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Prevalence and Epidemiological Patterns of Bovine Brucellosis in Africa: A Systematic Review and Meta-Analysis

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Title:

PREVALENCE AND EPIDEMIOLOGICAL PATTERNS OF BOVINE BRUCELLOSIS IN AFRICA: A SYSTEMATIC REVIEW AND META-ANALYSIS

ABSTRACT

Background: Bovine brucellosis is an important zoonotic and livestock disease with substantial implications for animal productivity and public health in Africa. However, evidence on its prevalence and epidemiological patterns remains geographically and methodologically heterogeneous.

Objective: To systematically synthesize evidence on the prevalence, epidemiological patterns, risk factors, and control-related findings of bovine brucellosis in Africa.

Methods: A systematic review was conducted in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines. Literature searches were performed in PubMed, Scopus, Web of Science, ScienceDirect, and Google Scholar. Following screening and eligibility assessment, 48 studies were included in the systematic review. Of these, 45 studies provided sufficient prevalence data for quantitative synthesis. A DerSimonian-Laird random-effects meta-analysis of logit-transformed prevalence estimates was performed, with subgroup analyses by country, geographical region, diagnostic approach, and publication year. Epidemiological risk factors and control-related findings were synthesized narratively because of substantial differences in definitions, study designs, and reported effect measures.

Results: The 45 studies included in the quantitative synthesis comprised 337,705 animals, of which 12,725 were seropositive. The crude sample-size-weighted prevalence was 3.77%, whereas the pooled random-effects prevalence was 6.13% (95% CI: 4.49-8.32%). Between-study heterogeneity was extremely high ($Q = 6713.1$, $df = 44$, $p < 0.001$; $I^2 = 99.34\%$; $\tau^2 = 1.2017$), indicating substantial variation in prevalence estimates across studies. Country-level estimates also varied markedly, with particularly high pooled estimates reported in South Sudan, Sudan, Namibia, Ghana, Somalia, and Egypt. Subgroup analyses demonstrated differences according to geographical region and diagnostic approach, although these comparisons should be interpreted cautiously because of differences in study populations, settings, diagnostic algorithms, and sampling strategies. Reported epidemiological factors included herd size, animal age and sex, breed, abortion history, herd management, production systems, livestock movement, and human-livestock interaction.

Conclusion: Bovine brucellosis shows substantial geographical and methodological heterogeneity across the available African evidence. The pooled prevalence of 6.13% provides a summary of the included evidence but should not be interpreted as a uniform continent-wide prevalence estimate given the extreme between-study heterogeneity. Strengthening standardized diagnostic procedures, risk-based surveillance, vaccination programs and integrated One Health approaches is warranted. Future studies should use harmonized diagnostic algorithms, standardized risk-factor definitions, and comparable sampling frameworks to improve the reliability and comparability of prevalence estimates.

Keywords: Bovine brucellosis; *Brucella abortus*; Africa; seroprevalence; systematic review; meta-analysis; epidemiology; One Health; cattle.

INTRODUCTION

Bovine brucellosis, caused by primarily by *brucella abortus,* is a highly contagious zoonotic disease with profound implication for livestock health, food security, and human well-being in Africa [1]. The disease is characterized by reproductive failures in cattle including abortion, stillbirths, and reduced milk production leading to substantial economic losses in agrarian and pastoral communities [2]. In humans, brucellosis manifest as a debilitating febrile illness, often misdiagnosed due to its nonspecific symptoms, resulting in chronic infections and long-term disability if untreated [3]. Despite its significance, the epidemiology of bovine brucellosis in Africa remains understudied, with fragmented data and regional disparities in surveillance and reporting [4].

The context presents unique challenges for brucellosis control, including extensive livestock movement, communal grazing system, and limited access to veterinary services [5]. Pastoralist communities, which rely heavily on livestock for subsistence, are particularly vulnerable due to close human-animal interactions and consumption of raw dairy products [6]. Moreover, the lack of standardized diagnostic protocols and underreporting in many regions obscure the true burden of the disease [7]. While some countries have implemented control programs, such as vaccination campaigns and test-and-slaughter policies, their effectiveness is often hampered by logistical constraints, vaccine shortages, and low stakeholder awareness [7].

A critical research gap lies in the inconsistent methodologies used to estimate brucellosis prevalence across studies, leading to wide variations reported rates [8]. Many studies focus on seroprevalence without accounting for potential cross-reactivity with other pathogens or the limitations of serological tests in endemic settings [9]. Furthermore, there is limited synthesis risk factors dividing transmission, such as trade networks, climate variability, and co-infections with other abortifacient diseases. The interplay between bovine brucellosis in high risk occupational groups like farmers, butchers, and veterinarians [10].

This review is motivated by urgent need to consolidate existing knowledge on bovine brucellosis in Africa, providing a foundation for evidence- based interventions. By systematically analyzing epidemiological patterns, we aim to identify high-risk regions, livestock system, and human populations requiring targeted control measures. The findings will inform policymakers,

veterinarians, and public health practitioners in designing context-specific strategies to mitigate the dual burden of brucellosis on animal and health.

METHODOLOGY

Study Design

This systematic review and meta-analysis was conducted in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines. The review was registered on the Open Science Framework (OSF) under DOI 10.17605/OSF.IO/EVFDR. The OSF registration provides a publicly accessible record of the review. The review involved systematic literature searching, study selection, data extraction, and quantitative synthesis to assess the prevalence and epidemiological patterns of bovine brucellosis in Africa.

Search Strategy

A comprehensive literature search was performed across five electronica databases: PubMed, Scopus, Web of Science, ScienceDirect, and Google Scholar. The search aimed to identify studies reporting on the prevalence and epidemiological patterns of bovine brucellosis in Africa.

Search terms were developed using Boolean operators and induced combinations of keywords such as: “bovine brucellosis” OR “Brucella abortus” AND “prevalence” OR “epidemiology” AND “Africa”. Medical subject headings (MeSH) terms were applied where appropriate. The search was limited to peer-reviewed articles published in English. No restriction was placed on publication year to capture both historical and recent trends. Additionally, reference lists of relevant article were screened to identify further eligible studies.

Eligibility Criteria

Inclusion criteria comprised studies that provided primary epidemiological data on bovine brucellosis conducted within Africa countries, utilizing observational study design and validated diagnostic methods, including the Rose Bengal Test and ELISA. To enhance the robustness of the analysis, only studies with a minimum sample size of 50 animals and published in peer-reviewed journals in English were considered.

Exclusion criteria encompassed review articles, meta-analyses, editorials, and studies lacking field relevance or sufficient extractable data. Publication without accessible full texts were also excluded. These criteria were applied to ensure methodological consistency and reliability of the synthesized evidence.

Study Selection

All identified records were imported into the reference-management system, and duplicate records were removed. Titles and abstracts were independently screened by two reviewers against the predefined eligibility criteria. Full-text reports considered potentially eligible were retrieved and independently assessed for inclusion. Disagreements between reviewers were resolved through discussion and consensus. The study-selection process is summarized in the PRISMA flow diagram (Figure 1).

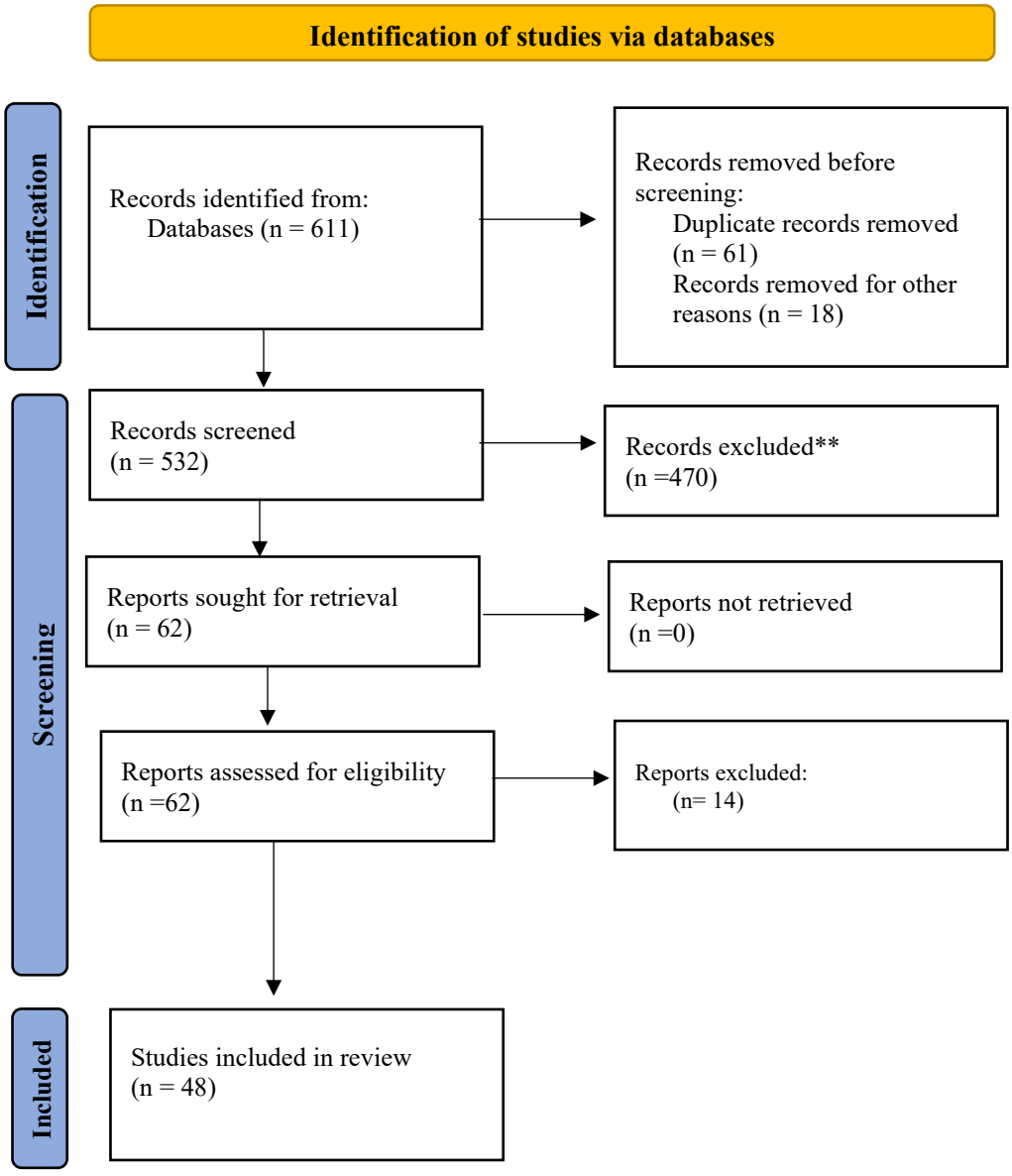


Figure 1. PRISMA flow diagram showing the identification, screening, eligibility assessment and inclusion of studies in the systematic review and meta-analysis of bovine brucellosis in Africa.

Data Extraction

Data were systematically extracted using a standardized and pilot tested data collection framework to ensure methodological consistency. Extracted variables included study characteristics (geographical location, design, and sample size), livestock species examined, and diagnostic techniques applied. Epidemiological outcomes, including prevalence estimates and associated risk factors, were recorded, alongside any reported data on human brucellosis. The extraction process was conducted independently by two reviewers to enhance reliability, with discrepancies resolved through discussion and consensus, thereby minimizing the risk of extraction bias.

Quality assessment

The methodological quality of included studies was assessed using a modified version of the Newcastle-Ottawa scale for observational studies. Studies were evaluated based on sampling strategy, diagnostic accuracy, data reporting and risk of bias. Only studies meeting minimum quality thresholds were included in the final analysis.

Data Synthesis and Statistical Analysis

A quantitative meta-analysis was conducted for studies reporting sufficient data to calculate Brucella seroprevalence. Of the 48 studies included in the systematic review, 45 reported both sample size and the number of seropositive animals and were therefore included in the quantitative synthesis. Three studies without usable positive-count data were retained in the systematic review but excluded from prevalence calculations.

