Epidemiology, risk factors and vector density of trypanosomosis in cattle in Ethiopia: Systematic review and meta-analysis

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A R T I C L E   I N F O

A B S T R A C T

Background: Bovine trypanosomosis remains a major barrier to livestock productivity, agricultural progress, and socioeconomic development in Ethiopia's large tsetse belt regions, threatening 70 million cattle. Therefore, this review examined published literature from the last ten years to estimate the pooled prevalence, risk factors, and vector density of bovine trypanosomosis. This systematic review followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines, using PubMed, Web of Science, HINARI, Google, and Google Scholar. Pooled prevalence and risk factors were calculated with a random effects model in R software, with a 95 % confidence interval. This meta-analysis included research published after 2015 on trypanosomosis in Ethiopian cattle, where *Trypanosoma* was classified at least to the genus level. Studies on other species, lacking specific prevalence data and published before 2015 were excluded.
Results: A total of 26 articles were included in this meta-analysis. The overall pooled proportion of bovine Trypanosomosis cases was 9 % (95 % CI: 8–9 %). Considerable heterogeneity was observed across the included studies ($I^2 = 94$ %; $P < 0.01$). The highest pooled prevalence of trypanosomosis was reported in Amhara and Oromia (8 %), followed by Benishangul Gumuz (BSGR) (7 %). Based on the subspecies analysis, the highest pooled proportion was 65 % (95 % CI: 58 %–71 %) for *T. congolense* ($I^2 = 81$ %: $p = 0.01$), followed by 32 % for *T. vivax* ($I^2 = 60$ %: $P = 0.61$) and 19 % for *T. brucei* (95 % CI: 7 %–41 %). Among the risk factors, poor body condition, black coat color, and packed cell volume (PCV) were found to be significant for the development of this disease. Black-coated animals were 2.36 and 3.48 times more susceptible to trypanosomosis than red- and white-coated animals, respectively. According to the pooled odds ratio, animals in poor body condition were 2.82 times more likely to have bovine trypanosomosis. Animals infected with *Trypanosoma* were 18 times more likely to have a lower packed cell volume (PCV) compared to non-infected animals. The study found that Tsetse flies were responsible for 72.32 % of bovine trypanosomosis cases, with *Glossina pallidipes* and *Glossina tachinoides* being the most common species. The remaining 27.68 % were due to other biting insects. The study highlights the need for science-based risk mitigation strategies to control *Trypanosoma* infections,

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emphasizing the crucial role of Tsetse flies, particularly *G. pallidipes* and *G. tachinoides*, in transmission.

1. Introduction

Animal Trypanosomosis is a significant animal health issue that has a substantial impact on settlement and socioeconomic development in large tsetse belt regions of Africa. Within sub-Saharan Africa, including East Africa, this vector is distributed across approximately 10 million km^2 of potential grazing lands in 37 countries. As a result, approximately 55 million people and 160 million cattle are at risk of contracting this disease (Kuzoe, 1993; Torgerson and Macpherson, 2011; Stijlemans et al., 2018). In Ethiopia, animal trypanosomosis is widely distributed across tsetse-infested belts, which are found in sub-Saharan Africa. In these regions, approximately 220,000 km^2 of fertile land is infested by *Glossina* spp. (Cecchi et al., 2008). Animal trypanosomosis is prevalent in Ethiopia, spanning the tsetse-infested belts typical of sub-Saharan Africa. Approximately 220,000 km^2 of arable land in these areas is affected by *Glossina* spp. (Cecchi et al., 2008; Eyasu et al., 2021). The presence of tsetse-borne trypanosomosis restricts approximately 180,000 to 200,000 km of potentially cultivable land in the western and southwestern regions of Ethiopia. This puts at risk 14 million cattle, an equivalent number of small ruminants, nearly 7 million equines, and 1.8 million camels, all of which are susceptible to contracting trypanosomosis at any given time (Abera et al., 2014).

Trypanosomosis is a complex protozoan disease caused by unicellular parasites (trypanosomes) found in the blood and other tissues of vertebrates, including cattle and humans (Tesfaye and Ibrahim, 2017). The most important trypanosome species affecting livestock in Ethiopia are *T. congolense*, *T. vivax* and *T. brucei* in cattle, sheep and goats; *T. evansi* in camels; and *T. equiperdium* in horses (Getachew et al., 2014). In Ethiopia, approximately five *Glossina* spp. were reported: *G. pallidipes*, *G. morsitans submorsitans*, *G. fuscipes, G. tachinoides,* and *G. longipennis (*Bitew et al., *2011)*. The most commonly reported and important *Trypanosoma* spp. affecting bovine in the southern and southwestern parts of the country include *T. congolense*, *T. vivax* and *T. brucei* (Duguma et al., 2015; Abebe and Jobre, 1996). The major clinical manifestations of bovine trypanosomosis are intermittent fever, anemia, dullness, anorexia, apathy, watery ocular discharge and superficial lymph node enlargement. Since then, the animals progressively become emaciated and cachectic and die (Seyoum et al., 2022). In cows, an irregular oestrus cycle and abortion are observed (Constable et al., 2016).

Bovine trypanosomosis leads to approximately 3 million fatalities annually, with approximately 35 million doses of trypanocidal drugs being administered each year to enable livestock to persist in tsetse-infested regions (Duguma et al., 2015; Hundessa et al., 2021). The economic losses in cattle production alone can reach up to US$1.2 billion, while the indirect impact of this disease on agriculture-livestock production is estimated to be approximately US$4.5 billion per year (Mattioli and Slingenbergh, 2013). The disease directly affects the productivity of animals in terms of milk and meat, diminishes birth rates, and increases abortion and mortality rates, ultimately reducing the size and composition of the herd. The projected maximum benefit per square kilometer of tsetse-infested area over 20 years amounts to US$10,000 (Shaw et al., 2014; Adugna et al., 2017). Consequently, the total maximum benefits from addressing bovine trypanosomosis in Ethiopia could reach US$1 billion over a 20-year timeframe (Adugna et al., 2017). Various diagnostic methods are available for identifying the disease, including wet mount, buffy coat examination, and the polymerase chain reaction (PCR) technique (Chagas et al., 2020; Momčilović et al., 2019). The application of PCR ensures accurate amplification of products from the specific disease agent of interest, thereby informing treatment options that can be promptly implemented in the field, thus facilitating improved control programs (Tsegaye et al., 2021a; Holand et al., 2004).

