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A systematic review and meta-analysis on prevalence of bovine trypanosomosis in East Africa

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ABSTRACT

Bovine trypanosomosis is an incapacitating and lethal ailment brought about by protozoan parasites of the genus Trypanosoma. The disease leads to losses in livestock and agricultural productivity, resulting in significant socio-economic repercussions. In East Africa, trypanosomosis has been endemic for an extensive period due to ecological factors and vector biology that facilitate the persistent circulation of trypanosomes. This investigation outlines the occurrence of bovine trypanosomosis in East Africa through a meta-analysis. A thorough search was conducted on PubMed, Google Scholar, Scopus, Web of Science and AJOL. Suitable studies were chosen using inclusion and exclusion criteria. The prevalence was estimated through a random effect model. Publication bias and the variation in prevalence estimates due to heterogeneity were also evaluated. The analysis was performed on 115 studies that contained relevant prevalence data. The collective estimate of bovine trypanosomosis prevalence across the studies stood at 12% (95% CI: 11, 13), ranging from 1% (95% CI: 0, 2) to 51% (95% CI: 45, 58). The subgroup analysis by country revealed considerable disparities in prevalence. The highest estimated prevalence was 24% (95% CI: 18, 30) in Somalia, whereas the lowest prevalence was observed in Ethiopia at 10% (95% CI: 9, 11). A significant level of heterogeneity was noted in most pooled estimates, even after conducting subgroup analysis. The visual examination of the funnel plot and the Egger's regression asymmetry coefficient (b = −5.13, 95% CI: −7.49, −2.76, $p = 0.00$) and Begg's plot ($p = 0.00$) indicate the presence of publication bias. In conclusion, bovine trypanosomosis is a pervasive and noteworthy malady affecting livestock. The findings of this investigation imply a high prevalence of bovine trypanosomosis in the majority of the countries under scrutiny. Despite the well-known hindrance that livestock trypanosomosis poses to livestock production in Africa, little attention has been devoted to the trypanosomosis situation, particularly in East African nations.

1. Introduction

African animal trypanosomiasis (AAT) is a parasitic ailment that leads to significant economic losses in livestock due to anemia, loss of condition, and emaciation. AAT is primarily found in regions of Africa where its biological vector, the tsetse fly, is present (CFSPH,

Abbrivations: AAT, African Animal Trypanosomosis; CFSPH, Center for Food Security and Public Health; CoCoPop, Condition, Context, Population; FAO, FOOD and Agricultural Organization; ILRI, International Livestock Research Institute.

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2009). Bovine trypanosomosis persists as the primary obstacle to livestock production in sub-Saharan Africa, posing a threat to the lives of 55 million individuals. The infection risk for both humans and domestic animals has profoundly impacted the social, economic, and agricultural development of communities residing within tsetse-infested areas, which encompass over 10 million square kilometers of Africa between 14°N and 29°S of the continent (FAO, 2002).

Bovine trypanosomosis represents a vector-borne affliction in cattle caused by trypanosome infection. In sub-Saharan Africa, there exist >50 million cattle that are susceptible to this ailment, thereby potentially incurring substantial economic losses (Leta et al., 2016; Holt et al., 2016). The prevalence of trypanosomosis in cattle hosts exhibits intricate variations due to diverse determinants, encompassing vector population density, ecological factors in a given area, livestock management systems, and the trypanotolerant status of the cattle (Sow et al., 2013; Lelisa et al., 2016).

The limitations and varying levels of sensitivity of the different diagnostic tools employed in epidemiological studies can also impact the true depiction of bovine trypanosomosis prevalence (Moti et al., 2014; Abdi et al., 2017). Moreover, studies conducted in multiple locations have unveiled heterogeneity, as evidenced by a cursory examination of prevalence data concerning bovine trypanosomiasis (Adam et al., 2012; Nakayima et al., 2012). Numerous factors and conditions might have contributed to these variations (Abdi et al., 2017). According to meta-analyzed data obtained from Ethiopia, the geographical location and year of the study might have influenced the heterogeneity observed in disease prevalence data (Leta et al., 2016). Additionally, meta-analyzed data from select African countries (2000–2018) demonstrates that the choice of diagnostic method served as the primary factor influencing heterogeneity, whereas sample size made only a minor contribution (Ebhodaghe et al., 2018).

Bovine trypanosomosis should be closely monitored in countries where it has been endemic for an extended period of time in order to establish a definitive pattern of prevalence both before and after implementing control measures. However, the scarcity of resources in Africa has resulted in this practice being rarely observed. Meta-analyses provide a viable solution to address this issue by amalgamating existing data and processing mean-prevalence data over a specified timeframe and in a designated area. This methodology proves invaluable in comprehensively evaluating the dynamics of the disease in Africa and serves as a guide to prioritize control efforts in all endemic regions (Holt et al., 2016).

Due to the disease's propensity to transcend national borders and the fact that control programs for bovine trypanosomosis are typically devised at the national level, the efficacy of control efforts may be compromised (Ahmed et al., 2016). A collaborative endeavor that spans national boundaries is imperative to eradicate the disease in Africa (Adam et al., 2012). Establishing the prevalence of the disease on a country-by-country basis and consolidating all pertinent and reliable published data from endemic countries to present a comprehensive prevalence overview for sub-Saharan Africa is a fundamental measure that has the potential to encourage the necessary cooperation in control efforts.

Several epidemiological investigations have been carried out on the occurrence of trypanosomosis in cattle. Various authors have conducted studies on the prevalence and incidence of trypanosomosis in different East African countries. These studies have reported a prevalence rate of 11.33% in Ethiopia (Dagnachew et al., 2011), 41% in Uganda (Angwech et al., 2015), 15.6% in Kenya (Okello et al., 2022), and 17.2% in Tanzania (Simwango et al., 2017). These epidemiological studies serve as evidence of the frequent occurrence of the disease, particularly in the humid and semi-humid regions of sub-Saharan Africa. Although there are limited reports of animal trypanosomosis in some East African countries, epidemiological research suggests that the disease is endemic, especially in nations with a significant vector population. Trypanosomosis affects both humans, causing sleeping sickness, and animals, causing nagana, and is prevalent in 37 sub-Saharan countries. Currently, approximately 60 million people and around 50 million cattle are at risk of infection (FAO, 2011). The International Livestock Research Institute (ILRI) has identified trypanosomosis as one of the top 10 global cattle diseases that have a significant impact on impoverished nations (Perry et al., 2002).

Considering that African Animal Trypanosomiasis (AAT) continues to pose a significant threat to livestock in sub-Saharan Africa, there is a dearth of comprehensive epidemiological data and effective prevention and control strategies for bovine trypanosomosis in East Africa (Morrison et al., 2016). Furthermore, no meta-analysis or systematic review incorporating multiple individual studies or addressing specific clinical inquiries has been conducted in East Africa. Therefore, the aim of this systematic review and meta-analysis was to provide a consolidated prevalence of bovine trypanosomosis based on the available literature in East Africa.

2. Methods

The PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-analysis) checklist was employed as a guiding tool for the systematic review conducted by Page et al. (2021). The purpose of employing this checklist was to ensure the inclusion of pertinent data from the selected studies. The primary outcome of interest in this study was the prevalence of bovine trypanosomosis in East Africa.

2.1. Literature search strategy and eligibility criteria

The time frame allocated for the literature search pertaining to the prevalence of bovine trypanosomosis spanned from September 2022 to December 2022. A comprehensive and meticulous search strategy was implemented to identify all relevant studies. Databases such as PubMed, Scopus, AJOL, Science Direct, Web of Science, and Google Scholar were utilized in order to conduct the literature searches and identify the studies that met the inclusion criteria. In this systematic review and meta-analysis, the CoCoPop (Condition, Context, and Population) framework was employed to ascertain the eligibility of the included articles. The condition under consideration was bovine trypanosomosis (Co), the context was East Africa (Co), and the population of interest was cattle (Pop). The search strategy encompassed Medical Subject Heading (MeSH) terms as well as a range of significant keywords. The research question guiding

this study was "what is the prevalence of bovine trypanosomosis in domestic cattle in East Africa?"

During the online search, title-related keywords were combined using the Boolean operator "OR/AND." The search terms employed were as follows: (trypanosomosis OR trypanosomiasis infection OR bovine trypanosomosis) AND (epidemiology OR prevalence OR infection rate OR spatial distribution) AND (cattle OR bovine OR animals infected) AND (East Africa). To avoid duplications, all identified studies were imported into the EndNote 20 software system.

2.2. Inclusion and exclusion criteria

The criteria for inclusion in this research were as follows: a research article had to be (i) published in a reputable scholarly journal, (ii) written in the English language, (iii) a cross-sectional study, (iv) conducted in the region of East Africa, (v) focusing on infected cattle as the species under investigation, with clear specifications regarding the size of the study population, the diagnostic technique employed, and the sampling method utilized, and (vi) published between the years 2000 and 2022 (Fig. 1). Experimental studies, outbreak reports, case series, traditional reviews, cohort studies, and case-control studies, as well as publications lacking detailed descriptions of the diagnostic tools employed, the study design, and/or the sources of the samples, and reports solely based on clinical signs, were excluded, despite their reporting of the disease's prevalence. Furthermore, studies that reported trypanosomosis infection across multiple species without providing a breakdown of the data at the species level were also excluded.

