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A Decade of Giardiasis and Cryptosporidiosis: Emerging Trends in Texas Hospitalizations (2012-2021)

Loni A. Taylor
ltaylor@tamu.edu
Texas A&M University
Derek Lemons
Independent Researcher
Kristi L. Allgood
Texas A&M University
Andrew Lam
Texas A&M University
Graciela M. Nogueras-Gonzalez
University of Texas MD Anderson Cancer Center
Timothy A. Erickson
Texas A&M University
Rebecca S.B. Fischer
Texas A&M University

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Authors and affiliations:

Loni A. Taylor[1-3*], Derek Lemons[4], Kristi L. Allgood[1], Andrew Lam[1,2], Graciela M. Nogueras-Gonzalez[5], Timothy A. Erickson[1,2], Rebecca S.B. Fischer[1,2,6]

[1]Department of Epidemiology and Biostatistics, School of Public Health, Texas A&M University, College Station, TX, USA

[2]Laboratory for Emerging and Tropical Disease Research, School of Public Health, Texas A&M University, College Station, TX, USA

[3]Center for Worker Health, College Station, TX, USA

[4]Independent Researcher, Huntsville, TX, USA

[5]Department of Epidemiology, University of Texas MD Anderson Cancer Center, Houston, TX, USA

[6]Division of Tropical Medicine, Department of Pediatrics, Baylor College of Medicine, Houston, TX, USA

***Corresponding author**: Loni A. Taylor ltaylor@tamu.edu

Author email addresses:
Derek Lemons: dereklemons6@gmail.com
Kristi L. Allgood: kallgood@tamu.edu
Andrew Lam: alam7lam@tamu.edu
Graciela M. Nogueras-Gonzalez: gmgonzalez@mdanderson.org
Timothy A. Erickson: timerickson@tamu.edu
Rebecca S.B. Fischer: rfischer@tamu.edu

Abstract

Background

Giardiasis and cryptosporidiosis contribute to a substantial but incompletely characterized burden of hospitalizations in Texas. We evaluated temporal, demographic, and geographic patterns of *Giardia* and *Cryptosporidium* associated hospitalizations to reveal the local epidemiology.

Methods

We analyzed Texas Inpatient Public Use Data File records from 2012–2021 containing ICD-9 or ICD-10 codes for giardiasis or cryptosporidiosis. We described temporal and geographic trends in hospitalizations from 2012–2019 using linear regression and assessed spatial clustering using complementary spatial methods, including Getis-Ord statistic [Gi*]. We analyzed patient characteristics to identify populations at greatest risk for high illness severity and risk of mortality using logistic regression.

Results

A total of 1,776 *Giardia* and 2,330 *Cryptosporidium* associated hospitalizations were identified for the 10-year period. From 2012 to 2019, hospitalization incidence increased significantly for both infections (*Giardia*: $\beta = 0.048$ hospitalizations per 100,000 population per year, $P = 0.005$; *Cryptosporidium*: $\beta = 0.084$ hospitalizations per 100,000 population per year, $P < 0.001$). In 2019, hospitalization incidence peaked and reached 0.84 per 100,000 population for *Giardia* and 1.16 per 100,000 population for *Cryptosporidium*. Spatial analyses identified geographic clustering in south Texas for *Giardia* and north Texas for *Cryptosporidium*. We identified groups

at high clinical risk of high illness severity and mortality risk. Adults aged 65 years and older had more severe illness (*Giardia*: OR 3.78, 95% CI: 2.72–5.28; *Cryptosporidium*: OR 2.61, 95% CI: 1.97–3.48) and higher mortality risk (*Giardia*: OR 6.60, 95% CI: 4.66–9.46; *Cryptosporidium*: OR 5.29, 95% CI: 3.90–7.23); individuals with a history of HIV or drug use also had more severe illness (*Giardia* OR 1.86, 95% CI: 1.48–2.34, P < 0.001; *Cryptosporidium* OR 2.63, 95% CI: 2.16–3.23, P < 0.001) and higher mortality risk (*Giardia* OR 1.62, 95% CI: 1.31–2.01, P < 0.001; *Cryptosporidium* OR 2.17, 95% CI: 1.82–2.58, P < 0.001).

Conclusions

We found temporal, demographic, and geographic variation in hospitalization burden across Texas, identifying populations and regions that may benefit from enhanced surveillance and targeted prevention. Increasing pediatric hospitalizations warrant monitoring, and routine surveillance for giardiasis should be considered.

Keywords: Giardiasis; Cryptosporidiosis; Hospitalization; Texas; Spatial Epidemiology; Disease Surveillance; Public Health Surveillance; Epidemiologic Trends

1. Background

Giardiasis and cryptosporidiosis are parasitic zoonoses of substantial public health importance worldwide. The causative agents, *Giardia duodenalis* (also known as *G. lamblia, G. intestinalis*) and *Cryptosporidium spp.*, infect humans and a wide variety of wild and domestic animal species, with environmental reservoirs, particularly fecally contaminated water sources, serving as important sources of transmission. *G. duodenalis* and *Cryptosporidium spp*. contribute substantially to the nearly 2.4 billion episodes of diarrheal disease occurring globally each year.

Global estimates suggest that they account for approximately 183.8 million and 64.0 million illnesses, respectively, each year [1].

Although most illnesses associated with these pathogens are asymptomatic or self-limiting, severe and life-threatening illnesses do occur. Most cryptosporidiosis illnesses are mild (91.0%), with 8.5% classified as moderate and 0.5% as severe; however, prolonged, severe, or life-threatening disease may occur in immunocompromised individuals, particularly those with impaired T-cell immunity [2–4]. Approximately 20–30% of individuals with giardiasis develop moderate to severe clinical disease. Both giardiasis and cryptosporidiosis can result in substantial morbidity and healthcare utilization in the U.S. National estimates suggest approximately 3,581 giardiasis and 2,725 cryptosporidiosis hospitalizations annually, with associated hospitalization costs of approximately US$34.4 million and US$45.8 million, respectively [5–8]. More recent estimates similarly demonstrate a substantial waterborne disease burden, with approximately 1,100 giardiasis and 1,120 cryptosporidiosis hospitalizations annually attributable specifically to domestically acquired waterborne transmission [9]. Together, these findings highlight the considerable clinical and economic burden associated with these preventable enteric infections.

Despite the endemicity of both parasites in the United States (U.S.) and periodic outbreaks [10,11], their epidemiologic dynamics have received limited attention in recent years, particularly at the local level. Giardiasis and cryptosporidiosis are among the most commonly reported enteric protozoal infections in the U.S., with annual reported incidence rates of approximately 6 and 4 cases per 100,000 persons, respectively; giardiasis incidence has remained

relatively stable in recent years, while cryptosporidiosis reports have increased approximately five-fold over the past two decades [11,12].

National surveillance for giardiasis and cryptosporidiosis, however, provides an incomplete picture. The U.S. Centers for Disease Control and Prevention rely on state-based reporting through the National Notifiable Diseases Surveillance System, but reporting requirements vary by state and disease. As a result, variation in surveillance practices can limit comparisons of disease burden nationally and across local jurisdictions. In Texas, cryptosporidiosis is a reportable condition, whereas giardiasis is not – a barrier to accurate and complete local epidemiologic understanding of two major enteric protozoal infections [13]. Consequently, the epidemiology of giardiasis in Texas remains poorly characterized. Nearby states with required giardiasis reporting provide little insight into the situation in Texas: Louisiana reported 5.5 cases per 100,000 population in 2019, whereas Arizona reported 2.0 cases per 100,000 population [11]. The incomplete reporting in Texas hinders public health action.

Passive surveillance through routine public health reporting is important for monitoring changing epidemiology, defining temporal trends and geographic hotspots, and detecting outbreaks. At the state level, public health agencies in Texas are operating with incomplete epidemiologic intelligence on *Giardia* and *Cryptosporidium* infections, which challenges efforts to develop targeted risk-management and disease-control strategies. This limitation may reduce clinical awareness for detection and diagnosis, as well as public-facing education on personal risk avoidance. In the absence of robust passive surveillance, information gleaned from individuals hospitalized with severe disease can provide insight into temporal and geographic patterns of

clinically significant disease and identify populations experiencing severe illness. Leveraging a robust data repository on hospitalizations in Texas, we sought to provide a local context for giardiasis and cryptosporidiosis over a 10-year period. Our objectives were to characterize hospitalization incidence and epidemiologic trends associated with giardiasis and cryptosporidiosis and identify populations at highest risk of illness severity and risk of mortality to reveal remaining opportunities for enhanced clinical recognition and public health action.

