Original Research

Journal of Advanced Veterinary Research
(2024) Volume 14, Issue 4, 735-741

Prevalence of camel trypanosomiasis in Gulf region: a systematic meta-analysis

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ARTICLE INFO

Recieved: 06 March 2024

Accepted: 09 April 2024

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Keywords:

Systematic review
T. evansi
Saudi Arabia
Parasite.

ABSTRACT

Trypanosomiasis in camels is a worldwide major clinical problem. The objective of this review was to present analysis of comprehensive studies on camel trypansomiasis in the Gulf region through meta-analytical investigation. This meta-analysis was conducted according to the rules of PRISMA. Data were extracted after complete search; then finally eligible articles were identified. Using comprehensive meta-analysis software program, the data were analyzed. The results of meta-analysis were effect size, confidence intervals (CI), heterogeneity, and publication bias. Out of 11720 camels in 18 accepted studies, 3177 were proved to be infected with *T. evansi* (27.1 %). At random, and fixed effects, a Z-value of -6.195 (P-value = 0.000) -30.186 (P-value = 0.000) was recorded, respectively. The Q-value (894.96), I-squared (98.038), and P- value (0.000) are the final heterogeneity variables. Additionally, the Tau-squared is 0.619 with a 0.39 Standard Error. Egger's linear regression test for asymmetry did not indicate publication bias, Intercept (-4.95), 95% confidence interval (from -9.91 to -0.07), t-value (2.27), and df = 16.00. The 1-tailed P-value (recommended) is 0.018, and the 2-tailed P-value is 0.036. The outcome of Kendall's tau with continuity correction (-0.313), with a 1-tailed P-value (recommended) of 0.030 and 2 -tailed P-value of 0.060. Duval and Tweedie's trim-and-fill method (no studies trimmed) resulted in an adjusted correlation from -0.718 to -0.630 (95% CI). In conclusion, the present results indicate that camel trypanosomiasis is a common infection in Gulf countries. Therefore, strict prevention and control policies should be formulated.

Introduction

Camels are extremely important in Arabian countries, as they have a fundamental place in Arab culture and economy (Faye and Bonnet, 2012). There are an estimated 35 million camels, with the majority living in developing nations (Stat, 2016). While hot and arid environments, desertification, and scarce natural resources pose significant challenges for many animal species, camels have evolved exceptional adaptations that enable them to thrive in such conditions (Faye, 2014). Although it was believed that camels were resistant to a variety of infectious diseases, a number of bacterial, viral, and parasitic infections have been documented in camels recently (Kassa *et al*., 2011a).

Camel trypanosomosis (Surra) is a worldwide veterinary concern caused by *Trypanosoma evansi* (*T. evansi*), a unicellular haemoprotozoan parasite (Eyob and Matios, 2013). This parasite is a member of the Trypanosomatidae family of the genus Trypanosoma (Sobhy *et al*., 2017). *T. evansi* is mostly spread by bloodsucking flies such as Tabanus spp. and Stomoxys spp. (Qudsiyati *et al*., 2023). *T. evansi* is a common infection in camels, causing significant economic losses owing to weight loss, abortion in pregnant animals, and a high fatality rate in untreated animals (Sobhy *et al*., 2017). Surra commonly presents chronically in camels, but when the animal is stressed, it may manifest acutely with a high fatality rate (Eyob and Matios, 2013). Reduced fertility (Sengupta *et al*., 2019), as well as broad loss of bodily condition, lower body edema, intermittent fever, anemia, hair loss, and abortion (Sivajothi *et al*., 2016) are characteristics of the chronic form.

Many techniques are available for surra laboratory diagnosis, including direct parasitological techniques that have low sensitivity when parasitaemia is low or aparasitemic periods occur, which are typical in chronic infection (Cadioli *et al*., 2015). Furthermore, a variety of serological tests are employed in the screening process for camel Trypanosomiasis. These tests include the antigen-ELISA test, which detects parasitic antigen (Sengupta *et al*., 2019; Sadek *et al*., 2021), or serological tests that detect antibodies, such as indirect -ELISA (Sivajothi *et al*., 2016), indirect fluorescent antibodies (Aquino *et al*., 2010), and card agglutination tests (Songa, 1988). To identify Tryoanosomal DNA, a variety of molecular tests, including conventional (Mohamed Elsiddig Mohamed *et al*., 2019; El-Sayed *et al*., 2021), quantitative real-time (Konnai *et al*., 2009), and multiplex polymerase chain reaction (Sawitri *et al*., 2015), can be used, in addition to being more sensitive than previous approaches, offer the added benefit of categorizing parasites at the subspecies level (Sawitri *et al*., 2015; Sadek *et al*., 2021).

