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Seroprevalence and risk factors of lumpy skin disease in cattle across Asia and Africa: a systematic review and meta-analysis, 2000-2025

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Abstract

Background: Lumpy skin disease (LSD), caused by lumpy skin disease virus, is an economically important transboundary cattle disease that has expanded from Africa into Asia in recent decades. Despite the substantial economic impact of LSD, sero-epidemiological evidence remains fragmented across Asia and Africa. Recurrent outbreaks and continuing geographic expansion highlight the need for pooled estimates that can guide surveillance, vaccination, and risk-based control.

Objectives: Therefore, this systematic review and meta-analysis aimed to estimate the pooled seroprevalence of LSD in cattle across Asia and Africa from 2000 to 2025 and to identify study-level and animal-level factors associated with variation in seropositivity.

Results: Twenty studies involving 13,356 cattle were included. The overall pooled seroprevalence of LSD was 31.2% (95% CI: 21.0-42.5), with substantial between-study heterogeneity (I^2 = 99.43%, $p < 0.001$). Pooled seroprevalence was higher in Asia (39.1%) than in Africa (22.2%) and was higher during outbreaks (44.0%) than in endemic settings (26.4%). By diagnostic method, the highest pooled estimate was observed for ELISA (36.1%), followed by virus neutralization test (33.5%) and indirect fluorescent antibody test (11.3%). Studies with smaller sample sizes showed higher pooled seroprevalence than larger studies. Meta-regression indicated that sampling year and sample size contributed significantly to heterogeneity. Risk-factor analysis showed higher odds of LSD seropositivity in cattle aged over two years (OR = 1.47; 95% CI: 1.01-2.15), females (OR = 1.32; 95% CI: 1.06-1.65), crossbred cattle (OR = 2.92; 95% CI: 1.41-6.05), and cattle managed under extensive rearing systems (OR = 1.63; 95% CI: 1.26-2.12).

Conclusions: LSD seroprevalence in cattle remains substantial across Asia and Africa, although estimates vary markedly by region, study design, sample size, diagnostic method, and management factors. The findings support the need for harmonized serological surveillance, standardized reporting, risk-based vaccination, and targeted control strategies, particularly in high-risk production systems and regions with active transboundary spread.

1. Background

Lumpy Skin Disease (LSD) is a highly infectious and economically important transboundary viral disease of a wide range of domestic animals including cattle, buffalo, and wild ruminants. It is caused by LSD virus (LSDV) that belongs to the *Capripoxvirus* genus in the Poxviridae family with a prototype strain of Neethling virus. This virus has strong similarity to sheep and goat pox viruses as they are serologically and antigenically indistinguishable but genetically dissimilar [1–4]. Lumpy Skin Disease (LSD) was first reported in Zambia in 1929 and became endemic in Sub-Saharan Africa, then it spread to Egypt in 1988 and Israel in 1989 [5, 6]. From the 1990s to the early 21st century, LSD spread over the Arabian Peninsula and in parts of Eastern Mediterranean countries. A significant transboundary spread occurred between 2012 to 2016, with the disease progressing through the broader Middle East into Turkey and parts of Eastern Europe, Russia, and even in several Balkan states [7, 8]. LSD was first reported in Central and South Asia in 2019, affecting China, Bangladesh, and India which swiftly expanded to South-East Asian countries by 2020-2022 [9–12].

LSD has become a major concern for livestock management and food safety in many countries of the world [11]. Cattle and water buffalo (*Bubalus bubalis*) serve as the main hosts for the LSDV. Besides, LSD cases have also been reported in some wildlife [13]. In cattle, the disease typically shows a morbidity rate ranging from 2 to 45% and the mortality rate generally remains below 10% [14]. In Asia, multiple factors including both legal and illegal transportation of livestock carrying the LSDV across borders, as well as the presence of LSD insect vectors in some areas, have contributed the transboundary LSD spread from one country to another [11] LSDV is predominantly transmitted by blood-sucking arthropods mainly mosquitoes and biting flies [15–17] also by lice, ticks, and wasps [18], however it can also be spread by contaminated feed, water, and direct contact via saliva, nasal secretions, and semen in later stages [15,19]. Most outbreaks occurred during the summer, when arthropods are most active, and this indicates that blood sucking insects play an integral part in virus transmission [20].

