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Review Article

Burden and spatio-temporal distribution of selected tick-borne diseases in the East African community from 2000 to 2024: A systematic review and meta-analysis

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ABSTRACT: Ticks and tick-borne diseases are a major challenge to livestock in the East African region. Several independent studies have been published from different countries; however, there are no meta-analysis studies conducted on their spatio-temporal distribution. Therefore, this study aimed to synchronise the reported burden and distribution to augment the existing data and guide targeted prevention measures. We conducted a systematic review and meta-analysis using PRISMA 2020 guidelines. A comprehensive literature search was conducted using free online databases: PubMed, Scopus, and Google Scholar for studies published between 2000 and 2024. All retrieved articles were screened based on predefined inclusion and exclusion criteria to determine their eligibility. The period was considered sufficient for temporal comparison with the reported increase in zoonotic diseases within the last two decades. Data variables were extracted, and pooled prevalence estimates and subgroup analysis were performed using R Console software. Publication bias was assessed using a funnel plot and Egger's test, which revealed no significant publication bias ($t = 0.3706$, $df = 3$, $p = 0.7356$). Out of the 4563 articles identified, only 72 were included in the final analysis. Most of the articles were from Kenya (39.9%), followed by Uganda, Tanzania, Rwanda, Burundi and Democratic Republic of Congo (DRC) at 27.8%, 26.9%, 2.2%, 1.8% and 1.4% respectively. Theileriosis (46.6%) is the most studied tick-borne disease followed by anaplasmosis, babesiosis and erhlichiosis at 27.8%, 21.5% and 4.9% respectively. Meta-analysis involving 100,519 samples revealed a pooled prevalence estimates of 24.3% (CI at 95% 24.0-24.5%). Sub-group analysis by different variables showed substantial heterogeneity; country ($I^2 = 99.3\%$, $R^2 = 3.8\%$, $P<0.01$), laboratory test ($I^2 = 99.2\%$, $R^2 = 21.1\%$, $P<0.01$), year of publication ($I^2 = 99.3\%$, $R^2 = 11.7\%$, $P<0.01$) and tick borne pathogen ($I^2 = 99.4\%$, $R^2 = 0.2\%$, $P<0.01$). Out of the 9,988 ticks screened, 2.0% were infected with Theileria, 1.0% Erlichia and 0.9% Anaplasma and 0.2% with Babesia pathogens. The pooled prevalence varied across the different countries. The number of studies has significantly increased recently with more research on theileria infections. There is need for consolidated scientific approach, technical and financial support to ensure effective and efficient targeted prevention and control measures.

Keywords: Distribution, East Africa Community, prevalence, meta-analysis, review, tick-borne disease.

Abbreviations: EAC, East African Community; TBDs, Tick Borne Diseases; **USD,** United States Dollar; **CDC,** Centers for Disease Control; **PRISMA,** Preferred Reporting Items for Systematic Reviews and Meta-Analyses; **PICO,** Population, Intervention, Comparison and Outcome; **NOS,** Newcasstle-Ottawa Scale; **DRC,** Democratic Republic of Congo; **CI,** Confidence Interval; **ELISA,** Enzyme-Linked Immunosorbent Assay; **IFAT,** Indirect Flourescence Antibody Test; PCR, Polymerase Chain Reaction; **OR,** Odds Ratio; RLBH, Reverse Line- Blot Hybridisation; **PM-** Post Mortem; COVID- Corona Virus Disease.

INTRODUCTION

The population of the East African Community (EAC) was estimated at 312,588,811 in 2024 by United Nations population estimates and projections (https://population.un.org (accessed on January 2025) and is rapidly growing. Food and nutritional security are a challenge facing the region, with increasing levels of malnutrition associated with insufficient animal source foods. Livestock contributes immensely to the economic status of the EAC countries. For instance, livestock contribute approximately 12% of Kenya's national Gross Domestic Product (GDP) and 42% of the Agricultural GDP (Jumba *et al*., 2020), with both rural and urban populations relying on them either directly or indirectly (Mugumaarhahama *et al*., 2021). In Tanzania, livestock contributes over 30% of the farm gate value of agricultural commodities and about 10% of the national GDP. In Rwanda, livestock is estimated to contribute approximately 14% to the agricultural GDP and is a critical source of livelihoods and food security for a large portion of the population. However, in Uganda, it is estimated at 4.0% of the national GDP. Livestock, especially cattle, play a critical role in the lives and livelihoods of cattle keepers in the East African Community (Gachohi *et al*., 2012). Milk and meat are the key products from cattle that contribute significantly to the total gross value of livestock in the agricultural sector (Ikaal *et al*., 2020). With the critical role livestock play, farmers are now moving to an intensive production system to increase production in limited space, which increases susceptibility to diseases. With the abundance of several tick species in the region, Tick-Borne Diseases (TBDs) are a major problem resulting in devastating effects on cattle keepers. Treatment and management of TBDs in developing countries have been estimated to cost approximately USD 20 billion annually (Karim *et al*., 2017). Similarly, they have been associated with a significant reduction in milk and meat production as well as the mortality of approximately 3 million animals every year.

Ticks are hematophagous arthropods distributed worldwide, with approximately 900 species out of which 700 are from the Ixodidae family (hard) and 200 from the Argasidae family (soft) (Muhammad *et al.*, 2018). They are the primary ectoparasites of wild and domestic animals, resulting in huge economic losses (Jongejan and Uilenberg, 2004) through transmission of Tick-Borne Pathogens (TBPs), resulting in TBDs. Ticks become infected when they feed on an infected host, where they then transmit the infection to the next host. Depending on the life cycle of the ticks, a single tick can infest several hosts, increasing the risk of disease transmission. The majority of the TBDs are zoonotic and their incidence has steadily increased in the last two decades (Chitanga *et al*., 2014; Estrada-Peña and Fuente, 2014; Sanchez-Vicente *et al*., 2019). For instance, the incidence of Lyme borreliosis was estimated at 365 cases per 100,000 person-years in Europe in 2018 (Burn *et al.*, 2023), whereas in the United States of America, a total of 62,551 cases were reported in 2022 (CDC, 2024). Similarly, emergence (thrombocytopenia syndrome, Heartland virus and Bourbon virus) (Kosoy *et al.*, 2015; Savage *et al*., 2013; Yu *et al*., 2011) and reemergence (Crimean-Congo haemorrhagic fever, tick-borne encephalitis) (Estrada-Peña *et al*., 2014; Al-Abri *et al*., 2017) of TBDs have been reported globally.

In the EAC, a wide variety of tick species have been reported and implicated to transmit bacterial (spirochetes, *Rickettsia*), viral (flaviviruses, nairoviruses) and parasitic (*Babesia*, *Theileria*) infections in animals and humans (Djiman *et al*., 2024). They cause significant challenges to rural populations in the tropics with extensive production systems and conducive climatic conditions (hot and humid) for their growth and survival. With the low-input extensive farming practices and transhumance exploitation of natural resources, cattle in EAC are exposed to tick-borne habitats, resulting in increased incidences of TBDs (Ouedraogo *et al*., 2021; Zannou *et al*., 2021). There are more than nine genera of ticks found in EAC that are involved in the epidemiology of various TBDs (Wanzala, 2023). For instance, the introduction of the invasive *Rhipicephalus microplus* tick has been accompanied by a surge in cases of bovine babesiosis (Biguezoton, 2016). Several independent studies have been conducted in the region to determine the burden and the risk factors of different TBDs in EAC. Notably, theileriosis, babesiosis, anaplasmosis and erlichiosis have been reported as the most common TBDs in cattle and the tick population in the region (Djiman *et al*., 2024). With the movement of cattle across the borders, there is a potential for the spread of TBDs from one country to the other. There is scarce literature that compares (meta-analysis) the burden of TBDs in different countries, and there is therefore a need to collate the individual studies to determine the correlation and the possible transboundary transmission. Despite the increasing presence of TBDs, there is scarce research looking at the burden and spatio-temporal distribution of these infections in the region. This systematic review seeks to provide a summary of the burden and distribution of TBDs in EAC, which will highlight the hotspots and dynamic changes over time. The findings will augment the existing epidemiological data and help to guide in resource mobilisation, designing and implementation of targeted control measures.

Research questions

1. Which tick-borne pathogen species have been detected in cattle and ticks in the East African community between 2000 and 2024?
2. What is the prevalence of TBDs, and which laboratory

tests are commonly used to detect them in the East African community between 2000 and 2024, and how do they compare across different countries?

3. What are the temporal trends and spatial distribution patterns of tick-borne diseases (TBDs) in the East African community from 2000 to 2024, and how do factors such as diagnostic methods influence these patterns?

