inferential strength of the canine-sentinel triangulation approach for tularemia. Whereas canine ehrlichiosis positivity is a relatively direct proxy for shared tick exposure, canine data are a weaker proxy for human tularemia risk, since human tularemia infections also may arise from nontick routes to which canines are not comparably exposed. Therefore, tularemia findings should be interpreted relative to reported case patterns rather than as a direct index of tick-borne transmission risk.

The diagnostic complexity surrounding TBDs in Oklahoma is compounded by the presence of STARI, an emerging lone star tick-transmitted condition that presents with an expanding erythema migrans (EM)–like rash clinically indistinguishable from early LD, accompanied by fatigue, headache, and myalgia [25,26]. The EM-like rash of STARI itself may lead to a LD misdiagnosis for some patients, as the presence of provider-diagnosed EM rash alone meets national surveillance case definition criteria for a diagnosis of LD without any additional confirmatory laboratory testing. Because the etiologic agent of STARI has not been definitively identified, no nationwide notifiable case definition exists, no commercial laboratory test is available, and STARI is not included in NNDSS reporting [25,26]. Patients with STARI who seek care for a LD-like presentation will test negative for *Borrelia burgdorferi* and may be dismissed without treatment, despite the documented clinical benefit of doxycycline in most reported cases [26]. This diagnostic gap emphasizes the urgent need for standardized TBD diagnostic protocols and improved clinician education regarding regional endemic patterns [4].

The overlap in symptom profiles among ehrlichiosis, RMSF/SFR, tularemia, and STARI (conditions that occur in Oklahoma but involve different vectors or transmission routes) means that a provider unfamiliar with local TBD epidemiology may not order appropriate tests, particularly in western counties where surveillance data have historically suggested low disease burden despite canine sentinel data pointing to the contrary. The variation in Oklahoma's public health TBD data formats over nearly a century (Textbox 1) illustrates how data inconsistency compounds this problem. Without reliable historical baseline data, clinicians and public health officials cannot accurately communicate risk levels to communities, and opportunities for early case detection are lost [4,13].

The One Health triangulation approach used in this study builds on an established and growing evidence base for canine sentinel surveillance as a complement to human TBD reporting [58-61]. Along with the present findings from Oklahoma, there appears to be a systemic expansion of canine sentinel data integration into state and federal TBD surveillance frameworks. However, this study also demonstrates that CAPC canine data already in the public domain can be better and more regularly used for this purpose. The NOAA layer supplies a coarse climatic comparison only; because it omits land cover, hosts, microclimate, and field validation, it cannot distinguish surveillance failure from ecological unsuitability [28,29]. The TBD surveillance gap is therefore not solely a data availability problem as such; it is also a data integration and communication issue that could be addressed within the existing public health infrastructure.

The heterogeneity of Oklahoma's historical TBD data, spanning handwritten mortality logs, printed narrative reports, tabular presentations, and modern electronic formats across nearly a century, illustrates a challenge that is common to TBD public health surveillance [12,13]. Addressing this challenge systematically would require substantial investment in data standardization and digitization. Emerging AI tools offer promising approaches for assisting in and accelerating this process, with implications for public health surveillance and integrating heterogeneous data sources, including historical records, electronic health records, and social media streams, and for reducing delays in outbreak detection [62,63], although there are also problems associated with their use, such as privacy violation concerns and other ethical challenges. In any case, applied to the archival TBD data challenges, AI assistance and tools appear to hold promise for data collection and engagement in relation to public health data and records, enabling more rigorous longitudinal analyses than are currently feasible.

Limitations

Noted here are particular limitations that should be considered when interpreting the findings.

First, some limitations may be associated with passive disease reporting, including differential case ascertainment, testing variability, and reporting completeness across counties and time periods [1,4]. It is also critically important to note that reported cases of both human and canine TBD often lack travel or exposure history and, in the datasets used here, are mapped exclusively by county of residence (for canines, the county of the testing veterinary clinic) rather than by county of exposure. Because ticks may be acquired during travel, recreation, or work outside the home county, and because canines frequently accompany their owners on such activities, county-level counts and percent-positive values may attribute infections to counties where exposure did not occur, which limits geographic interpretation of both the human and canine surveillance patterns presented here. This constraint bears directly on the small number of human anaplasmosis cases reported in Oklahoma, which cannot be assumed to have been locally acquired: *Anaplasma phagocytophilum* is transmitted by *I scapularis*, a vector not established across most of the state [8,18], and we identified no published case report establishing local acquisition through epidemiologic investigation. Human anaplasmosis is

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accordingly reported here as a surveillance count only and is not characterized as an endemic human TBD in Oklahoma.