Numerous studies have been conducted in Ethiopia since 2015 regarding bovine trypanosomosis incidence. Various prevalence rates of Trypanosomosis have been reported in different parts of the region, for example, 25.5 % by Tadesse (Tadesse et al., 2015), 15 % by Hundessa et al. (Hundessa et al., 2021), 13 % by Robi and Diriba (Robi and Diriba, 2021), and 12 % by Lemu et al. (Lemu et al., 2019). It is imperative to organize the existing epidemiological information and associated risk factors for trypanosomosis to identify challenging situations requiring intervention for disease control and prevention. As a result, future burdens will be minimized, and trypanosomosis patterns will be predicted. This study aimed to estimate the pooled prevalence of trypanosomosis, evaluate its associated risk factors, and assess the vector density of bovine trypanosomosis in Ethiopia using the available literature.

The research questions to be addressed in this meta-analysis are as follows: what is the pooled prevalence pattern of bovine trypanosomosis over the last ten years since 2015? Which vector species are denser in Ethiopia? What are the significant risk factors associated with trypanosomosis? Which species of *Trypanosoma* were highly endemic in the previous 10 years?

2. Methods

The literature search was carried out from August 12–20, 2023. A methodological assessment of published papers detailing the general prevalence, related risk factors, and vector density of trypanosomosis was carried out using the PRISMA checklist (Salameh et al., 2020) (Supplementary material −1).

2.1. Search strategy and source of information

A comprehensive search strategy was used to identify all relevant studies. Two authors (MD and AS) independently searched databases such as PubMed, HINARI, Web of Science, Google Scholar, and other manual methods. The research question was "What are the prevalence, vector density, and associated risk factors for trypanosomosis in cattle in Ethiopia? "The following MeSH terms were

used in the electronic database search: (Trypanosomias OR Trypanosomosis OR Bovine trypanosomosis OR Bovine Trypanosomiasis OR Animal Trypanosomosis OR Trypanosomosis in cattle) AND (epidemiology OR prevalence OR infection rate) AND (Ethiopia). The second objective MeSH terms were "risk factors", "predisposing factors", "associated factors", and "determinants". A restriction was placed on the language of publication as English. All identified studies were imported to End-Note 20 software to remove duplicates and scientific citations of the references.

2.2. Description of the study settings

Ethiopia, a nation in the Horn of Africa, is located between $3°$ $00'$–150 $00'$ N latitude and 320 30'–480 00' E longitude. This is where the study was carried out. Its total area of land is 1.04 million km^2. After Nigeria, Ethiopia is the second most populated country in Africa, with 120 million people (Genet, 2020; WHO, 2022). In addition to being a great place for agriculture, Ethiopia is home to an estimated 70, 25.5, and 24 million sheep, goats, and cattle, respectively (Volume, 2016). The varied terrain of the nation serves as the foundation for multiple agro-climatic zones. The region between 1500 and 2300 m above sea level (m.a.s.l.) is a temperate transition zone, while the areas above 2300 m.a.s.l. are referred to as highland regions with an altitude.

2.3. Study eligibility criteria

2.3.1. Inclusion criteria

The search was performed by three field experts (Veterinary Epidemiology, Veterinary Parasitology, and Veterinary Clinical Medicine) to avoid author bias. This meta-analysis includes all of the primary descriptive studies that have been published in the English language that document the occurrence of trypanosomosis in cattle. The inclusion criteria included articles with a clear estimation of the prevalence of trypanosomosis and its associated risk factors. Studies must be derived from observational studies and clear cuts of species of *Trypanosoma*. The study animals were restricted to domestic cattle. Samples had to be collected from naturally infected cattle that had not been experimentally infected. What study animal characteristics were included in this study? Which age group, breed, and any other included or excluded characteristics? *Trypanosoma* was identified at least down to the genus level, and the geographical location must be in Ethiopia. Articles that have been published were considered for inclusion if they were published after the year 2015.

2.3.2. Exclusion criteria

Studies of other species were excluded. Studies for which estimates of the proportion of each species with trypanosomosis were not clear or detailed were also excluded. Articles published before 2015 were excluded. Review articles, duplicates, abstracts only, qualitative studies, KAP (knowledge, attitudes, and practices) questionnaire-based studies, book chapters, case reports, editorials, short communications, opinions, or studies without original data were excluded. Intervention studies lacking baseline data on the association between animal exposure and disease were excluded from the meta-analysis.

2.3.3. Definition of the outcome variable

In our review, we have two outcome variables: 1) the prevalence/proportion/portion of *trypanosoma* spp. among the cattle population, 2) the odds ratio of risk factors, and 3) the density of the vector of *trypanosoma* (descriptive). Therefore, in the first case, the number of Trypanosomosis-positive individuals out of the total number of samples was used to estimate the proportion of trypanosomosis-infected individuals. In the second case, the outcome was calculated from the odds of the two risk factors.

2.3.4. Data extraction

The relevant data were independently extracted by two investigators (M.D. and A.S.). Quantitative and qualitative data were extracted from the included studies into two tables (for vector density and the prevalence of *Trypanosoma*) and an Excel spreadsheet. The extracted components included the name of the primary author, year of publication, year of study, region, and all species of *Trypanosoma* spp. (primary outcome interest), diagnostic methods, data collection techniques, and ethical considerations.