MATERIALS AND METHODS

Ethical approval

No ethical approval was obtained because this study did not involve laboratory animals and only involved screening of the published articles on TBDs in EAC. To carry out this systematic review, we used the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) checklist and guidelines.

Inclusion criteria

Observational studies with prevalence/incidence of TBDs in cattle as the outcome from any EAC country and written in English, published between 2000 and May 2024, were included. All the countries in the EAC region were included except South Sudan to avoid bias in the study period under consideration, as it was part of Sudan until 2011.

Exclusion criteria

Case reports, case series, review articles, experimental studies, studies not reporting prevalence/incidence as the outcome, unpublished/grey literature.

Literature search

The following databases were used to search for relevant studies: PubMed, Scopus, and Google Scholar. For each of the research questions, search terms were generated to identify as many articles as possible. Different TBDs were searched individually using Boolean operators “AND”, “OR” to combine the terms to return as many records as possible. For babesiosis, the following search string was used; (Prevalence OR Burden OR Impact OR Incidence OR Epidemiology) AND (Babesiosis OR "*Babaseia bigeminna*" OR "*Babesia bovis*") AND (cattle OR calves) AND (Kenya OR Uganda OR Tanzania OR Rwanda OR Burundi OR "Democratic Republic of Congo"). For anaplasmosis, (Prevalence OR Burden OR Impact OR Incidence) AND epidemiology AND (Anaplasmosis OR "*Anaplasma marginale*" OR "*Anaplasma centralle*") AND (cattle OR calves) AND (Kenya OR Uganda OR Tanzania OR Rwanda OR Burundi OR "Democratic Republic of Congo"). For theileriosis, (Prevalence OR Burden OR Impact OR Incidence) AND epidemiology AND (Theileriosis OR "*Theileria parva*" OR "East Coast fever") AND (cattle OR calves) AND (Kenya OR Uganda OR Tanzania OR Rwanda OR Burundi OR "Democratic Republic of Congo"). For ehrlichiosis, (Prevalence OR Burden OR Impact OR Incidence) AND epidemiology AND (Cowdriosis OR Heart water OR "*Ehrlichia ruminantium*") AND (cattle OR calves) AND (Kenya OR Uganda OR Tanzania OR Rwanda OR Burundi OR "Democratic Republic of Congo").

To find original papers we might have missed during the search process, we additionally manually searched for further relevant research using references from the retrieved articles and associated systematic reviews. The Rayyan platform was utilised to remove duplicate articles and organise search outcomes into either relevant or irrelevant studies based on the inclusion/exclusion criterion.

Selection of articles

We used the PICO approach to identify the relevant articles where Population (P): cattle or ticks, Intervention/Exposure (E): diagnostic/screening test such as serology, molecular to detect TBDs, and Outcome (O): Prevalence/incidence of TBDs in EAC country. Unfortunately, there were no comparisons for the groups investigated since all of the included articles were observational studies. Two researchers independently screened the articles, and any discrepancies were resolved through consensus. Two phases were used to select the articles, whereas phase one involved reviewing the title and abstract of the articles and categorising them based on the inclusion/exclusion criteria as either included, excluded or maybe. The articles that were unclear as to be included or not were downloaded for further screening and then classified accordingly. In the second phase, all the relevant articles were downloaded, and a full-text detailed review was done to select the appropriate articles.

Data extraction

Using the designed data extraction tool, data were extracted from the appropriate articles, including the following: Name of the first author, year of publication, study design, continent, country, laboratory method of identification, total sample size, sex distribution, overall prevalence of brucellosis and prevalence in different sex where applicable.

Data quality assessment

Three major domains were utilized to evaluate the quality of the data collected using the modified Newcastle-Ottawa

Scale (NOS) (Luchini *et al*., 2017; Kithuka *et al.*, 2025): Domain 1; During the cattle selection process, the study's randomization, description of inclusion/exclusion criteria, stratified sampling strategy, and representativeness (sample size >20) were examined in order to evaluate selection bias. Should all the issues be identified, this domain receives a maximum of four points. Domain 2; Outcome ascertainment: this evaluated the test that produced the results, the reliability of the data analysis, and selective reporting (just reporting the positive). A maximum of three points are awarded to this domain. Domain 3: Transparency and Reporting: This area evaluated the thorough explanation of the study's design, sampling techniques, recruitment strategy, and data collection processes. Additionally, if the authors openly acknowledged any selection bias-related limitations and explore how these would affect the study's conclusions. A maximum of four points is awarded to this domain. Each article could receive up to 11 points for quality. Publications with a total score of 9–11 points were considered high-quality, while those with a score of 5-8 points were considered moderate, and those with a score of 0–4 were considered low quality.

Every included study was evaluated and given a score, which was used to weigh the evidence in the systematic review, identify high-quality research, and summarise the quality of the evidence. The domain-specific scores help with the critical evaluation of the evidence by highlighting areas where studies may have possible biases, such as in comparability or selection. The Newcastle-Ottawa Scale is a robust and practical tool that provides a standardised method for assessing the quality and risk of bias in observational studies, facilitating the synthesis of reliable and valid findings in systematic reviews.

Data analysis

Data variables collected in Excel were exported to R statistical software (version R version 4.1.2, x86_64-apple-darwin17.0 (64-bit)) for statistical analysis using the *meta* and *metafor* packages. Tables and Figures containing frequencies, summaries, and proportions were produced. The percentage of all reported positive samples from all included studies was used to get the pooled prevalence. Since PCR is the most widely used sensitive test for TBDs, it was selected as the reference test in a pairwise comparison of other laboratory tests to evaluate the heterogeneity (both the residual heterogeneity, I^2 and that which can be explained by the variable, R^2) across the tests with $p<0.05$.

A Forest plot was used to estimate the individual effect size of each study, with their respective confidence interval to provide a visual summary of the data. In addition to visual inspection for symmetry of the plot, we also used Egger's regression test for quantitative evaluation of the possibility of publication bias. Meta-regression analysis was performed using individual study prevalence and their confidence interval to determine the source of statistical heterogeneity (I^2), which was categorised into no, low, moderate and high with 0, 25, 50, and 75% values respectively, and the level of significance was set at $p<0.05$.

RESULTS

A total of 4,563 articles were initially identified across the selected databases: 274 from PubMed, 791 from Scopus, and 3,498 from Google Scholar (Figure 1). Following the removal of 2,583 duplicates, 1,850 records were excluded after title and abstract screening for reasons including irrelevance and missing abstracts. Seven additional articles were excluded due to inaccessible full texts. The remaining 123 articles were assessed in full, resulting in the exclusion of 51 that did not meet the eligibility criteria. Ultimately, 72 articles were included in the final analysis. These articles yielded 223 individual entries, as several studies reported multiple observations based on the use of different diagnostic methods, the detection of multiple tick-borne pathogens, or the identification of more than one pathogen species. Each entry was treated as a distinct data point for the purposes of analysis. Out of these, most of the studies (39.9%) were from Kenya, followed by Uganda, Tanzania, Rwanda, Burundi and DRC at 27.8%, 26.9%, 2.2%, 1.8% and 1.4% respectively (Figure 2). The data for this study were collected from various regions across the East African region. In Burundi, the study was conducted in the Imbi zone. In the DRC, data were gathered from Ituri, North Kivu, and South Kivu. In Kenya, Uganda, and Tanzania, studies on TBDs were carried out across multiple regions within each country. However, the study conducted in Rwanda did not specify the region of focus. Most of the articles (89.2%; 199/223) were cross-sectional studies, with 9.4% longitudinal, and only 1.3% used secondary data. Depending on the TBD and the laboratory test used, a wide range of prevalence was reported from different studies (Figure 4). On the other hand, most of the samples tested in the studies (87.4%; 195/223) were collected from cattle, with the remaining (12.6%; 28/223) from ticks. Theileriosis (46.6%; 104/223) was the most studied tick-borne disease, followed by anaplasmosis, babesiosis and ehrlichiosis at 27.8%, 21.5% and 4.9% respectively (Table 1). According to our quality assessment criteria, 40 publications were of high quality with a score of 9-11, and 32 had a score of 5-8, indicating moderate quality (Table 2). The generated funnel plot showed that the data points are symmetrically distributed around the vertical line (pooled effect size), suggesting no substantial publication bias. The absence of a clear asymmetry indicates that smaller studies do not disproportionately report extreme effect sizes. However, a few points lie outside the triangular confidence region, which may indicate heterogeneity rather than bias (Figure 5). Egger's regression test conducted on the funnel plot's asymmetry revealed no significant publication bias (t =