2.3. Study quality assessment

The literature search was carried out independently by two researchers, and any disagreements were resolved through consensus based on standardized extraction forms in order to ensure consistency and accuracy. The data was subsequently extracted and stored in Microsoft Office Excel 2019.

2.4. Data extraction

The eligible studies provided the following information: the first author, publication year, study year, country, study design,

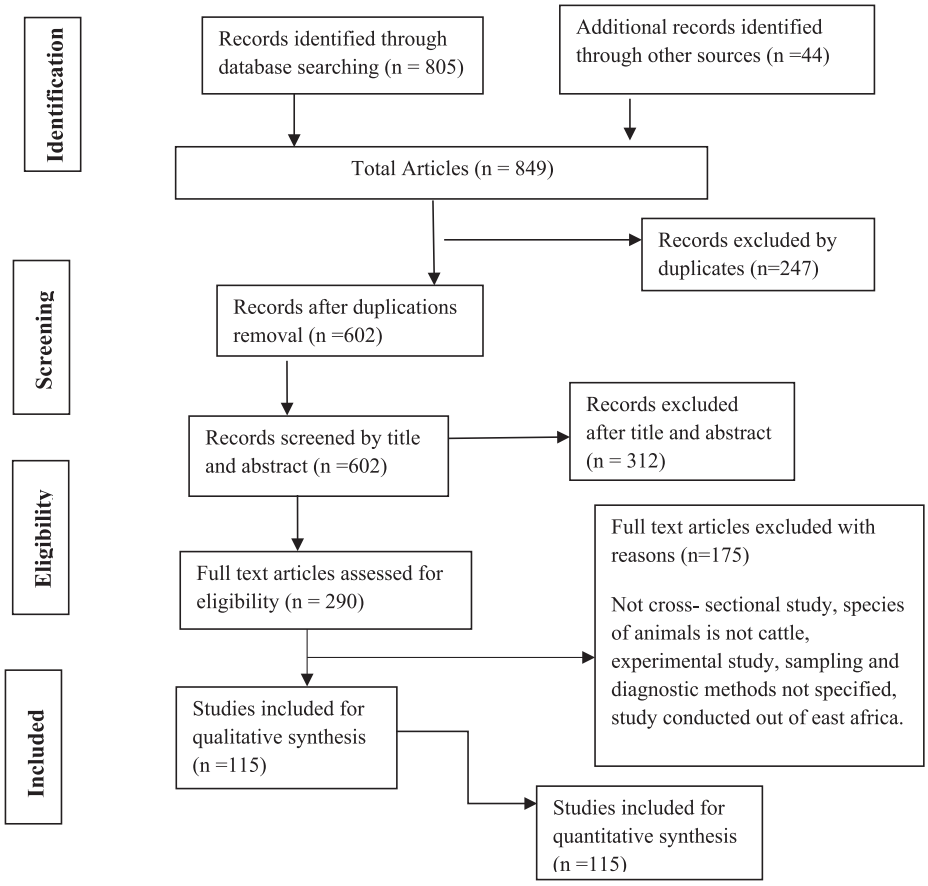

Fig. 1. PRISMA flow chart for selection of study for the Prevalence of Bovine trypanosomosis in East Africa from 2000 to 2022.

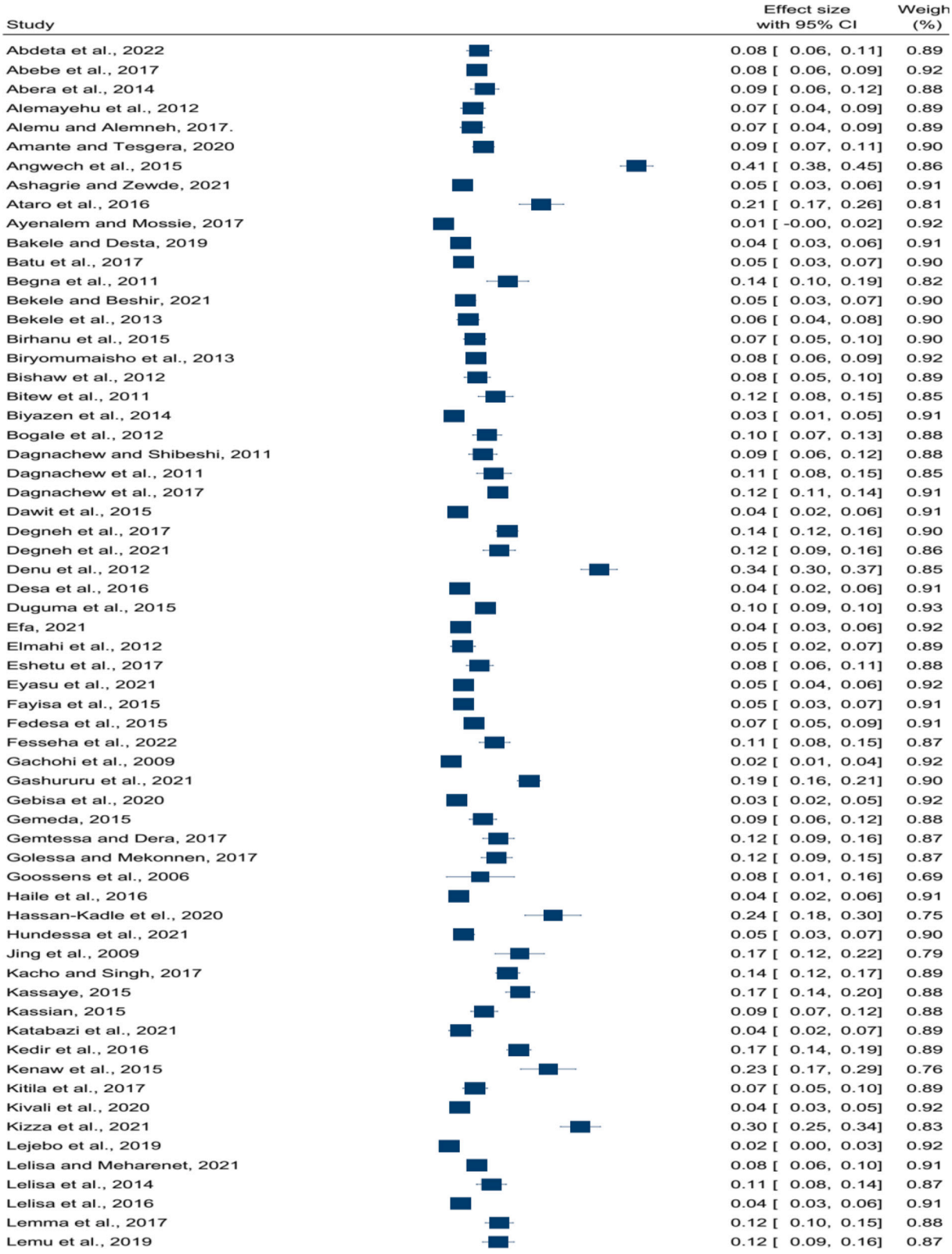

Fig. 2. Forest plot for pooled prevalence of bovine trypanosomosis in East Africa.