2.3.5. Study quality assessment

In this review of the eligible included studies, a quality assessment was performed to verify the methodological quality of this review. The quality of the included cross-sectional studies was assessed by the AXIS quality tool (Downes et al., 2016). This quality assessment tool includes 20 items, including justification of sample size, sample representativeness, a description of no responders, use of validated measures, diagnosis of statistical methods, discussion of nonresponse bias, reporting of funding and conflicts of interest.

2.3.6. Data synthesis and statistical analysis

A meta-analysis was carried out using R software with the "metaprop" function of the 'meta' package version 4.1.3 (Balduzzi et al., 2019) and "metafor" (Viechtbauer, 2010) in R Studio. The random effects model based on the restricted maximum likelihood method (REML), which calculates within- and between-study variability, was applied to estimate the pooled prevalence and 95 % CIs. The overall meta-analysis (overall effect size), pooled odds ratio, heterogeneity, and weight of each study were calculated. In addition, graphs and tables were used to describe the prevalence and risk factors. Considering that the outcome variable is binary (i.e., *Try-panosomosis* positive or negative and given only for single groups), the only possible parameter to measure effect size was the raw proportion with 95 % confidence intervals (Borenstein et al., 2009). Therefore, pooled proportions were estimated using a logit

transformation in a logistic-normal random-effect regression model as described by Nyaga et al. (Nyaga et al., 2014), while subgroup analysis was performed using a mixed-effect logistic regression model.

2.3.7. Investigation of heterogeneity

The Cochran's Q test (reported as the *p*-value), τ^2 (between study variance) and inverse variance index (I^2) were used to assess the sources of heterogeneity, which describes the percentage of observed total variation between studies that is due to heterogeneity rather than chance. As explained by Higgins and Thompson (Higgins et al., 2009), the I^2 index was estimated to represent low, moderate, and high heterogeneity if it corresponded to I^2 values of 25 %, 50 %, and 75 %, respectively. Heterogeneity was deemed to be statistically significant if the I^2 value exceeded 50 %, and the Q test revealed a *P* value of less than 0.10. The degree of study heterogeneity was evaluated using a forest plot diagram. Forest plots demonstrate the weights, magnitudes of effects, and 95 % confidence intervals for each study.

2.3.8. Subgroup sets

To determine specific between-study variability, a subgroup analysis *was* performed based on study year, study location or region, and species of the parasite.

2.3.9. Publication bias assessment

Publication bias is usually evaluated through funnel plots in which asymmetry may be assessed visually, Begg's rank, and Egger's test (Asgedom et al., 2024). Thus, in our case, publication bias was assessed using funnel plot diagrams and Egger's regression test.

3. Results

3.1. Article search results

According to the PRISMA 2020 flowchart (Fig. 1), 1619 articles were searched across a variety of electronic databases, of which 25 were excluded due to duplicate content assessment ($n = 25$), 53 were marked as ineligible due to the use of automation tools ($n = 53$), and 142 were removed for other reasons. In total, 1399 articles were screened for title and abstract, 629 studies were searched for retrieval, and 532 articles were not retrieved. Ninety-seven ($n = 97$) articles were reported before being reported for eligibility, and forty-five ($n = 59$) of them were excluded for various reasons. Ultimately, 26 studies ($n = 26$) were included in the meta-analysis.

3.2. Overview of included articles

The attributes of studies on trypanosomosis are intricately described systematically. The study animals included cattle of all ages,
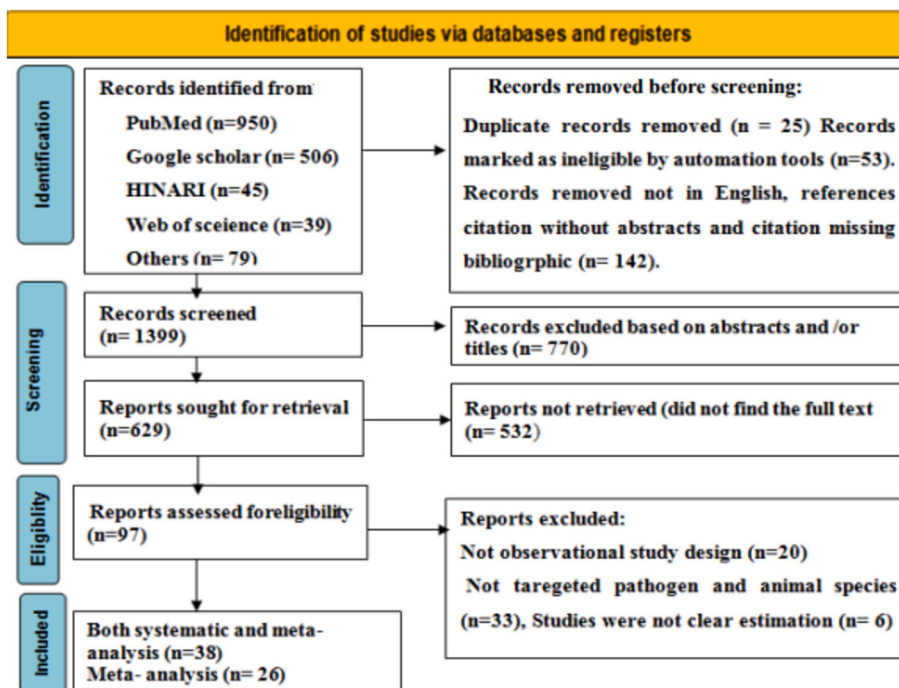

Fig. 1. PRISMA flow chart for the included studies.