Second, the use of aggregated multiyear CDC county-level data, available only in 4-year blocks for most TBDs studied, prevents analysis of year-to-year trends and may mask meaningful within-period variation, including, for example, the impact of the COVID-19 pandemic on health care usage and TBD testing [49]. The later study period (2019-2022) also coincides with the COVID-19 pandemic, which is known to have artificially depressed TBD reporting nationwide [49-51], such that observed declines in case counts cannot be interpreted as true reductions in disease burden.

Third, county-level case counts suppressed by the CDC for privacy (fewer than 5 cases per county per period) were treated as missing, which is the methodologically appropriate approach but means that an estimated 40%-50% of counties in the ehrlichiosis analysis had no usable human case data, limiting the geographic completeness of the human surveillance picture.

Fourth, CAPC canine data are derived from canines presenting to veterinary clinics and reflect testing practices and veterinary access patterns, not a random sample of the canine population; counties with fewer veterinary testing resources may have lower reported canine positivity independent of true disease burden [15,16]. An important related limitation is that canine ehrlichiosis serology has the potential to greatly overestimate human ehrlichiosis risk. Commercial canine assays detect antibodies to several *Ehrlichia* species without distinguishing among them, and where the majority of canine infections are caused by *E canis*, an agent that is not a recognized human pathogen, canine seropositivity has little bearing on human risk. *E canis* is transmitted by the brown dog tick (*Rhipicephalus sanguineus*) and the American dog tick (*D variabilis*), both of which are present in Oklahoma [46,47]. Although American dog ticks frequently bite people and brown dog ticks occasionally feed on humans, neither species transmits the human-pathogenic *Ehrlichia* species (*E chaffeensis* and *E ewingii*), which are vectored primarily by the lone star tick (*A americanum*) [44,46,47]. Consequently, canine ehrlichiosis resulting from *E canis* infection transmitted by either species of dog tick would not be an indicator of human ehrlichiosis risk. Because the CAPC canine data used here do not identify the infecting *Ehrlichia* species, the geographic extent of canine positivity, particularly in western counties with no reported human cases, should be interpreted as evidence of *Ehrlichia* exposure in the canine population rather than as a direct measure of human ehrlichiosis risk, and may in part reflect *E canis* transmission by dog ticks.

Fifth, the historical tularemia data (1928-1980) were manually extracted from archival records of heterogeneous quality and format, introducing the possibility of transcription error and limiting comparability across time periods. In addition, case definition criteria for human TBD surveillance changed at multiple points during the time frame examined, and pre-1990 archival counts were compiled without a standardized national case definition; such changes could account for a substantial portion of the dramatic variation in case counts across decades and cannot be separated from true changes in incidence using the available data [11,19].

Sixth, for tularemia specifically, the canine-sentinel triangulation approach is inherently limited because *F tularensis* is transmitted through multiple nontick routes (including ingestion, inhalation, and direct animal contact) to which canines are not comparably exposed, weakening canine data as a proxy for human tularemia risk [19,36,56].

Seventh, this study is geographically limited to Oklahoma as a use case and the ecological conditions, tick species distribution, and health care infrastructure specific to that state; findings may not be generalizable to other states without replication using locally appropriate data [18,64].

Eighth, no longitudinal county-level tick density data exist for Oklahoma across the study period, preventing direct assessment of whether changes in vector abundance contributed to observed case variation [33].

Ninth, regarding vector tick density specifically, the current county-level *A americanum* presence data from the CDC, while useful for establishing broad vector distribution, do not adequately contextualize the historical tularemia and ehrlichiosis surveillance information presented here. To our knowledge, no systematic, longitudinal, county-level dataset of *A americanum* or *D variabilis* density exists for Oklahoma across the full period represented in the graph set. The figures therefore do not treat climate or tick-distribution maps as direct evidence of tick density; instead, they summarize observed human and canine surveillance patterns through statewide, county, and regional graphs. This point underscores the need for dedicated, ongoing entomological surveillance to complement disease-based human and canine data streams [32,33]. Relatedly, the Tick Season Risk Index used as the environmental layer in this study is a simple two-variable construct based on county annual mean temperature and annual precipitation, with weights assigned by the authors rather than estimated from data. Although temperature and moisture variables are well established in the modeling literature as principal climatic correlates of *A americanum* distribution [5,30,31], the specific variables, weights, and 0-100 scaling used here have no published precedent, were not fitted to tick occurrence records, and were not ground-truthed against active surveillance for host-seeking ticks in Oklahoma counties. The index therefore cannot identify a threshold for tick establishment, and counties falling in its moderate range should not be assumed to support *A americanum* populations: land use, land cover, host community composition, and microclimate may render such counties unsuitable irrespective of county-average climate. The index should be interpreted only as a coarse, exploratory screen indicating that county-average climate does not obviously preclude tick activity, and validating it will require paired field collection of host-seeking ticks across the climatic gradient described here.