2. Methods

2.1 Data Source and Study Population

We analyzed hospital discharge records from the Texas Inpatient Public Use Data File (PUDF) for 2012–2021. Records with an ICD-9-CM diagnosis code for giardiasis (007.1; 2012–September 2015) or an ICD-10-CM diagnosis code (A07.1; October 2015–2021) were identified. Similarly, records with an ICD-9-CM diagnosis code for cryptosporidiosis (007.4; 2012–September 2015) or an ICD-10-CM diagnosis code (A07.2; October 2015–2021) were identified. All available diagnosis fields were screened for the relevant ICD codes, regardless of diagnosis position. These cohorts were analyzed separately. Potential co-infections were assessed by cross-referencing diagnosis fields in each dataset for ICD-9 and ICD-10 codes corresponding to the alternate infection, including the admitting diagnosis, principal diagnosis, and up to 24 additional diagnosis fields.

Statistical analyses were conducted in R (version 4.5.3; R Core Team, 2026) [14], with data management and statistical analysis performed using the packages described in Additional file 1 [15,16]. There were a total of 1,776 hospitalization records containing diagnosis codes for

Giardia infection and 2,330 for *Cryptosporidium* infection in Texas during the study period. For the purposes of estimating population incidence of hospitalizations in Texas, we excluded 91 *Giardia* records and 89 *Cryptosporidium* records on the basis that the patients were residents outside of Texas. Thus, the study population for that analysis is 1,685 *Giardia*-associated hospitalizations and 2,241 *Cryptosporidium*-associated hospitalizations.

2.2 Data Handling

Where possible, we used variables in the form recorded in the PUDF. Sex was categorized as male, female, or not specified. Records with missing values for sex or race-ethnicity were retained in the analyses to maximize sample size. HDU status, defined as drug or alcohol use or an HIV diagnosis, and age were recorded together as a single categorical variable in the PUDF [17]. This variable included 27 categories, with 22 categories representing age ranges for patients without HDU and only 5 categories representing age ranges for patients with HDU. To further explore the effects of age and HDU on hospitalization, we created four variables from the original, combined age-HDU variable: (1) a dichotomous age variable (0–44 vs. ≥45 years) for all patients; (2) a dichotomous HDU variable (HDU vs. non-HDU) that included all patients; (3) a new combined age-HDU variable with four groups: 0–44+non-HDU (age 0-44 years *and* no HDU), ≥45/non-HDU (age ≥45 *and* no HDU), 0–44/HDU (age 0-44 years *and HDU*), and ≥45/HDU (age ≥45 years *and* HDU) that included all patients; and (4) a five-category age variable (0–4, 5–14, 15–44, 45–64, and ≥65 years) for non-HDU patients since more granular age information was available for this sub-population.

The PUDF reports race and ethnicity as separate variables. For this analysis, we combined them into a single race-ethnicity variable with five categories: non-Hispanic White, Hispanic, non-Hispanic Black, non-Hispanic Other, and Not Specified. The non-Hispanic Other category

included individuals identified as a race other than White or Black, as well as those identified as multiracial.

Illness severity and risk of mortality were based on the All Patient Refined Diagnosis Related Group (APR-DRG) classifications provided in the PUDF, originally categorized as minor, moderate, major, or extreme. We created a dichotomized variable for each as low (minor or moderate) and high (major or extreme) for analysis.

Categorical variables are presented as frequencies (n) and percentages (%), whereas continuous variables (e.g., hospital charges [USD]) are summarized using medians and interquartile ranges (IQR).

2.3 Incidence Estimation and Temporospatial Trends Analysis

Annual hospitalization incidence per 100,000 population was calculated using county-level American Community Survey (ACS) 5-Year population estimates for 2012–2021. County estimates [18] were aggregated to Texas Public Health Regions (PHRs) [19] using the Texas Department of State Health Services county-to-region crosswalk. Cumulative incidence was calculated using total hospitalizations and corresponding cumulative population denominators.

Temporal trends in hospitalization incidence were assessed using linear regression from 2012–2019, overall and by sex, HDU status, age group, race-ethnicity, and PHR. Years 2020–2021 were excluded because of COVID-19-related disruptions to healthcare utilization [20,21]. Slopes (β) represented annual changes in hospitalization incidence per 100,000 population. HDU patients were excluded from age-stratified incidence analyses because appropriate population denominators were unavailable but were retained in severity and mortality models.

Spatial clustering was evaluated at the PHR level using cumulative 2012–2019 hospitalization incidence and Global Moran's I, Getis-Ord Gi*, and Kulldorff spatial scan statistics (Additional file 1: Supplementary Methods SM1).

2.4 Illness Severity and Mortality Risk Analysis

Logistic regression was used to model demographic characteristics associated with increased odds of high illness severity and high mortality risk, separately using the dichotomous outcomes described above. Unadjusted odds ratios (uORs), 95% Wald confidence intervals (CIs), and P values were estimated for each predictor relative to its designated reference category. In the illness severity model, the outcome variable was categorized as high (major or extreme) versus low (minor or moderate) illness severity. Similarly, in the mortality risk model, the outcome variable was classified as high (major or extreme) versus low (minor or moderate) mortality risk. Statistical significance was defined as $P < 0.05$. Sensitivity analyses are described in Additional file 1: Supplementary Methods (SM2).

3. Results

3.1 Overall Findings

We identified 1,776 *Giardia* and 2,330 *Cryptosporidium* associated hospitalizations during the study period (2012–2021) (Table 1 and Additional file 1: Table S1), including 91 hospitalizations with diagnostic codes for both infections. Males accounted for the largest proportion of *Giardia* associated hospitalizations (722, 40.7%), whereas females accounted for the largest proportion of *Cryptosporidium* associated hospitalizations (850, 36.5%) (Table 1). A high proportion of hospitalizations were among individuals with a history of HIV or drug use (HDU): 34.9% (812) of *Cryptosporidium* associated hospitalizations and 26.0% (461) of *Giardia* associated

hospitalizations (Table 1). Hospitalizations were common among older age groups: most *Giardia*-associated hospitalizations were among adults aged ≥65 years (369, 20.8%) or 45–64 years (356, 20.1%) (Table 1). Similarly, the largest age-group proportions of *Cryptosporidium*-associated hospitalizations were among adults aged ≥65 years (466, 20.0%) or 45–64 years (381, 16.4%), with adults aged 15–44 years (375, 16.1%) also accounting for a high proportion (Table 1). Median hospital charges increased over the study period for both infections (Table 1). For *Giardia*-associated hospitalizations, median hospital charges increased from $33,724.35 (IQR: $18,833.19–$69,317.97) in 2012 to $50,499.50 (IQR: $31,654.63–$93,021.98) in 2021. For *Cryptosporidium*-associated hospitalizations, median hospital charges increased from $29,364.20 (IQR: $19,009.90–$56,836.15) in 2012 to $55,937.51 (IQR: $33,748.34–$112,145.59) in 2021.

3.2 Temporal Trends

From 2012 to 2019, the incidence of hospitalizations associated with giardiasis and cryptosporidiosis in Texas increased (Figures 1 and Additional file 1: Figure S1 and Table S1). *Giardia*-associated hospitalizations increased from 0.56 per 100,000 population in 2012 to 0.84 per 100,000 population in 2019 ($\beta = 0.048$ per 100,000 population/year, 95% CI: 0.021–0.075, $P = 0.0049$), and *Cryptosporidium*-associated hospitalizations increased from 0.60 per 100,000 population in 2012 to 1.16 per 100,000 population in 2019 ($\beta = 0.084$ per 100,000 population/year, 95% CI: 0.065–0.104, $P < 0.0001$) (Figures 1 and Additional file 1: Figure S1 and Table S1).