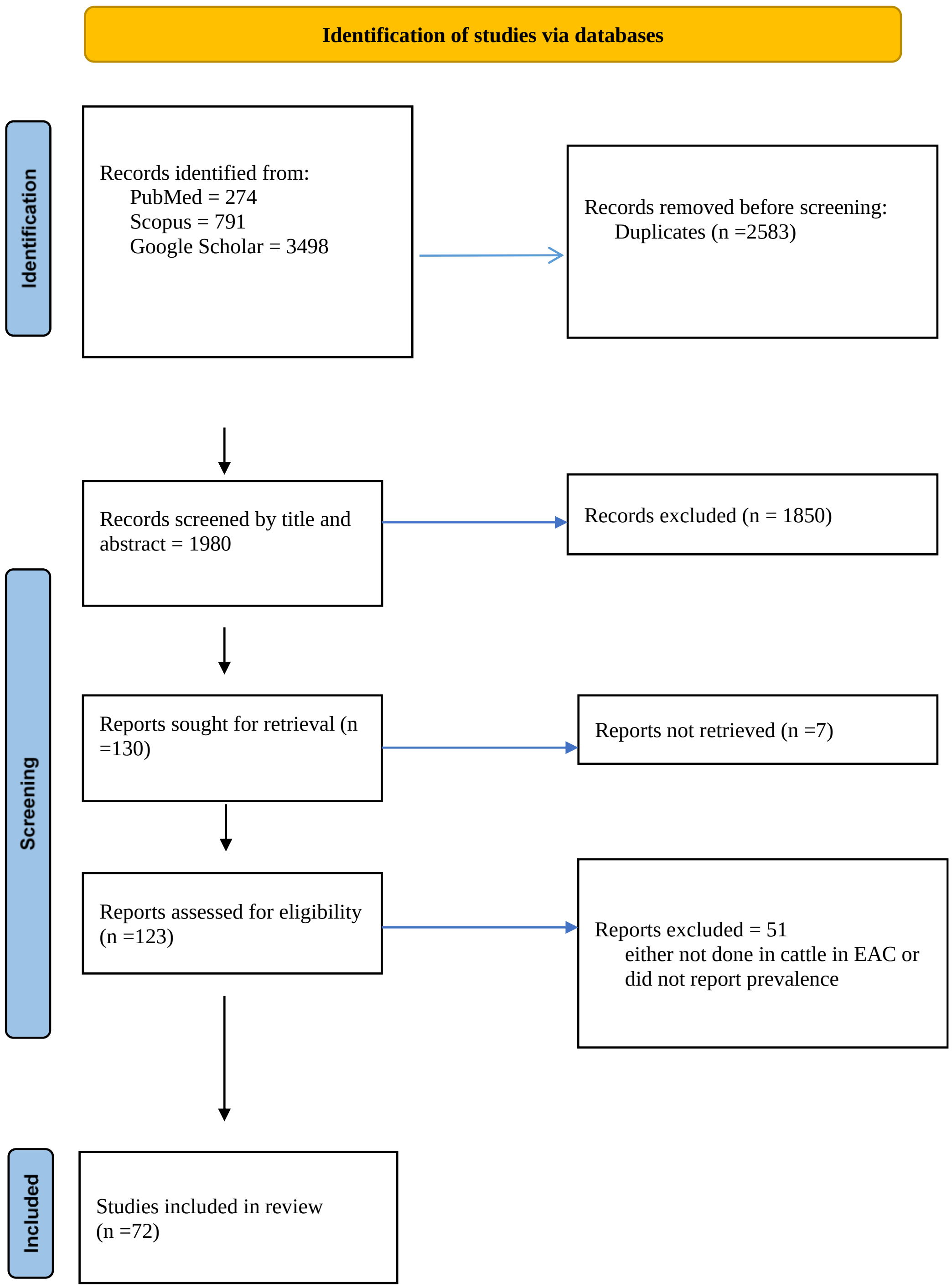

Figure 1. Flow diagram showing the articles retrieval process.

0.3706, df = 3, p = 0.7356). The estimated limit of the intercept as the standard error approaches zero was -1.6059 (95% CI: -8.0370, 4.8253), with a broad confidence interval that includes zero, indicating a lack of strong evidence for small-study effects. The elevated p-value suggests that the funnel plot is symmetric, which further reinforces the conclusion of no bias.

Pooled prevalence estimates and sub-group analysis of tick-borne diseases and heterogeneity

From the 223 observations included in this study, a total of 100,519 cattle were included in the studies to detect different TBDs (Table 2). Out of these, 24,393 were reported to be infected with one or more species of TBDs,

Table 1. Characteristics of the included studies from different EAC countries.

Variable	Kenya	Tanzania	Uganda	Rwanda	Burundi	DRC	Total	p_value
Publication period								
2000-2004	5 (5.6%)	4 (6.7%)	7 (11.3%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	16 (7.2%)	
2005-2009	4 (4.5%)	14 (23.3%)	3 (4.8%)	5 (100.0%)	0 (0.0%)	0 (0.0%)	26 (11.7%)	
2010-2014	20 (22.5%)	3 (5.0%)	14 (22.6%)	0 (0.0%)	0 (0.0%)	1 (33.3%)	38 (17.0%)	< 0.001
2015-2019	18 (20.2%)	13 (21.7%)	24 (38.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	55 (24.7%)	
2020-2024	42 (47.2%)	26 (43.3%)	14 (22.6%)	0 (0.0%)	4 (100.0%)	2 (66.7%)	88 (39.5%)	
TBDs								
Anaplasmosis	27 (30.3%)	11 (18.3%)	23 (37.1%)	0 (0.0%)	1 (25.0%)	0 (0.0%)	62 (27.8%)	
Babesiosis	19 (21.3%)	16 (26.7%)	10 (16.1%)	0 (0.0%)	1 (25.0%)	0 (0.0%)	46 (20.6%)	0.121
Ehrlichiosis	8 (9.0%)	1 (1.7%)	2 (3.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	11 (4.9%)	
Theileriosis	35 (39.3%)	32 (53.3%)	27 (43.5%)	5 (100.0%)	2 (50.0%)	3 (100.0%)	104 (46.6%)	
Study design								
Cross-sectional	73 (82.0%)	52 (86.7%)	62 (100.0%)	5 (100.0%)	4 (100.0%)	3 (100.0%)	199 (89.2%)	0.009
Longitudinal	16 (18.0%)	5 (8.3%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	21 (9.4%)	
Retrospective	0 (0.0%)	3 (5.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (1.3%)	
Sample source								
Cattle	76 (85.4%)	52 (86.7%)	56 (90.3%)	4 (80.0%)	4 (100.0%)	3 (100.0%)	195 (87.4%)	0.835
Ticks	13 (14.6%)	8 (13.3%)	6 (9.7%)	1 (20.0%)	0 (0.0%)	0 (0.0%)	28 (12.6%)	
Sample type								
Clinical specimen	0 (0.0%)	3 (5.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (1.3%)	
Postmortem	1 (1.1%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.4%)	
Serum	34 (38.2%)	15 (25.0%)	10 (16.1%)	0 (0.0%)	3 (75.0%)	2 (66.7%)	64 (28.7%)	0.003
Tick tissue	2 (2.2%)	7 (11.7%)	0 (0.0%)	1 (20.0%)	0 (0.0%)	0 (0.0%)	10 (4.5%)	
Whole blood	52 (58.4%)	35 (58.3%)	52 (83.9%)	4 (80.0%)	1 (25.0%)	1 (33.3%)	145 (65.0%)	
Laboratory test								
ELISA	32 (36.0%)	18 (30.0%)	8 (12.9%)	0 (0.0%)	2 (50.0%)	1 (33.3%)	61 (27.4%)	
IFAT	2 (2.2%)	0 (0.0%)	1 (1.6%)	1 (20.0%)	0 (0.0%)	1 (33.3%)	5 (2.2%)	
Microscopy	1 (1.1%)	3 (5.0%)	15 (24.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	19 (8.5%)	
PCR	43 (48.3%)	39 (65.0%)	21 (33.9%)	4 (80.0%)	2 (50.0%)	1 (33.3%)	110 (49.3%)	< 0.001
Postmortem	1 (1.1%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.4%)	
RLBH	10 (11.2%)	0 (0.0%)	17 (27.4%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	27 (12.1%)	