The disease is characterized by fever, circumscribed skin nodules ranging from 1 to 5 cm in diameter, lacrimation, lymph node enlargement, edema in the legs and brisket regions, conjunctivitis, anorexia, salivation, depression, and nasal discharge [3]. LSDV can be diagnosed through typical clinical signs, particularly the appearance of nodular lesions on the skin. These symptoms are quite prominent with the distinctive skin lumps often visible even from a far. Besides, several serological tests can be used to confirm the presence of antibodies against LSDV, including enzyme-linked immunosorbent assay (ELISA), virus neutralization test (VNT), indirect fluorescent antibody test (IFAT), and Western blotting etc. [11].

Lumpy skin disease leads to severe economic losses, primarily from reduced milk yield (10-85%) due to high fever, secondary mastitis, and damaged hides, reduced growth, infertility, abortions, treatment and vaccine costs, and mortality [21, 22]. A study in Ethiopia estimated losses of USD 141 per affected lactating cow, with median herd-level losses of USD 1,176 due to LSD outbreaks [23]. In Turkey, production losses from LSD infection were USD 886.34 per dairy cow and USD 1,066.61 per beef animal [24]. A study in Bangladesh reported an average loss of USD

110.40 per LSD case, with crossbred cattle incurring higher losses (USD 114.23) than indigenous breeds (USD 89.36) [25]. These findings highlight the significant economic impact of LSD across different regions and cattle breeds.

Despite highly significant economic impact of LSD, there is a limited number of research available on this highly destructive, arthropod-borne disease in South and East Asia, and Africa. The repeated outbreaks and re-emergence of LSDV worldwide emphasize the importance of understanding its prevalence in order to develop effective control and prevention strategies. A meta-analysis on seroprevalence data of LSD from two continents over the past 25-year period can offer a better understanding of the distribution of the disease, its impacts on animal production, and will be useful in disease control and prevention. The review on LSD has been conducted aiming to use a systematic review and meta-analysis approach to assess the current status of LSD, with a special focus on its prevalence and to evaluate the potential factors that contribute to the variability in the prevalence and distribution of the disease.

2. Materials and Methods

The study was carried out in accordance with the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines for systematic reviews and meta-analyses. The PRISMA 2020 checklist was followed to ensure the inclusion of all relevant information and to maintain the methodological quality and standard of the study [26].

2.1. Search Strategy

A systematic search of the papers was carried out to identify the published papers related to the prevalence of LSD in cattle. Four electronic web search engines: Scopus, PubMed, Web of science and Google Scholar, were used to search the published paper that published between January 2000 to May 2025. The search syntaxes were utilized to find related literature using these specified scientific keywords: “(Prevalence OR Outbreaks OR Frequency OR Detection OR Occurrence OR Identification OR Isolation OR Characterization OR Investigation OR Survey) AND (LSD OR LSDV OR Lumpy skin disease OR Lumpy skin disease virus OR Capripox Virus OR Capripoxvirus OR Neethling) AND (Cattle OR Bovine OR Cow OR Calf OR Bos taurus OR Bos indicus OR Bull OR Ox OR Ruminants) NOT (Review)”. The search covered “All fields” and the author’s manual searched to retrieve potential articles that might have been missed during the electronic database search, ensuring that no reports were left out.