For each study, prevalence was calculated as the number of seropositive animals divided by the total number of animals tested. The crude sample-size-weighted prevalence was calculated from the aggregate number of positive animals divided by the aggregate sample size. Because the included studies showed substantial variation in prevalence, sample size, study populations, and diagnostic approaches, the principal pooled estimate was obtained using a DerSimonian–Laird random-effects model applied to logit-transformed proportions, with estimates subsequently back-transformed to the prevalence scale. The random-effects estimate was considered the primary summary measure because the assumption of a common underlying prevalence across studies was not appropriate for the observed evidence base.

Between-study heterogeneity was assessed using Cochran's Q statistic, the I^2 statistic, and τ^2 (tau-squared). I^2 was used to describe the proportion of total variability attributable to between-study heterogeneity, while τ^2 represented the estimated between-study variance on the logit scale. Study-level prevalence estimates and their 95% confidence intervals were presented using forest plots.

Where sufficient data were available, subgroup analyses were conducted according to country, geographic region, diagnostic-test family, and publication year. These analyses were undertaken to explore potential sources of heterogeneity rather than to establish causal relationships between subgroup characteristics and seroprevalence. The diagnostic-test subgroup results were therefore interpreted cautiously because differences between diagnostic categories may reflect differences in study populations, sampling strategies, or indications for testing rather than differences in test performance.

Risk factors were synthesized narratively because the included studies used heterogeneous definitions, analytical methods, and effect measures, and did not provide sufficiently comparable data for a pooled risk-factor meta-analysis. Descriptive findings were therefore summarized according to the frequency with which individual risk factors were reported and the direction of associations identified in the original studies.

RESULT

Study Selection

The database search identified 611 records. After removal of 61 duplicate records and 18 records removed for other reasons, 532 records remained for title and abstract screening. Of these, 470 records were excluded because they did not meet the predefined eligibility criteria. A total of 62 reports were sought for retrieval, and all 62 reports were successfully retrieved and assessed for eligibility. Fourteen reports were subsequently excluded because they did not meet the eligibility criteria, including insufficient or non-extractable data and lack of relevance to the objectives of the review. Ultimately, 48 studies met the inclusion criteria and were included in the systematic review. The study-selection process is presented in the PRISMA flow diagram (Figure 1).

Study Characteristics

A total of 48 studies met the predefined eligibility criteria and were included in the systematic review. Of these, 45 studies reported sufficient quantitative information, including the total number of animals tested and the number of seropositive animals, to contribute to the meta-analysis. Three included studies were retained for the systematic review but were not incorporated into the quantitative prevalence synthesis because the reported data were insufficient for calculation of study-level prevalence.

The 45 studies included in the quantitative synthesis comprised a total of 337,705 cattle, of which 12,725 were reported as seropositive for Brucella infection. Study-level prevalence estimates varied substantially across the evidence base, reflecting differences in geographic setting, study populations, sample sizes, and diagnostic approaches. The characteristics of the included studies, including country, diagnostic method, sample size, number of positive animals, and prevalence estimate, are summarized in Table 1.

Table 1. Characteristics of Studies Included in the Quantitative Synthesis of Bovine Brucellosis Seroprevalence in Africa**.**

Study (Author, Year)	Country	Year	Sample size (n)	No. positive	Diagnostic test	Prevalence (%)
Akinseye (2016)	Nigeria	2016	8,105	315	RBPT ± CFT	3.89
Alhaji (2016)	Nigeria	2016	672	13	RBPT + confirmatory	1.93
Ebrahim (2016)	Sudan	2016	300	77	RBPT ± CFT	25.67
Miller (2016)	Uganda	2016	768	—	RBPT ± CFT	—
Tasiame (2016)	Ghana	2016	315	62	c-ELISA	19.68
Ayoola (2017)	Nigeria	2017	1,241	97	RBPT ± CFT	7.82
Fèvre (2017)	Kenya	2017	983	3	Serology (unspecified)	0.31
Asakura (2018)	Tanzania	2018	124	55	iELISA	44.35
Awah-Ndukum (2018)	Cameroon	2018	1,031	57	RBPT + confirmatory	5.53
Chaka (2018)	Ethiopia	2018	268	26	ELISA + CFT	9.70
Madut (2018)	South Sudan	2018	893	277	RBPT + confirmatory	31.02
Ogugua (2018)	Nigeria	2018	513	48	c-ELISA	9.36
Sagamiko (2018)	Tanzania	2018	1,211	113	c-ELISA	9.33
Yahyaoui-Azami (2018)	Morocco	2018	1,194	23	RBPT ± CFT	1.93

Abuom (2019)	Kenya	2019	398	67	*Brucella abortus* antibody	16.83
Nguna (2019)	Uganda	2019	345	4	iELISA	1.16
Robi (2019)	Ethiopia	2019	423	17	CFT ± ELISA	4.02
Selim (2019)	Egypt	2019	720	120	iELISA	16.67
Cadmus (2020)	Nigeria	2020	149	10	c-ELISA	6.71
Ntivuguruzwa (2020)	Rwanda	2020	1,907	141	RBPT ± CFT	7.39
Cadmus (2021)	Nigeria	2021	366	21	c-ELISA	5.74
Hassan-Kadle (2021)	Somalia	2021	201	39	RBPT ± CFT	19.40
Kiiza (2021)	Rwanda	2021	465	63	RBPT ± CFT	13.55
Mfune (2021)	Zambia	2021	1,712	127	RBPT + confirmatory	7.42
Ntirandekura (2021)	Tanzania	2021	426	—	RBPT + confirmatory	—
Ouared (2021)	Algeria	2021	63,284	213	ELISA	0.34
Megahed (2022)	Egypt	2022	400	84	iELISA	21.00
Okafor (2022)	Nigeria	2022	33	3	c-ELISA	9.09
Akoko (2023)	Kenya	2023	6,593	448	ELISA	6.80
Efrem (2023)	Eritrea	2023	2,740	34	RBPT ± CFT	1.24
Elhaig (2023)	Egypt	2023	989	205	RBPT ± CFT	20.73
Elisha (2023)	Tanzania	2023	400	2	c-ELISA	0.50

Kassa (2023)	Ethiopia	2023	352	2	RBPT + confirmatory	0.57
Marumo (2023)	South Africa	2023	770	—	CFT ± ELISA	—
Mengele (2023)	Tanzania	2023	2,048	49	c-ELISA	2.39
Warioba (2023)	Tanzania	2023	1,052	272	iELISA	25.86
Birhan (2024)	Ethiopia	2024	384	68	RBPT + confirmatory	17.71
de Boni (2024)	South Africa	2024	9,111	155	Serology (unspecified)	1.70
Erkyihun (2024)	Ethiopia	2024	426	2	RBPT + confirmatory	0.47
Lita (2024)	Sudan	2024	478	103	RBPT + confirmatory	21.55
Madzingira (2024)	Namibia	2024	371	84	CFT ± ELISA	22.64
Oyetola (2024)	Mali	2024	804	66	Serology (unspecified)	8.21
Getachew (2025)	Ethiopia	2025	490	7	iELISA	1.43
Madiba (2025)	South Africa	2025	1,133	9	RBPT + confirmatory	0.79
Mtinda (2025)	Tanzania	2025	380	24	RBPT + confirmatory	6.32
Seakamela (2025)	South Africa	2025	212,440	8,980	CFT ± ELISA	4.23
Bandara (2026)	Sri Lanka	2026	180	64	RBPT + confirmatory	35.56
Joseph (2026)	Tanzania	2026	10,081	76	Not reported	0.75
Total / Summary	**20 countries**	**2016–2026**	**339,669**	**12,725**	**—**	**3.746**

The crude aggregate prevalence, calculated by dividing the total number of seropositive animals by the total number tested, was 3.77%. However, because the prevalence estimates differed markedly among studies, the primary summary measure was the random-effects pooled prevalence rather than the crude aggregate estimate.

Research Trend

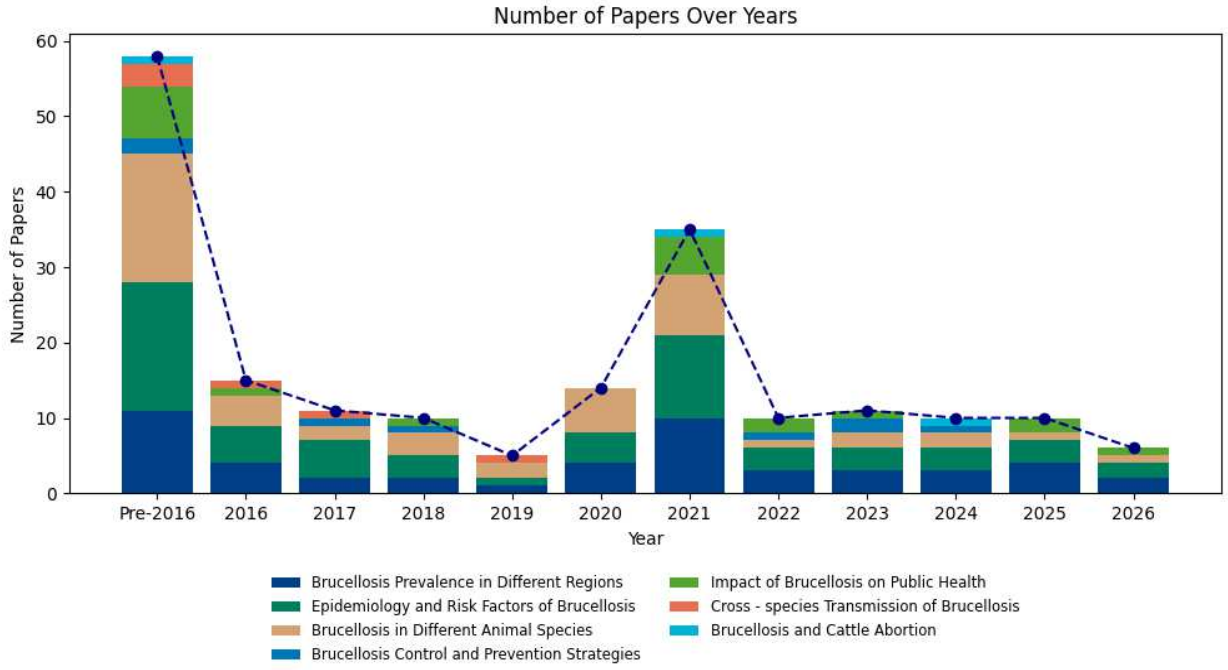


Figure 2. Research Trends in the Domain of Prevalence and Epidemiological Patterns Bovine Brucellosis in Africa

The temporal distribution of publications indicates a fluctuating but sustained research interest in bovine brucellosis across Africa. Prior to 2016, a total of 23 studies were published, primarily focusing on prevalence estimation and basic epidemiological patterns. Between 2016 and 2018, publication output remained relatively stable, averaging 5-6 studies per year. A decline was observed in 2019, followed by a notable increase during 2020-2021, when 19 studies were published. This surge may reflect increased attention to zoonotic diseases during the COVID-19 pandemic.

Post-2021, publication rates declined slightly but remained consistent. Despite the growing body of literature, notable gaps persist, particularly in studies addressing control strategies, knowledge, attitudes, and practices (KAP), and human brucellosis, which remain underrepresented compared to prevalence focused research.

Overall quantitative synthesis

Among the 48 studies included in the systematic review, 45 provided sufficient data for quantitative synthesis. These studies included 337,705 cattle, of which 12,725 were reported as seropositive for *Brucella*. The crude aggregate prevalence was 3.77%. Using a DerSimonian-Laird random-effects model with logit-transformed prevalence estimates, the pooled seroprevalence was 6.13% (95% CI: 4.49-8.32%).