and both sexes and included both local and crossbred varieties. A total of twenty-six independent articles were considered for the analysis of trypanosomosis prevalence (Table 1). In our investigation, we discovered that the majority of *trypanosoma* spp. were *T. congolens*, *T. vivax,* and mixed infections. The included studies for the meta-analysis were conducted and published in various regions of Ethiopia between 2015 and 2023. The majority of these studies took place in the southern Oromia regional states and central regions of Ethiopia. The diagnosis methods employed a microscope using the dark ground buffy coat technique to examine the presence of trypanosomes, following the procedures outlined by Paris et al. (Paris et al., 1982). The study designs were predominantly cross-sectional, and the type of sample collected was blood. This uniformity in study design and sample type served to decrease the variability between studies. The included studies in each region were 9 (35 %) in the SNNPR, 8 (30 %) in Oromia, 5 (19 %) in Amhara, 2 (7 %) in the BSGR, and 2 (7 %) in Sidama. The minimum sample size in this systematic review was 144 cattle (Takele and Gechere, 2019), while the maximum sample size was 2402 cattle (Sheferaw et al., 2019). In terms of the general geographical distribution, more than 50 % of the studies were conducted in the southern part of Ethiopia. The total number of studies included in the analysis of vector density was 13, with 10 (72.23 %) of them focusing on tsetse fly species and only 3 articles examining other biting species (Table 2). Among the 13 studies on tsetse fly species, 8 studies (Tsegaye et al., 2021a; Sheferaw et al., 2019; Efa, 2021; Bekele and Beshir, 2021; Yigzaw et al., 2017; Abebe et al., 2021; Ayele and Dagnachew, 2023; Abayneh and Tadesse, 2019) exclusively investigated *G. pallidipes.*

3.3. Pooled prevalence and publication bias

The meta-analysis incorporated a total of 26 articles to examine the pooled prevalence of trypanosomosis. The included studies displayed a high level of heterogeneity ($I^2 = 94$ %: $\tau^2 = 0.3727$; $P < 0.01$), and the estimated pooled prevalence among the cattle population was calculated to be 9 % (95 % CI: 8–9 %) (Fig. 2). There was statistically significant between-study variability ($Q = 207.94$, DF = 24, $p < 0.0001$). There was no publication bias ($P < 0.05$) according to funnel plots and/or Egger's regression asymmetry analysis (Fig. 3). The presence of publication bias was not suggested by funnel plots (Fig. 3) or Egger's regression asymmetry ($p > 0.05$).

3.4. Subgroup analysis

Due to the considerable heterogeneity and the need to conduct subanalyses based on study regions, study year wise, and *Trypanosoma* spp. wise, subgroup analysis by region revealed significant heterogeneity between studies (Supplementary material-2). Analysis of subgroup differences indicated a statistically significant subgroup effect ($p < 0.001$). The highest degree of heterogeneity ($I^2 = 97$ %; $p < 0.01$) in the subgroup analysis of trypanosomosis by region was observed in the Oromia region (Table 3). According to the regional subgroup, the highest pooled proportion of trypanosomosis was reported in Amhara and Oromia (8 %), followed by BSGR (7 %).

For the subanalysis of the study years, the studies were categorized into three groups: before 2018, between 2018 and 2021, and

Table 1
characteristics of included studies ($n = 26$).

Author	Study Region	Location	Species	Sample size	Positive	Prevalence (%)
(Abayneh and Tadesse, 2019)	SNNPRS	Southeren	Not stated	384	16	4
(Bekele and Beshir, 2021)	Oromia	Western	*T.congolense, mixed*	432	23	5
(Degneh et al., 2021)	Oromia	Southwestern	*T.congolense,T.vivax*	384	32	8
(Efa, 2021)	Oromia	Southwestern	*T.congolense,T.vivax*	819	36	4
(Degneh et al., 2021)	SNNPR	Southern	*T.congolense,T.vivax*	384	32	8
(Eyasu et al., 2021)	SNNPR	Southern	*T.congolense, T.vivax* and mixed	964	48	5
(Fesseha et al., 2022)	SNNPR	Southern	*T.congolense,T.vivax*	384	44	11
(Gebisa et al., 2020)	Oromia	Southwestern	*T.congolens,T.vivax*	1046	36	3
(Gona, 2016)	SNNPR	Southern	*T.congolense,T.vivax*	480	32	7
(Wondie and Alemneh, 2018)	Amhara	Western	*T.congolense,T.vivax*	164	25	15
(Hundessa et al., 2021)	SNNPR	Southern	*T.congolens,T.vivax*	400	20	5
(Mattioli and Slingenbergh, 2013)	Oromia	Northwestern	*T.congolense,T.vivax*	384	98	26
(Lemu et al., 2019)	Oromia	Western	*T.congolense,T.vivax*	384	47	12
(Robi and Diriba, 2021)	Oromia	Southwestern	*T.congolense. T.vivax* & mixed	2088	279	13
(Seyoum et al., 2022)	BSGR	Southrn	*T.congolense,T.vivax*	600	61	10
(Sheferaw et al., 2019)	BSGR	Southern	*T.congolense,T.vivax*	2402	123	5
(Takele and Gechere, 2019)	SNNPR	Southern	T.congolense only	144	3	2
(Tsegaye et al., 2021a)	Oromia	Western	*T.congolense,T.vivax*	428	26	6
(Yada, 2019)	SNNPR	Southern	*T.congolense,T.vivax*	242	13	5
(Haile et al., 2017)	Amhara	Northwestern	*T.congolense,T.vivax*	439	43	10
(Abebe et al., 2021)	Sidama	Southeren	*T.congolense,T.vivax*	384	24	6
(Yigzaw et al., 2017)	Sidama	Southeren	*T.congolense, T.brucei &mixed*	383	8	2
(Abiy, 2020)	SNNPRS	Southern	*T.congolense*	262	5	2
(Ashagrie and Zewde, 2021)	Amhara	Northwestern	*T.congolense,T.vivax*	571	27	5
(Alemu and Alemneh, 2017)	Amhara	Northwestern		384	26	7
(Lelisa and Meharenet, 2021)	Amhara	Northwestern	*T.congolense,T.vivax*	730	57	8

Table 2

Densities of vectors of *trypanosma* %OBS = Percentage of other biting species, FTD = Flies/ trap/ day.