Significant increases in hospitalization incidence were observed among both males and females for each infection (Additional file 1: Table S1 and Figures S2-4). For *Giardia*, hospitalization incidence increased among males ($\beta = 0.054$ per 100,000 population/year, 95% CI: 0.026–0.082, $P = 0.0032$) and females ($\beta = 0.034$ per 100,000 population/year, 95% CI: 0.009–0.059, P =

0.0158). Similarly, *Cryptosporidium* associated hospitalization incidence increased among males (β = 0.068 per 100,000 population/year, 95% CI: 0.046–0.090, P = 0.0003) and females (β = 0.069 per 100,000 population/year, 95% CI: 0.034–0.105, P = 0.0031). Among children aged 0–4 years, increases were observed for both *Giardia* (β = 0.185 per 100,000 population/year, 95% CI: 0.098–0.272, P = 0.0020) and *Cryptosporidium* (β = 0.250 per 100,000 population/year, 95% CI: 0.169–0.331, P = 0.0003) (Additional file 1: Table S1 and Figures S5-7). While *Cryptosporidium*-associated hospitalization incidence increased across most racial/ethnic groups, significant increases in *Giardia*-associated hospitalization incidence were observed only among Hispanic and non-Hispanic White individuals (Additional file 1: Table S1 and Figures S8-10).

3.3 Geospatial Trends

For *Giardia* hospitalizations, Global Moran's I indicated significant positive spatial autocorrelation across the 11 PHRs (I = 0.304, P = 0.027; Additional file 1: Table S2). Local Gi* analysis did not identify any PHRs as statistically significant hot or cold spots, although PHRs 8 and 11 had the largest positive Gi* Z-scores (PHR 8: Z = 2.17, P = 0.130; PHR 11: Z = 2.09, P = 0.092). The Kulldorff spatial scan identified PHRs 8 and 11 as the most likely cluster (388 observed, 251 expected; SMR = 1.54; P = 0.001; Additional file 1: Table S3). Aggregate Gi* results are presented in Figure 3, with exploratory annual results shown in Figure 4.

For *Cryptosporidium* hospitalizations, Global Moran's I did not identify significant spatial autocorrelation across PHRs (I = 0.097, P = 0.187; Additional file 1: Table S2). Local Gi* analysis identified PHR 1 as a nominally significant hot spot (Z = 2.49, P = 0.044), which was interpreted as exploratory. The Kulldorff spatial scan identified PHRs 1, 2, and 9 as the most likely cluster (237 observed, 138 expected; SMR = 1.71; P = 0.001; Additional file 1: Table S3). Aggregate and annual Gi* results are presented in Figures 3 and 4, respectively.

3.4 Temporospatial Trends

There was geographic heterogeneity in temporal trends (Figure 2). In PHR 11, hospitalization incidence increased for both *Giardia* (β = 0.271 per 100,000 population/year, 95% CI: 0.158–0.384, P = 0.0011) and *Cryptosporidium* (β = 0.223 per 100,000 population/year, 95% CI: 0.103–0.343, P = 0.0039) (Additional file 1: Table S1 and Figure S1). For *Cryptosporidium*, but not *Giardia*, hospitalization incidence also increased in PHR 1 (β = 0.243 per 100,000 population/year, 95% CI: 0.071–0.415, P = 0.0136) and PHR 3 (β = 0.101 per 100,000 population/year, 95% CI: 0.023–0.179, P = 0.0191) (Additional file 1: Table S1 and Figure S1). Within PHR 11, significant increases for both infections were also observed among children aged 0–4 years (Additional file 1: Table S1 and Figures S6-7), as well as among non-Hispanic White individuals for *Giardia* and non-Hispanic individuals of another race-ethnicity for *Cryptosporidium* (Additional file 1: Table S1 and Figures S9-10).

3.5 Demographic Associations with Illness Severity and Risk of Mortality

Across both study groups, older age, history of HDU, and non-Hispanic Black race-ethnicity were associated with greater odds of high illness severity and high mortality risk (Figures 5-8 and Additional file 1: Tables S4-5).

Age was one of the strongest predictors of high illness severity (Figures 5-6 and Additional file 1: Table S4) and high mortality risk (Figures 7-8 and Additional file 1: Table S5). Adults aged 65 years and older had significantly greater odds of high severity for both *Giardia* (uOR = 3.78, 95% CI: 2.72–5.28) and *Cryptosporidium* (uOR = 2.61, 95% CI: 1.97–3.48), compared to the referent age group, 15-44 years. Similarly, adults aged 65 years and older had greater odds of

high mortality risk for both *Giardia* (uOR = 6.60, 95% CI: 4.66–9.46) and *Cryptosporidium* (uOR = 5.29, 95% CI: 3.90–7.23).

Higher illness severity was also observed among individuals with a history of HDU, compared to those without, both for *Giardia* (uOR = 1.86, 95% CI: 1.48–2.34) and, to a greater extent, *Cryptosporidium* (uOR = 2.63, 95% CI: 2.16–3.23). This relationship was mirrored by higher mortality risk for *Giardia* (uOR = 1.62, 95% CI: 1.31–2.01) and, again even more so, with *Cryptosporidium* (uOR = 2.17, 95% CI: 1.82–2.58).

Combining these main risk groups, all had significantly greater odds of high illness severity and high mortality risk than patients aged 0–44 years without a history of HDU, with highest illness severity among adults aged 45 years and older who also had a history of HDU for both *Giardia* (uOR = 4.27, 95% CI: 2.91–6.38) and *Cryptosporidium* (uOR = 5.35, 95% CI: 3.81–7.64). This same group also had the higher mortality risk (*Giardia*: uOR = 4.84, 95% CI: 3.32–7.08; *Cryptosporidium*: uOR = 6.71, 95% CI: 4.96–9.12).

Finally, with respect to differences in risk by race-ethnicity, the non-Hispanic Black group had double the odds of high illness severity for both *Giardia* (uOR = 1.97, 95% CI: 1.45–2.70) and *Cryptosporidium* (uOR = 1.97, 95% CI: 1.53–2.54), compared to the non-Hispanic White referent group. Conversely, the non-Hispanic Black group had higher odds of high mortality risk for *Giardia* (uOR = 1.66, 95% CI: 1.25–2.20) and *Cryptosporidium* (uOR = 1.48, 95% CI: 1.19–1.84), though Hispanic was not identified as a separate risk group.

4. Discussion

In this decade-long analysis of *Giardia* and *Cryptosporidium* associated hospitalizations in Texas, we identified increasing hospitalization incidence, distinct geographic patterns, and populations at increased risk for high illness severity and risk of mortality. These findings complement national surveillance by providing insight into severe disease requiring hospitalization and may inform surveillance, prevention, and clinical recognition of high-risk populations.

In contrast to national surveillance patterns [11,12], we report increasing hospitalization incidence in Texas for both giardiasis and cryptosporidiosis during 2012–2019, with a more pronounced increase observed for cryptosporidiosis. This pattern was observed for both sexes, selected racial and ethnic populations and was particularly pronounced among children aged <5 years. Although national surveillance has not demonstrated comparable increases in reported *Giardia* and *Cryptosporidium* infections, hospitalized individuals reflect a clinically distinct subset of disease, typically characterized by greater severity or higher risk of complication [11,12]. The factors underlying the increases we observed are not made evident by our analyses but are likely multifactorial and may include increased environmental risk via contaminated drinking or recreational water, more frequent contact with infected animals, person-to-person transmission, foodborne exposure, population growth, and healthcare-seeking behavior [22–25].

Recent analyses of canine *Giardia* infections in Texas also identified substantial geographic variation, including high cumulative test positivity and an increasing temporal trend in Cameron County, within the South Texas region (PHR 11) where increased human *Giardia* associated hospitalization burden was observed in the present study [26]. Although these ecological findings do not establish zoonotic transmission, overlapping patterns in human and companion animal populations support a One Health approach to investigating shared environmental,

311 socioeconomic, and animal-related drivers of *Giardia* transmission in Texas. Our data may also,
312 in part, reflect healthcare access and utilization, as hospitalization risk and outcomes may vary
313 with patient age, underlying conditions, and clinical presentation, while changes over time may
314 additionally reflect improvements in diagnostic testing and clinical awareness and recognition
315 [27]. Given the uncertainties why hospitalizations are on the rise, our findings provide a
316 compelling narrative that reflects an increasing burden of severe, hospitalized disease affecting
317 broad population groups, emphasizing the importance of strengthening surveillance and
318 investigation while simultaneously seeking improved understanding of the drivers of severe
319 giardiasis and cryptosporidiosis.