yielding a pooled prevalence of 24.3% (CI at 95% 24.0-24.5%) with a range of 1.0% to 100% depending on the species of TBDs and laboratory test used. Serological studies (ELISA and IFAT) reported higher prevalence across the countries compared to other diagnostic tests. However, PCR is a more sensitive test to detect the genetic material of the pathogen with a narrow confidence interval (Figure 3). Sub-group analysis by country showed substantial heterogeneity (I^2 = 99.3%, R^2 = 3.8%, P<0.01). The pooled prevalence was higher in Burundi (73.1%; CI 95% 71.1-75.0%), with the lowest prevalence in Kenya of 22.0% (CI 95% 21.7-22.4%); however, there was no significant difference in the reported prevalence across the countries (Table 3). Similarly, there was significant heterogeneity by the laboratory test used (I^2 = 99.2%, R^2 = 21.1%, P<0.01), with approximately 21% (R^2) of this explained by the diagnostic method used. The studies that utilised IFAT (45.0%; CI 95%: 42.9-47.1%) and ELISA (44.5%; CI 95%: 43.9-45.1) were 6 and five times more likely to report higher pooled prevalence, respectively, compared to those that used PCR (Table 3). Sub-group analysis by year of publication showed substantial heterogeneity (I^2 = 99.3%, R^2 = 11.7%, P<0.01) with those published between 2005-2009 having 1.5 odds of reporting higher pooled prevalence compared to those published between 2000 and 2004. The pooled prevalence of TBDs between 2005 and 2009 was 36.2% (CI 95%: 35.4-37.0%) while it was 13.0% (CI 95%: 12.7-13.3%) for the studies published between 2020 and 2024. We also performed subgroup analysis by the source of samples and the result showed substantial heterogeneity (I^2 = 99.4%, R^2= 5.3%, P=0.02) where samples from cattle had a higher pooled prevalence (26.5%; CI 95%: 26.2-26.8%) compared to those from tick tissues (4.1%; CI 95%: 3.8-

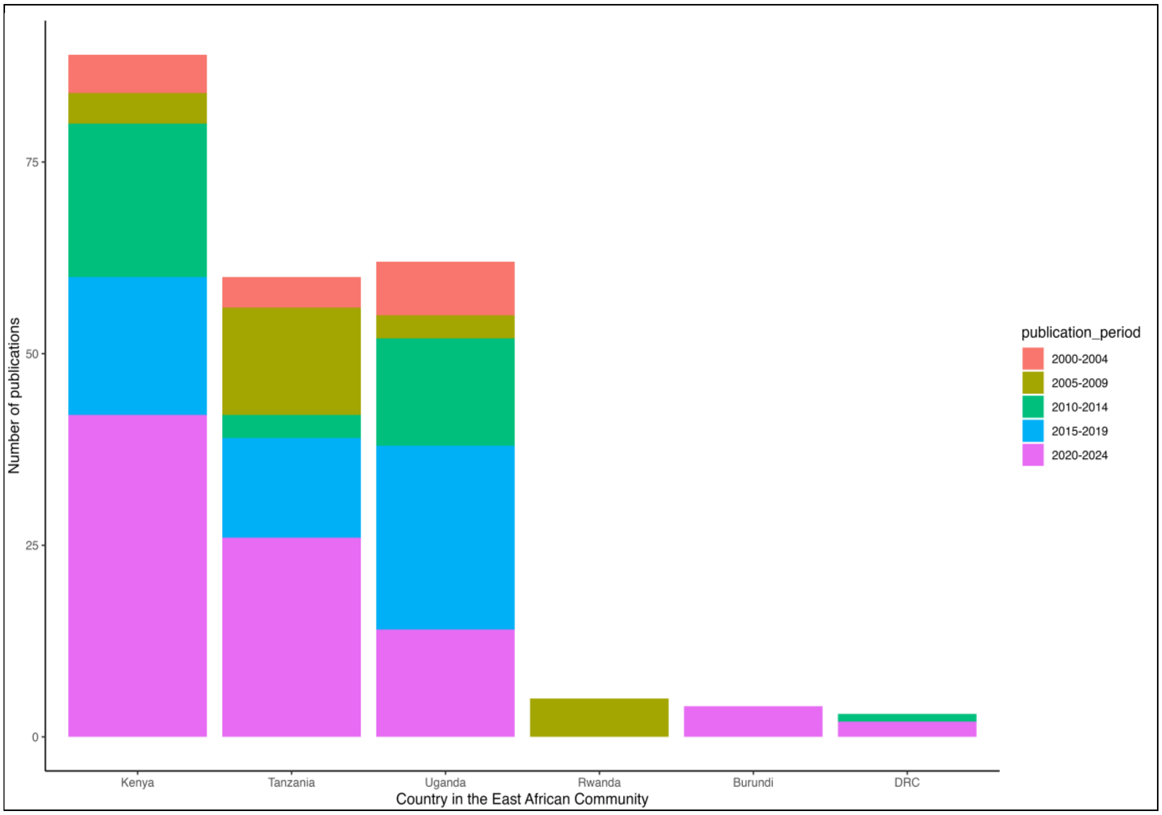

Figure 2. Number of TBDs studies in different East African countries between 2000-2024.

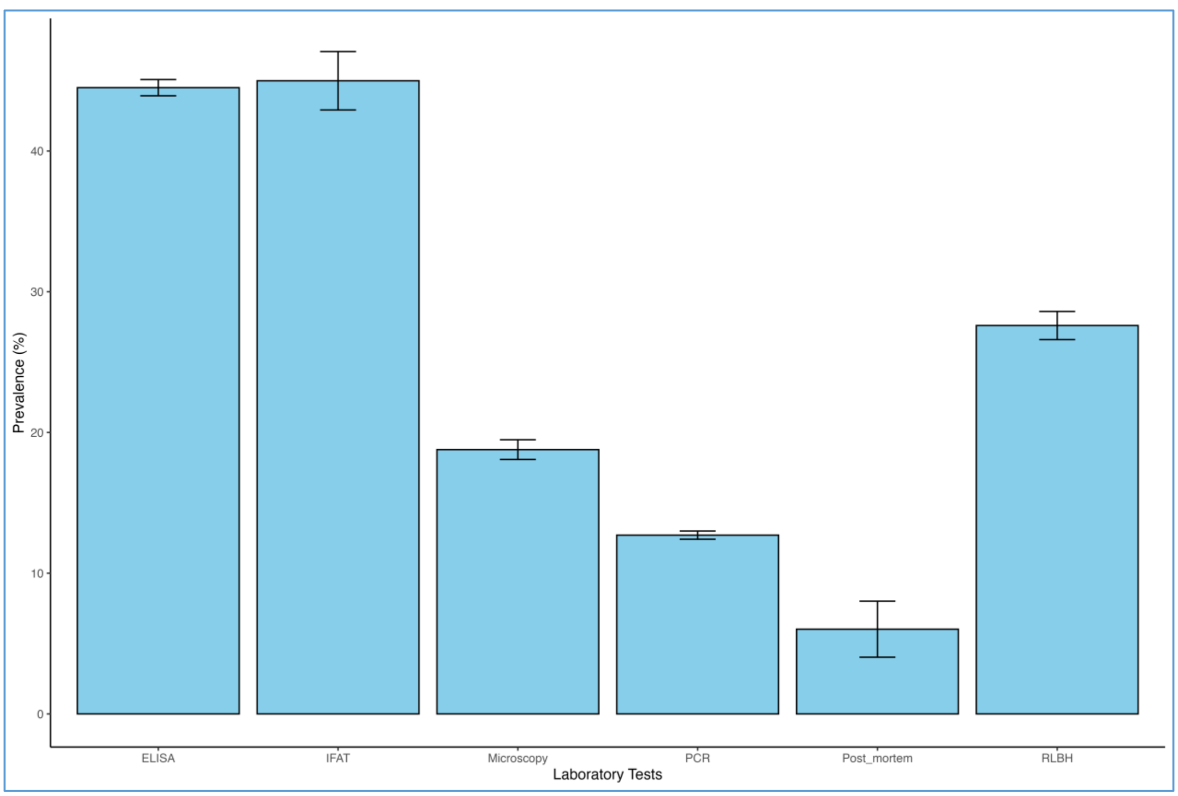

Figure 3. Comparison of reported prevalence of TBDs in EAC between 2000-2024 by diagnostic/laboratory test.

Table 2. Characteristics of the eligible studies on TBDs in East Africa community.