| Author	No strap	N	FTD	%tsetse(each spp)	Tsetse fly species	%OBS	other biting species
(Bekele and Beshir, 2021)	60	290	2.42	100	*G.pallidipes, .tachinoide, .m.submorsitance*	0	Not applicable
(Ayele et al., 2012)	41	1609	19.14	97.60	*G. pallidipes*	2.4	*Stomoxes, Tabanus*
(Abayneh and Tadesse, 2019)	20	1548	14.67	62.21(963)	*G.pallidipes*	37.9(319)	*Stomoxes, Tabanus*
(Haile et al., 2017)	55	1635	9.9	65.6	*G.tachinoide*	34.4	*Stomox,Tabanus ,Hematopao*
. (Sheferaw et al., 2019)	305	4113	4.5	39	*G. pallidipes*	61	*Stomoxes, Tabanus*
(Abebe et al., 2021)	36	1925	17.82	62.21	*G.pallidipes*	4.36	*Stomoxes, Tabanus*
(Habte et al., 2021)	70	1170	6.87	82.2	*Glossina morsitans submorsitans*	17.8	*Stomoxes, Tabanus*
(Robi and Diriba, 2021)	377	5290	5.27	75.14	*G. tachinoides, G. morsitans submorsitans*	24.0.86	*Stomoxy Tabanus*
(Efa, 2021)	90	1083	6.01	62.2	*G. Pallideps G. Morsistans G. Fascies,G. Tachnoids*	3.78	*stomoxes Tabanus*
(Tsegaye et al., 2021a)	100	2055	18.9	92	*G. morsitans submorsitans, G. pallidipes,G. fuscies*	8	*Stomoxes Tabanus*
(Gebisa et al., 2020)	160	1751	1.82	100	*G.morsitans and G. tachinoides*	0	Not applicable
, (Lelisa and Meharenet, 2021)	57	590	0.06	2	*G.tachnoide*	98	*Stomox,tetanus ,Hematopao*
(Yigzaw et al., 2017)	24	59	0.82	100(59)	*G. pallidipes*	0	Not applicable
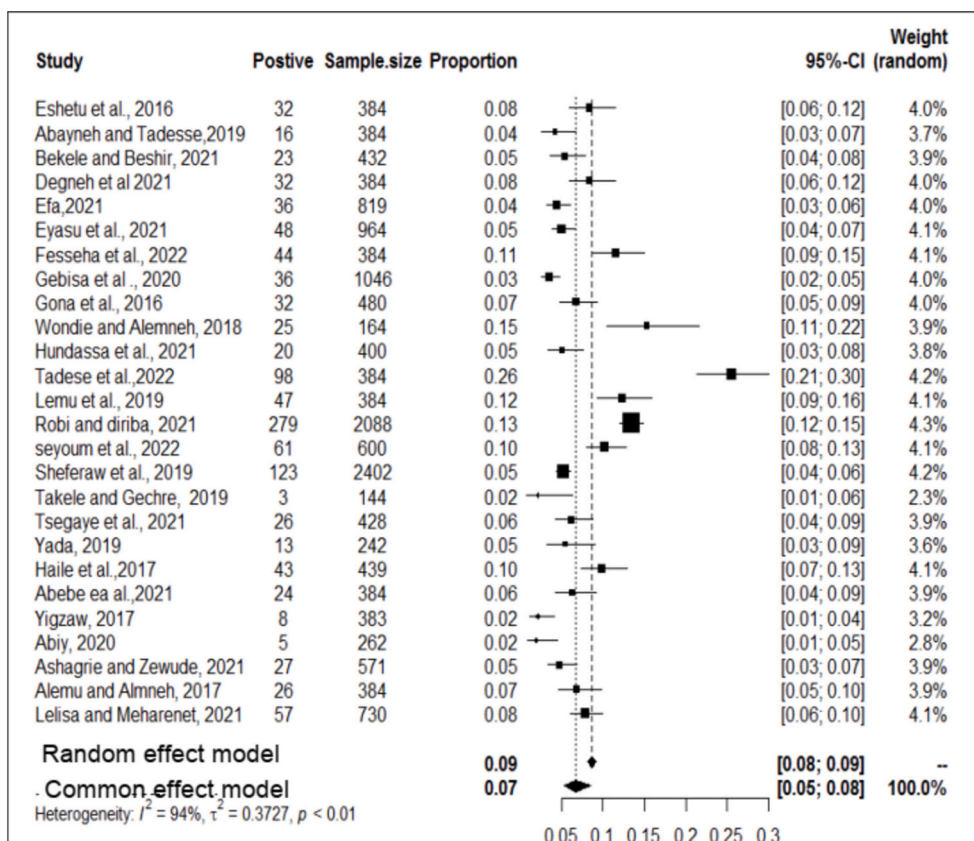
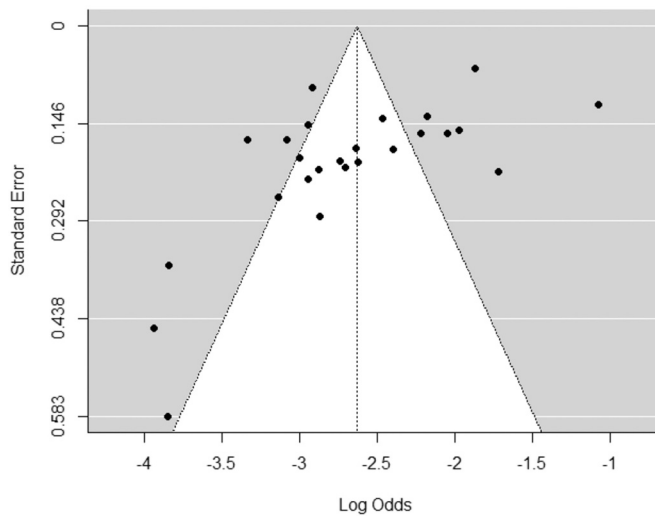**Fig. 2.** Forest plot for the pooled prevalence of bovine trypanosomosis in Ethiopia.

Fig. 3. Funnel plots of the standard error by log odds of the prevalence of bovine trypanosomosis.

Table 3
Pooled effect size estimates of trypanosomosis, stratified by subgroups.