Several investigations have been conducted to determine the prevalence of *T. evansi* in camels in the Gulf region. Using PCR, the prevalence rate of *T. evansi* in southern Saudi Arabia was 30.9% (Mohamed Elsiddig Mohamed *et al*., 2019), but it was 9.8% in Taif governorate, Makkah province, King Saudi Arabia (Al Malki and Hussien, 2022). Furthermore, in Abu Dhabi, United Arab Emirates, the prevalence of *T. evansi* was to be 60% using real-time PCR (Shameem *et al*., 2022). In Oman, the prevalence rate of *T. evansi* was 2.6% by PCR (Khalafalla and Al Mawly, 2020). Using microscopic examination of wet blood films, the prevalence rate in Kuwait was 1.7% (Al-Taqi, 1989).

The variances in *T. evansi* prevalence can be ascribed to several factors, including sample size, the method used for the examination, and the density of vectors in the studied area (Kyari *et al*., 2021). Several factors have been associated with the increased risk of *T. evansi* infection in

ISSN: 2090-6277/2090-6269/

camels, including the age of the examined camels; older camels are more prone to infection than younger ones (Selim *et al*., 2022a). Meanwhile, other several researchers reported that younger camels have a higher prevalence of *T. evansi* infection compared to older ones (Pathak *et al*., 1992; Ngaira *et al*., 2002; Lemecha *et al*., 2008; Kassa *et al*., 2011a). The prevalence of *T. evansi* may be influenced by the gender of the camel under examination. Numerous studies have revealed that females are more likely than males to become infected (Sobhy *et al*., 2017; Boushaki *et al*., 2019a) . On the other hand, many researchers reported higher rates of infection among males than females (Njiru *et al*., 2004; Bogale *et al*., 2012). Larger herds of camels are more prone to *T. evansi* infection than smaller ones, hence herd size is one of the management factors that has been linked to an increased risk of *T. evansi* (Delafosse and Doutoum, 2004; Benaissa *et al*., 2020b). Exposure to *T. evansi* was significantly influenced by the water supply. Higher infection rates were seen in camels that drank from rivers as opposed to wells (Benaissa *et al*., 2020b). There was a controversy about the prevalence of the camel trypanosomiasis in Gulf region. Therefore, the aim of the present study was to provide a systematic mata-analysis on the prevalence of camel trypanosomiasis in Saudi Arabia, Oman and United Arab Emirates.

Materials and methods

Ethical approval

The authors conducted analyses of all available scientific articles in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-analyses (PRISMA) guidelines. Therefore, the ethical committee for using animals in scientific investigations may not have been necessary in this research. Prior to starting the trial, the protocol of study was developed.

Selected studies

The present review adopted all published studies describing the prevalence of camel Trypanosomiasis in the Gulf Region specifically by collecting blood samples from infected camels with parasites.

Types of reference individuals

All examined camels characterized by fever, anorexia, listlessness, pale mucous membranes, dullness, a very thin hump and drop to one side, abortions in pregnant females, and death in untreated camels. The study's sample sizes were not restricted.

Inclusion and exclusion criteria

Inclusion criteria

- The publication's English version is accessible when articles are written in another language.
- Publication of studies between 1984 and 2023.
- Published in a reputable journal.
- Cross-sectional study.
- Studies on the blood sample collection from infected camel with trypanosomiasis have been conducted.
- Studies indicating the prevalence of trypanosomiasis regardless of the laboratory diagnostic method utilized are examples of outcomes.
- The number of animals with trypanosomiasis infection were used to determine prevalence.

Exclusion criteria

- Techniques for identifying trypanosomiasis other than prevalence.
- Foreign-language publications.
- Data from articles that have been published are incomplete.

Search plan and selection of studies

The objective was to search through all the publications that had been studied the prevalence of camel trypanosomiasis in the Gulf Region. We searched the PubMed, Ovid, Web of Science, Sage, EBSCO, CABI, Scopus, Mendeley, and ISI web of knowledge database with a combination of the following search terms ("CAMEL" "TRYPANOSOMIASIS") (title/ abstract) ("TRYPANOSOMIASIS") (title/ abstract)AND ("CAMEL") (title / abstract) AND ("TRYPANOSOMIASIS EVANSI") (title/ abstract) AND ("SURRA") (title/abstract) AND ("PREVALANCE" "INCIDENCE") (title/ abstract) OR ("GULF REGION") (title / abstract). The preliminary screening of the articles was based on the title and abstract from the earliest data available until December 2023. This procedure was supplemented by hand-searching, Google Scholar searching, expert recommendations, and citation reviews. We integrated the database outputs using a referencing program, EndNote (version X9; Thomson Reuters). The selection process of the studies' articles are shown in Figure 1.