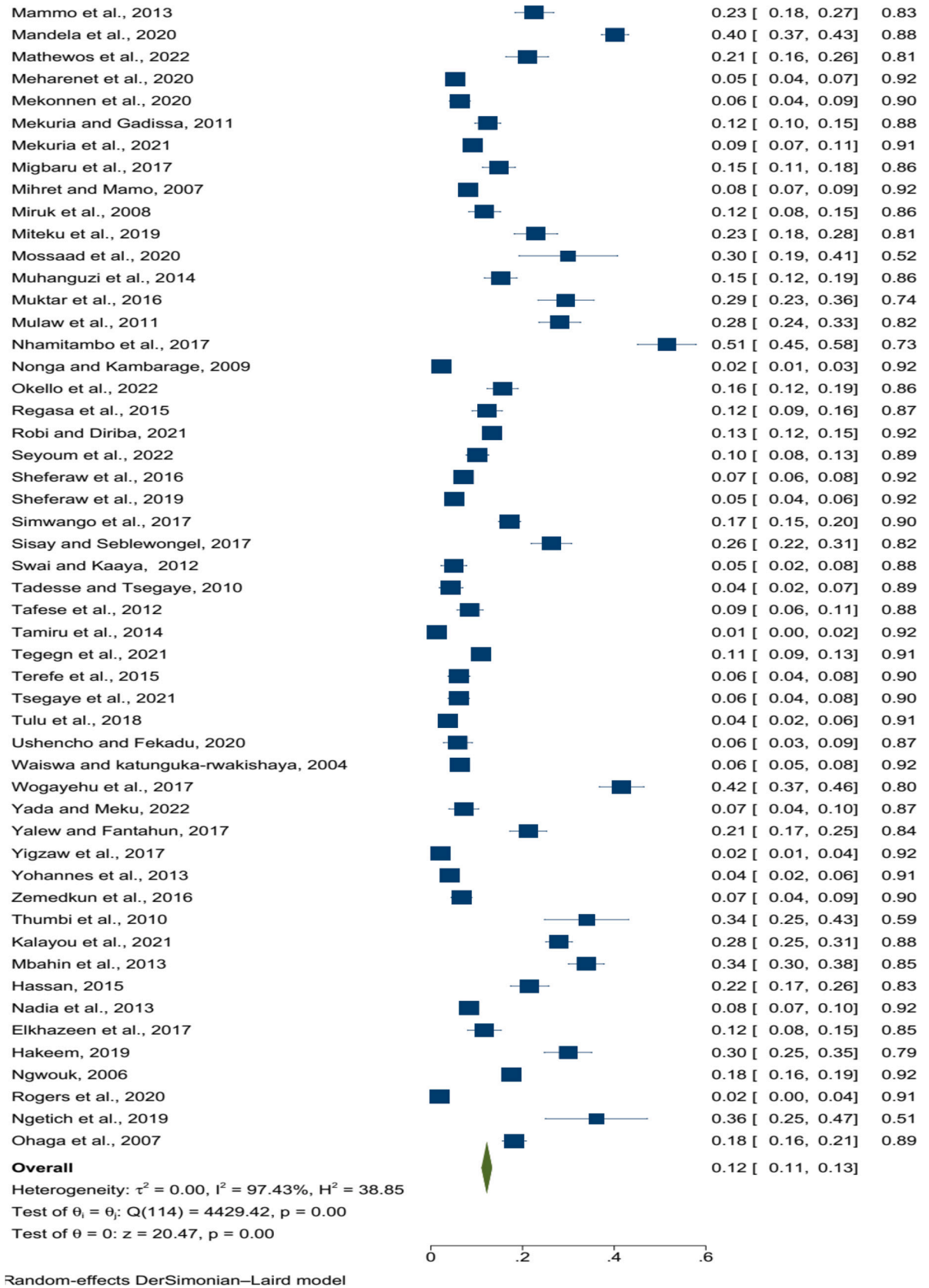
Mammo et al., 2013 0.23 [0.18, 0.27] 0.83
Mandela et al., 2020 0.40 [0.37, 0.43] 0.88
Mathewos et al., 2022 0.21 [0.16, 0.26] 0.81
Meharenet et al., 2020 0.05 [0.04, 0.07] 0.92
Mekonnen et al., 2020 0.06 [0.04, 0.09] 0.90
Mekuria and Gadissa, 2011 0.12 [0.10, 0.15] 0.88
Mekuria et al., 2021 0.09 [0.07, 0.11] 0.91
Migbaru et al., 2017 0.15 [0.11, 0.18] 0.86
Mihret and Mamo, 2007 0.08 [0.07, 0.09] 0.92
Miruk et al., 2008 0.12 [0.08, 0.15] 0.86
Miteku et al., 2019 0.23 [0.18, 0.28] 0.81
Mossaad et al., 2020 0.30 [0.19, 0.41] 0.52
Muhanguzi et al., 2014 0.15 [0.12, 0.19] 0.86
Muktar et al., 2016 0.29 [0.23, 0.36] 0.74
Mulaw et al., 2011 0.28 [0.24, 0.33] 0.82
Nhamitambo et al., 2017 0.51 [0.45, 0.58] 0.73
Nonga and Kambarage, 2009 0.02 [0.01, 0.03] 0.92
Okello et al., 2022 0.16 [0.12, 0.19] 0.86
Regasa et al., 2015 0.12 [0.09, 0.16] 0.87
Robi and Diriba, 2021 0.13 [0.12, 0.15] 0.92
Seyoum et al., 2022 0.10 [0.08, 0.13] 0.89
Sheferaw et al., 2016 0.07 [0.06, 0.08] 0.92
Sheferaw et al., 2019 0.05 [0.04, 0.06] 0.92
Simwango et al., 2017 0.17 [0.15, 0.20] 0.90
Sisay and Seblewongel, 2017 0.26 [0.22, 0.31] 0.82
Swai and Kaaya, 2012 0.05 [0.02, 0.08] 0.88
Tadesse and Tsegaye, 2010 0.04 [0.02, 0.07] 0.89
Tafese et al., 2012 0.09 [0.06, 0.11] 0.88
Tamiru et al., 2014 0.01 [0.00, 0.02] 0.92
Tegegn et al., 2021 0.11 [0.09, 0.13] 0.91
Terefe et al., 2015 0.06 [0.04, 0.08] 0.90
Tsegaye et al., 2021 0.06 [0.04, 0.08] 0.90
Tulu et al., 2018 0.04 [0.02, 0.06] 0.91
Ushencho and Fekadu, 2020 0.06 [0.03, 0.09] 0.87
Waiswa and katunguka-rwakishaya, 2004 0.06 [0.05, 0.08] 0.92
Wogayehu et al., 2017 0.42 [0.37, 0.46] 0.80
Yada and Meku, 2022 0.07 [0.04, 0.10] 0.87
Yalew and Fantahun, 2017 0.21 [0.17, 0.25] 0.84
Yigzaw et al., 2017 0.02 [0.01, 0.04] 0.92
Yohannes et al., 2013 0.04 [0.02, 0.06] 0.91
Zemedkun et al., 2016 0.07 [0.04, 0.09] 0.90
Thumbi et al., 2010 0.34 [0.25, 0.43] 0.59
Kalayou et al., 2021 0.28 [0.25, 0.31] 0.88
Mbahin et al., 2013 0.34 [0.30, 0.38] 0.85
Hassan, 2015 0.22 [0.17, 0.26] 0.83
Nadia et al., 2013 0.08 [0.07, 0.10] 0.92
Elkhazeen et al., 2017 0.12 [0.08, 0.15] 0.85
Hakeem, 2019 0.30 [0.25, 0.35] 0.79
Ngwouk, 2006 0.18 [0.16, 0.19] 0.92
Rogers et al., 2020 0.02 [0.00, 0.04] 0.91
Ngetich et al., 2019 0.36 [0.25, 0.47] 0.51
Ohaga et al., 2007 0.18 [0.16, 0.21] 0.89
Overall 0.12 [0.11, 0.13]
Heterogeneity: τ^2 = 0.00, I^2 = 97.43%, H^2 = 38.85
Test of $\theta_i = \theta_j$: Q(114) = 4429.42, p = 0.00
Test of θ = 0: z = 20.47, p = 0.00
0
.2
.4
.6
Random-effects DerSimonian–Laird model

Fig. 2. (*continued*).

sampling method, diagnostic method, sample size, and prevalence. In cases where multiple diagnostic techniques were used, the most sensitive technique was chosen. Trypanosomosis prevalence was defined as the frequency of cases caused by *T. congolense, T. vivax*, and/or *T. brucei* in a specific population over a specified period of time. From the extracted data, estimates and confidence intervals at the study level were generated.

2.5. Data synthesis and statistical analysis

Data analysis was conducted in a series of steps utilizing STATA version 17. Initially, the mean prevalence and event rate were computed by tallying the number of positive cases across all considered studies and dividing it by the total sample size. The 95% confidence interval was determined through the utilization of the exact binomial method. The combined prevalence estimates for bovine trypanosomosis in the general population, along with their corresponding 95% confidence intervals, were calculated employing the DerSimonian and Laird random effects model meta-analysis (Harris et al., 2008).

The evaluation of heterogeneity between studies involved the utilization of the Cochran's Q test, reported as a *p*-value, and the inverse variance index (I^2), which elucidates the proportion of observed total variation between studies attributed to heterogeneity rather than chance. I^2 values of 25, 50, and 75% signify low, moderate, and high degrees of heterogeneity, respectively. An I^2 value of 0% indicates the absence of observed heterogeneity. Q represents the weighted sum of squares on a standardized scale and is reported alongside a *p*-value, with lower *p*-values indicating the presence of heterogeneity. The presence of heterogeneity among studies was assessed through the implementation of a forest plot diagram and a Galbraith plot. The forest plot diagram visualized the outcomes of the meta-analysis, displaying the weight of studies and their corresponding confidence intervals for all included studies alongside the pooled effect size (Higgins and Thompson, 2002).

To identify the potential sources of heterogeneity among studies, sub-group analyses were conducted for the prevalence of bovine trypanosomosis. The variables considered in these sub-group analyses included the country of study, sample size, diagnostic technique, study year, and sampling method. The examination of publication bias initially involved a visual assessment using a funnel plot, followed by Egger's regression asymmetry test. Begge's test was employed to statistically evaluate the significance of the bias (Borenstein et al., 2009). Unbiased estimates were calculated using the Duval and Tweedie non-parametric 'fill and trim' linear random method (Duval and Tweedie, 2000). For each study, the prevalence with its corresponding 95% confidence interval, as well as the overall random-effects pooled estimate of all the studies, were presented (Fig. 2).

3. Results

3.1. Literature search results

A literature search was conducted from September to December 2022. A total of 805 studies were identified through an electronic search, and an additional 44 studies were identified through other sources in the regions of East Africa and cattle domain restrictions. After removing 247 duplicate studies, 602 articles remained and undergone screening based on their title and abstract. Out of these, 312 articles were determined to be unsuitable based on their title and abstract. The eligibility of the 290 full-text article abstracts was then assessed using predetermined criteria. 175 articles were excluded from the analysis because they did not meet the requirements of being cross-sectional studies, did not involve cattle as study animals, did not specify their sampling and diagnostic procedures, or were not conducted in East Africa. Unfortunately, a total of 115 studies met the inclusion criteria for the meta-analysis. The flowchart depicting the process of selecting eligible studies is presented in Fig. 1.