Moderators	K	Category	N	Case	ES (95 %CI)(RE)	Heterogeneity			Test for subgroup differences (RE)	
						I^2(%)	τ^2	p value	Q	p-value
Year wise	5	Pre-2018	3389	196	0.06[0.04; 0.10]	78	0.25	< 0.01	0.16	0.643
	7	2018–2021	4291	270	0.06 [0.03; 0.10]	90	0.56	<0.01		
	14	Post-2021	7986	718	0.07[0.05;0.10]	95 %	0.34	<0.01		
Region wise	8	Oromia	5965	577	0.08[0.05; 0.13]	97.0	0.54	<0.01	12	<0.001
	5	Amhara	2288	178	0.08 [0.06; 0.12]	82.0	0.17	<0.01		
	2	BSGR	6004	368	0.07[0.04; 0.14]	95.0	0.26	<0.01		
	9	SNNRP	3644	213	0.05[0.04; 0.08]	79.0	0.20	<0.01		
	2	Sidama	767	32	0.4[0.01;0.11] 87	0.56	<0.01			
	24	*T.congolense*	1328	744	0.65 [0.58; 0.71]	81	0.31	<0.01		
	19	*T. vivax*	1373	441	0.32 [0.27; 0.37]	60	0.11	<0.01		
Species wise	2	*T. brucei*	22	4	0.19[0.07; 0.41]	0	0.00	0.61	14.13	0.0014
	7	Mixed	723	131	0.18[0.16;21]	0	0.00	0.61		

K = Number of included studies, N = Total number of cattle population, Case = positive Animals, RE = Random effect, Mixed infection = both T. vivax and T.congolense.

after 2021. The highest degree of heterogeneity (I^2 = 95 %) in all cases was found in studies conducted after 2021 (Table 3). The highest sub pooled prevalence of trypanosomosis was reported in studies published after 2021 (7 %). The subgroup difference test (diagnostic approach) indicated no statistically significant group effect (Q = 0.16; DF = 2; p = 0.643).

According to the subanalysis based on the types of species of *Trypanosoma*, the included studies were categorized into four groups: *T. congolense* (n = 24), *T. vivax* (n = 19), *T. brucei* (n = 2), and mixed infection (n = 7). Significant discrepancies were found in the sub analysis of the prevalence of trypanosomosis by type of species. As shown Table 3, the subgroup analysis revealed that the pooled proportion of *T. congolense* was highest at 65 % (95 % CI: 58 %–71 %) and exhibited heterogeneity (I^2 = 81 %: τ2 = 0.315; p < 0.01). This was followed by *T. vivax* at 32 % (95 % CI: 27 %–37 %), with heterogeneity (I^2 = 60 %: τ^2 = 0.1147; P = 0.61), and *T. brucei* at 19 % (95 % CI: 7 %–41 %), with no heterogeneity (I^2 = 0 %: τ^2 = 0; P = 0.61).

3.5. Risk factor studies

Several risk factors have been studied in previous reports in Ethiopia and are presented in The risk factors considered to affect the occurrence of trypanosomosis infection in cattle are age, sex, coat color, season, agroecological condition and body condition. In this study, we evaluated coat color, age, sex, agroecological conditions, body condition, season, and packed cell volume (PCV) (Supplementary material-2 and Table 3).

3.6. Association of coat color with the prevalence of bovine trypanosomosis

Nine of the 26 studies examined the relationship between the incidence of trypanosomosis and coat color categories of animals

(Table 3). Meta-analyses of the pooled odds ratios of 9 studies were conducted to explore the associations between different coat color categories and the prevalence of trypanosomosis. As shown in Fig. 8a, the pooled odds ratio (OR = 1.2; $p = 0.67$) of red vs. white was not significantly associated with the incidence of trypanosomosis. However, animals with a red coat color had a 1.2 ($I^2 = 77$ %; $\tau^2 = 1.066$; $p < 0.01$) times greater likelihood of trypanosomosis than animals with a white coat color. Similarly, we performed a pooled odds ratio analysis to explore the relationship between black and red coat color and the prevalence of trypanosomosis. The pooled odds ratios, shows a significant association (OR = 2.36, $p < 0.01$) between the included studies. Moreover, the black-to-white odds ratio also showed a significant difference (OR = 3.48, $p = 0.02$) (Table 3).

3.7. Association of age with the incidence of bovine trypanosomosis

Eleven out of the twenty-six studies analyzed in the (previous report investigated) the correlation between the prevalence of trypanosomosis and different age categories of the animals. Among these studies, no statistically significant associations were found. These findings suggest that trypanosomosis was most prevalent in 2- to 5-year-old animals, followed by animals older than 5 years. To further explore the association between different age categories of animals and bovine trypanosomosis, a meta-analysis of the pooled odds ratio was conducted using the data from the eleven studies. Table 3 shows that there was no significant association ($p > 0.05$) between the infection rate of bovine trypanosomosis and the two age categories: animals younger than 2 years and animals aged 5 years (OR = 0.90, CI = 0.78–1.1; $P = 0.43$).

3.8. Association of PCV value with the prevalence of bovine trypanosomosis

Twenty-one of the identified studies examined the relationship between the prevalence of trypanosomosis and the mean packed cell value (PCV) in cattle. To explore this relationship further, a pooled odds ratio analysis was performed. Table 3 shows a significant association (OR = 18.4, 95 % CI; 10.04–31.7; $P < 0.01$) between the prevalence of trypanosomosis and PCV in cattle, with a high degree of heterogeneity (89 %).

3.9. The association between sex and the incidence of bovine trypanosomosis

Fourteen studies investigated the association between the prevalence of bovine trypanosomosis and the sex of the animals. Only one study reported a significant association between males and the incidence of bovine trypanosomosis (Mihret and Mamo, 2007), while the remaining thirteen studies showed no significant association. A meta-analysis of the fourteen included studies was conducted to examine the association between the prevalence of bovine trypanosomosis and the sex of the animals. The pooled odds ratio of bovine trypanosomosis incidence did not significantly differ between sexes in the cattle population (pooled OR = 1.13, 95 % CI = 0.92 to 1.40; $P = 0.24$), and the variability of the studies in both sexes was 47 % ($p < 0.03$) (Table 3).