2.2. Eligibility Criteria

The eligibility of the searched articles was evaluated using the following inclusion criteria: i. title and abstract must be related to Lumpy Skin Disease, ii. A paper of appropriate methodological quality (e.g., PRISMA), iii. Observational studies (cross-sectional, longitudinal, retrospective cohort) and data-rich surveys or surveillance reports, iv. articles presenting prevalence, morbidity, and risk factors of LSD; providing enough data to calculate effect size (prevalence, odds ratio); studying historical or emerging outbreaks, v. any country in the two continents as well as the world, vi. studying the population of cattle of any breed, age, and sex, vii. paper written in English, viii. published between January 2000 and May 2025. Reasons for exclusion were reviews, editorials, conference abstracts without full data, non-peer-reviewed theses/dissertations, duplicates, experimental trials (e.g., clinical/vaccine studies), laboratory-only studies (e.g., molecular characterization of LSDV), economic models, test performance/surveillance evaluations, and outbreak control or clinical signs reports. Studies of LSD other than cattle populations, non-LSD pathogens, non-English publications, studies published before 2000, and those with poor methodological quality (high bias, inadequate scoring) and lacking quantitative data (e.g., prevalence, OR) were excluded (**Table S1**).

2.3. Selection of Studies and Data Extraction

We initially screened the titles and abstracts of the retrieved papers, and those meeting the inclusion criteria were selected for full-text review. After the final selection of the paper, the data concerning author's name, title, country, year, disease occurrence, study design, study period, duration (month), sampling method, sample size calculation, prevalence, sample used, methods of detection, season, age group, sex group, production system, cattle source, vaccination status, breed, biosecurity measures, herd size, vector presence, clinical sign, and lactation were extracted.

2.4. Quality Assessment

To support objective interpretation of the pooled estimates, the methodological quality and risk of bias of each included study were assessed using a predefined quality-assessment checklist [27, 28]. The checklist included 13 parameters with "yes" and "no" applicable options. Operationally, "yes" was rewarded with a score of 1, while "no" was provided with 0 (**Table S2**). Five researchers individually assessed the quality of the selected paper. The mean quality score (out of 10) was calculated for each article. Articles were categorized as low, moderate, and high quality if scored <5, 5-7, and ≥8, respectively.

2.5. Statistical Analyses

All extracted data were arranged and stored in Microsoft Excel 2024. A random-effects model meta-analysis was used to estimate the pooled seroprevalence of Lumpy Skin Disease (LSD) in cattle, with corresponding 95% confidence intervals (CI), accounting for variability between studies. Subgroup analyses were performed to explore differences in prevalence estimates by several factors such as, country, study design, disease occurrence (outbreak vs. non-outbreak settings), and diagnostic method used. The heterogeneity among studies was assessed using Cochran's Q test and the I^2 statistic. I^2 values of 25%, 50%, and 75% were interpreted as indicators of low, moderate, and high heterogeneity, respectively, while I^2 of 0% indicated no observed heterogeneity. To further investigate sources of heterogeneity, both univariable and multivariable meta-regression analyses were performed. The variables that showed $p < 0.05$ in univariable meta-regression were considered for multivariable meta regression. The publication bias was evaluated through visual inspection of funnel plots and statistically tested using Begg's and Egger's methods. The forest plots were generated to show individual study estimates, pooled prevalence, and heterogeneity metrics. Additionally, several risk factors for LSD were also assessed among eligible studies. All statistical analyses were conducted using Stata version 18.0 (StataCorp LLC, College Station, TX, USA). Spatial distribution maps of LSD seroprevalence across Asia and Africa were created using ArcMap version 10.8 (Esri, Redlands, CA, USA) to visualize regional patterns and hotspots.

3. Results

The database search identified 3,199 records: PubMed (n = 702), Scopus (n = 761), Web of Science (n = 734), and Google Scholar (n = 1,002). After removing 1,379 duplicate records, 1,820 records were screened by title and abstract. Of these, 1,003 records were excluded, and 817 reports were sought for retrieval. Eleven reports could not be retrieved, and 621 reports did not provide individual prevalence data, leaving 185 full-text reports for eligibility assessment. A further 166 reports were excluded because they were case reports (n = 7), case-control studies (n = 23), experimental trials (n = 19), non-English articles (n = 8), prospective studies (n = 7), duplicate publications using the same dataset (n = 4), studies without confirmatory diagnosis (n = 17), molecular diagnostic studies only (n = 69), or other ineligible reports (n = 12) (Table S3). Finally, 19 eligible studies were identified through database searching, and one additional study was identified through manual reference-list screening, resulting in 20 studies included in the review and meta-analysis. The study selection process is shown in **Figure 1**. The characteristics of the eligible articles are shown in **Table 1**.