3.2. Descriptive characteristics of included studies

The studies included in this systematic review and meta-analysis were conducted in various East African countries, namely Ethiopia, Uganda, Tanzania, Kenya, Sudan, Somalia, and Rwanda, between the years 2000 and 2022. A total of 115 studies were conducted in these seven countries using a cross-sectional study design that employed cluster, multistage, purposive, simple random, stratified, or systematic sampling procedures. Ethiopia had the highest number of studies, with 83 out of the 115 included studies originating from this country. Uganda had 9 studies, Kenya had 8 studies, Sudan had 7 studies, Tanzania had 6 studies, while Rwanda and Somalia each had 1 study. No study was published from Eritrea, Djibouti, Burundi, South Sudan, and other East African nations. In each study, the presence of infection was determined using either parasitological or molecular diagnostic methods. A total of 77,407 cattle were included in the estimation of the pooled prevalence of bovine trypanosomosis in East Africa. The sample size of the studies ranged from 59 cattle (Goossens et al., 2006) to 7021 cattle (Duguma et al., 2015). Out of the total sample size, 8993 cattle were found to be positive for bovine trypanosomosis. The overall apparent infection rate of bovine trypanosomosis in cattle was 12%. Specific information about the characteristics of the included studies can be found in Table 1.

3.3. Meta- analysis and meta-regression

A comprehensive total of 115 research papers were included in the meta-analysis to ascertain the overall amalgamated prevalence

Table 1
Descriptive summary of the included studies in the systematic review and meta-analysis of the prevalence of bovine trypanosomosis in East Africa from 2000 to 2022

Authors	P. year	S. year	country	S. design	S. method	D. method	S. size	E	E. rate	LCI	UCI
Abdeta et al., 2022	2022	2020	Ethiopia	Cs	Simple random	Parasitological	440	36	0.082	0.056	0.107
Abebe et al., 2017	2017	2016	Ethiopia	Cs	Simple random	Parasitological	1508	118	0.078	0.065	0.092
Abera et al., 2014	2014	2013	Ethiopia	Cs	Simple random	Parasitological	384	36	0.094	0.065	0.123
Alemayehu et al., 2012	2012	2011	Ethiopia	Cs	Simple random	Parasitological	391	27	0.069	0.044	0.094
Alemu and Alemneh, 2017.	2017	2016	Ethiopia	Cs	Simple random	Parasitological	384	26	0.068	0.043	0.093
Amante and Tesgera, 2020	2020	2020	Ethiopia	Cs	Multistage sampling	Parasitological	638	58	0.091	0.069	0.113
Angwech et al., 2015	2015	2011	Uganda	Cs	Simple random	Molecular	816	338	0.414	0.380	0.448
Ashagrie and Zewde, 2021	2021	2021	Ethiopia	Cs	Simple random	Parasitological	571	27	0.047	0.030	0.065
Ataro et al., 2016	2016	2011	Ethiopia	Cs	Simple random	Parasitological	300	64	0.213	0.167	0.260
Ayenalem and Mossie, 2017	2017	2014	Ethiopia	Cs	Simple random	Parasitological	384	3	0.008	0.001	0.017
Bakele and Desta, 2019	2019	2018	Ethiopia	Cs	Simple random	Parasitological	544	23	0.042	0.025	0.059
Batu et al., 2017	2017	2014	Ethiopia	Cs	Simple random	Parasitological	445	22	0.049	0.029	0.070
Begna et al., 2011	2011	2011	Ethiopia	Cs	Simple random	Parasitological	246	35	0.142	0.099	0.186
Bekele and Beshir, 2021	2021	2021	Ethiopia	Cs	Simple random	Parasitological	432	23	0.053	0.032	0.074
Bekele et al., 2013	2013	2011	Ethiopia	Cs	Simple random	Parasitological	410	24	0.059	0.036	0.081
Birhanu et al., 2015	2015	2015	Ethiopia	Cs	Simple random	Molecular	493	36	0.073	0.050	0.096
Biryomumaisho et al., 2013	2013	2011	Uganda	Cs	Purposive sampling	Parasitological	1891	144	0.076	0.064	0.088
Bishaw et al., 2012	2012	2009	Ethiopia	Cs	Simple random	Parasitological	384	30	0.078	0.051	0.105
Bitew et al., 2011	2011	2009	Ethiopia	Cs	Simple random	Parasitological	300	35	0.117	0.080	0.153
Biyazen et al., 2014	2014	2014	Ethiopia	Cs	Simple random	Molecular	384	11	0.029	0.012	0.045
Bogale et al., 2012	2012	2011	Ethiopia	Cs	Simple random	Parasitological	384	38	0.099	0.069	0.129
Dagnachew and Shibeshi, 2011	2011	2009	Ethiopia	Cs	Simple random	Parasitological	368	33	0.090	0.060	0.119
Dagnachew et al., 2011	2011	2009	Ethiopia	Cs	Simple random	Parasitological	300	34	0.113	0.077	0.149
Dagnachew et al., 2017	2017	2012	Ethiopia	Cs	Multistage sampling	Parasitological	1435	175	0.122	0.105	0.139
Dawit et al., 2015	2015	2015	Ethiopia	Cs	Simple random	Parasitological	385	14	0.036	0.018	0.055
Degneh et al., 2017	2017	2016	Ethiopia	Cs	Purposive sampling	Parasitological	930	131	0.141	0.119	0.163
Degneh et al., 2021	2021	2018	Ethiopia	Cs	Simple random	Parasitological	370	46	0.124	0.091	0.158
Denu et al., 2012	2012	2008	Ethiopia	Cs	Multistage sampling	Parasitological	600	201	0.335	0.297	0.373
Desa et al., 2016	2016	2009	Ethiopia	Cs	Simple random	Parasitological	410	17	0.041	0.022	0.061
Duguma et al., 2015	2015	2012	Ethiopia	Cs	Simple random	Parasitological	7021	675	0.096	0.089	0.103
Efa, 2021	2021	2019	Ethiopia	Cs	Simple random	Parasitological	819	36	0.044	0.030	0.058
Elmahi et al., 2012	2012	2012	Sudan	Cs	Simple random	Parasitological	271	13	0.048	0.023	0.073
Eshetu et al., 2017	2017	2016	Ethiopia	Cs	Systematic random	Parasitological	384	32	0.083	0.056	0.111
Eyasu et al., 2021	2021	2019	Ethiopia	Cs	Systematic random	Parasitological	964	48	0.050	0.036	0.064
Fayisa et al., 2015	2015	2014	Ethiopia	Cs	Simple random	Parasitological	556	27	0.049	0.031	0.066
Fedesa et al., 2015	2015	2014	Ethiopia	Cs	Simple random	Parasitological	650	46	0.071	0.051	0.090
Fesseha et al., 2022	2022	2021	Ethiopia	Cs	Simple random	Parasitological	384	44	0.115	0.083	0.146
Gachohi et al., 2009	2009	2005	Kenya	Cs	Cluster sampling	Parasitological	477	11	0.023	0.010	0.037
Gashururu et al., 2021	2021	2021	Rwanda	Cs	Stratified sampling	Molecular	1037	194	0.187	0.163	0.211
Gebisa et al., 2020	2020	2019	Ethiopia	Cs	Multistage sampling	Parasitological	1046	36	0.034	0.023	0.045
Gemeda, 2015	2015	2011	Ethiopia	Cs	Simple random	Parasitological	400	36	0.090	0.062	0.118
Gemtessa and Dera, 2017	2017	2010	Ethiopia	Cs	Simple random	Parasitological	391	48	0.123	0.090	0.155
Golessa and Mekonnen, 2017	2017	2016	Ethiopia	Cs	Multistage sampling	Parasitological	395	47	0.119	0.087	0.151
Goossens et al., 2006	2006	2002	Tanzania	Cs	Simple random	Molecular	59	5	0.085	0.014	0.156
Haile et al., 2016	2016	2015	Ethiopia	Cs	Simple random	Parasitological	488	19	0.039	0.022	0.056
Hassan-Kadle et al., 2020	2020	2018	Somalia	Cs	Simple random	Molecular	202	48	0.238	0.179	0.296
Hundessa et al., 2021	2021	2020	Ethiopia	Cs	Simple random	Parasitological	400	20	0.050	0.029	0.071
Jing et al., 2009	2009	2008	Uganda	Cs	Simple random	Molecular	203	34	0.167	0.116	0.219
Kacho and Singh, 2017	2017	2008	Ethiopia	Cs	Simple random	Parasitological	780	111	0.142	0.118	0.167
Kassaye, 2015	2015	2013	Ethiopia	Cs	Simple random	Parasitological	599	101	0.169	0.139	0.199
Kassian, 2015	2015	2015	Tanzania	Cs	Simple random	Parasitological	420	39	0.093	0.065	0.121
Katabazi et al., 2021	2021	2020	Uganda	Cs	Simple random	Molecular	254	11	0.043	0.018	0.068
Kedir et al., 2016	2016	2015	Ethiopia	Cs	Simple random	Parasitological	862	143	0.166	0.141	0.191
Kenaw et al., 2015	2015	2015	Ethiopia	Cs	Simple random	Parasitological	202	46	0.228	0.170	0.286