References	Country	Study design	No. samples	Sample source	Pathogen	Cases for TBDs	Qualitys core
Nyabongo et al.,2021	Burundi	cross-sectional	828	cattle	Theileria, Babesia, Anaplasma	667	9
Kalume et al., 2012	DRC	cross-sectional	482	cattle	Theileria	194	8
Vyambwera et al., 2023	DRC	cross-sectional	756	cattle	Theileria	208	7
Wesonga et al.,2014	Kenya	cross-sectional	421	cattle	Theileria	172	9
Maloo et al., 2001	Kenya	longitudinal	195	cattle	Theileria	121	8
Ngeranwa et al., 2008	Kenya	cross-sectional	148	cattle	Anaplasma	142	5
Gachohi at el., 2010	Kenya	cross-sectional	440	cattle	Theileria, Babesia, Anaplasma	85	10
Shepelo et al., 2021	Kenya	cross-sectional	94	ticks	Anaplasma & Ehrlichia	8	9
Kiprono et al., 2011	Kenya	cross-sectional	197	cattle	Theileria, Babesia, Anaplasma	51	10
Chiuya et al., 2021	Kenya	cross-sectional	422	cattle	Theileria, Babesia, Anaplasma & Ehrlichia	7	9
Ngetich et al. 2024	Kenya	cross-sectional	318	cattle	Theileria	41	10
Maloo et al., 2001	Kenya	cross-sectional	939	cattle	Theileria, Babesia, Anaplasma	485	7
Kiara et al.,2014	Kenya	longitudinal	538	cattle	Theileria, Babesia	423	10
Okuthe and Buyu, 2006	Kenya	cross-sectional	760	cattle	Theileria, Babesia, Anaplasma	376	9
Nyawira et al.,2015	Kenya	longitudinal	453	cattle	Theileria, Babesia, Anaplasma	313	10
Thumbi et al., 2014	Kenya	longitudinal	548	cattle	Theileria	33	10
Okal et al., 2020	Kenya	cross-sectional	680	cattle	Theileria, Anaplasma	2	10
Shepelo et al., 2019	Kenya	cross-sectional	314	cattle	Ehrlichia	249	9
Chiuya et al., 2020	Kenya	cross-sectional	256	ticks	Theileria, Babesia, Anaplasma	1	7
Moumouni et al., 2015	Kenya	cross-sectional	192	cattle	Theileria, Babesia, Anaplasma	28	9
Shepelo et al., 2020	Kenya	cross-sectional	306	cattle	Anaplasma & Ehrlichia	61	9
Gachohi at el., 2003	Kenya	cross-sectional	440	cattle	Theileria	85	9
Wesonga et al.,2010	Kenya	cross-sectional	649	cattle	Theileria, Babesia, Anaplasma	428	8
Wesonga et al.,2013	Kenya	cross-sectional	399	cattle	Theileria, Babesia, Anaplasma	235	8
Githaka et al., 2022	Kenya	cross-sectional	506	cattle	Babesia	70	8
Oundo et al., 2024	Kenya	cross-sectional	1382	ticks	Theileria & Ehrlichia	6	9
Kibet et al., 2024	Kenya	cross-sectional	402	cattle	Babesia, Anaplasma	241	9
Wesonga et al., 2017	Kenya	cross-sectional	421	cattle	Babesia, Anaplasma	225	9
Oundo et al., 2022	Kenya	cross-sectional	1486	cattle	Theileria, Babesia, Anaplasma	162	8
Bazarusanga et al., 2008	Rwanda	cross-sectional	194	cattle	Theileria	97	8
Bazarusanga et al., 2008	Rwanda	cross-sectional	300	ticks	Theileria	56	8
Kerario et al.,2017	Tanzania	cross-sectional	648	cattle	Theileria	92	9
Haji et al., 2022	Tanzania	cross-sectional	520	cattle	Anaplasma	13	9
Haji et al., 2022	Tanzania	cross-sectional	520	cattle	Theileria, Babesia, Anaplasma	6	9
Allan et al., 2021	Tanzania	cross-sectional	770	cattle	Theileria	39	8
Laisser et al.,2014	Tanzania	cross-sectional	354	cattle	Theileria	98	5
Kazungu, 2015	Tanzania	cross-sectional	182	cattle	Theileria	179	8
Kimaro et al., 2017	Tanzania	cross-sectional	960	cattle	Theileria	264	9
Swai et al., 2007	Tanzania	cross-sectional	1395	cattle	Theileria	496	9
Ogden et al.,2003	Tanzania	cross-sectional	836	ticks	Theileria	22	9
Ringo et al., 2020	Tanzania	cross-sectional	236	cattle	Theileria, Babesia, Anaplasma	81	9

Table 2. Contd.

References	Country	Study design	No. samples	Sample source	Pathogen	Cases for TBDs	Qualitys core
Ringo et al., 2018	Tanzania	cross-sectional	245	cattle	Theileria, Babesia, Anaplasma & Ehrlichia	63	10
Swai et al., 2009	Tanzania	longitudinal	384	cattle	Theileria, Babesia, Anaplasma	182	9
Swai et al., 2004	Tanzania	cross-sectional	697	cattle	Babesia	42	8
Rukambile et al., 2014	Tanzania	cross-sectional	102	cattle	Theileria	19	7
Haji et al., 2023	Tanzania	cross-sectional	377	ticks	Theileria, Babesia	11	8
Magesa et al., 2023	Tanzania	cross-sectional	91	ticks	Theileria, Anaplasma	21	8
Ringo et al., 2022	Tanzania	cross-sectional	250	cattle	Theileria, Babesia, Anaplasma	64	9
Swai et al., 2005	Tanzania	cross-sectional	666	cattle	Anaplasma	346	8
Muhairwa et al., 2006	Tanzania	retrospective	241	cattle	Theileria, Babesia, Anaplasma	184	6
swai et al., 2006	Tanzania	cross-sectional	826	ticks	Theileria	22	7
Swai et al., 2007	Tanzania	cross-sectional	1329	cattle	Babesia	465	8
Muhanguzi et al.,2014	Uganda	cross-sectional	2658	cattle	Theileria	133	8
Chenyambuga et al., 2010	Uganda	cross-sectional	49	cattle	Theileria	37	8
Magona et al., 2001	Uganda	cross-sectional	98	cattle	Thileria & Anaplasma	33	6
Tayebwa et al., 2018	Uganda	cross-sectional	409	cattle	Theileria, Babesia, Anaplasma	189	9
Oura et al.,2011	Uganda	cross-sectional	143	cattle	Theileria, Anaplasma & Ehrlichia	100	8
Muhanguzi,2010	Uganda	cross-sectional	363	cattle	Theileria, Babesia	72	9
Palmfjord, 2015	Uganda	cross-sectional	130	cattle	Anaplasma	40	9
Anna, 2015	Uganda	cross-sectional	130	cattle	Babesia	35	9
Weny et al., 2017	Uganda	cross-sectional	186	cattle	Theileria, Anaplasma	28	7
Otim et al., 2004	Uganda	cross-sectional	454	cattle	Theileria, Anaplasma	3	8
Byaruhanga et al.,2015	Uganda	cross-sectional	397	cattle	Theileria, Anaplasma	58	9
Miyama et al., 2020	Uganda	cross-sectional	420	cattle	Theileria	190	9
Kabi et al., 2008	Uganda	cross-sectional	184	cattle	Theileria, Babesia, Anaplasma	183	8
Brayuhanga et al., 2021	Uganda	cross-sectional	40	ticks	Theileria & Ehrlichia	10	9
Brayuhanga et al., 2016	Uganda	cross-sectional	240	cattle	Theileria, Babesia, Anaplasma	49	9
Brayuhanga et al., 2023	Uganda	cross-sectional	240	cattle	Anaplasma	29	7
Magona and Mayende, 2001	Uganda	cross-sectional	98	cattle	Theileria, Anaplasma	33	7
Byamukama et al., 2021	Uganda	cross-sectional	208	cattle	Theileria, Babesia, Anaplasma	105	9
Kabuusu et al., 2013	Uganda	cross-sectional	131	cattle	Theileria, Babesia, Anaplasma	67	9
Lolli et al., 2016	Uganda	cross-sectional	3935	cattle	Babesia, Anaplasma	912	9

4.5%). Out of the 9,988 ticks screened in the included studies, 202 were infected with Theileria (2.0%; CI 95%: 1.8-2.3%), 97 (1.0%; CI 95%: 0.8-1.2%) with Ehrlichia, 92 (0.9%; CI 95%: 0.7-1.1%) with Anaplasma and 22 (0.2%; CI 95%: 0.1-0.3%) with babesia parasites. Univariate meta-regression analysis by the tick-borne pathogen as a predictor variable showed substantial heterogeneity (I^2 = 99.4%, R^2 = 0.2%, P<0.01) with approximately 99% of the variability unaccounted for and only less than 1% could be explained by the variable (Table 3). Despite study design reporting a substantial heterogeneity (I^2 = 99.4%, R^2 = 0.0%, P=0.4), this could not be explained by the specific

Table 3. Sub-group analysis by different variable on the burden of TBDs in EAC between 2000 and 2024.