3.10. Association of agro-ecology with the prevalence of bovine trypanosomosis

Six studies from previous reports addressed the association between agro-ecological conditions and the occurrence of trypanosomosis among cattle in Ethiopia. Two of these studies revealed a significant association between agro-ecological conditions and the prevalence of bovine trypanosomosis (Mekuria and Gadissa, 2011; Degneh et al., 2017), suggesting that it was more prevalent in the midland areas than in the lowland areas. However, four studies suggested no significant association between the prevalence of trypanosomosis and the agro-ecological condition of the animals (Robi and Diriba, 2021; Yada, 2019; Tsegaye et al., 2021b). To address these conflicting reports, a meta-analysis of the pooled prevalence odds ratio was conducted using a random effect model to examine the association between agro-ecological conditions and bovine trypanosomosis. Table 3 the prevalence of bovine trypanosomosis in relation to agro-ecological conditions.

3.11. Association of body condition with the prevalence of bovine trypanosomosis

Out of the twenty-six studies that were included, thirteen focused on the correlation between body conditions and the prevalence of trypanosomosis among the cattle population in Ethiopia. In ten of these studies, a statistically significant association ($p < 0.05$) was found between body condition and the prevalence of trypanosomosis in cattle. However, the remaining three studies concluded that there was no relationship between body condition and the occurrence of this trematode infection in cattle. The highest prevalence of trypanosomosis in cattle was observed in those with poor body condition (Eyasu et al., 2021; Seyoum et al., 2022; Sheferaw et al., 2019; Degneh et al., 2021; Fesseha et al., 2022; Tsegaye et al., 2021b), followed by those with medium body condition (Ayele and Dagnachew, 2023). Conversely, in other studies, there was no significant association between the prevalence of trypanosomosis and the body condition of the animals (Tadesse et al., 2015; Efa, 2021), which reported a prevalence of 24 % (95 % CI; 22 %–26 %; $p = 0.79$) and 57 % (95 % CI 38 %–85 %; $p = 0.073$).

In this meta-analysis, the pooled odds ratio indicated that poor body condition was significantly associated with the incidence of bovine trypanosomosis (OR: 2.82, 95 % CI: 1.38 to 5.77, $P < 0.01$; Table 3). This means that animals in poor body condition were 2.82 times more likely to have bovine trypanosomosis than were animals in good body condition. Similarly, as shown in Fig. 13b, animals in medium body condition were 1.96 times more likely to have bovine trypanosomosis than those in good body condition 57 % (95 % CI 38 %–85 %; p = 0.073).

3.12. Association of season with the prevalence of bovine trypanosomosis

Only three studies have examined the association between the prevalence of trypanosomosis and seasonal conditions. To investigate the relationship between season and the prevalence of trypanosomosis infection, a pooled odds ratio analysis was performed. Table 4 shows a significant association (OR = 2.00, 95 % CI; 1.48 to 2.70; P < 0.01) between the prevalence of trypanosomosis and wet vs. dry conditions in cattle.

4. Discussion

This meta-analysis included twenty-six observational studies that estimated the pooled prevalence of bovine trypanosomosis in Ethiopia. The overall prevalence of this blood parasitic infection was 9 %. This finding was similar to those of individual studies in Ethiopia (Degneh et al., 2021; Lelisa and Meharenet, 2021; Eshetu et al., 2017). The similarity in prevalence with the current results may be due to chance not having a specific explanation; means prevalence rate in the study might not be attributable to a specific cause or underlying factor. However, significantly higher prevalence values were also reported in Ethiopia (Mulaw et al., 2011; Kassaye, 2015). Furthermore, this finding was greater than that of the previous pooled prevalence (8 %) study conducted in the last decade by Leta et al. (Leta et al., 2016). This may be related to the increase in drug resistance genes, genetic drift of the pathogen, sample size representativeness of each included study, number of studies included, authors' methods of data manipulation techniques and the influence of climatic changes that favor vectors and help the distribution of trypanosomosis.

Subgroup analysis revealed that the pooled proportion of *T. congolense* was 65 %, followed by *T. vivax* at 32 % and *T. brucei* at 19 %. In our current meta-analysis, the highest pooled proportion of *T. congolense* among the other species might be associated with effective transmission of *T. congolense* by a dominant cyclical vector in the area, *Glossina pallidipes*. This might also be associated with increased trypanocidal drug resistance by *T. congolense*, which makes it dominant during parasitological surveys. Similarly, the greater proportion of *T. congolense* in this study (65 %) was similar to previous results (Duguma et al., 2015; Mekuria and Gadissa, 2011; Degneh et al., 2017) for Southwest Ethiopia (76 %), Western Ethiopia (62 %) and Northwest Ethiopia (77.6 %). Moreover, in several studies conducted in sub-Saharan Africa, *T. congolense* was the most prevalent trypanosome species in cattle (Ameen et al., 2008; Simo et al., 2015). In contrast, *T. vivax* infections were dominant in the Amhara region of the Chilga district (Zewdu and Dessie, 2016). This could be due to the mechanical transmission of various biting flies and the diagnostic methods used by experts. This is attributed to the fact that as the distance from the known tsetse infestation area increases, *T. vivax* becomes more frequent and eventually predominates (Mihret and Mamo, 2007).

During the study period, there was an increase in the occurrence of trypanosomosis after 2018. This increase can be attributed to the impact of climatic changes on the transmission rate of the disease through vectors, the increase in drug resistance over time, and the decrease in the number of trypanosomosis-resistant animal breeds as the number of exotic animal breeds increases. According to the regional subgroup analysis, the greatest proportion of trypanosomosis was found in Amhara and Oromia. This prevalence variation among different study regions can be linked to the geographical location of each study site and their proximity to suitable habitats for the *Glossina* vector in the district. This may also be influenced by the number of studies conducted in each region. Additionally, the movement of livestock from tsetse-infested areas to non-tsetse-infested areas during the summer season for better feeding conditions and their return to native areas during winter could contribute to the infection of healthy animals. Furthermore, the presence of higher fly density in lowlands may also play a role in the infection of healthy animals. Moreover, the differences between regions indicate variations in efforts and attitudes toward tsetse and trypanosomosis control and eradication.