Table 1: Included studies for metanalysis of seroprevalence of Lumpy Skin Disease of cattle

Author's and publication year	Country	Disease pattern	Study design	Sampling Period	Sampling method	Detection test	No. of total	No. of Positive	Prevalence	Quality score
Asia										
[29]	Bangladesh	Endemic	Cross-sectional	2021-2025	Random	Ab-ELISA	1104	289	0.262	8.46
[30]	Bangladesh	Endemic	Cross-sectional	2021-2025	Random	Ab-ELISA	184	52	0.283	9.23
[31]	Bangladesh	Endemic	Cross-sectional	2021-2025	Random	Ab-ELISA	736	181	0.246	10.00
[32]	Cambodia	Endemic	Cross-sectional	2021-2025	Purposive	Ab-ELISA	300	224	0.747	10.00
[33]	India	Endemic	Longitudinal Cross-sectional	2021-2025	Random	Ab-ELISA	184	36	0.196	7.69
[34]	India	Endemic	Cross-sectional	2011-2020	Purposive	Ab-ELISA	478	267	0.559	7.69
[35]	India	Outbreak	Longitudinal Cross-sectional	2021-2025	Purposive	Ab-ELISA	86	9	0.105	6.15
[36]	Indonesia	Outbreak	Survey	2021-2025	Purposive	Ab-ELISA	906	94	0.104	7.69
[8]	Oman	Outbreak	Cross-sectional	2000-2010	Purposive	Ab-ELISA	34	30	0.882	4.61
[37]	Pakistan	Endemic	Cross-sectional	2021-2025	Random	Ab-ELISA	400	152	0.380	9.23
[38]	Thailand	Outbreak	Not mentioned	2021-2025	Purposive	Ab-ELISA	460	312	0.678	4.61
Africa										
[39]	Egypt	Outbreak	Cross-sectional	2021-2025	Random	Ab-ELISA	84	46	0.548	6.15
[40]	Egypt	Sporadic	Cross-sectional	2011-2020	Random	IFAT	382	68	0.178	6.15
[41]	Egypt	Endemic	Cross-sectional	2011-2020	Random	Ab-ELISA	1000	180	0.180	10.00
[42]	Ethiopia	Endemic	Cross-sectional	2011-2020	Multi-stage	IFAT	1592	100	0.062	10.00
[43]	Ethiopia	Endemic	Cross-sectional	2011-2020	Random	SNT	384	29	0.076	9.23
[44]	Ethiopia	Endemic	Cross-sectional	2021-2025	Multi-stage	VNT	368	150	0.408	9.23

[45]	Ethiopia	Endemic	Cross-sectional	2000-2010	Multi-stage	VNT	2368	640	0.270	8.46
[46]	Sudan	Outbreak	Cross-sectional	2011-2020	Purposive	Ab-ELISA	43	18	0.419	7.69
[47]	Uganda	Endemic	Survey	2011-2020	Multi-stage	Ab-ELISA	2263	185	0.0818	8.46

3.1. Pooled Seroprevalence of LSDV Infection

The primary outcome of this meta-analysis was the pooled seroprevalence of LSDV antibodies in cattle, while secondary outcomes included subgroup-specific prevalence estimates, sources of heterogeneity, and animal-level risk factors for seropositivity. Among the selected 20 studies on antibody detection, 11 articles scored above 8 points, 7 articles scored between 5 and 7 points, and 2 articles received a score below 5. A total of 13,356 cattle from various geographical regions across Asia and Africa were examined for Lumpy Skin Disease Virus (LSDV) (**Figure 2**). Among them, 3,062 animals were confirmed positive using several serological diagnostic methods, including ELISA, Virus Neutralization Test (VNT), Indirect Fluorescent Antibody Test (IFAT), and Serum Neutralization Test (SNT). Based on the random-effects meta-analysis, the overall pooled seroprevalence of LSDV infection in cattle in the study period was estimated at 31.2% (95% CI: 21.0–42.5%) (**Figure 3**). A significant degree of heterogeneity was observed among the studies, with a Q statistic of 21,194.63 (df = 19), $P < 0.001$, and an I^2 value of 99.43% (**Figure 4**).