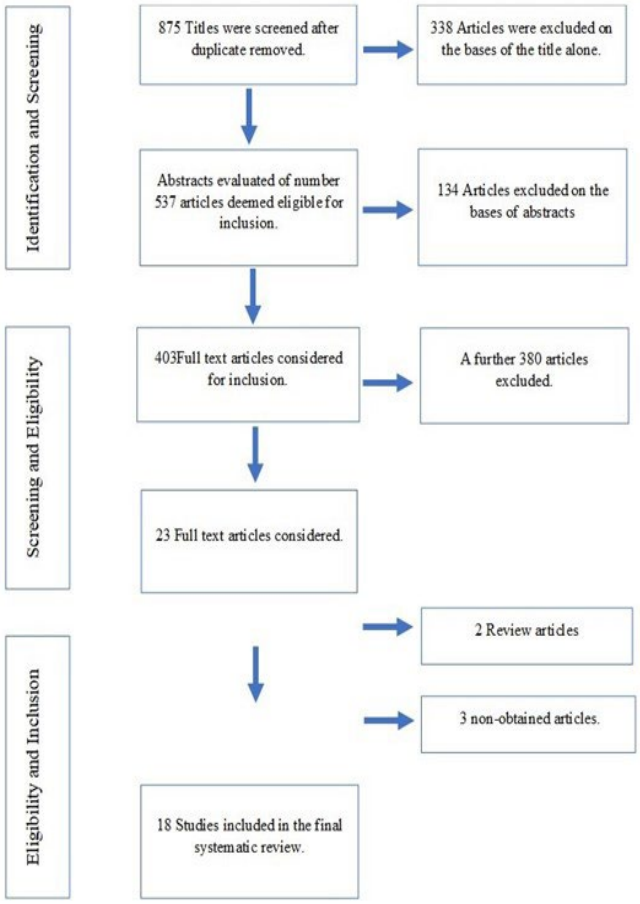

Figure 1. Results of the literature search and disposition of articles on prevalence of camel trypanosomiasis in Gulf region.

Data extraction and analysis

The data extracted included: year of publication, study area (i.e. administrative region and district), diagnostic method, sample size, trypanosomiasis types and positive cases with reported summary statistics (as prevalence or incidence rate) was added to a data extraction form.

Quality assurance

According to (PRISMA) (Moher *et al*., 2010), the current systematic review and meta-analysis was carried out. All the available published

publications on the assessment of the prevalence of camel Trypanosomiasis in gulf region based on blood sample collection from infected camels with parasites were incorporated, to diminish the publication bias.

Statistical analysis

Firstly, the overall pooled prevalence, the number of positive cases divided by the number of all animals tested (Marzok and El-khodery, 2017). A commercially available Meta-Analysis software was used for all data analysis. (Comprehensive Meta-Analysis software version 2, Biostat, Englewood, NJ, USA). The fixed and random effect model, 95% confidence intervals, effect size, heterogeneity, and the between-study variance using the tau-square (t2), relative weight and publication bias were the main outputs of the analysis. These variables were used in our study to assess the prevalence of camel Trypanosomiasis in the gulf region. Effect size was calculated using a standardized Z-statistic and p- value (Duffield *et al*., 2008) Cochrane's Q test was utilized to measure the heterogeneity with a significant value of $p < 0.05$, and the I2 statistic was used to determine the percentage of true heterogeneity among analyses. The Q-statistic and the number of trials (K) were used to determine the degree of heterogeneity, which describes the total variation. I2 statistics with a negative value set to zero and a range of 0 to 100% that is equal to or greater than 50% are really considered heterogeneous (Chen *et al*., 2011). Low, moderate, and high degrees of heterogeneity were identified with values of 25%, 50%, and 75%, respectively (Higgins *et al*., 2003). The relative weight of study was calculated as base inverse square of the standard error of each trial's effect. With the use of meta-regression, the forest plot, which graphically displays the means and their confidence intervals, was used to examine the degree of heterogeneity (Duffield *et al*., 2012). To determine the degree of publication bias, we investigated the funnel plot by graphing each study's effect size against its standard error and precision by logit event rate (Higgins *et al*., 2011). Egger's linear regression intercept (Egger *et al*., 1997) , Begg–Mazumdar rank correlation test (Kendall's statistic (P-Q) with continuity correction were used to assess the significance of funnel plot asymmetry (Begg and Mazumdar, 1994). Duval and Tweedie's trim and fill method was used to estimate potentially missing studies due to publication bias in the funnel plot and to modify the overall effect estimate for both fixed and random effects (Shi and Lin, 2019). The fail-safe N was used to calculate the number of studies with a zero-effect size that are necessary to eliminate the funnel plot's overall effect size (Robert G. Orwin, 1983).