Individual study prevalence estimates varied substantially across the included studies. The forest plot in Figure 2 presents the study-specific prevalence estimates with their corresponding 95% confidence intervals and the overall random-effects pooled estimate. The difference between the crude aggregate prevalence and the random-effects pooled estimate reflects the substantial variation in prevalence and study size across the evidence base. Therefore, the pooled estimate should be interpreted as an overall summary of the included studies rather than as a uniform estimate applicable to all cattle populations in Africa.

Quantitative synthesis and pooled seroprevalence

Among the studies with usable prevalence data, 45 studies contributed to the quantitative synthesis, comprising 337,705 animals and 12,725 seropositive animals. The crude sample-size-weighted prevalence was 3.77% (95% CI: 3.70-3.83%). Because this estimate was strongly influenced by a small number of very large surveys, a DerSimonian–Laird random-effects model based on logit-transformed proportions was used as the principal summary measure. The pooled seroprevalence was 6.13% (95% CI: 4.49-8.32%). The individual study estimates showed substantial variation, demonstrating considerable differences in seroprevalence across study settings (Figure 2).

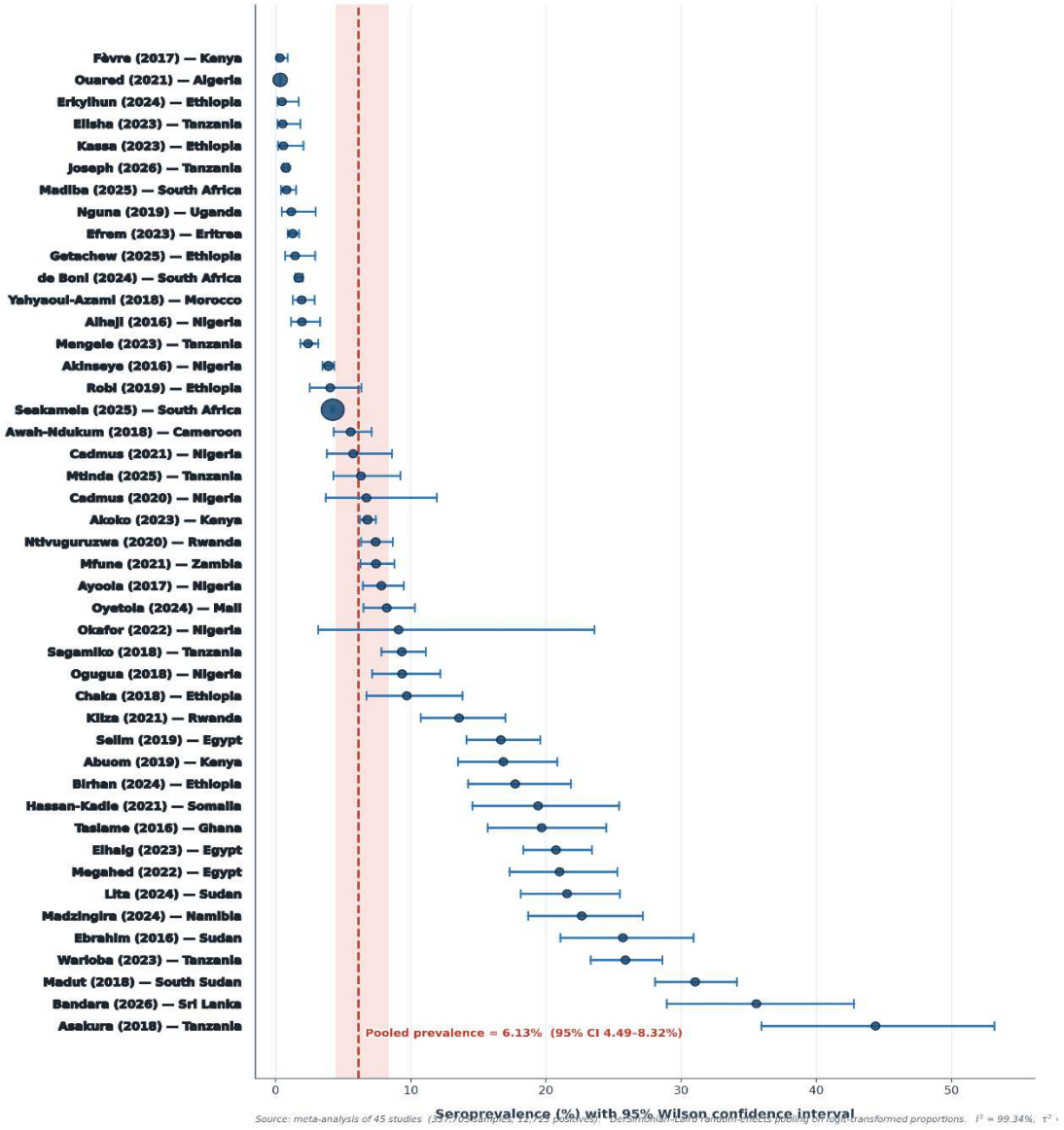


Figure 2. Forest plot of study-level Brucella seroprevalence with 95% confidence intervals and the random-effects pooled estimate.

The forest plot demonstrates marked variability in reported Brucella seroprevalence across the included studies. Study-level estimates ranged from approximately 0.3% to 44.4%, indicating substantial epidemiological variation between study populations. The random-effects pooled estimate of 6.13% should therefore be interpreted as an overall summary across heterogeneous study settings rather than as a uniform prevalence applicable to all African livestock populations. The difference between the crude prevalence (3.77%) and the random-effects estimate (6.13%) is

largely attributable to the influence of very large studies reporting relatively low prevalence and the contribution of smaller studies with higher prevalence.

Between-Study Heterogeneity

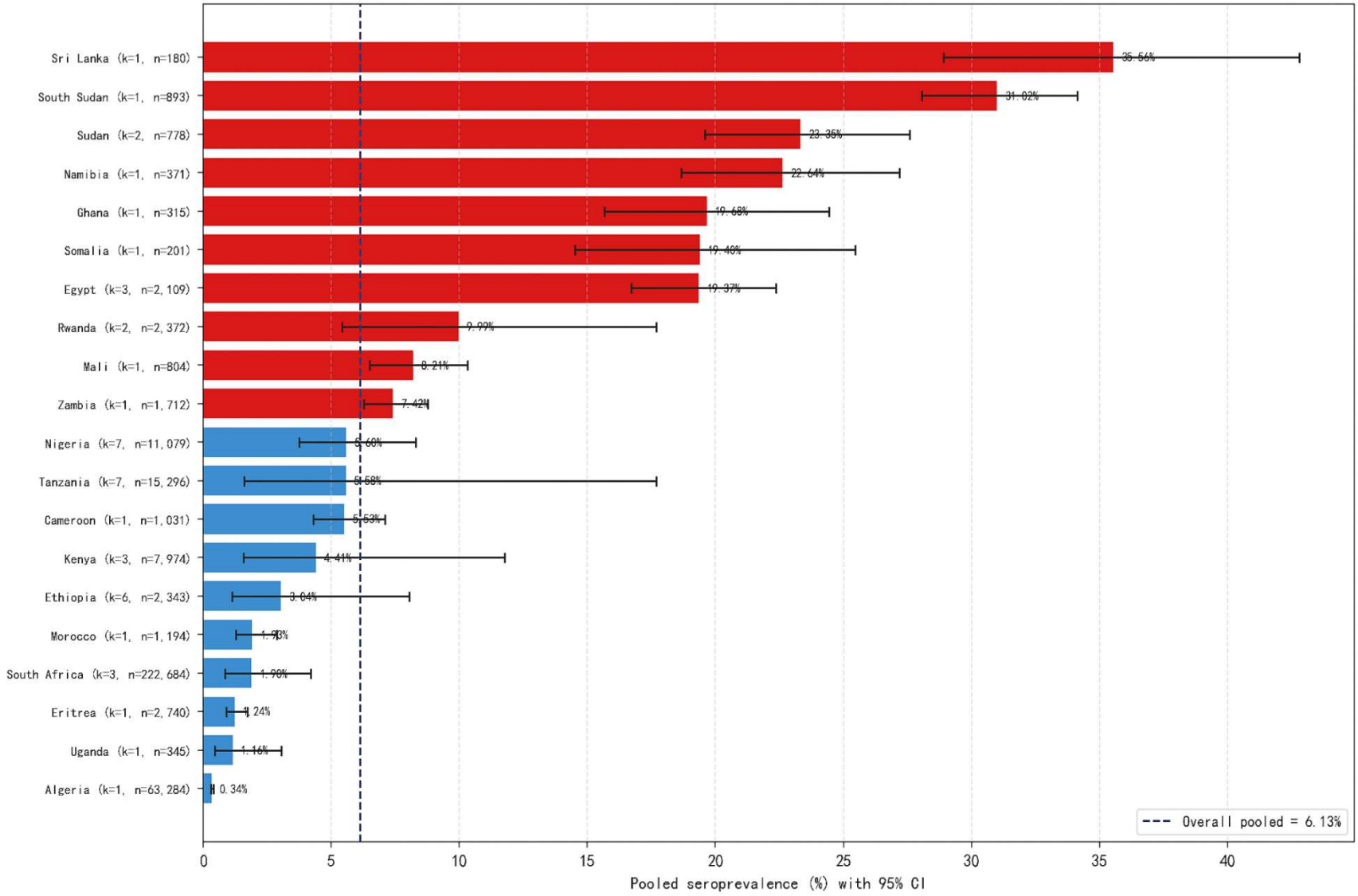
Substantial heterogeneity was observed among the 45 studies contributing to the quantitative synthesis. Cochran's Q statistic was 6713.1 with 44 degrees of freedom ($p < 0.001$), while the I^2 statistic was 99.34%, indicating that almost all observed variability in the study estimates was attributable to between-study heterogeneity rather than sampling error. The estimated between-study variance was $\tau^2 = 1.2017$ on the logit scale. These findings indicate considerable variation in *Brucella* seroprevalence across the study settings and support the use of a random-effects model. This level of heterogeneity is common in seroprevalence meta-analyses and reflects real biological and operational differences across countries, host species, husbandry systems, and diagnostic algorithms. The pooled estimate should therefore be interpreted as the average of a highly dispersed distribution, not as a single value applicable to any particular setting.

Country-Level Pooled Prevalence

Country level random effects analyses demonstrated substantial variation in *Brucella* seroprevalence among the African countries represented in the quantitative dataset. The highest pooled estimates were observed in South Sudan (31.02%), Sudan (23.35%), Namibia (22.64%), Ghana (19.68%), Somalia (19.40%), and Egypt (19.37%). Lower pooled estimates were observed in countries including Algeria, South Africa, Uganda, Eritrea, and Morocco.

These country-level estimates should be interpreted cautiously because the number of contributing studies varied considerably between countries. In particular, 11 of the 20 countries represented in the quantitative analysis were informed by only a single study. Consequently, the country-level estimates should not be interpreted as definitive national prevalence estimates or as evidence that one country has a uniformly higher prevalence than another. Rather, they represent pooled estimates based on the available studies included in this review. The country specific random effects pooled prevalence estimates and their corresponding 95% confidence intervals are presented in (Figure 3) and Shown on supplement (Figure S1).

Figure 3. Random-effects pooled Brucella seroprevalence by country, with 95% confidence intervals.



The country-level analysis demonstrates pronounced geographic heterogeneity in reported Brucella seroprevalence. South Sudan had a pooled estimate of 31.02% (95% CI: 28.07-34.13%), followed by Sudan at 23.35% (95% CI: 19.59-27.57%) and Namibia at 22.64% (95% CI: 18.67-27.18%). Ghana, Somalia, and Egypt also showed pooled estimates close to 20%. In contrast, several countries had substantially lower estimates, with Algeria representing the lowest pooled estimate among the African countries included in the analysis. However, country-level estimates should be interpreted cautiously because 11 of the 20 countries were represented by only a single study. In such countries, the pooled estimate is effectively the estimate from that individual study rather than a robust country-wide estimate.