Regarding the analysis of risk factors, the pooled odds ratio revealed that poor body condition was significantly associated with the occurrence of bovine trypanosomosis. Animals in poor body condition are 2.82 times more likely to have bovine trypanosomosis than are animals in good body condition, as trypanosomosis is characterized by progressive weight loss. This finding is consistent with a similar study by Dinka and Abebe (Dinka and Abebe, 2005). In terms of coat color, the pooled odds ratio showed a significant difference in the likelihood of individual animals being infected with this parasitic disease. Black animals were 3.48 and 2.36 times more likely to be infected than white and red-coat animals, respectively. The greater prevalence of trypanosomosis in black-colored animals may be attributed to the preference of the *Glossina* vector for feeding on black animals, as tsetse flies are more attracted to black color due to their shade-loving behavior during flight from one area to another (Eshetu et al., 2017). To the best of our knowledge, continuously reviewing and providing comprehensive findings related to the epidemiology, risk determinants, and vector population density of Trypanosomosis in bovines within Ethiopia illuminate critical domains necessitating concentrated intervention.

The study highlights the need for improved livestock management to combat trypanosomosis in Ethiopia. Crucial strategies include implementing integrated pest management to reduce tsetse fly populations, using insecticide-treated cattle, establishing routine screening programs for early detection, educating farmers on best husbandry practices, and promoting vaccines and new treatments through research collaborations. The zoonotic nature of trypanosomosis poses significant public health concerns.

In the context of Public Health Implications, essential interventions encompass the promotion of awareness regarding the zoonotic transmission from livestock to humans, the advancement of health infrastructure to improve diagnostic capabilities and therapeutic interventions, as well as the encouragement of mutually beneficial collaboration among veterinary services, public health authorities, and environmental agencies via a One Health paradigm.

The present results have significant implications for policy development in Ethiopia. Key actions include developing and enforcing comprehensive trypanosomosis control policies, creating regulations for vector control, animal health, and public health interventions, and effectively allocating resources for research, campaigns, and veterinary services. Engaging local communities in policy development ensures interventions are culturally appropriate and feasible, while establishing monitoring mechanisms will help evaluate

Table 4
Association between various variables with the prevalence of bovine trypanosomosis (OR, 95 %CI, I^2 and *P*-value).

Moderator Category		OR &95 %CI	I^2(%)	P-value
Coat color	White	**Ref.**		
	Red	1.2[0.520,2.780]	77	0.67
	Black	**2.36[1.37, 4.07]**	83	<0.01
Age	Adult	**Ref.**		
	young	0.93[0.78,1.1]	17	0.43
PCV	parasitic	**Ref.**		
	Aparasitic	**18.4[10, 31.7]**	89	< 0.01
BCS	Good	**Ref.**		
	medium	**1.96[1.16,3.32]**	84	< 0.01
	Poor	**2.82 [1.38, 5.77]**		
Sex	Female	Ref.		
	Male	1.3[0.92, 1.40]	47	0.24
Season	dry	Ref.		
	Wet	2.00[1.48,2.70]	0.00	< 0.01
Altitude	lowland	Ref.		
	midland	0.90[0.51,1.58]	72	< 0.01

and refine strategies to meet the needs of affected populations.

In general, addressing trypanosomosis in Ethiopia requires a multifaceted approach that incorporates improved livestock management, improved breed of animals, public health initiatives, and supportive policies. By focusing on innovative research and collaborative efforts, it is possible to make significant progress in controlling this debilitating disease and improving the quality of life for affected communities.

5. Conclusion and Future perspectives

As demonstrated by the current meta-analysis, the Amhara and Oromia regions had the highest overall pooled prevalence of trypanosomosis. Notably, among the different species of Trypanosoma, *T. congolence* accounted for the greatest proportion. This study also confirmed a strong positive correlation between the coat color of animals and poor body condition and the prevalence of tsetse fly vectors transmitting trypanosomosis. Furthermore, the percentage of tsetse fly vectors with trypanosomosis resistance was much greater in Ethiopia (72.23 %) than other biting insects (27.77 %). Consequently, based on these findings and the existing evidence, it is crucial to implement a comprehensive prevention and control strategy. In particular, measures should include the exchange of treatments and breeding of animals, the selection of animals with specific coat colors in endemic areas, and a heightened focus on tsetse fly sterilization, particularly in the Amhara and Oromia regional states in Ethiopia. Aside from ongoing efforts at eradicating the tsetse fly, efforts should be directed at controlling other potential mechanical vectors, such as tabanids and stomoxys, that transmit trypanosomosis. In nutshell, this systematic review and meta-analysis highlight the pressing necessity for focused future inquiries aimed at closing prevailing knowledge deficiencies and investigating innovative methodologies for the effective management of Trypanosomosis. Such research trajectories are essential for augmenting our comprehension and devising more efficacious strategies to mitigate and diminish the repercussions of Trypanosomosis in Ethiopia.

CRediT authorship contribution statement

Melkie Dagnaw Fenta: Writing – review & editing, Writing – original draft, Methodology, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Atsede Solomon Mebratu:** Writing – review & editing, Writing – original draft, Formal analysis, Data curation, Conceptualization. **Kalkidan Getnet:** Writing – original draft, Visualization, Validation, Conceptualization. **Moges Maru:** Writing – review & editing, Writing – original draft, Methodology, Investigation, Data curation, Conceptualization. **Bemrew Admassu Mengistu:** Conceptualization, Methodology, Writing – original draft, Writing – review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this article.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.parepi.2024.e00388.

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