Results

Search results and eligible studies

From databases and published articles, a total of 875 items were discovered. After exclusion criteria, 18 acceptable studies were included in this meta-analysis (Table 1, Figure 1).

Meta-analysis

The overall prevalence of camel Trypanosomiasis was 27.1 % in all 18 acceptable studies in the present meta-analysis. The examination of 11720 camels revealed 3177 to be positive for trypanosomiasis. The lowest prevalence (0.03%) was recorded in the study of Wernery *et al*., (2001). However, the highest prevalence (52.18 %) was reported by Al-Kharusi *et al*. (2021).

The final meta-analysis model of the size effect and null test for the prevalence of camel trypanosomiasis at fixed and random effect is shown in Table 2. At random, and fixed effects, a Z-value of -6.195 (P-value = 0.000) -30.186 (P-value = 0.000) was recorded, respectively.

Table 1. Location of *Trypanosoma evansi* investigations in Gulf region.

Location (Country)	Study
Sultanate of Oman	Srivastava *et al*. (1984)
	Kumar *et al*. (2012)
	Al-Kharusi *et al*. (2021a)
	Al-Kharusi *et al*.(2022a)
	Al-Harrasi *et al*. (2023)
	Khalafalla and Al Mawly (2020)
	Al-Kharusi *et al*.(2023)
Saudi Arabia	Hussein *et al*. (1991)
	Omer *et al*. (1998)
	El Wathig and Faye (2013)
	Al-Afaleq *et al*. (2015)
	Elwathig *et al*. (2016)
	Alanazi *et al*. (2018)
	Mohamed Elsiddig Mohamed *et al*. (2019)
	Metwally *et al*. (2021)
	Elobaid *et al*. (2021)
United Arab Emirates	Wernery *et al*. (2001a)
	Wernery *et al*. (2020)

Degree of Heterogeneity

A forest plot was used to evaluate and illustrate the degree of heterogeneity in the selected research on both fixed and random effects. Additionally, the outcome of relative weight for both fixed and random effects is shown in Figure 2.

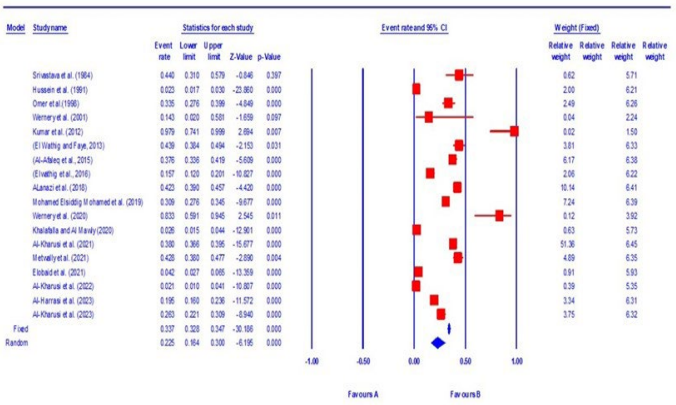

Figure 2. Forest Plot of the prevalence of camel trypanosomiasis shows the event rate, 95% confidence interval, Z- value, P- value, and relative weight on both Fixed and Random models of 19 observed studies.

Figure 3. shows the standard error, variance, logit event rate and 95% CI on both fixed and random effects of 18 individual studies using a forest plot. The Q-value (894.96), I-squared (98.038), and P- value (0.000) are the final heterogeneity variables. Additionally, the Tau-squared is 0.619 with a 0.39 Standard Error (Table 3).

Publication bias

Effect sizes (x axis) are represented against their standard errors and precisions (y axis) (the inverse of standard errors) in the funnel plot by logit event rate for the prevalence of camel trypanosomiasis (Figure 4,5).

The Egger's regression intercept, Begg's rank test, Duval and Tweedie's trim-and-fill method and conducted a classic fail-safe N analysis are designed to adjust estimates for the potential impact of publication bias under some explicit model of publication selection.