320 It is important to remember that since most *Giardia* and *Cryptosporidium* infections are mild, our
321 data can be interpreted as representing only cases in the severe end of the clinical spectrum (or
322 those for which complications were anticipated); our data must not be interpreted as infection
323 incidence. National surveillance data indicate that young children experience the highest burden
324 of reported giardiasis and cryptosporidiosis infections [11,12]. In contrast, most patients in our
325 hospital analysis were adults. Thus, pediatric infections resulting in mild disease are likely
326 substantially underrepresented in our hospitalization data. Despite this likely
327 underrepresentation, children <5 years exhibited the most pronounced increases in
328 hospitalization incidence. This is notable given the potential consequences of severe or recurrent
329 enteric infection in children, including malnutrition, growth faltering, and adverse developmental
330 outcomes [6,28,29].

331 Hospitalization data cannot directly estimate the risk of infection or hospitalization among those
332 infected, nor determine how these risks vary across subpopulations. Factors contributing to the
333 increasing number of hospitalizations among young children in Texas remain uncertain, but since

infections arise mainly from environmental contamination, prevention efforts focused on settings where children may be preferentially exposed would be strategic, including childcare facilities, splash pads, recreational water venues, drinking water systems, and environments involving contact with infected animals [22,24].

Adults in our study, particularly older adults, experienced more severe and life-threatening illnesses, consistent with what would be expected with age-related physiologic changes [30–33]. This could also reflect differences in hospitalization practices, underlying susceptibility, and the clinical course of disease across age groups [34,35]. However, this relationship was complicated by being classified as having a history of HIV infection or drug use (HDU). The nature of the data available for our HDU subpopulation limited our ability to examine this relationship beyond two large age groupings, <45 years and 45+ years. Furthermore, we cannot distinguish HIV-infected individuals in this group, let alone viral suppression or immune parameters. Despite these limitations, our findings identify both older age and a history of HDU as important markers of clinical risk. Adults aged ≥45 years with a history of HDU had particularly high odds of severe illness for both infections, while older age was strongly associated with mortality risk regardless of HDU status [2,27,36,37]. Comparable information on severe giardiasis is, again, limited, but our findings demonstrate a similar pattern. These relationships are less well established for HIV-uninfected substance users, but limited data suggest they are at heightened risk for infection and consequential disease, owing to behavioral, environmental, and physiologic consequences [38–40]. These high-risk populations may benefit from heightened clinical suspicion, early diagnostic evaluation, and timely treatment when presenting with diarrheal illnesses consistent with giardiasis and cryptosporidiosis, as well as research to pinpoint risk in these complicated and sometimes overlapping risk groups.

The burden of giardiasis and cryptosporidiosis is influenced by complex social and environmental factors. Although we found that hospitalized, non-Hispanic Black individuals also were at risk of more severe and life-threatening conditions, the literature is scant on factors contributing to racial and ethnic disparities in severe parasitic gastroenteritis. Poverty and other social inequities are intricately tied to structural influences on exposure sources (e.g., contaminated food, water, and environment), proximity and frequency of exposures, and availability of resources required to avoid exposure. Malnutrition, particularly in children, aggravates disease severity. At the same time, healthcare access and utilization are important considerations, since delayed diagnosis can translate to prolonged or complicated disease for some individuals. Although our data did not provide sufficient information to ascertain socioeconomic status of individual patients or specific barriers, broader evidence on inequities of healthcare access, underlying comorbidities, socioeconomic conditions, environmental exposures, and other social determinants of health can contribute to what we observed for these parasitic infections [41]. Further investigation is needed to determine whether disparities in exposure, delayed diagnosis, access to care, or other structural factors contribute to the elevated risk observed in this group.

Distinct geographic clustering of *Giardia* and *Cryptosporidium* associated hospitalizations was observed across Texas. For *Giardia*, significant global spatial autocorrelation was detected, with PHRs 8 and 11, encompassing the lower Rio Grande Valley and South Texas, identified as the most likely cluster. Although local Gi* analysis did not identify a statistically significant hot spot, these regions had the largest positive Gi* Z-scores, providing complementary evidence of elevated hospitalization burden. The lower Rio Grande Valley is characterized by extensive cross-border movement, substantial agricultural activity, and variable water and wastewater

infrastructure in some communities, which may contribute to exposure to enteric pathogens. Domestic and companion animals may also serve as sentinels of shared environmental and zoonotic risks, as previous studies have documented infectious disease exposures and zoonotic transmission cycles among dogs and cats in this region [26,42,43]. In contrast, *Cryptosporidium* exhibited geographically concentrated rather than global spatial clustering, with elevated hospitalization burden identified across West Texas and the Panhandle (PHRs 1, 2, and 9). These regions include extensive cattle and dairy production, and cattle are well-recognized reservoirs of *Cryptosporidium*. Livestock density, occupational agricultural exposures, agricultural wastewater, and environmental contamination may therefore contribute to regional transmission [44,45]. Future studies integrating environmental and animal sampling, exposure assessment, genomic epidemiology, and transmission modeling could help identify regional drivers of infection and severe disease.

Beyond the clinical burden, the economic burden of each hospital stay is daunting. Hospital charges were substantially higher at the end of the study period, reaching approximately $50,000 or more per hospitalization. Although our records do not reflect insurance payments, out-of-pocket costs, or unpaid costs absorbed by facilities, the substantial increase demonstrates a broader impact of infections, beyond a mild, self-limiting acute illness to severe, life-threatening disease and the resulting growing economic and healthcare resource burden [46,47]. Given that a substantial proportion of patients were older or had complex histories (e.g., HDU), alongside an increasing hospitalization incidence among young children, the economic burden stands to impact already vulnerable populations.

The nature of the administrative dataset we leveraged does warrant some important final considerations. First, these hospital discharge data reflect diagnoses associated with

hospitalization but do not establish the primary reason for presentation or admission. Clinical and laboratory records are not part of these PUDF records, meaning that laboratory confirmation is presumed but is not directly verifiable; we also cannot rule out parasite detection as an incidental or concomitant finding. For these reasons, we refer to our results as hospitalizations associated with *Giardia* and *Cryptosporidium* infection, rather than attributable to them. Even if not the drivers of admission, gastrointestinal parasites can aggravate other illnesses, cause dehydration or malabsorption, complicate treatment, and transmit to others, making them important in our analysis [28]. Second, the PUDF enumerates hospital discharge events rather than unique patients and lacks identifiers that could be used to link records. This means that individuals with repeat hospitalizations would be represented each time. Unfortunately, this precludes assessment of recurrent infection, readmission due to prolonged disease, or incomplete treatment effectiveness. Because repeat hospitalizations cannot be identified, we cannot determine the extent to which recurrent admissions contributed to the observed hospitalization burden or temporal trends. Accordingly, rates should be interpreted as hospitalization-event incidence rather than incidence among unique individuals. With these important considerations in mind, we stress that our findings provide an important component of understanding the epidemiology of human giardiasis and cryptosporidiosis in Texas, and complement public health surveillance data, which remain limited in Texas.

These hospitalization data are descriptive and cannot establish causality or determine whether observed trends reflect changes in transmission, reservoirs, susceptibility, or other factors. Advances in multiplex PCR have improved the accuracy and availability of testing for gastrointestinal pathogens [23] and changing diagnostic practices may have contributed to the observed trends. However, we cannot distinguish changes in disease burden from changes in

detection, healthcare utilization, or other factors. Nevertheless, our findings identify populations and geographic areas that warrant further investigation and targeted public health attention.

Strengthening surveillance in Texas, including adding giardiasis to existing surveillance efforts, could improve outbreak detection and characterization of changing epidemiologic patterns. Improved surveillance could also inform targeted investigations of environmental reservoirs and transmission pathways and support evidence-based strategies to reduce infections and associated hospitalizations.

5. Conclusions

Our analysis characterized a decade of *Giardia* and *Cryptosporidium* associated hospitalizations in Texas, identifying increasing hospitalization incidence, particularly among young children, and distinct geographic clustering. Among hospitalized patients, older age and HDU status were important markers of high illness severity and high mortality risk. Although these data capture only the more severe spectrum of disease, the increasing hospitalization burden and associated costs underscore the value of strengthened surveillance and prevention. These findings provide insight into severe protozoal gastroenteritis and highlight the need for continued investigation of the environmental, behavioral, and clinical factors underlying severe disease.