3.2. Source of Heterogeneity

A subgroup meta-analysis was conducted based on continent, country, quality score, quality score, disease pattern, study design, sampling year, sampling duration, sampling technique, sample size, and diagnostic methods. According to continent, the pooled prevalence of LSD was higher in Asia (39.1%; 95% CI: 23.3 to 56.2) than Africa (22.2%; 95% CI:12.0-34.4). By disease occurrence, the pooled prevalence of LSD was 26.4% (95% CI: 17.0 to 37.1) in endemic areas and 44.0% (95% CI: 18.3 to 71.5) during outbreaks (**Table 2**).

Table 2: Pooled seroprevalences and estimated sources of heterogeneity in the seroprevalence of LSD in cattle

Variable	No. of study	No. of tested	No. of positive	Pooled prevalence % (95% CI)	Heterogeneity		
					I^2	χ^2	P value
Continent							
Asia	11	4872	1646	39.1 (23.3-56.2)	99.28%	996.72	<0.001
Africa*	09	8484	1416	22.2 (12.0-34.4)	99.29%	684.45	<0.001
Quality Score							
High*	11	10699	2182	25.4 (14.8-37.8)	99.46%	1248.90	<0.001
Low	02	494	342	77.5 (55.6-93.6)	86.17%	7.23	0.007
Moderate	07	2163	538	28.2 (14.4-44.3)	98.12%	394.18	<0.001
Disease Pattern							
Endemic*	13	11361	2485	27.1 (17.0-38.6)	99.62%	1533.27	<0.001
Outbreak	06	1613	509	44.0 (18.3-71.5)	99.18%	602.68	<0.001
Sporadic	01	382	68	17.8 (14.1-21.8)	-	0.00	-
Study Design							
Cross sectional	15	9341	2238	31.1 (20.8-42.4)	99.18%	950.66	<0.001
Survey*	02	3169	279	9.1 (7.1-11.4)	73.76%	3.81	0.051
Longitudinal**	03	846	545	49.9 (11.4-88.5)	99.30%	139.55	<0.001
Sampling Year							
2000-2010	02	2402	670	58.6 (4.4-99.0)	98.30%	58.85	<0.001
2011-2020*	07	6142	847	19.6 (7.1-11.4)	99.36%	628.23	<0.001
2021-2025	11	4812	1545	34.8 (22.2-48.6)	98.91%	862.35	<0.001
Study Duration							
<6 months	05	1843	606	48.4 (21.0-76.3)	99.22%	573.02	<0.001
6-12 months*	10	6557	1087	23.2 (12.6-35.8)	99.13%	897.25	<0.001
>12 months	05	4956	1369	32.3 (14.2-53.7)	99.51%	347.90	<0.001
Sampling Technique							
Simple Random	09	4458	1033	24.8 (16.8-33.8)	97.60%	187.10	<0.001
Multi-stage*	04	6591	1075	18.5 (5.6-36.6)	99.62%	575.06	<0.001
Purposive	07	2307	954	48.8 (24.6-73.3)	99.23%	887.64	<0.001
Sample Size							
≤ 100	4	247	103	48.1 (15.7-81.3)	96.68%	86.64	<0.001
101-500	9	3140	1290	37.7 (22.5-54.3)	98.89%	743.93	<0.001
More than 500*	7	9969	1669	16.3 (10.1-23.7)	98.83%	596.21	<0.001
Detection Test							
Ab-ELISA	15	8262	2075	36.1 (23.3-49.9)	99.34%	1678.75	<0.001
IFAT*	2	1974	168	11.3 (2.6-24.9)	97.57%	41.21	<0.001
SNT	1	384	29	7.6 (5.1-10.4)	-	0.00	-
VNT	2	2736	790	33.5 (20.9-47.5)	96.32%	27.16	<0.001