Variable	No. studies	Sample	Cases	Pooled prevalence (CI 95%)	P-value	OR	I^2
Country					<0.01		99.4
Kenya	89	47482	10465	22.0 (21.7-22.4)	**Ref**	**Ref**	
Tanzania	60	25183	5719	22.7 (22.2-23.2)	0.5	0.8	
Uganda	62	22516	5684	25.2 (24.7-25.8)	0.09	1.6	
Rwanda	5	1322	463	35.0 (32.5-37.7)	0.3	2.0	
Burundi	4	2022	1478	73.1 (71.1-75.0)	0.01	8.7	
DRC	3	1994	584	29.3 (27.3-31.3)	0.6	1.6	
Lab Test					<0.01		99.2
PCR	110	49597	6301	12.7 (12.4-13.0)	**Ref**	**Ref**	
ELISA	61	28554	12707	44.5 (43.9-45.1)	0.01	5.9	
IFAT	5	2207	993	45.0 (42.9-47.1)	0.03	5.2	
RLBH	27	7656	2113	27.6 (26.6-28.6)	0.02	2.1	
PM	1	548	33	6.0 (4.2-8.4)	0.5	0.4	
Microscopy	19	11957	2246	18.8 (18.1-19.5)	0.03	2.2	
Year of publication					<0.01		99.3
2000-2004	16	7265	2448	33.7 (32.6-34.8)	**Ref**	**Ref**	
2005-2009	26	13219	4784	36.2 (35.4-37.0)	0.4	1.5	
2010-2014	38	14449	4920	34.1 (33.3-34.8)	0.9	1.1	
2015-2019	55	24358	6938	28.5 (27.9-29.1)	0.6	0.8	
2020-2024	88	40774	5303	13.0 (12.7-13.3)	0.01	0.3	
TBDs					<0.01		99.4
Theileria	104	44664	12455	27.9 (27.5-28.3)	**Ref**	**Ref**	
Anaplasma	62	28001	7111	25.4 (24.9-25.9)	0.2	0.7	
Babesia	46	22808	4326	19.0 (18.5-19.5)	0.1	0.7	
Ehrlichia	11	5046	501	9.9 (9.1-10.8)	0.2	0.5	
Sample source					0.02		99.4
Cattle	195	90531	23980	26.5 (26.2-26.8)	**Ref**	**Ref**	
Ticks	28	9988	413	4.1 (3.8-4.5)	0.02	0.3	
Overall	223	100519	24393	24.3 (24.0-24.5)			

Key: CI- confidence interval at 95%, I^2 residual heterogeneity statistics.

design. However, the longitudinal studies were 1.6 times more likely to report higher pooled prevalence estimates compared to cross-sectional studies.

Prevalence of TBDs by species

Theileria infection

Nearly half (46.6%) of the included studies focused on assessing the prevalence of *Theileria* species in the region, with 33.6% of these originating from Kenya. Of the 104 *Theileria*-related studies, the majority (57.7%; 60/104) targeted *Theileria parva*, the most pathogenic species, while the remaining studies investigated other species such as *T. mutans*, *T. taurotragi*, *T. velifera*, and *T. buffeli.* The 104 studies included 44,664 samples out of which 12,455 were infected with theileria parasites, yielding a pooled prevalence estimate of 28% (95% CI: 27.5-28.3). Comparatively, a higher overall prevalence (75.1%; CI95% 72.6-77.5) was reported in Burundi compared to 35.0% (95% CI: 32.5-37.7), 29.3% (95% CI: 27.3-31.3), 27.9% (95% CI: 26.9-28.9), 26.9% (95% CI: 26.2-27.7) and 24.8% (95% CI: 24.1-25.4) from Rwanda, DRC, Uganda, Tanzania and Kenya, respectively. The number of studies on theileriosis has steadily increased over time, where only 9 papers published between 2000 and 2004, compared to 36 between 2020 and 2024. All the included studies from DRC and Rwanda were estimating the burden of Theileria infection. Most of the studies (87.5%; 91/104) used a cross-sectional design, with 11.5% using longitudinal and only 0.9% using secondary data. Regardless of the laboratory test used, the prevalence ranged from 0.1 to 100%. The laboratory test was statistically significant across the different countries (p<0.05).

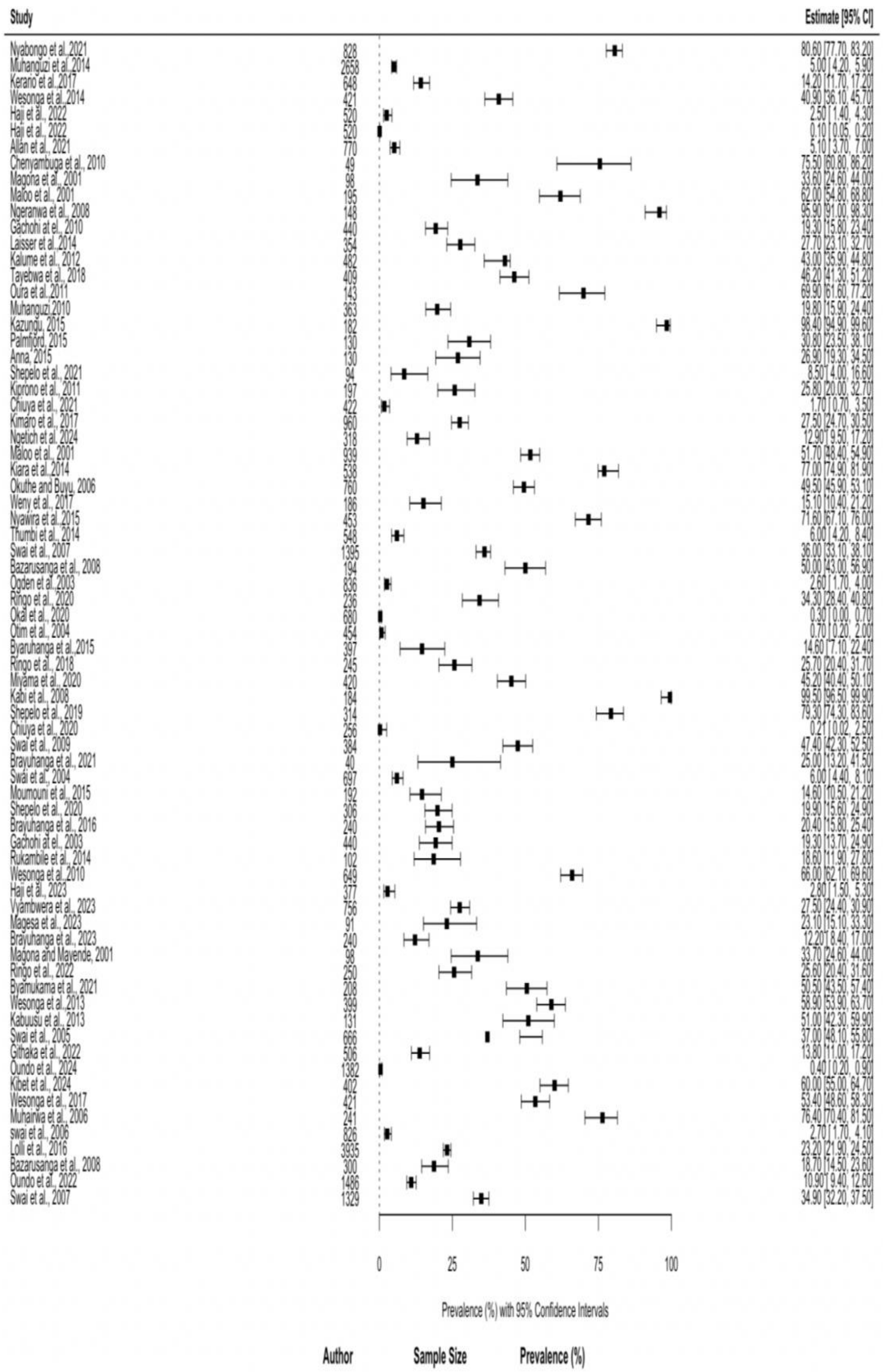

Figure 4. Forest plot showing reported prevalence and 95% confidence interval of selected TBDs from eligible studies.