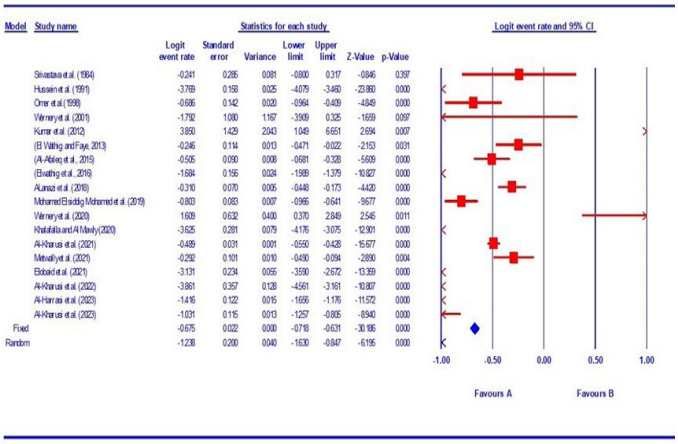

Figure 3. Forest Plot of the prevalence of camel trypanosomiasis shows the logit event rate, 95% C, standard error, and variance on both Fixed and Random models of 19 observed studies.

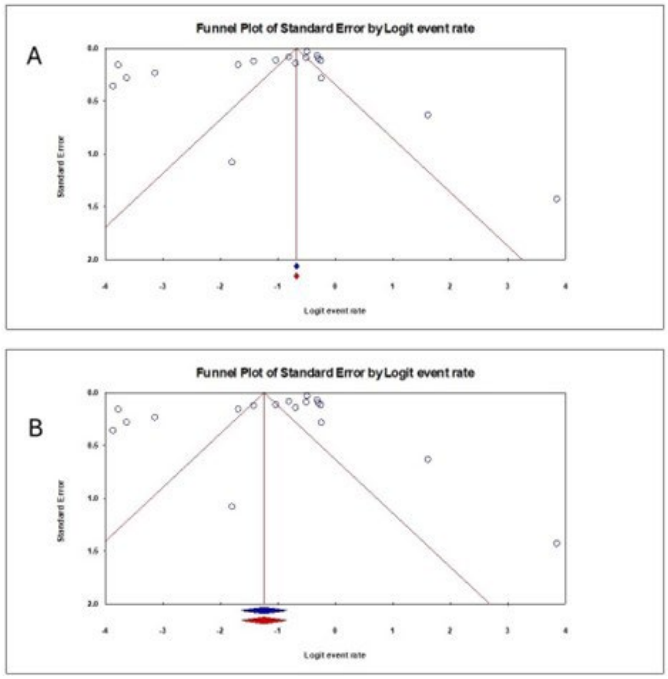

Figure 4. Funnel plot of the prevalence of camel trypanosomiasis shows standard error by logit event rate on fixed (A) and random (B) models of 19 observed and imputed studies.

Egger's linear regression test for asymmetry did not indicate publication bias, Intercept (-4.95), 95% confidence interval (from -9.91 to -0.07), t-value (2.08), df = 16.00. The 1-tailed P-value (recommended) is 0.018, and the 2-tailed P-value is 0.036.

The outcome of Kendall's tau with continuity correction (-0.313), with a 1-tailed P-value (recommended) of 0.030 and 2 -tailed P-value of 0.060.

Duval and Tweedie's trim-and-fill method (no studies trimmed) resulted in an adjusted correlation from -0.718 to -0.630 (95% CI).

The fail-safe N estimated the number of studies with an effect size of zero that are required to nullify the overall effect size for the funnel plot (Figure 4, 5). The classic fail-safe N suggested that 4713.00 missing studies are needed for the result of this meta-analysis to be non-significant (p-value > .050). Also, the orwin's fail-safe N suggested that -0.67 event rate in observed studies and 0.000 mean event rate in missing studies.

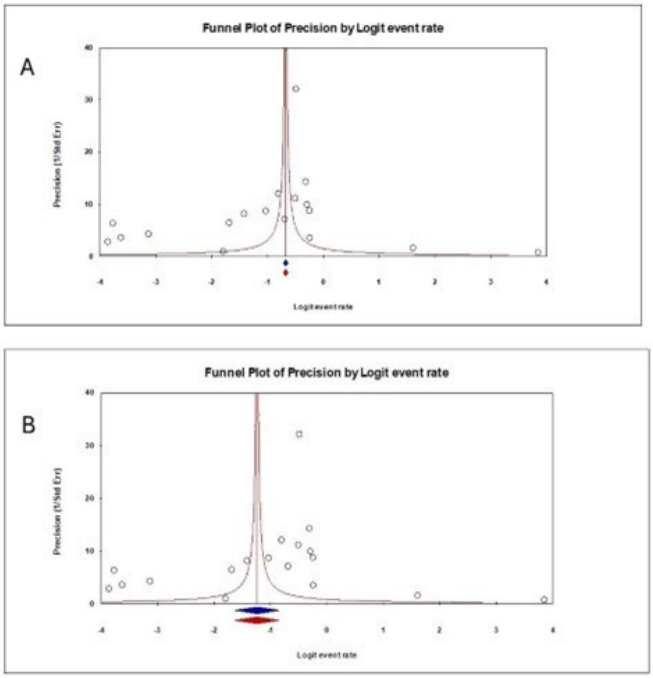

Figure 5. Funnel plot of the prevalence of camel trypanosomiasis shows precision by logit event rate on fixed (A) and random (B) model of 19 observed and imputed studies.