Supplementary information

Additional file 1 (.docx): Supplementary Methods, Tables, and Figures.

Supplementary Methods SM1–SM2; Tables S1–S5; and Figures S1–S10 supporting the temporal, spatial, and demographic analyses presented in the main manuscript.

Abbreviations

ACS: American Community Survey; APR-DRG: All Patient Refined Diagnosis Related Group; CI: confidence interval; HDU: history of HIV or drug use; IQR: interquartile range; PHR: Public Health Region; PUDF: Texas Inpatient Public Use Data File; SMR: standardized morbidity ratio; uOR: unadjusted odds ratio.

Declarations

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Availability of data and materials

The Texas Inpatient Public Use Data Files analyzed during this study are available from the Texas Department of State Health Services (DSHS/THCIC), subject to applicable data-use

agreements and request procedures. The authors are not permitted to redistribute the underlying patient-level data.

Authors' contributions

L.A.T.: Conceptualization, Methodology, Investigation, Project administration, Supervision, Visualization, Writing – original draft, Writing – review & editing. D.L.: Formal analysis, Methodology, Software, Writing – review & editing. K.L.A.: Writing – review & editing. A.L.: Data curation, Writing – original draft. G.M.N.-G.: Formal analysis, Methodology, Validation, Writing – review & editing. T.A.E.: Writing – review & editing. R.S.B.F.: Conceptualization, Supervision, Writing – review & editing.

Ethics approval and consent to participate

The Texas A&M University Institutional Review Board determined that this study does not constitute human subjects research (STUDY2026-1277).

Consent for publication

Not applicable

Competing interests

The authors declare that they have no competing interests.

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611

Tables

Table 1: Characteristics of *Giardia*- and *Cryptosporidium*- Associated Hospitalizations in Texas, 2012-2021

Variable	Categories	*Giardia* N (%)	*Cryptosporidium* N (%)
Number of Hospitalizations	2012	144	151
	2013	133	163
	2014	125	184
	2015	139	228
	2016	192	226
	2017	204	296
	2018	220	309
	2019	250	343
	2020	162	204
	2021	207	226
	Total	1776	2330
Incidence (per 100,000)	2012	0.56	0.60
	2013	0.51	0.62
	2014	0.46	0.68
	2015	0.51	0.83
	2016	0.68	0.81
	2017	0.70	1.05
	2018	0.74	1.03
	2019	0.84	1.16
	2020	0.54	0.69
	2021	0.62	0.73
	Total	0.62	0.83
Sex	Male	722 (40.7)	662 (28.4)
	Female	588 (33.1)	850 (36.5)

Variable	Categories	*Giardia* N (%)	*Cryptosporidium* N (%)
	Not Specified	466 (26.2)	818 (35.1)
History of HIV or Drug Use (HDU)	No	1315 (74.0)	1518 (65.2)
	Yes	461 (26.0)	812 (34.9)
Age[a] (years)	0-44	886 (50.0)	1192 (51.2)
	45+	890 (50.1)	1138 (48.8)
Age (years)	0-44 & HDU	296 (16.7)	521 (22.4)
	45+ & HDU	165 (9.3)	291 (12.5)
	0-44 & non-HDU	590 (33.2)	671 (28.8)
	45+ & non-HDU	725 (40.8)	847 (36.4)
Age[b] (years)	0-4	167 (9.4)	152 (6.5)
	5-14	125 (7.0)	144 (6.2)
	15-44	298 (16.8)	375 (16.1)
	45-64	356 (20.1)	381 (16.4)
	65+	369 (20.8)	466 (20.0)
Race-Ethnicity	Non-Hispanic White	776 (43.7)	1024 (44.0)
	Hispanic	604 (34.0)	700 (30.0)
	Non-Hispanic Black	262 (14.8)	476 (20.4)
	Another Non-Hispanic race-ethnicity	131 (7.4)	126 (5.4)
	Not Specified	3 (0.2)	4 (0.2)
Illness Severity	Minor	328 (18.5)	377 (16.2)
	Moderate	360 (20.3)	385 (16.5)
	Major	725 (40.8)	1075 (46.1)
	Extreme	361 (20.3)	489 (21.0)
	Not Specified	2 (0.1)	4 (0.2)
Mortality Risk	Minor	626 (35.3)	603 (25.8)
	Moderate	491 (27.7)	727 (31.2)
	Major	434 (24.4)	708 (30.4)

Variable	Categories	*Giardia* N (%)	*Cryptosporidium* N (%)
	Extreme	223 (12.6)	288 (12.4)
	Not Specified	2 (0.1)	4 (0.2)
Charges, per hospital stay (USD$)	**Year**	**Median (IQR)**	**Median (IQR)**
	2012	33724.35 (18833.19 - 69317.97)	29364.20 (19009.90, 56836.15)
	2013	33936.07 (19706.89, 68185.00)	30507.36 (18090.53, 63404.11)
	2014	34769.35 (21096.50, 69572.00)	37859.22 (21315.70, 75033.75)
	2015	27100.27 (16115.37, 61324.00)	32185.50 (22522.04, 63759.15)
	2016	41502.15 (23810.45, 85197.74)	33361.56 (19524.56, 59528.40)
	2017	38326.80 (21612.75, 76230.75)	42767.92 (24883.54, 74276.65)
	2018	39125.92 (21705.24, 72752.33)	43429.00 (26487.10, 85426.00)
	2019	43400.30 (20688.20, 89297.00)	45454.02 (27451.54, 85659.50)
	2020	52174.67 (26715.94, 115677.22)	51470.89 (28343.59, 87188.44)
	2021	50499.50 (31654.63, 93021.98)	55937.51 (33748.34, 112145.59)
	All Years	39375.25 (22123.18, 80095.06)	40792.74 (23996.94, 78507.75)

[a]Including individuals with history of HIV or Drug Use (*i.e.,* both HDU and non-HDU)

[b]Excluding individuals with history of HIV or Drug Use (*i.e.,* non-HDU only)

615

616

Figures

Figure 1: Incidence of *Giardia* and *Cryptosporidium* Hospitalizations in Texas, 2012-2019