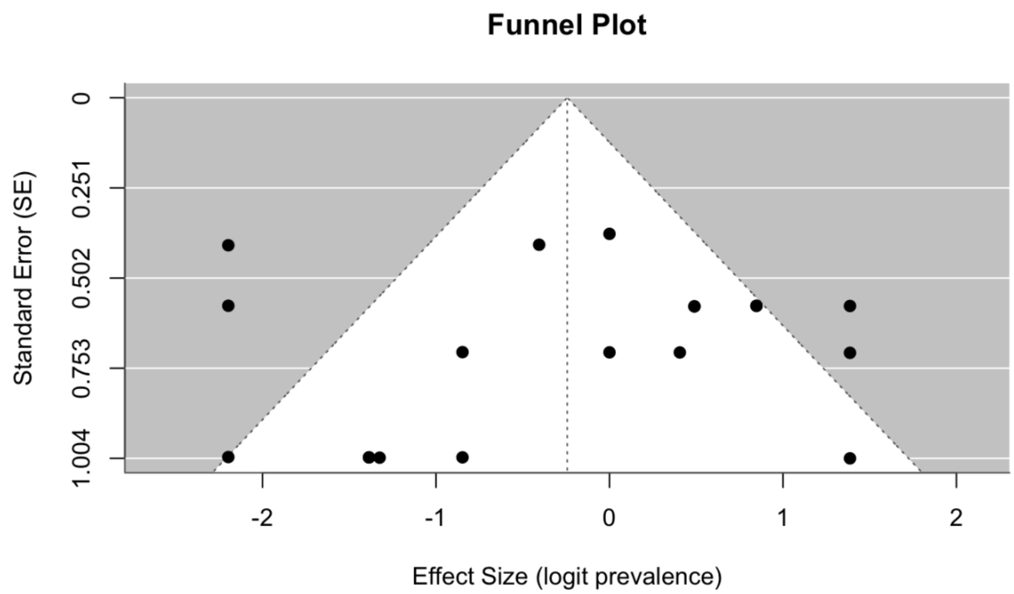

Figure 5. Publication bias assessment funnel plot for the included studies.

Anaplasma infection

Sixty-two studies consisting of 28,001 samples reported a pooled prevalence estimate of anaplasma infection at 25.4% (95% CI: 24.9-25.9). *Anaplasma marginale* and *Anaplasma centrale* are the two species that were mainly targeted in 79% of the studies, with others incidentally reported *A. bovis, A. platys, A.ovis, A. lambwe* or *A. omatjenne.* Twenty-seven studies on anaplasma infection were carried out in Kenya, with 23, 11 and 1 from Uganda, Tanzania and Burundi, respectively. A higher prevalence (76.4%; 95% CI: 71.8-80.4) was reported in Burundi, followed by 27.0% (95% CI: 26.1-28.0) in Uganda, 23.9% (95% CI: 22.6-25.3) from Tanzania and 23.6% (95% CI: 22.9-24.2) from Kenya. Studies have increased steadily from 4 between 2000 and 2004, seven each for the period between 2005 and 2009 and 2010 and 2014, 17 from 2015 to 2019 and 27 between 2020 and 2024. However, for this period, there was no study on anaplasma infection in cattle from DRC and Rwanda. Approximately 92% of these studies employed a cross-sectional design, with 6% using a longitudinal design and 2% using retrospective data. Regardless of the laboratory test used and the country of study, the prevalence reported ranged from 0.1-95.9%.

Babesia infection

Forty-six of the included studies, consisting of 22,808 samples, have reported a pooled prevalence estimate of 19.0% (95% CI:18.5-19.5) of babesia infection. However, varied pooled prevalence was reported from different countries: 20.5% (95% CI:19.7-21.3), 19.0% (95% CI: 18.0-20.0) and 14.6% (95% CI: 13.8-15.4) from Kenya, Uganda and Tanzania, respectively. There was only one study from Burundi with a prevalence of 63.6% (95% CI: 58.6-68.3). Approximately 97.0% of these studies were cross-sectional and only 3.0% longitudinal, with a reported prevalence range of 0.1-100%. *Babesia bigemina* and *Babesia bovis* were the target species in 95.6% of the studies, with only two reported *B. caballi* and *B. vogeli*. The number of studies on babesia infection has linearly increased with 3, 6, 7, 12 and 18 studies published between 2000-2004, 2005-2009, 2010-2014, 2015-2019 and 2020-2024, respectively. However, for this period, there was no study on babesia infection in cattle from DRC and Rwanda.

Ehrlichia infection

For the period under consideration for this systematic review, only 11 studies on Ehrlichia infection were included, with a pooled prevalence estimate of 9.9% (95% CI: 9.1-10.8). The studies were from Kenya (8), Uganda (2) and Tanzania (1), with 7 published between 2020-2024, 3 between 2015-2019 and only 1 between 2010-2014. Eight (72.3%) of these studies targeted *E. ruminantium,* with 2 reporting *E. minasensis* and 1 reporting *E. bovis*. The prevalence reported from each country ranged from 0.4-79.4% in Kenya, 7.5-30.8% in Uganda and 7% from the single study in Tanzania. All were cross-sectional studies, with 91% using molecular diagnosis and the rest through microscopy.

DISCUSSION

The purpose of this study was to summarise the burden and to map the spatio-temporal distribution of the selected

TBDs to support the efforts undertaken to control them. The results will supplement the already existing epidemiological data with the potential to guide a comprehensive approach to control TBDs in highly endemic areas with greater urgency. We were interested in the studies on Theileria, Babesia, Anaplasma and Ehrlichia parasites reported between 2000 and 2024. The number of studies on these pathogens differs significantly from one country to another other with more studies from Kenya. This could be attributed to several factors, including the economic impacts on livestock and humans (Bastos *et al.*, 2019), necessitating the need to understand their risk factors and vector dynamics to postulate preventive and control measures (Diarra *et al*., 2023; Djiman *et al*., 2024). The findings of this review have revealed that the EAC region is a reservoir of a wide range of tick-borne pathogens that can impact the livestock sector negatively.

The results from this review revealed that there is an increasing burden of TBDs, and the number of studies has significantly increased in the last decade. This can be attributed to climate change, that has resulted in humans and livestock invading areas heavily infested by ticks in search of feed and water (Mutai *et a*l., 2022). Similarly, the increasing human population has led to a reduction in the available grazing fields, and people are keeping few exotic breeds that are more susceptible than the indigenous breeds (Ullah *et al*., 2022). In the recent past, diseases and vectors have been reported in areas which were not previously attributed to uncontrolled animal movements across the border without proper screening measures. For instance, *Theileria parva* has been isolated from cattle in Cameroon, where the principal tick vector, *R. appendiculatus* has not been reported (Silatsa *et al*., 2020). On the other hand, *Anaplasma centrale* has currently been detected in Burkina Faso without the presence of the tick vector (Ouedraogo *et al*., 2021). Approximately 4% of the screened ticks included in the studies harboured at least one species of TBDs. This highlights the critical role the ticks play in the transmission and maintenance of pathogens in the EAC countries. Additionally, a recent study on the distribution of zoonotic TBDs in sub-Saharan Africa revealed a surge in interest in studying TBDs, including bacterial, viral and parasitic in the last decade, associated with climate change (Djiman *et al*., 2024). Elsewhere, the emergence and re-emergence of human and animal diseases have led to increased caution and a need for active surveillance, catalysed by COVID-19. For instance, diseases such as thrombocytopenia syndrome in China (Yu *et al*., 2011), Heartland virus and Bourbon virus in the United States of America (Kosoy *et al*., 2014; Savage *et al*., 2013), and the geographical expansion of Crimean-Congo hemorrhagic fever and tick-borne encephalitis have received more attention (Estrada-Peña and Fuente, 2014).

The prevalence of the selected TBDs included in this study varied significantly. Theileria infection has been studied widely in the region compared to other TBDs, and this could be attributed to its severity and the high chemotherapeutic cost of clinical cases. Theileria parva has been ranked as the most important TBD with high mortalities, especially in exotic cattle breeds (Allan *et al*., 2021). Unlike babesiosis and anaplasmosis, where infection in calves causes mild clinical disease, allowing establishment of an endemic stability state, there is no age-related resistance for theileriosis (Johnsson *et al*., 2012). To some degree, the role of wildlife in the maintenance and spread of highly pathogenic theileria species increases the risk of infection of cattle with theileria than other TBDs (Allan *et al*., 2021). The tick species responsible for the transmission of the pathogen to a greater extent determines the presence and spread of the infection. Three-host ticks, such as Rhipicephalus appendiculatus that transmit Theileria, have been reported to be difficult to control, unlike one-host ticks (*Rhipicephalus decolaratus, R. microplus and R. annulatus*) that transmit Babesia and Anaplasma parasites. There is a higher likelihood of missing three host ticks when an animal is sprayed, as it spends a few days on one animal before dropping down, unlike one host that spends its entire life on one host. The findings agree with what has been reported in a similar systematic review of Tick-Borne Pathogens in Egypt, where approximately 74% of the included studies were on theileria infection (El-Alfy *et al*., 2022). However, several studies have reported co-infection with Babesia and Anaplasma infections. Because of the asymptomatic nature of Ehrlichia infection, a few studies have been carried to determine its prevalence, with no single study from Burundi, Rwanda and DRC within the study period under consideration for this review.