Discussion

The camel is a crucial livestock animal of great economic contribution to pastoralists and endowed with prestigious social value. They are also playing significant role in the livelihood of the pastoralists and agro-pastoralists living in the fragile environments (Desie Sheferaw, 2018). It is in many regions, including the Gulf, so understanding the prevalence of surra in them is vital for both animal health and economic reasons (Selim *et al.*, 2022b).

The prevalence of trypanosomiasis in camels is high and has a severe impact on general health, productivity, and market value, posing a significant threat to food safety and the economy. Camel trypanosomiasis "Surra" caused by *Trypanosoma evansi* (*T. evansi*) which is a member of the Trypanosomatidae family, genus Trypanosome, and subgenus Trypanozoon (Desquesnes *et al.*, 2013). The disease of Surra is mechanically transmitted through biting of flies such as Stomoxys, Tabanids, and Hippoboscids (Tamarit *et al.*, 2010). The clinical finding courses of Surra varied from acute infection with high mortality to chronic infection with reduction in body weight, anemia, infertility (Boushaki *et al.*, 2019b). The objective of the current study was to use meta-analyses to determine the pooled prevalence of Camel trypanosomiasis "Surra" in gulf region. To reduce the publication bias, the current systematic meta-analysis was

Table 2. Final Meta-analysis model of the effect of size and test of null (2-tail) for 19 observed studies on the prevalence of camel trypanosomiasis.

Model	Effect size and 95% Confidence Interval				Test of null (2-Tail)	
	Number of studies	Point estimate	Lower limit	Upper limit	Z-value	P-value
Fixed	18	-0.68	-0.72	-0.63	-30.18	0
Random	18	-1.23	-1.63	-0.48	-6.19	0

Table 3. Heterogeneity and Tau-squared for 19 observed studies on the prevalence of camel trypanosomiasis.

Model	Heterogeneity					Tau-squared	
	Number of studies	Q-value	df (Q)	P-value	I-squared	Tau-squared	Standard Error
Fixed	18	894.96	17	0	98.1	0.62	0.39
Random	18	-	-	-	-	-	-

carried out in accordance with the PRISMA guidelines.

In the current study, 18 studies met the criteria of selection. The examination of 11720 diseased camels with trypanosomiasis revealed 3177 to be positive, the pooled prevalence of Camel trypanosomiasis was determined to be 27.1%. According to the meta-analysis's findings, Al-Kharusi *et al*. (2021a) in in North Al-Sharqiya governorate in the Sultanate of Oman had the greatest prevalence (52.18%, and 95% CI: 0.366-0.395). But Wernery *et al*., 2001 study in Dubai, United Arab Emirates recorded the lowest prevalence (0.03%, 95% CI: 0.020-0.581). Studies on the prevalence of Camel trypanosomiasis have been conducted with varying degrees of results (Gerem *et al*., 2020;Aden and Kula, 2020; Benaissa *et al*., 2020a).

The variation in the prevalence of Camel trypanosomiasis may be due to difference in agro-ecology of the study areas, management system, production system, population density, different sensitivity of different test methods used and new techniques such as PCR. In addition, seasons of the year when the studies were conducted which have a direct effect on the distribution of biting flies responsible for the mechanical transmission of *T. evansi* also cause variation in prevalence (Kassa *et al*., 2011b). In the selected studies, the prevalence of Camel trypanosomiasis was examined using Parasitological examination and molecular methods (thin blood smear (TBS), the Card Agglutination Test for *T. evansi* (CATT/*T. evansi*), DNA extraction and PCR) both fixed and random effects were assessed (Hassan-Kadle *et al*., 2019).

This research included 18 studies; 8 out of 18 depended on traditional and molecular techniques for Camel trypanosomiasis identification and 10 out of 18 depended on molecular ones either the Card Agglutination Test for *T. evansi* (CATT/*T. evansi*), DNA extraction and PCR for identification on *T. evansi*. The molecular and serological prevalence (Combining CATT/*T. evansi* and ITS1-PCR) has increased the prevalence of Camel trypanosomiasis, which are known to have a high sensitivity and specificity for detection of VBD pathogens can be achieved using different diagnostic methods (Maggi *et al*., 2014). Meanwhile, Parasitological examination for detection of Camel trypanosomiasis has some disadvantages as they are not sensitive but can be used in the field with a low amount of equipment (Al-Kharusi *et al*., 2022b).