(*continued on next page*)

Table 1 (*continued*)

Authors	P. year	S. year	country	S. design	S. method	D. method	S. size	E	E. rate	LCI	UCI
Kitila et al., 2017	2017	2015	Ethiopia	Cs	Simple random	Parasitological	408	30	0.074	0.048	0.099
Kivali et al., 2020	2020	2012	Kenya	Cs	Simple random	Molecular	888	37	0.042	0.029	0.055
Kizza et al., 2021	2021	2020	Uganda	Cs	Simple random	Molecular	460	136	0.296	0.254	0.337
Lejebo et al., 2019	2019	2019	Ethiopia	Cs	Simple random	Parasitological	384	7	0.018	0.005	0.032
Lelisa and Meharenet, 2021	2021	2018	Ethiopia	Cs	Purposive sampling	Parasitological	730	57	0.078	0.059	0.098
Lelisa et al., 2014	2014	2010	Ethiopia	Cs	Systematic random	Parasitological	389	42	0.108	0.077	0.139
Lelisa et al., 2016	2016	2015	Ethiopia	Cs	Simple random	Parasitological	566	24	0.042	0.026	0.059
Lemma et al., 2017	2017	2015	Ethiopia	Cs	Simple random	Parasitological	498	62	0.124	0.096	0.153
Lemu et al., 2019	2019	2018	Ethiopia	Cs	Simple random	Parasitological	384	47	0.122	0.090	0.155
Mammo et al., 2013	2013	2012	Ethiopia	Cs	Simple random	Parasitological	385	87	0.226	0.184	0.268
Mandela et al., 2020	2020	2020	Uganda	Cs	Purposive sampling	Molecular	1090	438	0.402	0.373	0.431
Mathewos et al., 2022	2022	2021	Ethiopia	Cs	Simple random	Parasitological	300	63	0.210	0.164	0.256
Meharenet et al., 2020	2020	2018	Ethiopia	Cs	Stratified sampling	Parasitological	1517	82	0.054	0.043	0.065
Mekonnen et al., 2020	2020	2017	Ethiopia	Cs	Purposive sampling	Parasitological	460	29	0.063	0.041	0.085
Mekuria and Gadissa, 2011	2011	2009	Ethiopia	Cs	Simple random	Parasitological	540	67	0.124	0.096	0.152
Mekuria et al., 2021	2021	2019	Ethiopia	Cs	Simple random	Parasitological	1280	116	0.091	0.075	0.106
Migbaru et al., 2017	2017	2014	Ethiopia	Cs	Simple random	Parasitological	384	57	0.148	0.113	0.184
Mihret and Mamo, 2007	2007	2006	Ethiopia	Cs	Multistage sampling	Parasitological	3360	275	0.082	0.073	0.091
Miruk et al., 2008	2008	2006	Ethiopia	Cs	Purposive sampling	Parasitological	341	40	0.117	0.083	0.151
Miteku et al., 2019	2019	2014	Ethiopia	Cs	Simple random	Parasitological	310	71	0.229	0.182	0.276
Mossaad et al., 2020	2020	2019	Sudan	Cs	Simple random	Molecular	70	21	0.300	0.193	0.407
Muhanguzi et al., 2014	2014	2011	Uganda	Cs	Cluster sampling	Molecular	401	61	0.152	0.117	0.187
Muktar et al., 2016	2016	2015	Ethiopia	Cs	Simple random	Parasitological	217	64	0.295	0.234	0.356
Mulaw et al., 2011	2011	2010	Ethiopia	Cs	Systematic random	Parasitological	384	108	0.281	0.236	0.326
Nhamitambo et al., 2017	2017	2016	Tanzania	Cs	Stratified sampling	Molecular	237	122	0.515	0.451	0.578
Nonga and Kambarage, 2009	2009	2009	Tanzania	Cs	Simple random	Parasitological	691	16	0.023	0.012	0.034
Okello et al., 2022	2022	2022	Kenya	Cs	Purposive sampling	Molecular	454	71	0.156	0.123	0.190
Regasa et al., 2015	2015	2014	Ethiopia	Cs	Simple random	Parasitological	391	48	0.123	0.090	0.155
Robi and Diriba, 2021	2021	2019	Ethiopia	Cs	Multistage sampling	Parasitological	2088	279	0.134	0.119	0.148
Seyoum et al., 2022	2022	2019	Ethiopia	Cs	Purposive sampling	Parasitological	600	61	0.102	0.077	0.126
Sheferaw et al., 2016	2016	2015	Ethiopia	Cs	Systematic random	Parasitological	1838	133	0.072	0.061	0.084
Sheferaw et al., 2019	2019	2016	Ethiopia	Cs	Simple random	Parasitological	2402	123	0.051	0.042	0.060
Simwango et al., 2017	2017	2016	Tanzania	Cs	Multistage sampling	Molecular	1002	172	0.172	0.148	0.195
Sisay and Seblewongel, 2017	2017	2015	Ethiopia	Cs	Simple random	Parasitological	384	101	0.263	0.219	0.307
Swai and Kaaya, 2012	2012	2011	Tanzania	Cs	Simple random	Parasitological	239	12	0.050	0.023	0.078
Tadesse and Tsegaye, 2010	2010	2009	Ethiopia	Cs	Simple random	Parasitological	250	11	0.044	0.019	0.069
Tafese et al., 2012	2012	2011	Ethiopia	Cs	Simple random	Parasitological	386	33	0.085	0.058	0.113
Tamiru et al., 2014	2014	2013	Ethiopia	Cs	Simple random	Parasitological	436	6	0.014	0.003	0.025
Tegegn et al., 2021	2021	2019	Ethiopia	Cs	Systematic random	Parasitological	1284	142	0.111	0.093	0.128
Terefe et al., 2015	2015	2014	Ethiopia	Ls	Simple random	Parasitological	409	25	0.061	0.038	0.084
Tsegaye et al., 2021	2021	2016	Ethiopia	Cs	Simple random	Parasitological	428	26	0.061	0.038	0.083
Tulu et al., 2018	2018	2017	Ethiopia	Cs	Simple random	Parasitological	384	14	0.036	0.018	0.055
Ushencho and Fekadu, 2020	2020	2019	Ethiopia	Cs	Simple random	Parasitological	220	13	0.059	0.028	0.090
Waiswa and katunguka-rwakishaya, 2004	2004	2003	Uganda	Cs	Simple random	Parasitological	1309	84	0.064	0.051	0.077
Wogayehu et al., 2017	2017	2007	Ethiopia	Cs	Cluster sampling	Parasitological	399	166	0.416	0.368	0.464
Yada and Meku, 2022	2022	2020	Ethiopia	Cs	Simple random	Parasitological	250	18	0.072	0.040	0.104
Yalew and Fantahun, 2017	2017	2015	Ethiopia	Cs	Simple random	Parasitological	400	85	0.213	0.172	0.253
Yigzaw et al., 2017	2017	2016	Ethiopia	Cs	Simple random	Parasitological	383	8	0.021	0.007	0.035
Yohannes et al., 2013	2013	2012	Ethiopia	Cs	Simple random	Parasitological	500	21	0.042	0.024	0.060
Zemedkun et al., 2016	2016	2014	Ethiopia	Cs	Simple random	Parasitological	480	32	0.067	0.044	0.089

(*continued on next page*)

Table 1 (*continued*)

Authors	P. year	S. year	country	S. design	S. method	D. method	S. size	E	E. rate	LCI	UCI
Thumbi et al., 2010	2010	2010	Kenya	Cs	Simple random	Molecular	103	35	0.340	0.248	0.431
Kalayou et al., 2021	2021	2019	Kenya	Cs	Cluster sampling	Parasitological	952	266	0.279	0.251	0.308
Mbahin et al., 2013	2013	2011	Kenya	Cs	Simple random	Parasitological	584	198	0.339	0.301	0.377
Hassan, 2015	2015	2015	Sudan	Cs	Multistage sampling	Parasitological	380	82	0.216	0.174	0.257
Nadia et al., 2013	2013	2010	Sudan	Cs	Simple random	Parasitological	1852	156	0.084	0.072	0.097
Elkhazeen et al., 2017	2017	2014	Sudan	Cs	Simple random	Molecular	300	35	0.117	0.080	0.153
Hakeem, 2019	2019	2016	Sudan	Cs	Simple random	Parasitological	304	91	0.299	0.248	0.351
Ngwouk, 2006	2006	2005	Sudan	Cs	Simple random	Parasitological	2400	422	0.176	0.161	0.191
Rogers et al., 2020	2020	2018	Uganda	Cs	Simple random	Parasitological	200	4	0.020	0.001	0.039
Ngetich et al., 2019	2019	2019	Kenya	Cs	Simple random	Molecular	72	26	0.361	0.250	0.472
Ohaga et al., 2007	2007	2006	Kenya	Cs	Purposive sampling	Parasitological	879	160	0.182	0.157	0.208

Keys: P. year = publication year, S. design = study design, S. year = study year, S. method = sampling method, D. method = diagnostic method, S. size = sample size, E. = event, E. rate = event rate, LCI = lower confidence interval, UCI = upper confidence interval.