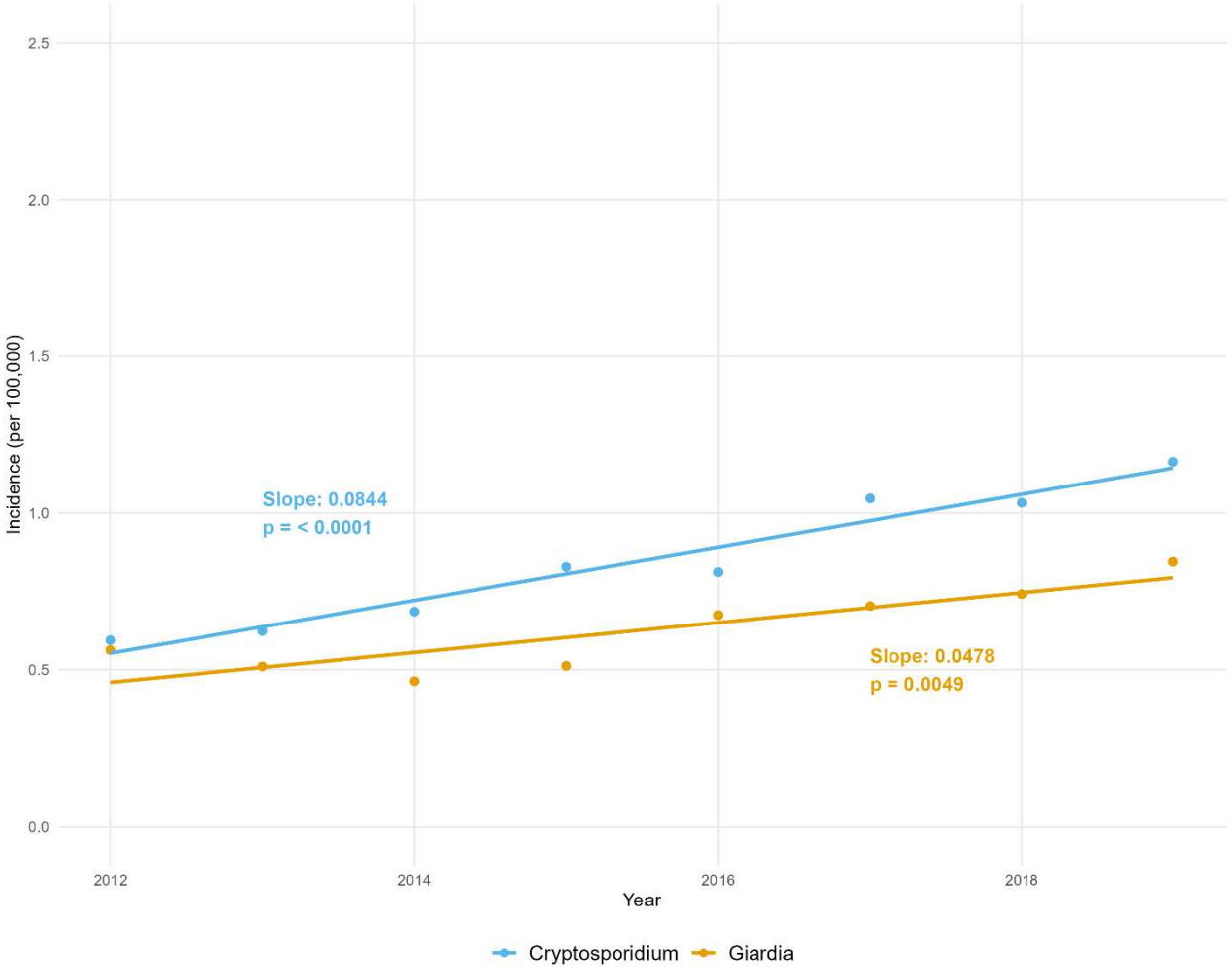


Figure 2: Incidence of *Giardia* and *Cryptosporidium* Hospitalizations in Texas, by Public Health Region, 2012-2019

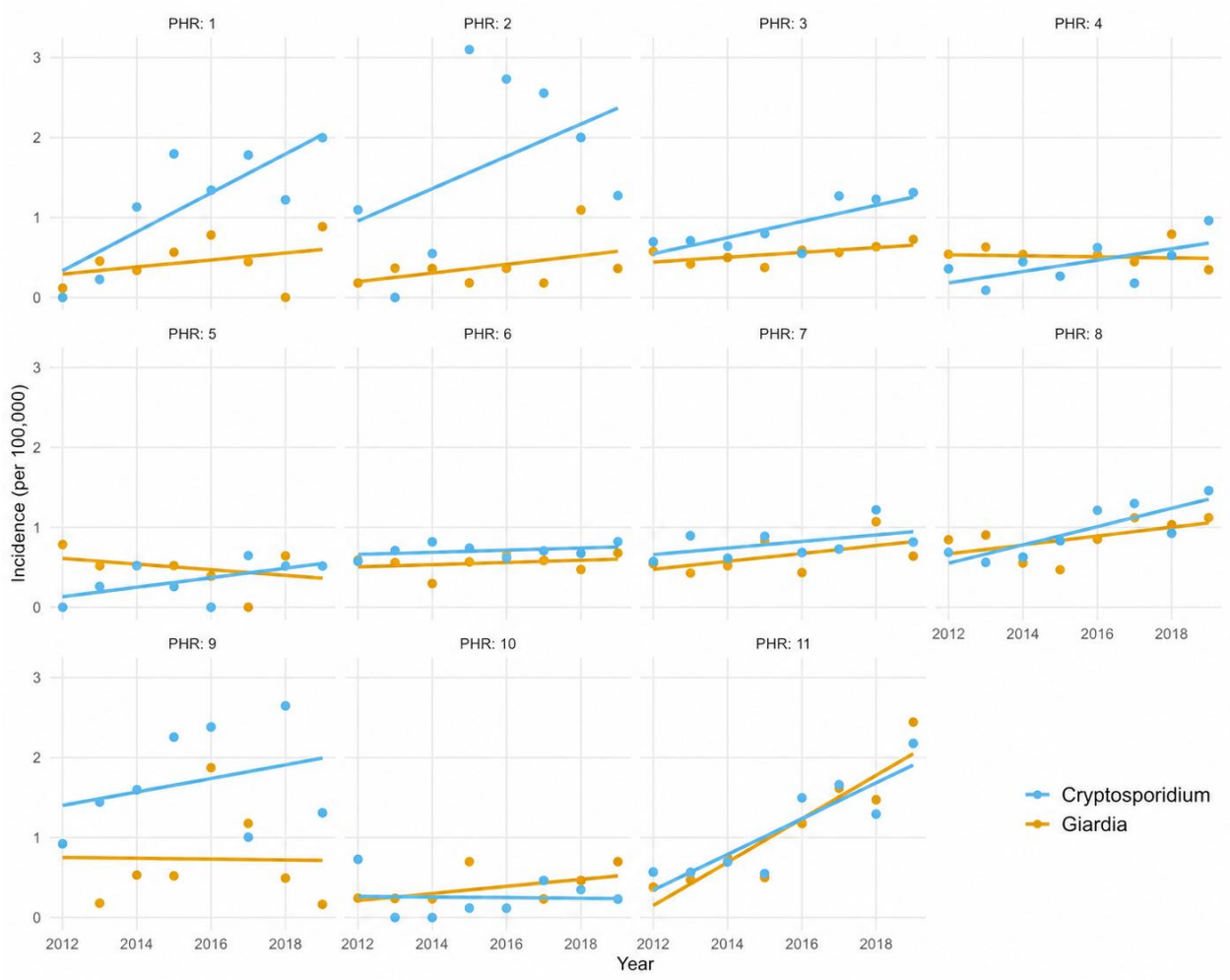


Figure 3: Hotspot analysis of (a) *Giardia* and (b) *Cryptosporidium* hospitalizations in Texas, 2012-2019

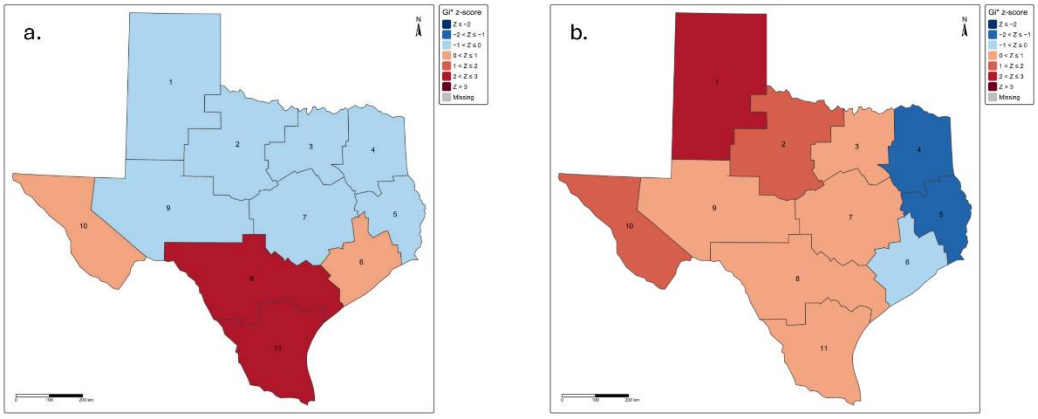
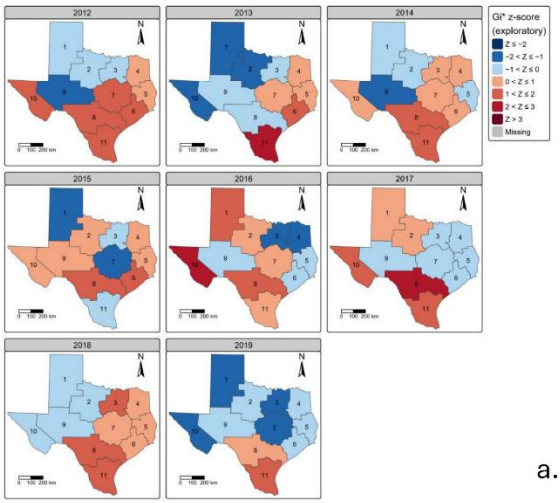
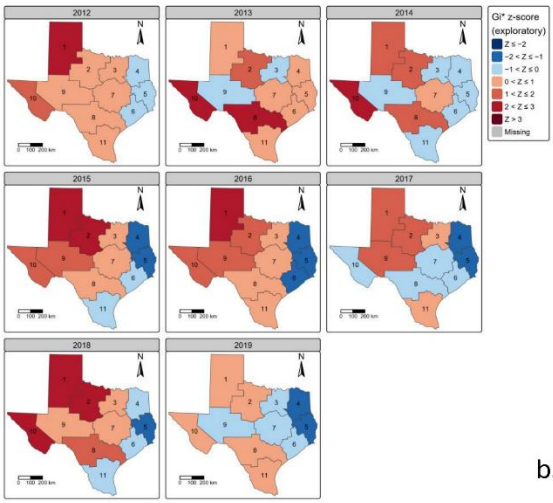


Figure 4: (a) *Giardia* and (b) *Cryptosporidium* Hot/Cold Spots by PHR by year



a.



b.