Regional Subgroup Analysis

A subgroup analysis was conducted according to geographic region to explore variation in *Brucella* seroprevalence between major African regions. Among the 45 studies contributing to the quantitative synthesis, 37 studies representing 270,160 cattle were classified as Sub-Saharan Africa. The pooled seroprevalence in this group was 5.50% (95% CI: 4.11-7.32%), with substantial heterogeneity (I^2 = 99.0%). Seven studies representing 67,365 cattle were classified as North Africa. The pooled seroprevalence was 8.94% (95% CI: 1.86-33.76%), with very high heterogeneity (I^2 = 99.8%). Although the pooled estimate was numerically higher in North Africa than in Sub-Saharan Africa, the wide confidence interval and extreme between-study heterogeneity indicate considerable uncertainty around the regional estimate. Therefore, the difference should not be interpreted as evidence of a definitive regional effect.

One additional study from Sri Lanka was classified separately as non-African and was therefore excluded from the African regional comparison. This study reported a prevalence of 35.56% (95% CI: 28.91–42.81%). It was not considered representative of either African region. The regional subgroup estimates, including the number of contributing studies, animals tested, positive animals, pooled prevalence, 95% confidence intervals, and between study heterogeneity, are summarized in (Table 2).

Table 2. Random-effects pooled *Brucella* seroprevalence by geographic region

Region	Studies (k)	Animals tested (N)	Positive (n)	Pooled prevalence (%)	95% CI	I^2 (%)
Sub-Saharan Africa	37	270,160	11,836	5.50	4.11-7.32	99.0
North Africa	7	67,365	825	8.94	1.86-33.76	99.8

The regional analysis suggests a higher pooled seroprevalence in North Africa than in Sub-Saharan Africa; however, this difference should be interpreted cautiously. The confidence interval for North Africa was substantially wider than that for Sub-Saharan Africa, and heterogeneity was extremely high within both regions. These findings indicate that broad geographic classification does not adequately account for the differences in seroprevalence between individual study populations. Country-specific epidemiological conditions, livestock production systems, diagnostic approaches, sampling strategies, and other study-level characteristics may contribute to the remaining heterogeneity.

Diagnostic-Method Subgroup Analysis

Subgroup analysis by diagnostic method demonstrated variation in pooled *Brucella* seroprevalence across diagnostic categories. Studies using RBPT with a confirmatory test had a pooled prevalence of 6.19% (95% CI: 3.24-11.51%), whereas studies using RBPT with or without confirmatory testing had a pooled prevalence of 7.87% (95% CI: 4.25-14.12%). Studies using c-ELISA had a pooled prevalence of 6.17% (95% CI: 3.43-10.85%), while those using iELISA had a higher pooled estimate of 12.34% (95% CI: 6.99-20.86%).

Other diagnostic categories showed lower pooled estimates, including serology with unspecified methodology (1.84%; 95% CI: 0.46-7.03%) and ELISA (1.55%; 95% CI: 0.08-24.17%). Studies using CFT with or without ELISA had a pooled prevalence of 7.57% (95% CI: 2.06-24.18%).

These differences should be interpreted cautiously. Diagnostic-method subgroup estimates may reflect differences in study populations, geographic settings, sampling strategies, disease risk, study objectives, and the specific diagnostic algorithms used, rather than differences in diagnostic-test performance alone. Therefore, the subgroup analysis does not provide sufficient evidence to conclude that one diagnostic method consistently produces higher or lower prevalence than another. The pooled seroprevalence estimates and corresponding 95% confidence intervals for the different diagnostic method categories are summarized in (Table 3).

Table 3. Random effects pooled *Brucella* seroprevalence according to diagnostic method

Diagnostic method	**Studies (k)**	**Animals tested (N)**	**Positive (n)**	**Pooled prevalence (%)**	**95% CI**
RBPT + confirmatory test	11	7,641	746	6.19	3.24-11.51
RBPT ± CFT	9	17,142	994	7.87	4.25-14.12
c-ELISA	8	5,035	308	6.17	3.43-10.85
iELISA	6	3,131	542	12.34	6.99-20.86
Serology unspecified	3	10,898	224	1.84	0.46-7.03
CFT ± ELISA	3	213,234	9,081	7.57	2.06-24.18
ELISA	2	69,877	661	1.55	0.08-24.17

The diagnostic subgroup analysis demonstrates that reported seroprevalence varied according to the diagnostic approach used; however, these differences should not be interpreted as evidence that one diagnostic test intrinsically produces higher or lower prevalence. The relatively high pooled estimate observed among iELISA studies may reflect differences in the populations selected for testing, study objectives, epidemiological risk, or other study-level characteristics rather than a direct effect of the assay itself. Similarly, the lower estimate observed in studies where the serological method was unspecified cannot be attributed to superior diagnostic performance. Therefore, diagnostic method should be considered an important source of methodological heterogeneity and potential confounding in comparisons of seroprevalence across studies.

Publication-Year Subgroup Analysis

A subgroup analysis was conducted according to publication year to examine variation in reported *Brucella* seroprevalence across the publication period. The pooled estimates varied across years, ranging from 1.66% in 2017 to 16.33% in 2022. However, the estimates differed considerably in the number and characteristics of contributing studies, sample sizes, geographic settings, and study populations.

Therefore, the variation in pooled prevalence across publication years should not be interpreted as evidence of a temporal increase or decrease in bovine brucellosis prevalence. Rather, the observed differences may reflect changes in the composition of the available evidence over time, including differences in countries studied, diagnostic approaches, study populations, and sample sizes.

The publication-year subgroup results are presented in Supplementary Figure S2.

Relationship between Sample Size and Prevalence

A scatterplot was used to examine the relationship between study sample size and reported *Brucella* seroprevalence among the studies included in the quantitative synthesis. Smaller studies showed a wide dispersion of prevalence estimates, whereas studies with larger sample sizes tended to cluster toward lower prevalence values, with most large studies reporting estimates below approximately 8%. This pattern suggests that study size may be associated with the magnitude and variability of reported prevalence estimates. The greater dispersion among smaller studies may reflect differences in study populations, geographic settings, sampling strategies, or other sources of between-study heterogeneity. It may also be compatible with small-study or publication

asymmetry. However, the observed pattern alone is insufficient to establish the presence of publication bias, particularly given the extreme heterogeneity observed in the meta-analysis. The relationship between sample size and reported prevalence is presented in (Figure 4).

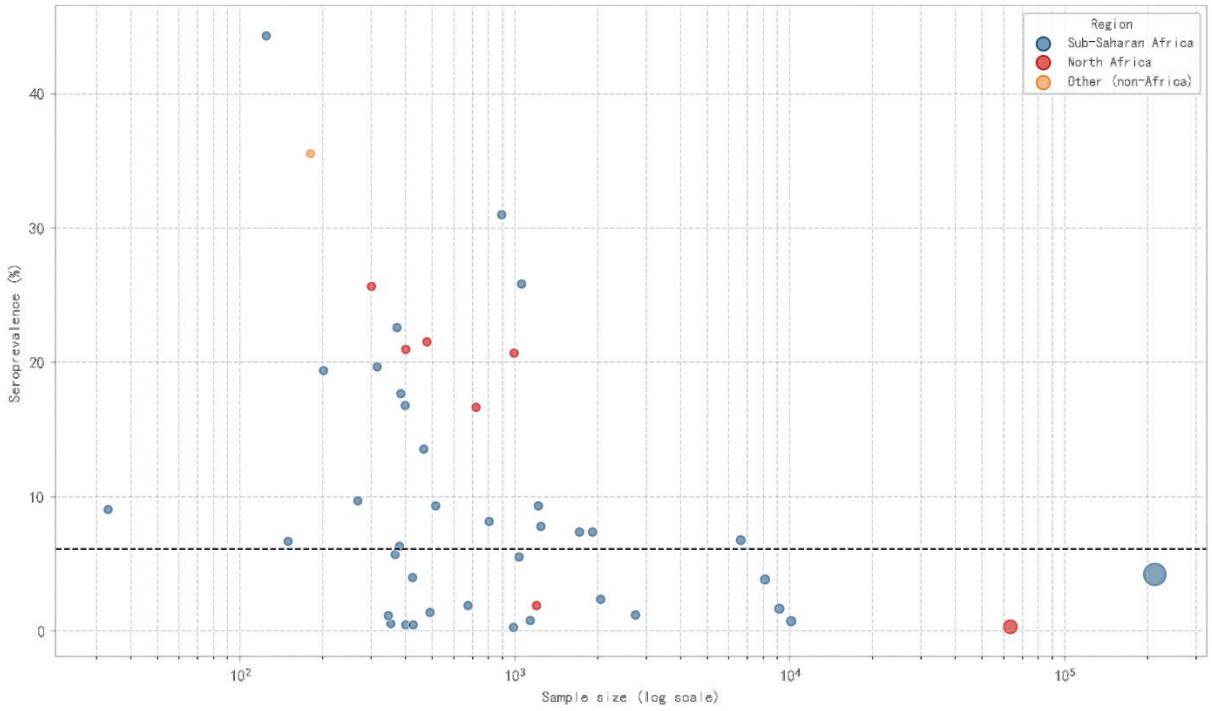


Figure 4. Relationship between study sample size and reported Brucella seroprevalence among studies included in the quantitative synthesis.

The distribution suggests that study size may be related to the magnitude and variability of reported seroprevalence. Studies with smaller sample sizes showed greater dispersion of prevalence estimates, including several high-prevalence observations, whereas large studies generally produced lower and more narrowly distributed estimates. This pattern may reflect differences in study design and population selection: smaller studies may be more frequently conducted in targeted, high-risk, or outbreak-related populations, while larger surveys may provide broader population coverage. The observed asymmetry may also be compatible with selective publication of positive findings from smaller studies; however, the available data do not establish publication bias as the cause of the observed pattern.

Risk Factor analysis

Risk-factor information was available from 34 of the 48 studies included in the systematic review. The most frequently investigated factors were sex and age, each reported in eight studies, followed by herd size in seven studies and breed in six studies. Abortion history was assessed in four studies. Other reported factors included geographic location, previous infection, hygiene practices, veterinary-service use, farm origin, calving practices, and reproductive events. Because the included studies differed substantially in their definitions of exposures, study populations, analytical approaches, and reported effect measures, a pooled meta-analysis of risk factors was not performed. The associations presented in (Table 4) therefore represent findings reported by individual studies and should not be interpreted as pooled effect estimates.

Among the reported associations, retained fetal membranes were associated with increased odds of seropositivity (OR = 32.74), as were frequency of birth (OR = 20.00), farm origin (OR = 16.67), combined age/breed/herd-size factors (OR = 14.60), and medium-scale farm status (OR = 11.30). Veterinary-service use was associated with lower odds of seropositivity in one study (OR = 0.39). Other factors, including abortion history, previous infection, herd size, and calving on pasture, were also reported as study-specific associations.

These findings suggest that reproductive history, herd characteristics, management practices, and veterinary-service factors may be relevant to bovine brucellosis epidemiology. However, differences in study design and exposure definitions prevent direct comparison of the reported effect estimates, and causal relationships cannot be inferred from these study-specific associations.

Table 4. Study-specific risk factors associated with bovine brucellosis seropositivity

Risk factor	Reported association/effect	Interpretation
Retained fetal membranes	OR = 32.74	Increased odds
Frequency of birth	OR = 20.00	Increased odds
Farm origin	OR = 16.67	Increased odds
Combined age/breed/herd-size factors	OR = 14.60	Increased odds
Medium-scale farm status	OR = 11.30	Increased odds
Veterinary-service use	OR = 0.39	Lower odds
Abortion history	Study-specific association	Not pooled
Previous infection	Study-specific association	Not pooled
Herd size	Study-specific association	Not pooled
Calving on pasture	Study-specific association	Not pooled

Several potentially important risk factors were associated with Brucella seropositivity across individual studies. Among the reported numerical estimates, particularly large associations were observed for retained fetal membranes (OR 32.74), frequency of birth (OR 20.00), farm origin (OR 16.67), combined age/breed/herd-size factors (OR 14.60), and medium-scale farm status (OR 11.30). Veterinary-service use was associated with lower odds of seropositivity in one study (OR 0.39). These estimates should, however, be interpreted as study-specific associations rather than pooled effects because the studies differed in exposure definitions, reference categories, populations, and analytical approaches. Therefore, no overall quantitative effect estimate was calculated for individual risk factors.