of trypanosomosis infection in cattle. To determine the effect size, a standardized mean difference accompanied by a 95% confidence interval was employed. The overall pooled prevalence was found to be 12% (95% CI: 11–13%) (Fig. 2). The apparent overall prevalence ranged from 1% (Alemu and Alemneh, 2017; Tamiru et al., 2014) to 51% (Nhamitambo et al., 2017). The studies encompassing bovine trypanosomosis in cattle revealed a substantial amount of heterogeneity ($I^2 = 97.43\%$, $p = 0.00$). The analysis of the Galbraith plot for studies on the infection rate of trypanosomosis in cattle also demonstrated that roughly 13.04% of the included studies deviated from the 95% confidence limits, thereby confirming the presence of relative variability between studies. It was anticipated that the two confidence interval lines would encompass 95% of the studies (Fig. 3). By utilizing subgroup analysis, it was determined that the heterogeneity of studies was attributable to the study year, study country, sample size, sampling method, and diagnostic method ($p = 0.00$). In the subsequent meta-regression, an examination was carried out to identify factors that could account for some of these variances. Based on the outcomes of the univariable meta-regression analyses involving coefficients and p values, it was observed that country and diagnostic method exhibited a univariable p value of <0.05, signifying significant variability between studies. A meta-regression of bovine trypanosomosis by country (b = −2.34, 95% CI = −2.50, −2.18; $p = 0.00$) and diagnostic method

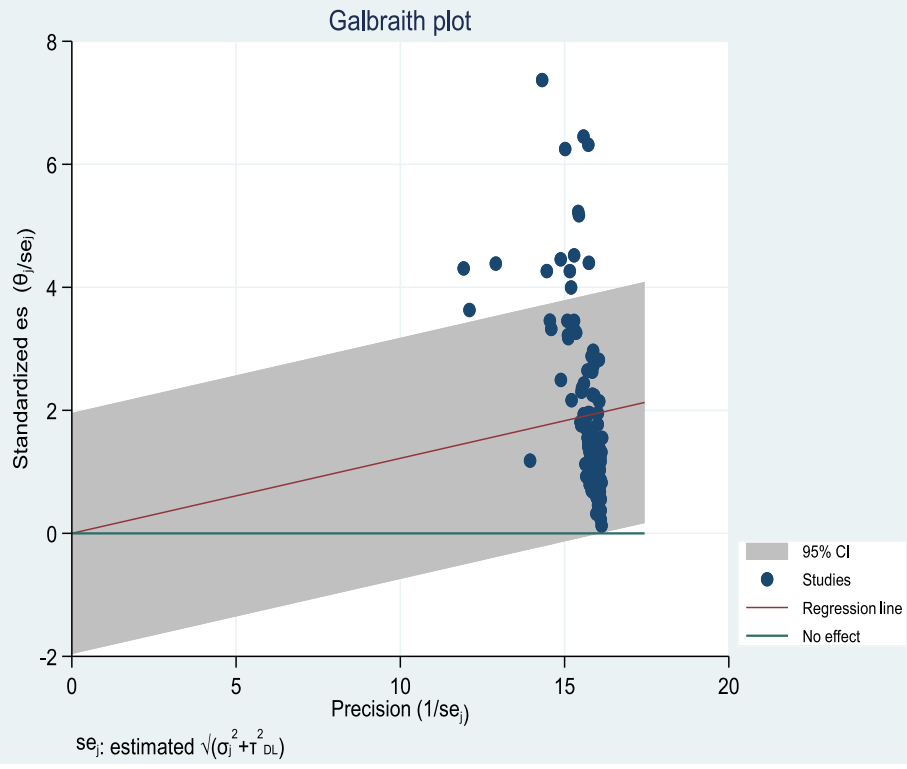

Fig. 3. Galbraith plot for prevalence of bovine trypanosomosis in East Africa.

(b = −2.30, 95% CI = −2.45, −2.15; $p = 0.00$) demonstrates a notable reduction in prevalence (Figs. 4–7).

3.4. Subgroup analysis

The analysis of subgroups was conducted to evaluate the heterogeneity among studies based on the study year, country, sampling method, diagnostic method, and sample size. The presence of statistically significant heterogeneity was observed across all categories of study years, including 2000–2007, 2008–2015, and 2016–2022, as well as country codes 1–7 and sampling methods 1–6. Furthermore, the subgroup analysis also revealed statistically significant heterogeneity among studies when considering sample sizes categorized as 59–384, 385–595, 596–1000, and > 1000, as well as diagnostic methods coded as 1 and 2. Notably, the highest degree of heterogeneity was observed in the study period 2000–2007 ($I^2 = 99.19\%$; $p = 0.00$), the nation of Uganda ($I^2 = 99.17\%$; $p = 0.00$), the sampling method of cluster sampling ($I^2 = 99.33\%$; $p = 0.00$), the diagnostic method of molecular ($I^2 = 98.61\%$; $p = 0.00$), and the sample size of 385–595 ($I^2 = 97.77\%$; $p = 0.00$) (Table 2).

The prevalence of bovine trypanosomosis has shown significant variations among different countries. These variations suggest discrepancies in the efforts and attitudes towards the control and eradication programs for tsetse and trypanosomosis. Notably, Somalia has the highest prevalence rate at 24%, followed by Kenya at 21%, Rwanda at 19%, Uganda at 18%, Sudan at 17%, Tanzania at 15%, and Ethiopia at 10%.

3.5. Publication bias

Funnel plot asymmetry observation and bias coefficients for the studies published on bovine trypanosomosis were conducted to prove the presence of publication bias and small-study effects. The result of the funnel plot showed that there was asymmetrical distribution of articles which depicts that smaller studies were missed to be reported for the scientific community. Likewise, the results of Egger's test and Begg's test plot showed that there was statistically significant publication bias in estimating the prevalence of trypanosomosis infection in cattle (Egger's test: b = −5.13, 95% CI: −7.49%, −2.76, $p = 0.00$ and Begg's test: $p = 0.00$). Egger's test is also called linear regression method which was used to test the funnel-plot symmetry, in which a regression model is built, using the standardized estimate of the effect size as a dependent variable and the inverse of the standard error (1/SE) as an independent variable. If the intercept is significantly different from zero, the estimate of the effect is considered biased (Shi et al., 2017).

The nonparametric Trim and Fill method were used for estimating the number of missing studies that might exist in a meta-analysis and the effect that these studies might have had on its outcome. Trim and fill are a popular method of accounting for publication bias in meta-analysis. The idea of the trim-and-fill method is to first *trim* the studies that cause a funnel plot's asymmetry so that the overall effect estimate produced by the remaining studies can be considered minimally impacted by publication bias, and then to *fill* imputed missing studies in the funnel plot based on the bias-corrected overall estimate (Shi and Lin, 2019).

The findings from the funnel plot analysis revealed an asymmetrical distribution of articles, indicating that smaller studies were not

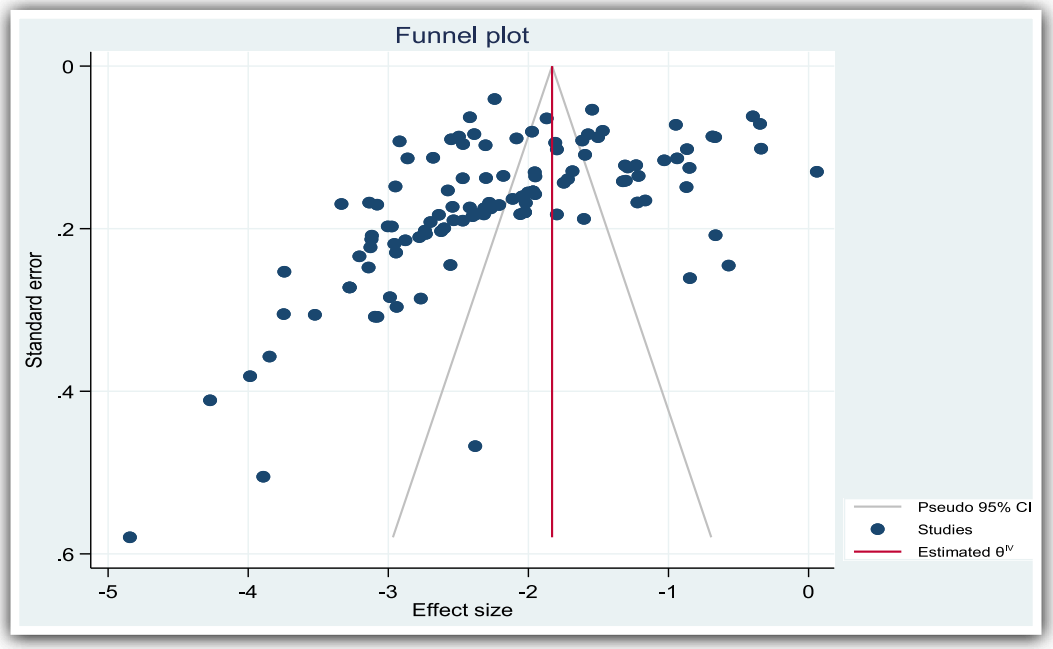

Fig. 4. Funnel plot with pseudo 95% limits of pooled prevalence of bovine trypanosomosis in East Africa. The individual plots are located asymmetrically.