According to the meta-analysis's findings, from the logit event rate of the fixed effect model in the current study, large study by (Al-Kharusi *et al*., 2021b) have a relative weight of 51.31 %, while the small studies by (Kumar *et al*., 2012) and (Wernery *et al*., 2001b) are given about 0.02 % and 0.04% of the relative weight, respectively. The common effect is well estimated by the larger studies, while the common effect is poorly estimated by the small study, hence the small studied are given a low weight. Small studies have a negligible effect on the total value, which is calculated in the range of 0.02 to 0.04% of the relative weight. In contrast, each study's effect size under the random effect model is estimated for a specific population, hence each study's estimate must be assigned the proper weight in the analysis.

In the current study, the "Relative weights" under random effect each of the large study carried out by (Al-Kharusi *et al*., 2021b) are given about 6.22 % of the relative weight (rather than 51.31 %), even though the small studies by Kumar *et al*. (2012) and Wernery *et al*. (2001b) are given about 1.47 % and 2.19% of the relative weight, respectively (rather than 0.02 % and 0.04%).

In contrast to the fixed effect model, when the small study had essentially no influence, it has a much greater impact effect. Concretely, it receives a relative weight in range of 1.47% and 2.19%, which is virtually the same as the weight given to any of the larger study (51.31%). As a result, studies that are larger and have smaller standard errors are given greater weight than those that are smaller and have larger standard errors. The pooled effect estimate's uncertainty is reduced by this selection of weights.

For heterogenicity in the current study, the Q-value (894.96), I-squared (98.038), and P- value (0.000) are the final heterogeneity variables for 18 observed studies on the prevalence of camel trypanosomiasis. Additionally, the Tau-squared is 0.619 with a 0.39 Standard Error.

Heterogeneity analysis is the measure that demonstrates how the effect width differs between studies. This statistic test determines whether the effects reported by the various studies are mainly attributed to sampling error or also to systematic difference between the studies in addition to a sampling error (Hedges and Olkin, 1985). It is crucial to determine the magnitude of the variance between the distributions since the studies included in the meta-analyses have varying effect sizes. Therefore, Statistical heterogeneity tests are conducted to determine the conformity of the normal distribution of effect sizes. The observed impact value between studies differs for two reasons. The first reason is related to the actual heterogeneity of the effect size, and the second reason is tied to errors within the studies (Borenstein *et al*., 2009) . In consideration of heterogeneity, the null hypothesis was that the effect would be zero for both fixed (common) and random (true) effects. The Hedges' g/standard error (G/SE) for the relevant model was used to calculate the z-value, which was used to test the null hypothesis (Higgins, 2019).

Statistical methods, such as the Cochran's Q test or the index of heterogeneity I2 (I-squared), can be used to quantify the level of heterogeneity in meta-analysis research. The eyeball test (graphical method at forest plot) is a less formal alternative to assess the heterogeneity (Huedo-Medina *et al*., 2006).

In the current study, the z-values of the prevalence of Camel trypanosomiasis were -30.186 (P -value < 0.000) and -6.195 (P-value < 0.000) for both the fixed and random effects, respectively.

In the present study, the Q-statistic for the prevalence of Camel trypanosomiasis was 894.96, compared with the expected value of 18 (P-value < 0.000).

The Q-statistic implied the observed dispersion, while the null hypothesis for heterogeneity suggested that the studies assigned a common effect size. Therefore, it was assumed that the degrees of freedom were equal to the Q-statistic (Thompson, 1994). While the null hypothesis that there is no effect size dispersion is tested using the Q-statistic, the I-squared and tau-squared parameters are useful for evaluating (Schulz *et al*., 1995).

The prevalence of Camel trypanosomiasis had an I-squared value of 98.038, indicating that the actual differences in effect sizes accounted for 99 % of the apparent variance between the studies. Only 1% of the observed variation can be predicted using random error. However, the tau-squared of the prevalence of Camel trypanosomiasis was 0.619. This is the variance "between studies" that was utilized to calculate the weights. Fixed-effect model often includes Q- statistic and tau-squared, whereas random-effect model does not typically provide the Q-statistic or tau-squared.