Brucellosis Prevalence across Livestock Species in Africa

Although the primary focus of this review was bovine brucellosis, the included literature also reported *Brucella* seroprevalence in other livestock species. These data provide additional epidemiological context but were not combined with the bovine prevalence estimates in the primary meta-analysis. Among cattle, reported seroprevalence varied considerably between study settings, ranging from approximately 1.2% in Malawi [11] to 27.6% in Ethiopia [12]. Substantial variation was also reported among other livestock species, including sheep, goats, camels, donkeys, and buffalo. The variation across species and countries likely reflects differences in geographic setting, animal populations, management systems, sampling strategies, and diagnostic approaches. Because these estimates were derived from heterogeneous studies and different livestock populations, they should be interpreted as descriptive evidence rather than as directly comparable pooled prevalence estimates. The species-specific findings are summarized in (Table 5).

Cattle

Cattle were the most extensive studied species and exhibited the highest and most variable prevalence rates. Elevated seroprevalence was consistently reported in pastoral and agro-pastoral systems, particularly in east Africa. In Ethiopia, prevalence estimates ranged from 3.8% in localized districts [13] to as high as 27.6% in certain agro-ecological zones [12], largely attribute to communal grazing practices and limited vaccination coverage. Similarly, Uganda's cattle corridor reported prevalence levels between 12.4% to 18.9%, influenced by Tran's boundary livestock movements and extensive herd mixing [14].

In contrast relatively lower prevalence was observed in more controlled production system. For instance, South Africa reported a prevalence of approximately 8.3% where structured veterinary services and regulated livestock management practices are more established [15]. Urban and peri-urban dairy system in countries such as Nigeria and Tanzania demonstrated intermediate prevalence levels (approximately 14.5% -16.2%), often linked to intensified production, animal trade networks, and marked driven livestock movement [16], [17].

Small Ruminants and Camels

Although less frequently studied, small ruminants and camels exhibit epidemiologically relevant infection rates, suggesting their role as secondary reservoir. Seroprevalence in sheep and goats ranges from 1.8% to 4.3% in Nigeria [18] and approximately 2.1% in Ethiopia [19]. Camels in pastoral regions of Ethiopia show prevalence between 3.7% and 5.2%, with risk factors including migratory grazing and close contact with infected cattle population [20].

These findings highlight the importance of incorporating multi-species surveillance approaches in brucellosis control programs.

Equines and Wildlife

Equines and wildlife species demonstrates lower but epidemiologically significant levels of infection. Donkeys and horses in Nigeria exhibits seroprevalence rates of 2.4% and 1.9%, respectively [21], [22]. In contrast, African buffalo (*syncerus caffer*) populations in Kenya show higher seroprevalence (6.8%), indicating the presence of wildlife reservoirs and potential spillover at livestock-wildlife interface [23].

Table 5. Brucellosis Seroprevalence across Livestock Species in Africa

Species	**Country**	**Prevalence %**	**Key risk factor**	**Sources**
cattle	Ethiopia	3.8-27.6	Communal grazing, low vaccination	[12], [13]
	South Africa	8.3	Wildlife interface	[15]
	Uganda	12.4-18.9	Trans boundary trade	[14]
Sheep/Goats	Nigeria	1.8-4.3	Mixed farming system	[18]
	Ethiopia	2.1	Abattoir exposure	[19]

Camels	Ethiopia	3.7-5.2	Migration, cattle contact	[20]
Donkeys	Nigeria	2.4	Shared water source	[21]
African buffalo	Kenya	6.8	Wildlife-livestock overlap	[23]

Epidemiology and Risk Factors of Bovine Brucellosis

The epidemiology of bovine brucellosis in Africa reflects the interaction of host characteristics, livestock management systems, geographic conditions, and broader animal–human interfaces. The included literature described epidemiological patterns at several levels, including geographic distribution, host characteristics, husbandry practices, zoonotic exposure, temporal patterns, and strain diversity. Because these factors were assessed using different study designs, definitions, and analytical approaches, they were synthesized narratively rather than quantitatively. The hierarchical categorization of the epidemiological studies, including geographic distribution, host specific patterns, transmission dynamics, temporal trends, and strain diversity, is presented in (Table 6).

Table 6. Hierarchical Categorization of Epidemiological Studies on Bovine Brucellosis in Africa

Epidemiological focus	Risk factor category	Specific risk factor or patterns	Sources
Prevalence and distribution	Geographic variation	Regional seroprevalence differences	[12], [13], [14], [15], [17], [18], [19], [20], [24], [25], [26], [27], [28], [29], [30], [31], [32], [33], [34], [35], [36], [37]
		Spatial clustering (GIS/outbreak mapping)	[34], [38], [39], [40], [41]
	Host-specific patterns	Cattle (dairy/beef, indigenous Vs commercial	[12], [15], [17], [26], [30], [33], [36]
		Wildlife-livestock interface (buffalo, bush meat)	[42], [43], [44], [45]
		Small ruminants (sheep/goats)	[18], [38], [46], [47]
Transmission dynamics	Husbandry practices	Pastoral Vs. agro-pastoral Vs. intensive system	[12], [26], [28], [30], [33], [38], [43], [48]
		Herd size/management (communal Vs. private)	[15], [49]
	Zoonotic linkages	Human-livestock seropositivity correlations	[29], [34], [35], [37], [43], [50], [51]
		Abattoir/occupational exposure	[18], [19], [20], [39]
Temporal and molecular trends	Seasonal/ time-series patterns	Non-seasonal (year-round) transmission	[15], [17], [35]
		Long term seroprevalnce trends	[14], [35]
	Strain diversity	Biovar/genotype distribution (*b. abortus* biovar 3)	[6], [36], [45], [52]

Geographic and Spatial Patterns

The included studies reported substantial geographic variation in bovine brucellosis seroprevalence across African settings. Spatial analyses additionally described clustering of cases and associations with particular livestock-production and wildlife-interface environments [47]. These findings indicate that the distribution of bovine brucellosis is not uniform and that local ecological and production-system characteristics may influence observed transmission patterns [14].

Host and Production-System Patterns

Host-related and production-system characteristics were frequently considered in the included studies. Differences were reported between indigenous and commercial cattle populations and between dairy and beef production systems. Several studies also examined interactions between livestock and wildlife, including buffalo populations, while others considered the epidemiology of brucellosis in small ruminants alongside cattle [25].

Livestock management was another recurring epidemiological theme. Pastoral, agro-pastoral, and more intensive production systems were represented in the literature, with several studies examining herd size, communal versus private management, grazing practices, and animal movement. These observations support the importance of production-system context when interpreting differences in reported seroprevalence [12], [35].

Livestock Trade and Trans-boundary Movement

Trans-boundary livestock movement is key driver of disease spread across regions. Studies highlight that informal cross border trade networks facilitate the introduction and persistence of brucellosis in previously low prevalence areas [14], [35]. The absence of coordinated regional control policies further exacerbates this risk.

Zoonotic and Animal-Human Linkages

Several studies examined the relationship between livestock infection and human exposure. Reported themes included occupational exposure, abattoir-related exposure, and interactions between human and livestock populations. These findings reinforce the importance of considering bovine brucellosis within a broader One Health framework, while recognizing that the present meta-analysis primarily quantified bovine prevalence rather than human disease burden [19], [29].

Temporal and Molecular Patterns

The reviewed literature also included studies examining temporal patterns and Brucella strain diversity. Some studies reported year-round or non-seasonal transmission patterns, whereas others assessed longer-term changes in seroprevalence [15], [17], [35]. Molecular and strain-focused studies described variation in biovars or genotypes, including reports involving *Brucella abortus* biovar 3 [6], [35], [52] These findings provide additional epidemiological context but were not sufficiently comparable across studies to be incorporated into the quantitative prevalence meta-analysis.

Overall, the qualitative evidence indicates that bovine brucellosis in Africa is influenced by multiple interacting epidemiological domains rather than by a single dominant risk factor [17]. The heterogeneity in study populations, exposure definitions, diagnostic approaches, and analytical methods limits direct comparison of individual risk factors across studies. Therefore, the associations summarized below should be interpreted as study-level findings rather than pooled causal effects.

The principal epidemiological domains, reported patterns, associated risk factors and supporting studies are summarized in (Table 7).

Table 7. Qualitative Categorization of Epidemiological Patterns and Risk Factors Reported in Studies of Bovine Brucellosis in Africa

Epidemiological domain	Category	Specific pattern or factor reported	Sources
Prevalence and distribution	Geographic variation	Differences in regional seroprevalence	[12], [13], [14], [15], [17], [18], [19], [20], [24], [26], [27], [28], [29], [30], [31], [32], [33], [34], [35], [36], [37], [49], [53]
Prevalence and distribution	Spatial patterns	Spatial clustering and GIS/outbreak mapping	[34], [39], [40], [41], [47]
Host and production systems	Cattle characteristics	Differences involving dairy/beef and indigenous/commercial cattle populations	[12], [15], [17], [26], [30], [33], [36]
Host and production systems	Wildlife livestock interface	Associations involving buffalo and wildlife/livestock interactions	[23], [43], [44], [45]
Host and production systems	Other livestock hosts	Co-occurring patterns involving sheep and goats	[18], [38], [46], [47]

Epidemiological domain	Category	Specific pattern or factor reported	Sources
Transmission and management	Production system	Pastoral, agro-pastoral, and intensive production systems	[12], [26], [28], [30], [33], [38], [43], [48], [54]
Transmission and management	Herd management	Herd size and communal versus private management	[15], [32], [54]
Zoonotic interface	Human–livestock interaction	Human and livestock seropositivity relationships	[29], [34], [35], [37], [43], [50], [51]
Zoonotic interface	Occupational exposure	Abattoir and occupational exposure	[18], [19], [20], [39]
Temporal patterns	Seasonal/time-series patterns	Non-seasonal or year-round transmission patterns	[15], [17], [34], [35]
Temporal patterns	Long-term trends	Changes in seroprevalence over time	[14], [35]
Molecular epidemiology	Strain diversity	Biovar/genotype distribution, including *B. abortus* biovar 3	[6], [36], [45], [52]

Human Brucellosis and Livestock-Human Epidemiological Linkages

Human brucellosis represents an important zoonotic dimension of bovine brucellosis in Africa. The included literature describes human infection in occupationally exposed populations, pastoralist communities, children involved in livestock activities, and other populations with livestock contact. Reported findings identify occupational exposure, direct contact with livestock, and consumption of raw or unpasteurized animal products as important exposure contexts. Because the human studies differed substantially in population, outcome definition, diagnostic approach, and study design, their estimates are presented descriptively and were not included in the quantitative meta-analysis of bovine brucellosis.

Occupational and Demographic Risk Factors

Occupational exposure was frequently reported among the human populations investigated. Cattle handlers in Ghana had a reported seroprevalence of 12.4%, compared with 3.1% among non-exposed individuals [19]. Similarly, pastoralist communities in Nigeria had a reported seropositivity of approximately 9.8%, with an association between human infection and herd seroprevalence [28].

Children in pastoralist settings may also experience substantial exposure. In Kenya, school-age children had a reported seroprevalence of 14.7%, with livestock-related activities and consumption of unpasteurized milk identified as relevant exposure contexts [55]. In Uganda, higher infection rates among males were reported in association with occupational activities involving livestock handling and meat processing [39].

Dietary and Behavioral Risk Factors

Consumption of raw or unpasteurized dairy products represents an important potential pathway for zoonotic exposure. In an Ethiopian study, raw-milk consumption was associated with an approximately 5.8-fold increase in the risk of human brucellosis. Cultural practices and limited access to pasteurization may further increase exposure, particularly in rural and pastoral communities[29].