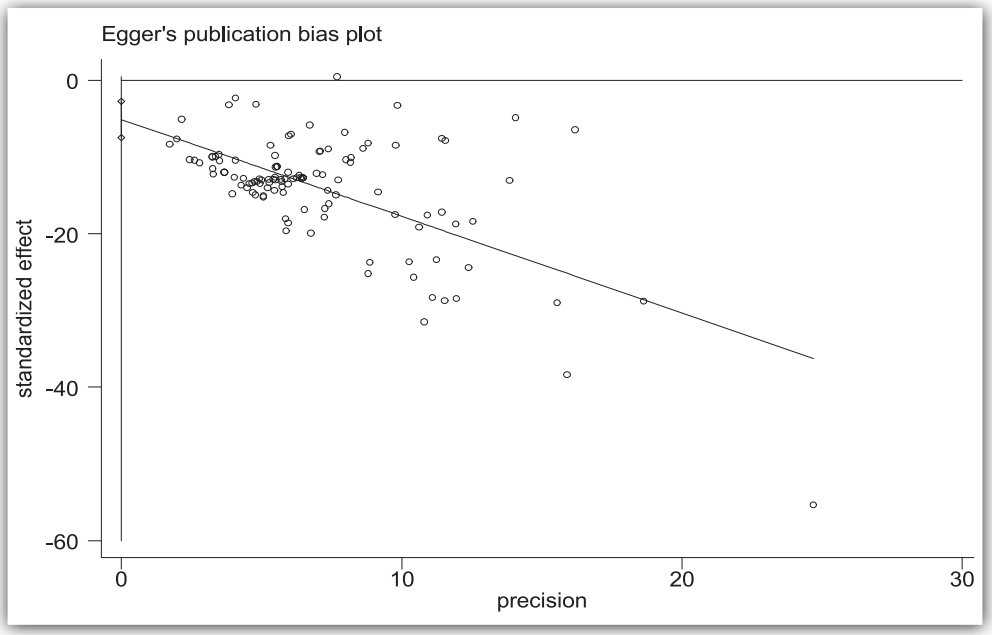

Fig. 5. Egger's publication bias plot.

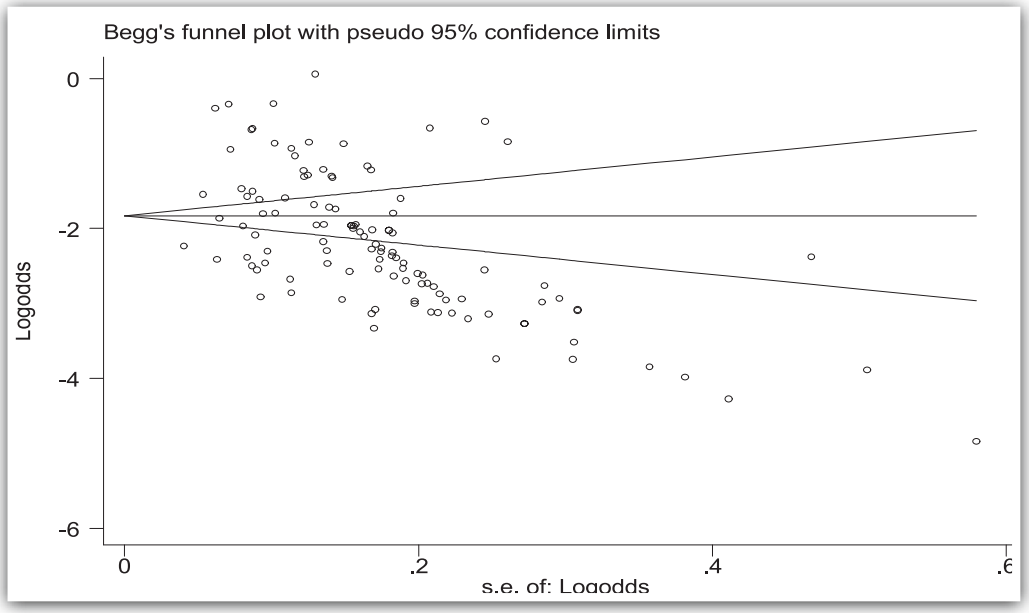

Fig. 6. Begg's funnel plot with pseudo 95% confidence limits.

reported within the scientific community. Additionally, the results obtained from Egger's test and Begg's test plot indicated a statistically significant publication bias in estimating the prevalence of trypanosomosis infection in cattle (Egger's test: b = −5.13, 95% CI: −7.49%, −2.76, $p = 0.00$ and Begg's test: $p = 0.00$).

4. Discussion

A comprehensive and systematic review followed by a meta-analysis was conducted in order to determine the aggregate prevalence

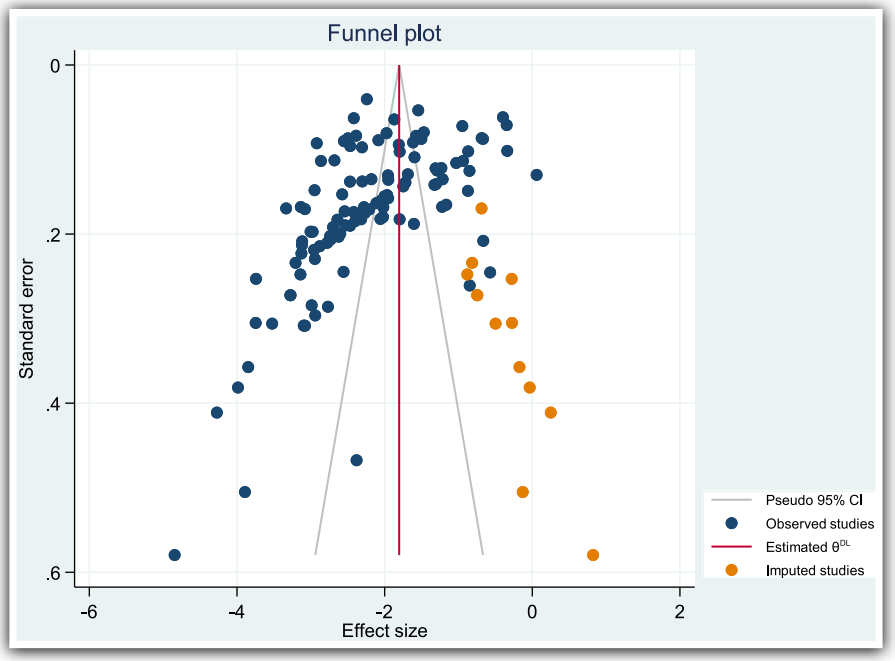

Fig. 7. Funnel plot with imputed studies using Trim and Fill method.

Table 2
Pooled prevalence estimates of bovine trypanosomosis in East Africa, stratified by sub-groups.

Characteristics	No. of studies	Prevalence (%)	95% CI	I^2%	Heterogeneity test *p*-value
Overall	115	12	11–13	97.43	0.00
Study year					
2000–2007	8	15	9–21	98.19	0.00
2008–2015	65	12	11–14	97.01	0.00
2016–2022	42	12	10–14	97.77	0.00
Country					
Ethiopia	83	10	9–11	95.88	0.00
Kenya	8	21	13–29	98.82	0.00
Rwanda	1	19	16–21	–	–
Somalia	1	24	18–30	–	–
Sudan	7	17	11–22	96.85	0.00
Tanzania	6	15	7–24	98.49	0.00
Uganda	9	18	10–26	99.17	0.00
Sampling method					
Cluster	4	22	5–39	99.33	0.00
Multistage	9	14	10–18	97.96	0.00
Purposive	9	15	9–20	98.36	0.00
Simple random	84	11	10–12	96.64	0.00
Stratified	3	25	8–42	99.27	0.00
Systematic	6	11	7–15	95.55	0.00
Diagnostic method					
Parasitological	96	11	10–12	96.71	0.00
Molecular	19	21	15–27	98.61	0.00
Sample size					
59–384	43	13	11–15	97.18	0.00
385–595	38	12	10–15	97.77	0.00
595–1000	16	12	9–15	97.57	0.00
>1000	18	10	8–12	96.33	0.00

of bovine trypanosomosis in East Africa. The results of the 115 included studies indicated a pooled prevalence of 12% (95% CI: 0.11, 0.13) for bovine trypanosomosis in East Africa. This finding was lower than the pooled prevalence observed in a study encompassing various African countries from 2000 to 2018, which reported a prevalence of 15.10% (Ebhodaghe et al., 2018), but higher than the pooled prevalence obtained from a meta-analyzed study conducted solely in Ethiopia, which reported a prevalence of 8.12% (Leta

et al., 2016). Furthermore, in the current meta-analysis, the subgroup analysis indicated that Somalia demonstrated the highest prevalence at 24%, followed by Kenya at 21%, Rwanda at 19%, Uganda at 18%, Sudan at 17%, Tanzania at 15%, and Ethiopia at 10%. The current subgroup findings were lower than those reported by individual studies conducted in different East African countries, including Ethiopia (34%; Denu et al., 2012), Sudan (30%; Mossaad et al., 2020), Tanzania (51%; Nhamitambo et al., 2017), and Uganda (41%; Angwech et al., 2015). Meanwhile, the current subgroup prevalence report of Kenya is higher than the reports of Okello et al. (2022) in Kenya who reported prevalence of 16%. Conversely, when compared to various individual studies, the subgroup prevalence was significantly higher than the reported prevalence of 1% (Alemu and Alemneh, 2017; Tamiru et al., 2014); 4% (Bakele and Desta, 2019; Efa, 2021); 5% (Batu et al., 2017); 3% (Biyazen et al., 2014); 2% (Gachohi et al., 2009); and 4% (Kivali et al., 2020).