Figure 5: Characteristics Associated with High Illness Severity in *Giardia* in Texas, 2012-2021

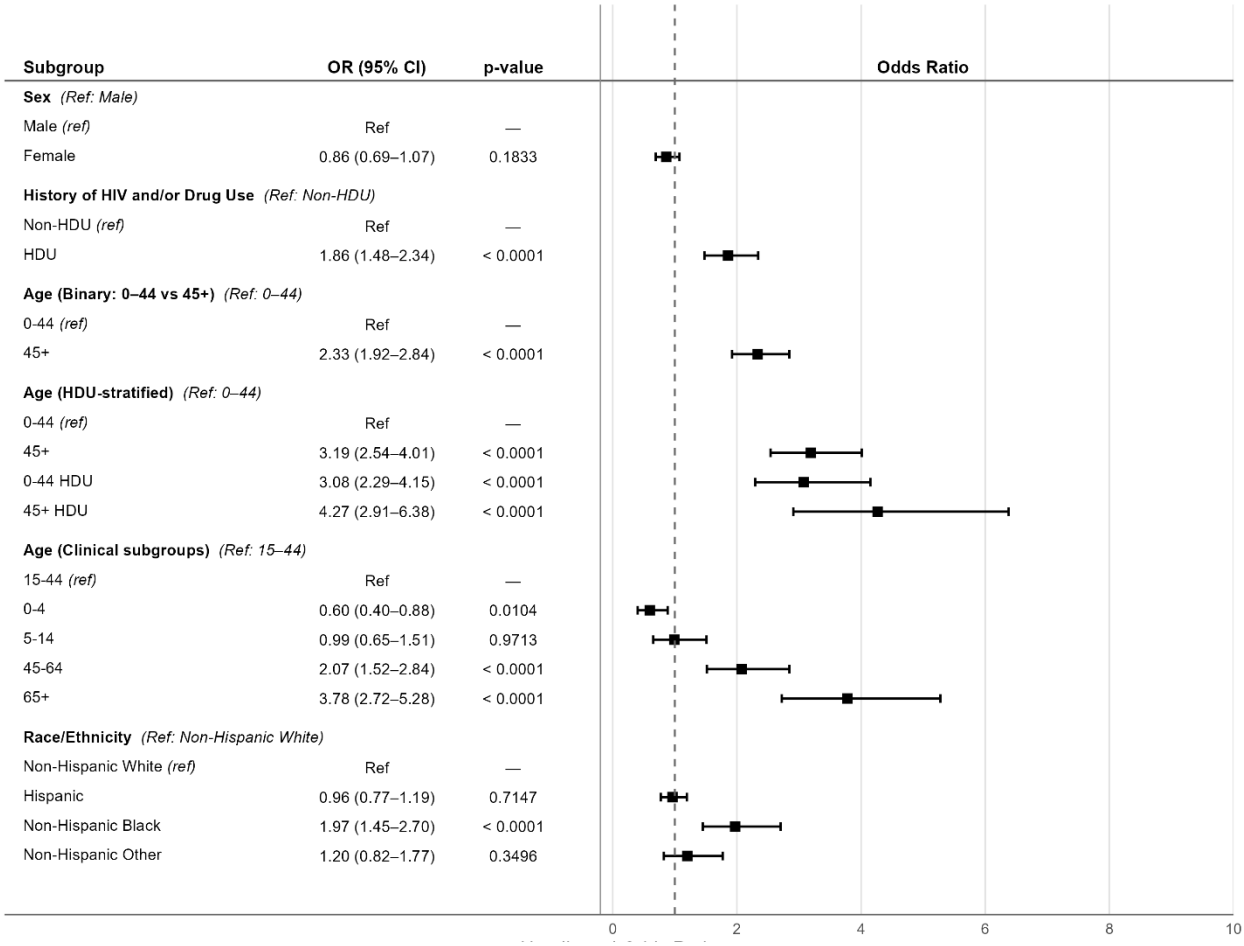


Figure 6: Characteristics Associated with High Illness Severity in *Cryptosporidium* in Texas, 2012-2021

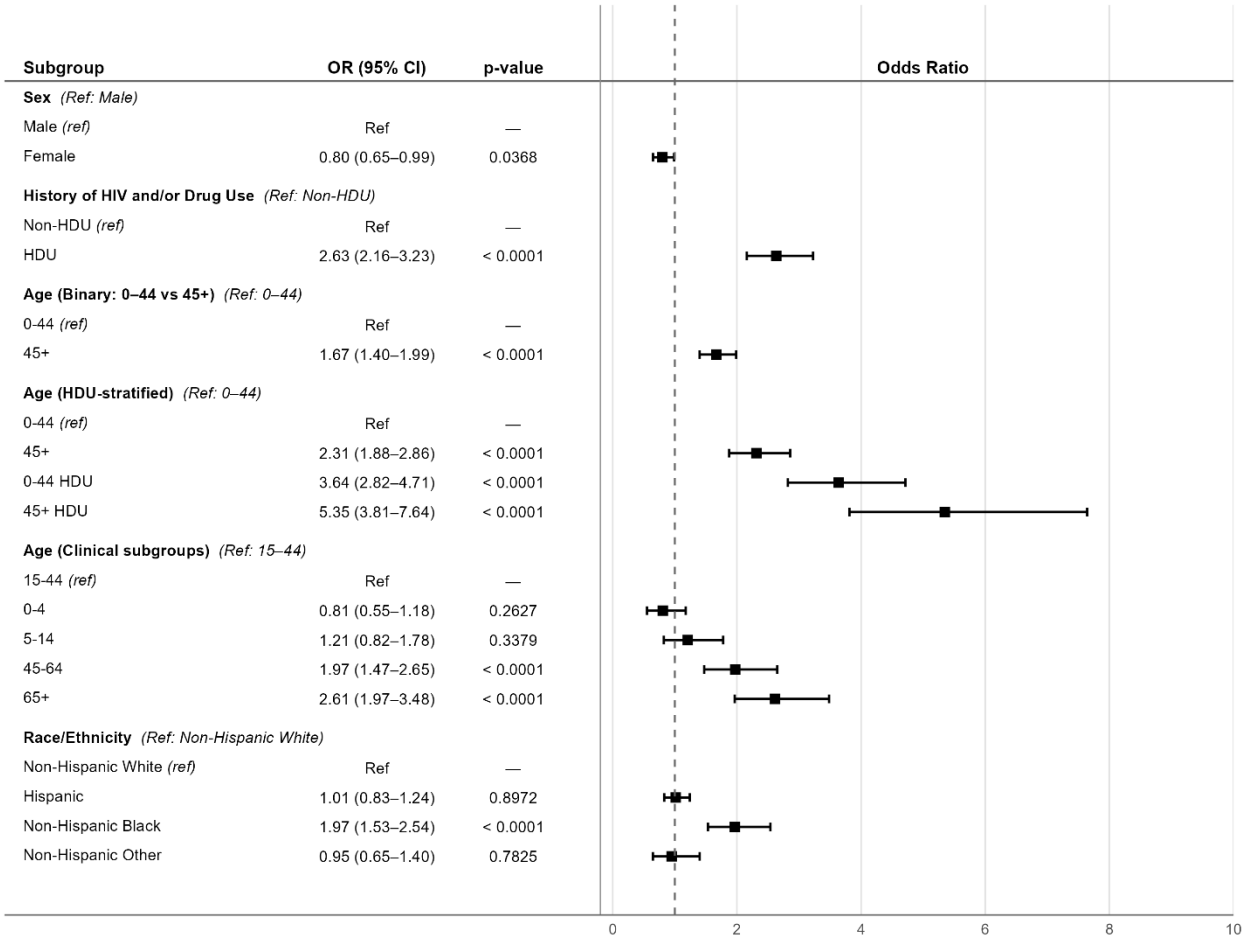


Figure 7: Characteristics Associated with High Mortality Risk in *Giardia* in Texas, 2012-2021