Finally, future research also should address demographic factors within the human case data, such as age, sex, occupation, or race or ethnicity, which are known to be associated with differentiating socioeconomic health determinants affecting both TBD exposure risk and access to diagnosis and care [19,21,23].

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Generalizability

Oklahoma is presented as a use case. The workflow can be replicated where comparable human and animal surveillance data exist, but the observed rankings and discordance should not be generalized to other states without local data, harmonized periods, and locally appropriate vector and ecological information. While dependent on data availability, the method itself is broadly transferable. As noted, CAPC canine test summaries are published at the county level nationwide [15], NOAA Climate Normals are available for all US counties [28], and most state health departments maintain current and archival notifiable disease records. The specific findings, however, are conditioned on Oklahoma's setting, including the dominance of *A americanum* and the endemic status of ehrlichiosis, RMSF/SFR, and tularemia rather than LD [18], a large rural population with uneven access to medical and veterinary care, extensive tribal lands [22], and the particular years and formats in which county data were released. States where LD predominates, and *I scapularis* is the principal vector, or where county data are released on different schedules, would be expected to show different patterns of human and canine concordance. The approach is likely most directly transferable to neighboring states with similar tick ecology and tularemia burden, such as Arkansas, Missouri, and Kansas [19], and to states into which *A americanum* is expanding [5,9], where canine positivity may become detectable before human cases are recognized [16].

Conclusions

Oklahoma is one of the highest-burden states for several non-Lyme TBDs, consistently ranked among the states contributing the greatest share of national case counts for spotted fever group rickettsioses (including RMSF), ehrlichiosis, and tularemia [3,11,19]. More than 75% of spotted fever rickettsiosis cases nationally occur in just 7 states, with Oklahoma standing alongside Arkansas, Missouri, North Carolina, Virginia, Alabama, and Tennessee [11]. Oklahoma, along with Arkansas, Missouri, and Kansas, collectively accounts for approximately 50% of all nationally reported tularemia cases [19]. The lone star tick (*A americanum*) is the primary driver of this burden; it is the most abundant tick infesting both animals and humans across the southern United States. [32]. In Oklahoma, its peak activity has historically concentrated in late spring and early summer, though recent entomological data from north-central Oklahoma indicate a shift in adult peak activity approximately 1 month earlier than historical norms, likely reflecting ongoing climatic changes [32].

Beyond the notifiable diseases tracked in this study, *A americanum* in Oklahoma is also the implicated vector for Heartland virus infection, Bourbon virus disease, AGS, and STARI. These conditions are not nationally notifiable, have little-known or no commercially available diagnostic tests, and are essentially invisible in standard surveillance systems [25,26,65,66]. AGS alone has seen a documented spike from approximately 12 confirmed US cases in 2009 to more than 34,000 by 2019, with Oklahoma among the states with the highest per-capita positive antibody rates [66]. While not establishing the magnitude or location of unobserved human disease burden, the findings (that human TBD case counts in Oklahoma are geographically concentrated) show geographic discordance among available surveillance measures. They support evaluating ascertainment and exposure attribution, especially in low-density counties.

This study has implications that extend well beyond Oklahoma. The NNDSS continues to make most TBD data publicly available only at the aggregate state level, a structural constraint that hinders the localized risk assessments necessary for effective clinical decision-making, public health communication, and targeted prevention [11-13]. This limitation is particularly consequential in high-burden states such as Oklahoma, where the full scope of TBD risk, including nonnotifiable conditions such as STARI and AGS, substantially exceeds what passive surveillance records indicate. Noting the lack of a systematic, standardized mechanism for collecting, reporting, and integrating TBD data within and across states at the county-level and below, the identified interpretive challenges illustrate the practical cost of surveillance gaps. For example, the marked declines in reported ehrlichiosis and tularemia cases between the 2 study periods cannot be confidently attributed to any single cause, because the available data cannot disentangle a true reduction in transmission from the well-documented effects of the COVID-19 pandemic on health care–seeking and reporting [49-51], from possible improvements in prevention behavior [52,53], or, in the case of tularemia, from shifts in the relative frequency of the disease's multiple nontick transmission routes [19,36,56]. The inability to distinguish among such explanations, each plausible and each supported by the published literature, is itself a key finding, demonstrating that current surveillance infrastructure is inadequate for evaluating whether disease burden or public health interventions are genuinely changing over time. As lone star tick ranges expand northward and westward under ongoing climate and ecological change [5,9], states not yet considered endemic for ehrlichiosis, tularemia, or STARI will face the same surveillance blind spots experienced in Oklahoma.