According to the current statistical meta-analysis, there is >75% great heterogeneity in the prevalence of Camel trypanosomiasis, and only two individual studies have an overall effect that indicates there is data heterogeneity. The overall effect estimated by the random effects model corresponds to the mean of the distribution of the true effect. The sample size, diagnostic technique, study's area in our study may be responsible for the statistical discrepancies between the studies.

Publication bias assumes that not all studies on a study's results are published depending on the direction or significance of the study's findings. Studies with small sample sizes, insufficient power, no discernible difference between groups, and a higher incidence of complications or adverse events in the research study are thought to have a detrimental impact on the overall effect or to introduce bias by increasing the average effect size (Joober *et al*., 2012). Therefore, detecting of the publication bias is a crucial issue because such bias may lead to incorrect conclusions of systematic reviews (Sutton *et al*., 2000). A funnel plot is frequently used in systematic reviews and meta-analyses to examine the existence of publication bias or systematic heterogeneity in individual studies. Effect size is typically displayed against standard errors or precisions in this type of funnel plot (Light and Pillemer, 1986). Because the funnel plot in the current study is asymmetric, there is a systematic distinction between studies with higher and lower precision.

Several statistical tests, including the Egger's regression test (Egger *et al*., 1997) and Begg's rank test (Begg and Mazumdar, 1994), have been proposed to examine publication bias in the funnel plot. Egger's regression test is a statistical tool for measuring funnel plot asymmetry through the standardized effect sizes on their precisions; in the absence of publication bias, the regression intercept is expected to be zero (Egger *et al*., 1997).

There is no indication of publication bias in the current study, according to the results of the Egger's linear regression test, for asymmetry result, which include intercept (-4.95), 95% confidence interval (from -9.91 to -0.07), t-value (2.08), df = 16.00. The 1-tailed P-value (recommended) is 0.018, and the 2-tailed P-value is 0.036. From the statistical meta-analysis, this regression is equal to a weighted regression of the effect sizes on their standard errors, weighted by the inverse of their variances; the weighted regression's slope, rather than the intercept, is predicted to be zero in the absence of publication bias (Rothstein, 2005).

The Begg and Mazumdar rank correlation test examines the correlation between the effect sizes and their corresponding sampling variances; a strong correlation implies publication bias (Begg and Mazumdar, 1994). The outcome of rank test in the present study is Kendall's Tau with continuity correction (-0.313), with a 1-tailed P-value (recommended) of 0.030 and 2 -tailed P-value of 0.060. This outcome provides the Egger regression test results with no indication of publication bias.

Additionally, the trim and fill method are another attractive tool that modifies the predicted total effect size in addition to testing for publication bias (Duval and Tweedie, 2000). It uses a repeated method to remove small studies at the extreme ends of the positive end of the funnel plot. The trimming and filling process is repeated until the funnel plot is symmetric in regard to the effect size (Duval, 2005).

In the current study, the results of the trim-and-fill method appear

as the closed dots indicate the missing studies (no studies trimmed), and the open dots indicate the observed studies (about 18 studies) imputed which depend greatly on the selected estimator (R0, L0, or Q0) for imputing missing studies and its result in an adjusted correlation from -0.718 to -0.630 (95% CI).

The fail-safe N or file drawer number strategy is another tool created by Rosenthal in 1979 (Rosenthal, 1979) to counteract publication bias. It assumes that it is possible to calculate the actual number of missing studies and argues that finding studies to include in a meta-analysis is necessary before determining whether the p value is significant. The use of fail-safe N assumes that the main effect of missing studies has no effect.

In the current study, the meta- analysis incorporates data from 18 studies, which yield a z-value for observed studies of -32.22988 and corresponding 2-tailed p-value of 0.00000. The classic fail-safe N suggested that 4713 missing studies are needed for the result of this meta-analysis to be non-significant (p-value > .050). This means that we would need to locate and include 4713 'null' studies for the combined 2-tailed P-value to exceed 0.050. From another method, the orwin's fail-safe N suggested that 0.336 event rate in observed studies and 0.500 mean event rate in missing studies. Although being frequently used in meta-analysis applications, these publication bias tests may have high type I error rate or low power in certain simulation settings (Peters *et al*., 2006, 2007; Rücker *et al*., 2008; Sterne *et al*., 2000; Terrin *et al*., 2003).

Conclusion

The results of the present study indicate that trypanosomiasis in camels exists in Gulf countries with varying prevalence. Strict measures should be taken for control of such disease in camels and other animals.

Acknowledgments

'This work was supported through the Annual Funding track by the Deanship of Scientific Research, Vice Presidency for Graduate Studies and Scientific Research, King Faisal University, Saudi Arabia (Funding number: 5909)

Conflict of interest

Authors declare that there is no conflict of interest.

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