These findings support the importance of food-safety interventions alongside livestock-focused control measures. However, the magnitude of individual risk estimates should be interpreted within the population and study design from which they were derived.

Spatial and Temporal Patterns

Geospatial analyses have described clustering of human brucellosis in areas characterized by high livestock density and close human–animal interaction. In Botswana, proximity to wildlife habitats was associated with increased human seropositivity, while spatial relationships between peri-urban dairy farms and hospital-related cases were reported in Uganda [39].

Temporal patterns varied among the reported settings. Localized seasonal increases were described in Algeria, particularly in relation to livestock husbandry and breeding periods [35]. In contrast, sustained endemic transmission without a clear seasonal pattern was reported among pastoralist communities in Kenya [55].

These observations provide epidemiological context but do not establish a uniform temporal or seasonal pattern of human brucellosis across Africa.

Livestock-Human Epidemiological Linkages

Several studies examined relationships between infection in livestock and humans. Associations between human and livestock seropositivity were reported in multiple settings, supporting the importance of integrated animal and human surveillance [28], [43].

However, these findings should be interpreted as evidence of epidemiological linkage rather than proof of direct transmission from cattle to humans. Differences in exposure patterns, diagnostic methods, sampling strategies, and population characteristics may contribute to the observed associations.

Surveillance Gaps and Underreporting

Human brucellosis may be substantially under recognized in settings where diagnostic capacity is limited and clinical presentation is nonspecific. The manuscript identifies diagnostic limitations and restricted laboratory capacity as important contributors to underreporting [41]. In Ethiopia,

limited routine testing of febrile illnesses was reported as an additional challenge, potentially contributing to misdiagnosis and underestimation of disease burden [43].

The available evidence therefore supports strengthening integrated surveillance systems that incorporate both livestock and human health sectors. Such approaches are particularly relevant in communities where occupational exposure and consumption of unpasteurized animal products are common [28], [43].

The reported human brucellosis prevalence and incidence findings, together with the associated epidemiological factors and populations studied, are summarized in (Table 8)

Table 8. Human Brucellosis Prevalence and Associated Epidemiological Factors Reported in Africa

Country	Population studied	Reported prevalence/incidence	Epidemiological factors reported	Reference
Ghana	Cattle handlers	12.4%	Direct contact with infected cattle	[19]
Nigeria	Pastoralists	9.8%	Raw-milk consumption; herd seropositivity	[28]
Kenya	School-age children	14.7%	Unpasteurized milk; livestock-care activities	[55]
Uganda	Hospital-diagnosed cases	6.2% annual incidence	Abattoir work; dairy farming	[39]
Algeria	General population	5.1%	Seasonal livestock-husbandry practices	[35]
Botswana	Bush meat consumers	8.9%	Buffalo contact; undercooked meat	[56]

Brucellosis Control Strategies: Current Approaches and Implementation Challenges

Control of bovine brucellosis in Africa involves a combination of vaccination, surveillance, targeted risk mapping, One Health interventions, movement and slaughter controls, and regional coordination. The reviewed literature indicates that these approaches have potential to reduce transmission or improve disease detection, but implementation is frequently constrained by limited veterinary infrastructure, financial resources, cold-chain requirements, weak enforcement, and coordination challenges. The available evidence is heterogeneous and largely consists of individual intervention studies, observational assessments, or modeling exercises; therefore, these findings should not be interpreted as a pooled estimate of intervention effectiveness.

Risk Mapping and Surveillance

Spatial risk mapping has been used to identify areas requiring targeted surveillance and control. A Kenyan study used spatial analysis to identify high-risk areas and inform allocation of control resources. Such approaches may improve the efficiency of surveillance by concentrating limited resources in areas where transmission risk is greatest. However, their effectiveness depends on the availability and quality of surveillance data and on sustained implementation of control activities.

Vaccination and Adjuvant Innovations

Vaccination remains an important component of bovine brucellosis control. The manuscript describes the use of *Brucella abortus* strain 19 and RB51 vaccines and reports variable outcomes between settings. An Ethiopian intervention reported a 40% reduction in seroprevalence in pilot areas [37], whereas implementation in Nigeria was reported to have limited impact in the context of cold-chain and programmatic constraints [57].

The literature also describes thermostable adjuvant formulations intended to improve vaccine stability under pastoral production conditions. However, the manuscript reports cost and adoption barriers that may limit field-scale implementation. These findings suggest that vaccine effectiveness in practice depends not only on biological efficacy but also on coverage, delivery systems, cold-chain capacity, and program continuity.

One Health Integration

Integrated human–animal surveillance and community-based interventions represent another important control strategy. The manuscript reports an Ethiopian program in which integrated surveillance and community education were associated with a 28% reduction in reported human brucellosis cases over three years [37], [58].

Although this finding suggests potential benefit from integrated interventions, the observed reduction should be interpreted in the context of the specific program and study design rather than generalized as an expected effect size for One Health interventions across Africa. Sustained implementation also requires effective coordination between animal-health, public-health, and other relevant sectors.

Regional Coordination and Trans-boundary Control

Trans-boundary livestock movement creates challenges that may require coordination beyond individual national programs. A proposed North African strategy involving Libya, Tunisia, and Algeria emphasized collaborative surveillance, while inconsistent national policies and differences in livestock-movement regulations and compensation mechanisms were identified as implementation barriers.

These findings support the need for harmonized surveillance and control frameworks in regions where livestock movements cross national borders. However, the cited strategy represents a proposed regional approach rather than evidence of a completed intervention with measured population-level effectiveness.

Abattoir and Food Safety Measures

The manuscript also describes control activities focused on abattoir screening and milk pasteurization in Nigeria [57]. These measures are relevant to both animal-health surveillance and reduction of human exposure. However, informal slaughter practices and limited enforcement were reported as important implementation barriers [57].

Mathematical Modeling

Mathematical and network-based models may help identify important transmission pathways and prioritize intervention points. The manuscript reports a network-control model that predicted a 60% reduction in spillover under 70% vaccination coverage [59]. However, the model relied on incomplete livestock-movement data, limiting the direct applicability of the prediction to real-world control programs. Accordingly, the modeled 60% reduction should be presented explicitly as a model-derived prediction, not as an observed intervention effect.

Implementation Challenges

Across the reviewed literature, the principal challenges to effective control include inadequate surveillance infrastructure, insufficient vaccination coverage, cold-chain limitations, and inconsistent enforcement of regulations, limited funding, and weak inter-sectoral coordination. These constraints indicate that successful control is unlikely to depend on a single intervention. Instead, sustainable programs will require context-specific combinations of vaccination, surveillance, risk-based targeting, food-safety measures, and coordinated animal–human health activities.

The control strategies, their implementation levels, specific approaches, reported evidence, and supporting references are summarized in (Table 9).

Table 9. Control Strategies for Bovine Brucellosis Reported in Africa

Control strategy	Implementation level	Specific approach	Evidence reported in the manuscript	Reference
Risk mapping and surveillance	National/regional	Spatial risk mapping for targeted surveillance and control	High-risk areas identified in Kenya to inform allocation of control resources	[60]
Vaccination	Livestock population	Use of *B. abortus* strain 19/RB51 and vaccination campaigns	A 40% reduction in seroprevalence was reported in an Ethiopian pilot intervention	[37]
Vaccine/adjuvant innovation	Livestock population	Thermostable adjuvant formulations	Improved vaccine stability was reported, with cost and adoption barriers	[61]
One Health integration	Multi-sectoral	Integrated human–animal surveillance and community education	A 28% reduction in reported human cases was reported in an Ethiopian program	[62]
Regional coordination	Transboundary	Collaborative surveillance and harmonized control policies	Proposed Libya –Tunisia -Algeria coordination; implementation challenges included inconsistent policies	[51]
Abattoir and food-safety control	National/local	Abattoir screening and milk pasteurization	Implementation was constrained by informal slaughter practices and enforcement gaps	[57]
Mathematical modeling	Analytical/planning	Network-based transmission and vaccination modeling	Model predicted a 60% reduction in spillover at 70% vaccination coverage; incomplete movement data limited applicability	[59]

Co-infections and Syndemic Interactions

Bovine brucellosis may occur alongside other zoonotic and livestock diseases, creating diagnostic and epidemiological challenges. The included literature reported co-occurrence of brucellosis with Q fever, leptospirosis, bovine tuberculosis, and mastitis-associated bacterial infections. These findings suggest that overlapping transmission pathways and reproductive or clinical syndromes may complicate disease recognition and management. However, the available studies differed in population, diagnostic methods, and definitions of co-infection; therefore, the reported associations are presented as study-specific findings rather than pooled estimates.

Q fever and Leptospirosis

Q fever and leptospirosis were among the most frequently reported infections occurring alongside brucellosis. In Northern Togo, brucellosis-Q fever co-infection among pastoralist populations was associated with more severe clinical manifestations, with an odds ratio of 3.1 (95% CI: 1.8-5.4) compared with single infection [50]. In Sokoto State, Nigeria, concurrent seropositivity for brucellosis and Q fever was reported in 18.3% of cattle and was associated with reproductive problems [28].

In Cameroon, 14.7% of cattle in the reported *Bos indicus* population were positive for brucellosis, leptospirosis, and Q fever concurrently [36]. The occurrence of multiple infections in the same population suggests that shared environmental or management exposures may contribute to overlapping transmission, although the available evidence does not establish a common reservoir or causal interaction.

Brucellosis and Bovine Tuberculosis

Co-occurrence of bovine brucellosis and bovine tuberculosis (bTB) has also been reported. In Sidi Kacem Province, Morocco, an 11.2% co-infection rate was reported among cattle, with lesions involving both pathogens identified in lymph nodes [27]. In African buffalo, one study reported lower transmission potential among individuals co-infected with brucellosis and bTB than among individuals carrying a single pathogen [42]. This finding represents a study-specific epidemiological observation and should not be generalized as evidence that co-infection reduces overall herd-level prevalence.

Brucellosis and Mastitis

Brucellosis was also reported in association with mastitis and bacterial pathogens affecting dairy cattle. In Uganda, *Staphylococcus aureus* isolates from brucellosis-positive cows showed higher reported penicillin resistance than isolates from brucellosis-negative animals. In Cameroon, mastitis-associated bacterial infections involving *E. coli* and *Streptococcus* spp. were reported among brucellosis-positive dairy herds, with a reported co-infection frequency of 37% [63].

These findings suggest that concurrent reproductive and mammary infections may complicate clinical management and antimicrobial decision-making. However, the available evidence does not establish that brucellosis itself caused the observed antimicrobial-resistance differences.

Diagnostic Implications

Co-infections are particularly important because several reproductive diseases can produce overlapping clinical presentations. In Southwest Ethiopia, the manuscript reports that some abortion cases initially attributed to brucellosis were subsequently associated with Q fever or leptospirosis [60]. This finding highlights the potential limitations of relying on a single diagnostic test or clinical presentation when investigating reproductive disease in high-risk cattle populations.

The evidence therefore supports consideration of differential and, where appropriate, multiplex diagnostic approaches in settings where several abortifacient or zoonotic pathogens are circulating. Nevertheless, the available studies do not permit estimation of a pooled co-infection prevalence or a common effect size across pathogens.

Implications for Disease Control

The occurrence of co-infections supports a broader approach to bovine reproductive and zoonotic disease surveillance. In areas where brucellosis, Q fever, leptospirosis, and bTB coexist, diagnostic algorithms that consider multiple pathogens may improve case attribution and reduce misclassification. Integrated surveillance may also provide a more complete understanding of transmission networks and reproductive losses.

Importantly, these observations should be distinguished from the primary prevalence meta-analysis. Co-infection findings were not incorporated into the pooled bovine brucellosis

prevalence estimate because the studies used heterogeneous populations, diagnostic approaches, and outcome definitions.