The triangulation approach demonstrated here, integrating archival human surveillance data with publicly available canine serological data and environmental climate data from a One Health perspective, offers a scalable, low-cost model for improving geographic TBD risk assessment using data already in the public domain [6,16,58,60]. A principal contribution of this study lies in the reporting of case counts, incidence rates, and percent positivity separately and combining them in a standardized comparative index at the county level. It differs from existing studies, which have relied largely on aggregate reporting at the state level or on canine sentinel data for LD, by applying the approach to ehrlichiosis, RMSF/SFR, and tularemia across nearly a century of archival records. For clinicians practicing in or near known *A americanum* habitats, including most of Oklahoma, the implication is clear: aggregate state-level TBD data cannot resolve county-level heterogeneity. At this point, canine positivity data can provide a more geographically sensitive signal for TBD exposure in the community, provided such data are interpreted with attention to their limitations, including geolocation by residence rather than exposure, the absence of travel history, and the inability of canine serology

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to distinguish *Ehrlichia* species pathogenic to humans from those that are not [6,16,46,58]. Additionally, treatment arguably should not be withheld pending confirmatory testing in suspected rickettsial or ehrlichial illness, given that outcomes worsen significantly with delayed treatment and that the overlap between these conditions and STARI, RMSF, and tularemia makes differential diagnosis on clinical grounds alone unreliable [4,65]. For public health practitioners and policymakers, this study reinforces the case for federal investment in standardized county-level (and below) TBD reporting and the formal integration of relevant animal health data into human disease surveillance frameworks [13]. Moreover, a One Health perspective, in which human, animal, and environmental health data are routinely integrated, is an operational necessity for understanding and managing the full, and largely undercounted, array and burden of TBD in the United States [14,16,62].

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Generative AI Use

The authors declare the use of generative AI in the research and writing process. Generative AI was not used to generate the original manuscript. After submission, the tools assisted with reviewer-response drafting, manuscript language editing, abstract condensation, terminology and citation formatting, figure-code revision, and source-data spot checks. The authors reviewed and verified the AI-assisted output and take responsibility for the accuracy and integrity of the final paper. According to the GAIDeT (Generative AI Delegation Taxonomy; 2025), the following tasks were delegated to generative AI tools under full human supervision: literature search and systematization; code generation; process automation; creation of algorithms for data analysis; validation; data analysis; visualization; reproducibility testing; text generation; proofreading and editing; summarizing text; reformatting; quality assessment; identification of limitations; recommendations; and publication support. The tools used were Claude (Anthropic; Fable 5) and ChatGPT Codex (OpenAI). Responsibility for the final paper lies entirely with the authors.

Conflicts of Interest

None declared.

Multimedia Appendix 1

Canine ehrlichiosis percent-positive, top Oklahoma counties, 2012-2026. Counties are limited to those with at least 500 total ehrlichiosis tests across the period.
[PNG File , 121 KB-Multimedia Appendix 1]

Multimedia Appendix 2

Human county reported cases, top 15 Oklahoma counties, 2004-2007. Totals combine parsed county rows for ehrlichiosis, Rocky Mountain spotted fever (RMSF)/spotted fever group rickettsiosis (SFR), and tularemia; raw counts are influenced by population and reporting patterns.
[PNG File , 58 KB-Multimedia Appendix 2]

Multimedia Appendix 3

Human county average reported incidence rate, top 15 Oklahoma counties, 2004-2007. Incidence rates are per 100,000 population and are averaged across printed disease-year rate rows for ehrlichiosis, Rocky Mountain spotted fever (RMSF)/spotted fever group rickettsiosis (SFR), and tularemia.
[PNG File , 46 KB-Multimedia Appendix 3]

Multimedia Appendix 4

Canine positive tests, top 15 Oklahoma counties, 2012-2026. Totals combine canine Lyme disease, anaplasmosis, and ehrlichiosis positive tests; 2026 values are year-to-date.
[PNG File , 61 KB-Multimedia Appendix 4]

Multimedia Appendix 5

Tick Season Risk Index by Oklahoma region. Values are an exploratory ordering derived from National Oceanic and Atmospheric Administration (NOAA) 1991-2020 county annual mean temperature (55%) and annual precipitation (45%). The index is not a validated habitat-suitability model, was not ground-truthed, and does not define a threshold for Amblyomma americanum establishment.
[PNG File , 57 KB-Multimedia Appendix 5]

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Abbreviations

AGS: alpha-gal syndrome
CAPC: Companion Animal Parasite Council
CDC: US Centers for Disease Control and Prevention
EM: erythema migrans
EPA: US Environmental Protection Agency
HHS: US Department of Health and Human Services
LD: Lyme disease
NNDSS: National Notifiable Diseases Surveillance System
NOAA: National Oceanic and Atmospheric Administration
PCR: polymerase chain reaction
RMSF: Rocky Mountain spotted fever
SFR: spotted fever group rickettsiosis
STARI: Southern tick-associated rash illness
STROBE: Strengthening the Reporting of Observational Studies in Epidemiology
TBD: tick-borne disease

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