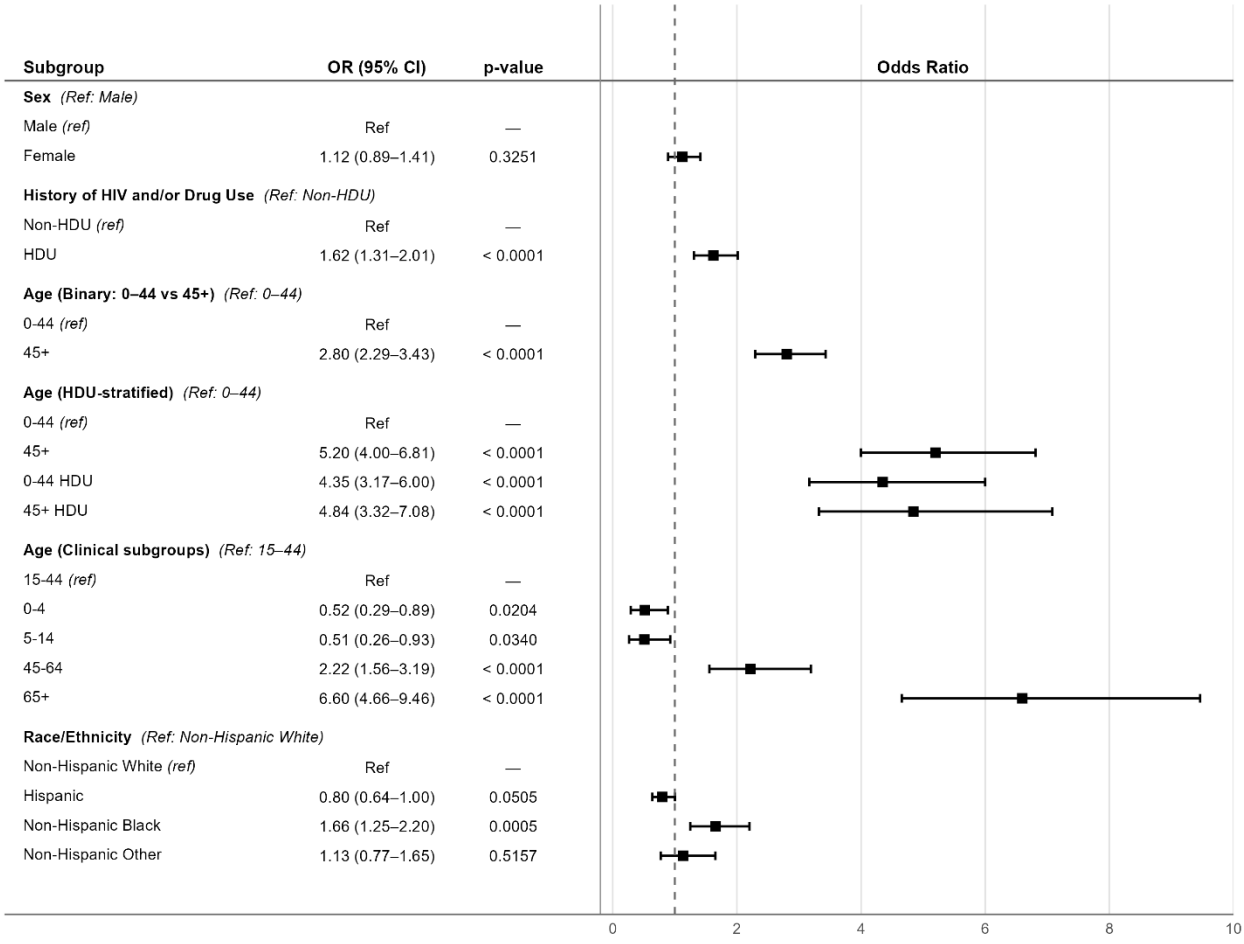
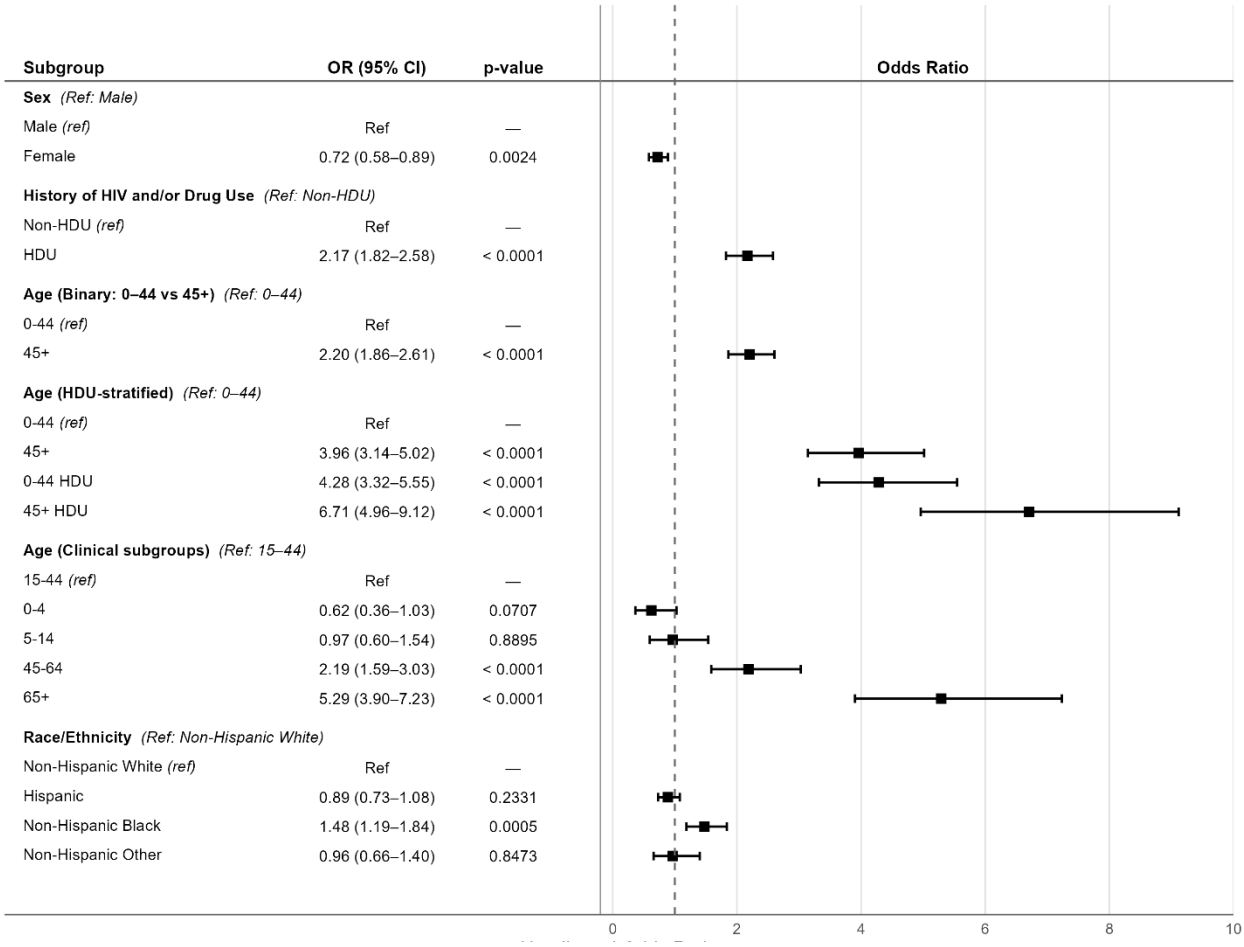


Figure 8: Characteristics Associated with High Mortality Risk in *Cryptosporidium* in Texas, 2012-2021



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