The reported co-occurrence patterns involving bovine brucellosis and other infectious agents, including the study settings and principal findings, are summarized in (Table 10)

Table 10. Disease Co-occurrence Patterns Reported with Bovine Brucellosis in Africa

Primary disease	Co-infecting pathogen	Country/setting	Key finding	Reference
Brucellosis	Q fever (*Coxiella burnetii*)	Northern Togo	Brucellosis-Q fever co-infection was associated with more severe clinical manifestations among pastoralists; OR 3.1 (95% CI: 1.8-5.4)	[50]
Brucellosis	Q fever (*Coxiella burnetii*)	Sokoto State, Nigeria	18.3% concurrent seroprevalence in cattle; associated with reproductive problems	[28]
Brucellosis	Bovine tuberculosis (*Mycobacterium bovis*)	Sidi Kacem, Morocco	11.2% co-infection rate in cattle; lesions involving both pathogens reported in lymph nodes	[27]
Brucellosis	Leptospirosis + Q fever	Cameroon	14.7% triple positivity for brucellosis, leptospirosis, and Q fever in *Bos indicus* cattle	[36]
Brucellosis	Q fever + leptospirosis	Southwest Ethiopia	Co-occurrence reported among cattle with abortion; potential for diagnostic misclassification	[60]
Brucellosis	*Staphylococcus aureus*	Uganda	Higher reported penicillin resistance among isolates from brucellosis-positive cows	[40]

Primary disease	Co-infecting pathogen	Country/setting	Key finding	Reference
Brucellosis	*E. coli* + *Streptococcus* spp.	Cameroon	Mastitis-associated bacterial infection reported in 37% of brucellosis-seropositive dairy herds	[63]

Knowledge, Attitudes and Practices among Livestock Keepers

Knowledge, attitudes, and practices (KAP) among livestock keepers are important contextual determinants of brucellosis prevention and control. The two KAP studies included in the review demonstrated substantial differences between communal cattle keepers in South Africa and dairy farmers in Malawi. Despite these differences, both studies identified gaps between knowledge of brucellosis and adoption of preventive practices. Because only two studies were available and their populations, production systems, and assessment methods differed, the findings were synthesized narratively rather than quantitatively.

Knowledge Gaps and Misconceptions

Knowledge of the zoonotic nature of brucellosis varied considerably between the two study populations. In South African communal cattle systems, only 23% of respondents correctly identified brucellosis as a zoonotic disease, while 68% associated the disease primarily with reproductive losses in cattle [64]. In contrast, 81% of Malawian dairy farmers recognized that brucellosis could be transmitted to humans, although 42% incorrectly believed that transmission could occur through the air [11].

These findings indicate that awareness of brucellosis does not necessarily imply accurate understanding of its transmission pathways. The reported confusion between brucellosis and other cattle diseases, particularly in relation to abortion and reproductive signs, further highlights the importance of context-specific disease education [11] [64].

Risk Perception and Protective Practices

Attitudes toward the importance of brucellosis also differed between production systems. Among South African communal cattle keepers, brucellosis was reportedly considered a lower priority than other livestock threats such as predators or drought, and only 12% of respondents expressed willingness to voluntarily cull infected animals [64]. In Malawi, 63% of dairy farmers considered brucellosis economically important or devastating, indicating greater perceived economic consequences; nevertheless, preventive practices remained inconsistent [11].

Reported behavioral practices included both protective and potentially risky practices. Among Malawian dairy farmers, 89% reportedly boiled milk for household consumption, but only 31%

used protective gloves during calving assistance [11]. In the South African communal system, raw-milk consumption and use of shared calving areas were reported as important risk practices [64]. These findings illustrate the gap that can exist between awareness of disease and consistent adoption of preventive measures.

Structural and Economic Barriers

Both KAP studies identified structural and economic constraints that may limit the ability of livestock keepers to translate knowledge into preventive action. South African communal cattle keepers reported limited alternative income sources as an important reason for retaining potentially infected breeding animals, while Malawian farmers identified the cost of milk-pasteurization equipment as a barrier to adoption [11], [64].

These findings suggest that educational interventions alone are unlikely to be sufficient where farmers face substantial economic or infrastructural constraints. Effective behavioral interventions may need to be accompanied by accessible veterinary services, practical food-safety options, appropriate compensation mechanisms, and feasible disease-control measures.

Implications for Brucellosis Control

The available KAP evidence supports the use of context-specific education and community engagement as components of brucellosis control. Educational interventions should address both zoonotic transmission and practical prevention, including safe handling of animals and reproductive materials, appropriate management of aborted materials, and safe consumption of animal products.

At the same time, interventions should recognize differences between communal, pastoral, and commercial dairy production systems. The limited number of KAP studies means that their findings should not be generalized to all livestock keepers in Africa. Additional standardized KAP research across different production systems and geographic regions would help identify which behavioral and structural barriers are most important for successful implementation of control programs. The comparative findings of knowledge, attitudes, preventive practices, and reported barriers among the livestock-keeper populations studied are presented in (Table 11).

Table 11. Comparative Knowledge, Attitudes, and Practices Related to Bovine Brucellosis

Study population	Knowledge finding	Attitudinal finding	Reported practices/barriers	Reference
South African communal cattle keepers	23% correctly identified brucellosis as zoonotic; 68% associated it primarily with livestock reproductive losses	Brucellosis perceived as a lower priority than predators or drought; 12% willing to voluntarily cull infected animals	Raw-milk consumption; shared calving areas; limited alternative income sources	[64]
Malawian dairy farmers	81% recognized zoonotic transmission; 42% incorrectly believed airborne transmission was possible	63% regarded brucellosis as economically devastating	89% boiled milk; 31% used protective gloves during calving assistance; cost of pasteurization equipment was a reported barrier	[11]

Brucellosis and Cattle Abortion: Epidemiological Links and Diagnostic Challenges

Abortion is an important reproductive manifestation associated with bovine brucellosis and an important contributor to livestock-production losses. The studies included in this review indicate that brucellosis is frequently identified or suspected among causes of cattle abortion in Ethiopian production systems. However, the available evidence uses different approaches to attribute abortions to brucellosis, including participatory ranking, veterinary assessment, serological testing, and limited molecular confirmation. These differences should be considered when interpreting the reported estimates.

Brucellosis as a Reported Cause of Cattle Abortion

In southwestern Ethiopia, brucellosis was ranked among the leading perceived causes of cattle abortion by local informants, accounting for 34% of reported abortion cases [60]. In the same region, serological evidence indicated that brucellosis-positive herds experienced abortion rates approximately 2.8 times higher than seronegative herds [60].

In Jimma Zone, Ethiopia, both farmers and veterinarians identified brucellosis as an important suspected cause of abortion, particularly during the third trimester of pregnancy [65]. A higher frequency of reported abortions during wet periods was also described, although this seasonal observation should be interpreted as a study-specific finding rather than evidence of a uniform seasonal pattern across Africa.

Diagnostic and Reporting Limitations

Attribution of abortion to brucellosis remains challenging because the clinical presentation is not pathognomonic. In Jimma Zone, only 18% of reported abortion cases underwent laboratory confirmation, while most diagnoses were based primarily on clinical assessment [65]. This limited confirmation creates potential for both underdiagnosis and misclassification of brucellosis-associated abortions.

Participatory studies also reported alternative explanations for abortion among farmers, including nutritional problems and culturally based explanations. Such perceptions may influence whether veterinary services are sought and whether abortion material is submitted for laboratory investigation. Consequently, surveillance based solely on farmer reports or clinical recognition may underestimate the contribution of brucellosis.

Economic and Reproductive Consequences

The reviewed Ethiopian evidence also indicates substantial reproductive and economic consequences associated with brucellosis-related abortion. In southwestern Ethiopia, herds with reported brucellosis-associated abortions had 42% lower calf-crop yields than unaffected herds, with estimated losses of approximately USD 189 per cow over the production cycle [60].

These findings illustrate the potential economic importance of reproductive losses in smallholder dairy systems. However, the reported economic estimate comes from a specific study population and should not be extrapolated as a continent-wide estimate of the economic burden of bovine brucellosis.

Participatory Surveillance and Diagnostic Integration

The Ethiopian studies illustrate the potential value of combining local knowledge with laboratory-based diagnosis. Farmer observations concerning reproductive signs and abnormal placental findings may provide useful information for identifying cases requiring further investigation. The manuscript reports that combining participatory observations with serological testing improved detection compared with clinical assessment alone in the reported study [65].

Nevertheless, this finding should be interpreted as evidence from an individual study rather than as a validated diagnostic-performance estimate applicable to all African production systems. Standardized laboratory confirmation remains important when estimating the contribution of brucellosis to cattle abortion.

The reported epidemiological links between bovine brucellosis and cattle abortion, together with the associated diagnostic and reporting challenges, are summarized in (Table 12).

Table 12. Epidemiological and Diagnostic Characteristics of Brucellosis-Associated Cattle Abortion Reported in Ethiopia

Study location	Type of abortion attribution/evidence	Reported finding	Relevant factors	Diagnostic/assessment approach	Reference
Southwestern Ethiopia	Farmer-reported attribution	Brucellosis accounted for 34% of reported abortion causes	Wet-season grazing; shared calving areas	Participatory ranking and Rose Bengal Test serology	[60]
Southwestern Ethiopia	Serological epidemiological evidence	Abortion rate approximately 2.8 times higher in brucellosis-positive than seronegative herds	Brucellosis seropositivity	Serological assessment	[60]
Jimma Zone, Ethiopia	Veterinarian-suspected attribution	28% of abortion cases attributed/suspected to brucellosis	High herd density; introduction of replacement heifers	Clinical assessment with limited PCR confirmation	[65]
Jimma Zone, Ethiopia	Laboratory-confirmation assessment	Only 18% of reported abortion cases underwent laboratory confirmation	Diagnostic limitations and reliance on clinical assessment	Clinical assessment; limited laboratory confirmation	[65]
Southwestern Ethiopia	Economic/reproductive impact	42% lower calf-crop yield and estimated loss of USD 189 per cow over the production cycle	Brucellosis-associated abortion	Production/economic assessment	[60]

DISCUSSION

This systematic review and meta-analysis synthesized evidence on bovine brucellosis seroprevalence across Africa and included 48 studies in the systematic review, of which 45 provided usable prevalence data for quantitative synthesis. Across these 45 studies, 337,705 animals were tested and 12,725 were reported as seropositive. The crude sample-size-weighted prevalence was 3.77%, whereas the DerSimonian-Laird random effects model produced a pooled prevalence of 6.13% (95% CI: 4.49-8.32%). The random-effects estimate is considered the principal summary measure because the evidence base showed extreme between-study heterogeneity.

The magnitude of heterogeneity was substantial, with Cochran's $Q = 6713.1$ ($df = 44$, $p < 0.001$), $I^2 = 99.34\%$, and $\tau^2 = 1.2017$ on the logit scale. Accordingly, the pooled estimate should be interpreted as average across a highly heterogeneous evidence base rather than as a single prevalence applicable to all African cattle populations. The very high I^2 indicates that differences between studies are much greater than would be expected from sampling error alone and supports interpretation according to geographic setting, diagnostic approach, and study population and production system.

Geographic variation was one of the most prominent findings of the quantitative synthesis. Among the African countries represented in the analysis, pooled estimates were highest in South Sudan (31.02%), Sudan (23.35%), Namibia (22.64%), Ghana (19.68%), Somalia (19.40%), and Egypt (19.37%). In contrast, substantially lower estimates were observed in Algeria, South Africa, Uganda, Eritrea, and Morocco. These differences should not be interpreted simply as evidence that some countries have intrinsically higher or lower levels of infection. Eleven of the 20 countries represented in the dataset were based on a single study, meaning that their country-specific pooled estimates are effectively estimates from individual studies rather than robust national estimates. Differences in sampling frames, production systems, geographic coverage, diagnostic methods, and study objectives may therefore contribute substantially to the observed country-level variation.