The overall pooled prevalence estimate was 24.3% (95% CI: 24.0-24.5), but varied significantly across the countries, which can be attributed to the differences in the sensitivities and specificities of the laboratory tests used and the number of studies from each country. Similarly, differences in the environmental factors such as temperature, humidity, vegetation cover, as well as cattle management factors that influence the presence and distribution of ticks, resulting in varied results (Gachohi *et a*l., 2012).

Subgroup analysis showed that serological studies produced a higher prevalence level compared to molecular techniques because they indicate exposure rather than actual infection. These methods are usually recommended for screening purposes as they provide historical information on exposure to pathogens. However, approximately 61% of the studies used molecular diagnostics techniques to detect TBDs, which agrees with other studies that these techniques have increased in the recent past due to high sensitivity and accuracy (Dong *et al*., 2008; Schreeg *et al*., 2016; Uilenberg *et al*., 2018; Springer *et al*., 2021; Mans *et al*., 2022).

Across the EAC, the pooled prevalence estimates for different TBDs ranged from 9.9% for Ehrlichia, 19.0%

babesia, 25.4% anaplasma to 27.9% theileria infection. From a similar study in Egypt, anaplasma infection reported the highest pooled prevalence of 43.9%, followed by theileria infection at 36.0% and 16.0% for babesia, with no reports on ehrlichia infection (El-Alfy *et al*., 2022). However, the study in Egypt included more tick-borne pathogens such as *Coxiella bruneti*, Rickettsia, Borrelia, and Crimean–Congo hemorrhagic fever and included several animal species; sheep, goats, equines, camels and buffaloes. However, in the EAC, *T. parva,* which causes severe and economically significant ECF diseases, calls for more investigation than the circulating *T. annulata* in Egypt.

The high pooled prevalence of Theileria in this study underscores the significance of the infection in cattle. Bovine theileriosis, caused by *T. parva* and *T. mutans,* is the leading TBD in East Africa, causing East Coast fever (ECF), which is confined to 15 countries in East and Southern Africa (Gharbi *et al.*, 2020). It causes huge economic losses of more than USD 300 million and mortality of approximately 1 million cattle annually (Nene *et al*., 2016). However, the infection has been detected in Cameroon even without the presence of the vector (Silatsa *et al*., 2020). Otherwise, it has neither been detected in cattle nor ticks in West Africa (Diarra *et al*., 2023), but a study in Uganda revealed the presence of the pathogen in ticks that are also widely distributed in West Africa (Byamukama *et al*., 2021). The hypothesis proposes that these ticks can acquire the infection but are incapable of transmitting it (Djamin *et al*., 2024). This calls for an investigation of the tick population to assess the pathogens and the potential risk that ticks pose to cattle. Tick studies have shown that 25% of *A. variegatum*, 40% of *R. decoloratus* and 25% *H. truncatum* were infected with *T. parva* (Djamin *et al*., 2024). The infection with other Theileria parasites has been reported to offer some protection against *T. parva* infection (Ahmed *et al*., 2022; Woolhouse *et al*., 2015). In contrast, a study in Kenya showed that animals previously infected with *T. parva* have been reported to come down with severe *T. mutans* infection (Irvin *et al*., 1972). This scenario emphasises the need for active surveillance, especially on less pathogenic species, both in animals and ticks, to assess their potential change in virulence as well as possible outbreaks.

Anaplasmosis, mainly caused by *A. marginalle* and *A. centrale,* which caused mild infection, was reported in the included studies. *A. marginalle* has been reported in more than 18 countries in sub-Saharan Africa, resulting in reduced production performance and high mortality in cattle (Djamin *et al*., 2024). On the other hand, *A centrale* has been utilised to produce live vaccine to control infections caused by the pathogenic *A. marginalle* (Hove *et al*., 2018). *A. ovis* causes a severe disease in sheep and goats and has been reported in South Africa (Chatanga *et al*., 2021; Ringo *et al*., 2022), Ethiopia (Teshale *et al*., 2018), East Africa (Ringo *et al*., 2019) and Senegal (Dahmani *et al.*, 2019). Most of the studies have detected Anaplasma parasites from animals and a few cases from ticks, which underscores the underutilization of ticks to assess the distribution of TBDs (Adjou Moumouni *et al*., 2018). The lack of studies to determine the role of tick vectors in the transmission of TBDs will severely compromise the effectiveness of control measures, which may not fully consider the role of ticks (Djamin *et al*., 2024).

Babesia bigemina and *B. bovis* are the primary causes of bovine babesiosis and have been reported to cause up to 80% mortality in exotic cattle breeds (Jacob *et al.*, 2020). In this study, bovine babesiosis was investigated in forty-one studies from cattle samples compared to only six from tick tissues. This agrees with what Djamin *et al*. (2024) reported, that 21 studies investigated babesia in animals and only four in ticks. Babesiosis has been reported in approximately 15 countries in sub-Saharan Africa (Djamin *et al*., 2024). Research has shown that *B. bovis* is more virulent and causes economic losses up to 20 times more than *B. bigemina* (Bock *et al*., 2004). The abundance of *R. annulatus* and *R. microplus* ticks in the EAC and the reports that they are the primary vectors of babesia parasites expose a research gap to begin utilising tick sources to assess their role in the transmission dynamics of babesiosis.

In contrast with the findings of this study, Djamin *et al*. (2024) reported that Ehrlichia infection was the most commonly studied zoonotic tick-borne disease in sub-Saharan Africa and attributed it to the widespread Amblyomma tick distribution and the zoonotic nature. *Ehrlichia ruminantium* is responsible for heartwater disease, which causes huge losses in exotic breeding ruminants (Hurtado *et al*., 2018). The involvement of the *Rhipicephalus microplus* tick species, a highly invasive and resistant to acaricides, poses a great challenge to livestock farming in sub-Saharan Africa (Yessinou *et al*., 2018; Vilela *et al*., 2020; Some *et al*., 2023). The increased attention on heartwater investigation stems from the high abundance of the tick vector in the region (Allsopp, 2010). On the other hand, large ruminants being the definitive hosts and early indicators of disease provide a platform for monitoring their epidemiology and public health implications (Van Heerden *et al*., 2004; Gajadhar *et al*., 2010). Therefore, future studies should prioritise investigating animals, ticks and humans using the "One Health" approach to better understand the transmission dynamics. Ticks being the natural reservoirs for several pathogens underscores the need for screening of ticks to elucidate the potential risks and the possible effective and sustainable preventive measures.

Our review's strengths include a thorough search of many databases to find relevant research on TBD-infected cattle populations and generate information that policymakers might utilise to improve or modify their region's already-existing control and prevention measures. In order to support efforts to achieve the Sustainable Development Goals of the UN, we also evaluated the spatio-temporal distribution and pointed out risk areas that should be given priority for prevention and control activities. This review also emphasised the necessity of surveys in places like Burundi, Rwanda, and the Democratic Republic of the Congo, where data is insufficient. The limitations of this study should be taken into consideration when interpreting its results. For example, the prevalence reported in various studies was derived from laboratory tests with varying specificities and sensitivities. The detection rate and the true prevalence of the burden of infections is influenced by serological tests that only identify antibodies against TBDs rather than the infection itself. Furthermore, the varied number of research studies and samples examined in many nations is likely to produce inaccurate comparison results. There is a chance that the prevalence could be overestimated or underestimated because the WOAH advises using sensitive molecular testing for routine diagnosis in order to get accurate data on the true status of TBDs. However, these methods are costly and demand specialised knowledge; therefore not easily accessible in many EAC nations with limited resources. Rather than using representative national surveillance data, the included papers were from academic research that is impacted by academic activities within a nation.

Conclusion

The findings of this review highlight the burden and distribution of tick-borne pathogens in the East African Community with potential economic significance, underlining the importance of their investigation. With the endemicity of theileriosis in EAC, it was studied more than other TBDs. For the studied pathogens, cattle were the main population of focus, with a few investigating their abundance in ticks. The number of studies has significantly increased, but there are some countries with limited studies on these significant pathogens. Despite several efforts to control TBDs in livestock, they are still a major problem across the East African countries with varying degrees of severity. Therefore, there is a need for more in-depth studies to elucidate the actual burden of TBDs and the role of large ruminants as reservoirs of some of these pathogens to humans. There is also a need to utilise ticks to assess the distribution of pathogens in surveillance studies in the region.

CONFLICT OF INTEREST

The authors declare that they have no conflicts of interest

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