The prevalence of bovine trypanosomosis exhibits notable variations across different countries. Notably, Somalia boasts the highest prevalence rate at 24%, whereas Ethiopia records the lowest at 10%. Despite the establishment of the National Tsetse and Trypanosomosis Control Project (NTTCP) in the 1980s and the funding support provided by the International Committee of the Red Cross (ICRC) for a tsetse and trypanosomosis (T & T) control project in select regions of Somalia (ICRC International Committee for the Red Cross, 2017), no additional measures aimed at reducing trypanosomosis losses in wider coverage areas have been implemented (Hassan-Kadle et al., 2020). This lack of intervention may be attributed to the observed increase in prevalence. Although this meta-analysis incorporates a total of 83 studies conducted in Ethiopia, the aggregated prevalence rate in this country remains relatively lower compared to other nations. Previous and ongoing tsetse control initiatives implemented in affected regions of Ethiopia may account for the reduction in bovine trypanosomosis prevalence. The Ethiopian government, in collaboration with the Pan-African Tsetse Eradication Campaign (PATEC) and the International Atomic Energy Agency (IAEA), has committed significant resources and efforts towards mitigating the tsetse fly challenge in Ethiopia. The utilization of deltamethrin-impregnated targets and the Deltamethrin pour-on formulation has been widely employed in Ethiopia to curb the tsetse fly challenge and minimize the impact of trypanosomosis (Leta et al., 2016).

Different findings from various nations within the East African region have indicated that the prevalence of bovine trypanosomosis exhibits substantial variation between countries. The high prevalence of bovine trypanosomosis in East Africa has been associated with numerous factors and conditions. These include the existence of small ruminant reservoirs of trypanosomes in areas where cattle are reared (Sinshaw et al., 2006), as well as a high abundance of vectors that prefer cattle over other types of livestock (Mulaw et al., 2011; Abebe et al., 2017). Additionally, the proximity of cattle populations to tsetse-belts (Bitew et al., 2011), compromised immunity in cattle due to strenuous activities (Denu et al., 2012; Kitila et al., 2017), and the emergence of drug-resistant trypanosomes have all been identified as contributing factors (Kassaye, 2015; Bitew et al., 2011). The prevalence may also be influenced by the low population of trypanotolerant cattle breeds and the high population of trypano susceptible cattle breeds. The impact of control efforts on disease burden has been relatively limited, potentially due to the lack of structured and systematic control strategies employed (Diall et al., 2017). Furthermore, the absence of control activities in certain countries may also be a contributing factor. In light of these circumstances, it is crucial for endemic countries to collaborate and intensify their control efforts, given the movement of tsetse flies and pastoral activities across national boundaries.

The subgroup analysis results revealed varying prevalence of bovine trypanosomosis in different categories of the aforementioned factors. The category of "study year" indicated that the period from 2000 to 2007 exhibited the highest heterogeneity of included studies in terms of the prevalence of bovine trypanosomosis ($I^2 = 98.19\%$; $p = 0.00$), while the period from 2008 to 2015 had the lowest heterogeneity among the studies ($I^2 = 97.01\%$; $p = 0.00$). The fluctuation in seasons across the years of the conducted studies and the number of studies included in each category might account for this variation. Furthermore, the subgroup analysis of studies by "country" revealed significant heterogeneity in the prevalence of bovine trypanosomosis. Uganda exhibited the highest study heterogeneity ($I^2 = 99.17\%$, $p = 0.00$), whereas Ethiopia reported the lowest study heterogeneity ($I^2 = 95.88\%$, $p = 0.00$). This variation might stem from the diverse study methodologies, diagnostic techniques, and geographic scope of the reports in each nation. The "sample size category" showed that studies with a range of 385 to 595 had the highest level of heterogeneity ($I^2 = 97.77\%$; $p = 0.00$), whereas studies with a sample size >1000 had the lowest level of heterogeneity ($I^2 = 96.33\%$, $p = 0.00$). This disparity could be attributed to the number of studies conducted in each category across different nations and time periods, employing various sampling and diagnostic techniques. Additionally, the analysis of sampling methods revealed that cluster sampling technique exhibited the highest level of heterogeneity ($I^2 = 99.33\%$, $p = 0.00$), whereas systematic sampling technique displayed the lowest level of heterogeneity ($I^2 = 95.55\%$, $p = 0.00$). This discrepancy might arise from the fact that cluster sampling is more prone to sampling error and less precise compared to other methods.

Additionally, an analysis was conducted on subgroups based on the diagnostic techniques used in the studies. These techniques were categorized as either parasitological or molecular. The parasitological method exhibited relatively low heterogeneity ($I^2 = 96.71\%$, $p = 0.00$), whereas the molecular method displayed the highest heterogeneity ($I^2 = 98.61\%$, $p = 0.00$). The reason for this discrepancy is that a significant portion (50–80%) of infections in the field are chronic and cannot be detected using the parasitological method due to the absence of detectable levels of parasitemia (Aregawi et al., 2019). Although quick and relatively inexpensive, parasitological tests lack sensitivity and specificity. Conversely, the molecular approach offers high specificity and sensitivity, enabling the identification of trypanosomes specific to multiple species in a single PCR (Salim et al., 2011).

To visually assess publication bias, a funnel plot was employed. Subsequently, Egger's regression asymmetry test and Begg's test were conducted. The funnel plot illustrated an asymmetrical distribution of articles. Similarly, both Egger's test and Begg's test demonstrated statistically significant publication bias in estimating the prevalence of trypanosomosis infection in cattle (Egger's test: b = −5.13, 95% CI: −7.49%, −2.76, $p = 0.00$, and Begg's test: $p = 0.00$). This bias may be attributed to the omission of smaller studies in reporting, inadequate methodological quality, selection bias, variations in effect size based on sample size, sampling variation, or chance. Unbiased estimates were calculated using Duval and Tweedie's non-parametric "fill and trim" linear random method.

The study possesses certain constraints. Initially, the data unveiled notable heterogeneity across studies, which persisted even subsequent to sub-group analysis. Consequently, the outcomes may not precisely reflect the overall condition of the ailment throughout the entire nation. Other limitations stem from the publications' provision of inaccurate or incomplete information. Despite conducting an exhaustive investigation, it is probable that certain studies remain undiscovered due to their absence from journals indexed by PubMed. The tests exhibited a significant inclination towards publication bias among studies. Moreover, the research was conducted within the time frame of 2000 and 2022. The elongated duration was imperative owing to the restricted accessibility of data, which to a certain extent may impede the interpretation of the findings.

5. Conclussion and recommendations

The present systematic review and meta-analysis adhered to the fundamental principles outlined by the Preferred Reporting Items for Systematic Reviews and Meta-analysis (PRISMA). The collective prevalence rate of 12% revealed in this systematic review and meta-analysis signifies that bovine trypanosomosis is a pervasive and noteworthy malady affecting livestock in terms of economic consequences. The findings of this investigation imply a high prevalence of bovine trypanosomosis in the majority of the countries under scrutiny. However, the scarcity of epidemiological data has emerged as a significant impediment to achieving reasonably accurate estimations of the disease burden. The incongruity in prevalence rates could be elucidated by disparities in variables such as the season of study, methodology employed, geographic location, and the abundance of vectors. In addition, heterogeneity in sample sizes, study years and seasons, diagnostic techniques, and sampling methods across different prevalence studies might also contribute to this inconsistency. Bovine trypanosomosis is the principal factor contributing to losses in livestock and agricultural productivity, thereby exerting negative socioeconomic effects on East Africa. Consequently, it is recommended that collaborative control endeavors be implemented across national borders, and the government should devise comprehensive nationwide programs aimed at disease control and eradication.

Ethical approval

Ethical approval is not applicable. No animal or human experimentation was undertaken.

Consent to publication

Not applicable.

Funding

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Authors' contribution

The idea was conceived, designed and data collected by GM, ZST and HD. Formal analysis: GM, MM, ZST and HD; Writing original draft: GM; Writing review & editing: GM, MM, ZST and HD. The authors read and approved the final manuscript.

CRediT authorship contribution statement

Getie Mulat: Conceptualization, Data curation, Formal analysis, Writing – original draft, Writing – review & editing. **Moges Maru:** Data curation, Methodology, Software, Validation, Writing – review & editing. **Zewdu Seyoum Tarekegn:** Conceptualization, Data curation, Formal analysis, Software, Visualization, Writing – review & editing. **Haileyesus Dejene:** Conceptualization, Data curation, Formal analysis, Methodology, Software, Writing – review & editing.

Declaration of competing interest

Authors have no competing interests.

Data availability

All data generated or analyzed during this study are available upon the request of the corresponding author.

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