The regional analysis similarly demonstrated substantial variation. The pooled prevalence was 5.50% in Sub-Saharan Africa and 8.94% in North Africa, but heterogeneity remained extremely

high within both groups (I^2 = 99.0% and 99.8%, respectively). Thus, geographic grouping alone does not adequately explain the observed variation. The single Sri Lankan study should not be interpreted as evidence concerning an African regional burden. It was retained because it was present in the quantitative dataset but represents a non-African study and should be considered separately from the African regional comparisons.

The difference between the crude prevalence of 3.77% and the random effects estimate of 6.13% is informative. The crude estimate is heavily influenced by very large surveys, particularly the South African and Algerian studies, whereas the random effects approach gives greater relative influence to smaller studies with higher observed prevalence. Neither estimate should therefore be interpreted as a direct estimate of the prevalence in the average African cattle population. Rather, the 6.13% random-effects estimate summarizes the distribution of prevalence represented by the included studies. The wide dispersion of study-level estimates and the extreme heterogeneity indicate that surveillance and control decisions should rely more heavily on local and regional evidence than on the overall pooled estimate alone.

Differences between diagnostic-test groups were also observed. Studies using iELISA had a pooled prevalence of 12.34%, compared with 6.19% for RBPT plus confirmatory testing, 7.87% for RBPT ± CFT, and 6.17% for c-ELISA. These differences should not be interpreted as evidence that one diagnostic test produces a particular prevalence or that the tests have directly comparable epidemiological performance. The studies using different diagnostic methods may also differ systematically in geographic location, study population, sampling strategy, disease-risk profile, and study objectives. The higher estimate observed among iELISA studies may therefore reflect differences in study populations and indications for testing rather than a simple diagnostic effect.

This interpretation is particularly important because diagnostic algorithms were incompletely standardized across the evidence base. Future studies should report the complete screening and confirmatory testing algorithm so that prevalence estimates can be compared more reliably.

The qualitative synthesis identified several recurring epidemiological factors, including sex, age, herd size, breed, abortion history, previous infection, farm origin, calving practices and veterinary-service use. However, the studies differed substantially in how these factors were defined and analyzed. Consequently, the reported odds ratios should be regarded as study-specific associations rather than pooled estimates or universally applicable effect sizes.

This limitation is important when interpreting apparently large associations such as those reported for retained fetal membranes, birth frequency, farm origin, herd characteristics or reproductive history. Without harmonized definitions and comparable effect measures, these estimates cannot be combined reliably. The present evidence therefore supports identification of recurring epidemiological hypotheses rather than definitive ranking of causal risk factors.

A marked relationship between sample size and reported prevalence was observed. Smaller studies showed much wider dispersion, including both very low and very high prevalence estimates, whereas large studies tended to cluster at lower prevalence. This pattern may reflect differences in study purpose and sampling design. Large national or regional surveys may include broad populations with relatively low background prevalence, while smaller studies may deliberately target high-risk herds, particular production systems, or outbreak-associated populations. The observed pattern is also compatible with small-study or publication effects, but the present evidence does not establish publication bias definitively. Therefore, the possibility should be treated as an important source of uncertainty rather than as a confirmed explanation.

The systematic review also identified an important livestock human interface. Occupational exposure, livestock contact, and consumption of raw or unpasteurized animal products were repeatedly described in the human brucellosis literature [19], [28], [29], [55]. Diagnostic limitations and restricted surveillance may further contribute to under recognition of human infection [41], [43]

The presence of Q fever, leptospirosis, and bovine tuberculosis alongside brucellosis further complicates diagnosis and surveillance [27], [36], [50], [60]. These findings support a One Health perspective in which livestock surveillance, human health surveillance, food safety, and occupational-health interventions are considered together. However, the present meta-analysis quantitatively evaluated bovine seroprevalence and did not estimate a pooled human disease burden. The reviewed evidence supports an important association between bovine brucellosis and reproductive losses. Ethiopian studies reported increased abortion occurrence among brucellosis-positive herds and identified brucellosis as an important suspected or reported cause of cattle abortion [60], [65]. Economic consequences were also reported, including reduced calf production and financial losses in affected production systems [60].

However, attribution of abortion to brucellosis remains challenging because many reported cases are based on clinical assessment or farmer attribution rather than laboratory confirmation. Consequently, abortion surveillance should incorporate appropriate laboratory investigation and differential diagnosis for other abortifacient pathogens.

The findings have several implications for control. First, the marked geographic heterogeneity indicates that surveillance should be risk-based rather than relying exclusively on broad national averages. High-prevalence settings and populations with limited veterinary infrastructure warrant particular attention, while large national surveys should not obscure potentially important high-risk subpopulations.

Second, vaccination remains an important component of control, but program effectiveness depends on adequate coverage, vaccine delivery, cold-chain capacity, surveillance, and sustained implementation. The intervention studies included in the review provide evidence of potential benefit in specific settings, but they do not provide a pooled estimate of vaccination effectiveness [37], [58], [57].

Third, integrated One Health interventions may improve control by addressing both animal infection and human exposure. Community education, safe handling of reproductive materials, milk pasteurization, occupational protection, and coordinated veterinary and public-health surveillance should therefore complement animal-level interventions [37], [58].

A major strength of this review is the inclusion of evidence from multiple African countries and the quantitative synthesis of 45 studies with usable prevalence data. The use of a random effects model, subgroup analyses, and explicit assessment of heterogeneity provides a more informative synthesis than reporting prevalence ranges alone. Several limitations should nevertheless be considered. First, heterogeneity was extremely high ($I^2 = 99.34\%$), substantially limiting the extent to which the pooled estimate can be generalized to individual countries or production systems. Second, eleven of the 20 countries were represented by a single study, limiting the precision and representativeness of country-level estimates.

Third, diagnostic approaches varied substantially among studies, and the complete testing algorithms were not consistently reported. Fourth, risk-factor definitions and effect measures were insufficiently standardized to permit quantitative pooling. Fifth, the apparent relationship between

small study size and higher prevalence raises the possibility of small-study or publication effects, although the available evidence is insufficient to establish publication bias conclusively.

Finally, the restriction of the systematic review to English-language publications may have introduced language bias. The inclusion of studies from heterogeneous production systems and geographic settings also means that the evidence base should not be interpreted as a uniformly representative sample of African cattle populations.

Future studies should prioritize representative sampling within countries and clearly document production system, herd characteristics, geographic coverage, and animal-selection procedures. Standardized reporting of diagnostic algorithms is also needed, including both screening and confirmatory tests. Risk-factor studies should report standardized effect measures with 95% confidence intervals and clearly defined reference categories. This would allow future systematic reviews to perform quantitative synthesis of major risk factors such as age, sex, herd size, breed, abortion history, and previous infection.

Additional longitudinal studies are also needed to distinguish persistent endemic transmission from localized outbreaks and to evaluate temporal changes in prevalence. Finally, intervention studies should report standardized outcome measures and implementation characteristics so that the effectiveness and feasibility of vaccination, surveillance, and One Health approaches can be evaluated more rigorously.

CONCLUSION

Bovine brucellosis remains an important zoonotic and livestock-health problem in Africa, with substantial variation in reported seroprevalence across geographic settings, production systems, and study populations. This systematic review included 48 studies, of which 45 provided usable prevalence data for quantitative synthesis. Across these studies, 337,705 animals were tested and 12,725 were reported as seropositive. The crude sample-size-weighted prevalence was 3.77%, while the DerSimonian–Laird random-effects model estimated a pooled seroprevalence of 6.13% (95% CI: 4.49–8.32%).

The very high between-study heterogeneity ($I^2 = 99.34\%$) indicates that the pooled estimate should be interpreted as a summary of a highly heterogeneous evidence base rather than as a uniform prevalence for African cattle populations. Country-level and regional differences were substantial, and many countries were represented by only one study. These findings emphasize the importance of interpreting bovine brucellosis burden at the local and regional level rather than relying exclusively on a continent-wide summary estimate. The qualitative evidence further indicates that bovine brucellosis is associated with diverse epidemiological contexts, including herd and animal characteristics, livestock-management practices, reproductive events, livestock–wildlife interactions, occupational exposure, and human consumption of unpasteurized animal products. However, differences in definitions, diagnostic methods, study populations, and analytical approaches prevented quantitative pooling of most individual risk factors.

The findings also demonstrate the importance of considering bovine brucellosis within a One Health framework. Human exposure, co-infections with other zoonotic and reproductive pathogens, cattle abortion, and limitations in diagnostic and surveillance capacity highlight the interconnected nature of animal, human, and environmental health. Effective control will require context-specific combinations of risk-based surveillance, standardized diagnostic algorithms, appropriate vaccination strategies, improved veterinary services, food-safety measures, community education, and coordination between animal-health and public-health sectors. Particular attention should be given to settings where surveillance capacity is limited and where livestock movement, communal production systems, or close human–animal contact increase opportunities for transmission.

Future research should prioritize representative longitudinal studies, harmonized diagnostic reporting, standardized definitions of epidemiological risk factors and rigorous evaluation of vaccination and integrated One Health interventions. Improving the quality and comparability of primary data will be essential for reducing uncertainty and developing more reliable estimates of bovine brucellosis burden across Africa.

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APPENDIX (SEARCH STRATEGY)

PubMed search strategy

((“prevalence”[title/abstract] AND (“epidemiological pattern” [title/abstract] OR “epidemiology” [MeSH Terms]) AND (“bovine brucellosis” [title/abstract] OR “brucellosis, bovine “[MeSH Term]) AND (“Africa”[MeSH Terms) Or “Africa” [title/abstract] NOT (review[publication type] OR “systematic review” [title/abstract] OR “meta-analysis” [publication type] OR survey [title/abstract])).

Scopus Search strategy

(TITLE-ABS-KEY (“bovine brucellosis” OR “Brucella abortus”) AND TITLE-ABS-KEY (“prevalence” OR “epidemiology”) AND TITLE-ABS-KEY (“Africa”)) AND (LIMIT-TO (DOCTYPE, “ar”))

Web of Science search strategy

TS=(“bovine brucellosis” OR “Brucella abortus”) AND TS= (“prevalence” OR “epidemiology”) AND TS=(“Africa”)

sciencDirect search strategy

(“bovine brucellosis” OR “Brucella abortus”) AND (“Prevalence” OR “epidemiology”) AND (“Africa”)

Google scholar search strategy

(“bovine brucellosis” AND “prevalence” AND “Africa”)

ABBREVIATIONS

Abbreviation	Full meaning
bTB	Bovine tuberculosis
CFT	Complement fixation test
CI	Confidence interval
c-ELISA	Competitive enzyme-linked immunosorbent assay
df	Degrees of freedom
E. coli	Escherichia coli
ELISA	Enzyme-linked immunosorbent assay
GIS	Geographic information system
iELISA	Indirect enzyme-linked immunosorbent assay
KAP	Knowledge, attitudes, and practices
OR	Odds ratio
PCR	Polymerase chain reaction
PRISMA	Preferred Reporting Items for Systematic Reviews and Meta-Analyses
RB51	Brucella abortus RB51 vaccine strain
RBPT	Rose Bengal plate test
spp.	Species (plural; used when referring to multiple or unspecified species within a genus)
USD	United States dollar

STATISTICAL SYMBOLS AND NOTATION

Symbol	Meaning
I^2	Percentage of total variation across studies attributable to heterogeneity
T^2	Between-study variance
Q	Cochran's Q statistic for assessing heterogeneity
p	p-value
n	Number of positive animals or observations, depending on context
N	Total number of animals or observations
k	Number of studies included in a synthesis

DECLARATIONS

Ethics Approval and Consent to Participate

Ethical approval and informed consent were not applicable to this systematic review and meta-analysis because the study synthesized data from previously published research and did not involve the recruitment of human participants or the collection of new animal specimens.

Consent for Publication

Not applicable.

Availability of Data and Materials

The data extracted from the studies included in this systematic review and meta-analysis are presented in the article and its supplementary materials, where applicable. Further information may be requested from the corresponding author.

Competing Interests

The authors declare that they have no competing interests.

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Registration

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