Total	**20**	**13356**	**3062**	**31.2 (21.0-42.5)**	**99.43%**	**21194.63**	**<0.001**

**Longitudinal Cross Sectional Study, *Base line, Ab-ELISA= Antibody Enzyme-Linked Immunosorbent Assay, IFAT= Indirect Fluorescent Antibody Test, SNT= Serum Neutralization Test, VNT= Virus Neutralization Test.

Based on study design, the estimated pooled prevalence was 49.9% (95% CI: 11.4 to 88.4) for longitudinal cross-sectional studies, 31.1% (95% CI: 20.8 to 42.4) for cross-sectional studies, and 9.1% (95% CI: 7.1 to 11.4) for survey, indicating that longitudinal cross-sectional designs yielded higher prevalence estimates. According to sampling year, the estimated pooled prevalence was 58.6% (95% CI: 4.4 to 99.0) for 2000-2010, 34.8% (95% CI: 22.2 to 48.6) for 2021-2025, and 19.6% (95% CI: 7.1 to 11.4) for 2011-2020. Considering sampling technique, the estimated pooled prevalence was 48.8% (95% CI: 24.6 to 73.3) for purposive, 24.8% (95% CI: 16.8 to 33.8) for simple random, and 18.5% (95% CI: 5.6 to 36.6) for multi-stage cluster sampling. Regarding sample size, studies with ≤100 samples showed a pooled prevalence of 48.1% (95% CI: 15.7–81.3), compared to 37.7% (95% CI: 22.5–54.3) for 101–500 and 16.3% (95% CI: 10.1–23.7) for >500 samples. Diagnostic methods varied, with Ab-ELISA being the most frequently applied, yielding a pooled prevalence of 36.1% (95% CI: 23.3–49.9). Country-specific analysis showed the highest prevalence in Oman (88.2%; 95% CI: 74.9 to 97.3) and the lowest in Uganda (8.2%; 95% CI: 7.1–9.3) (**Table 3**). Notably, most studies originated from Egypt, India, Bangladesh and Ethiopia.

Table 3: Estimated pooled prevalence of LSD in cattle by country

Country	No. of study	No. of tested	No. of positive	Pooled prevalence % (95% CI)	Heterogeneity		
					I^2	χ^2	P value
Bangladesh	03	2024	522	25.8 (23.9-27.7)	0.04%	1.25	0.535
Cambodia	01	300	224	74.7 (69.6-79.4)	-	0.00	-
Egypt	03	1466	190	28.6 (9.2-53.3)	98.52%	49.58	<0.001
Ethiopia*	04	4712	919	18.3 (5.4-36.7)	99.43%	461.09	<0.001
India	03	768	312	27.1 (5.8-56.5)	98.17%	127.53	<0.001
Indonesia	01	906	94	10.4 (8.5-12.4)	-	0.00	-
Oman	01	34	30	88.2 (74.9-97.3)	-	0.00	-
Pakistan	01	400	152	38.0 (33.3-42.8)	-	0.00	-
Sudan	01	43	18	41.9 (27.4- 57.0)	-	0.00	-
Thailand	01	460	312	67.8 (63.5-72.0)	-	0.00	-
Uganda	01	2263	185	8.2 (7.1-9.3)	-	0.00	-
Total	**20**	**13356**	**3062**	**31.2 (21.0-42.5)**	**99.43%**	**21194.63**	**<0.001**

*Base line for comparison

3.3. Meta-regression

Continent, country, quality score, disease pattern, study design, sampling year, sampling duration, sampling technique, sample size, and diagnostic methods were evaluated by meta regression analysis. Initially, univariable meta retrogression was performed, followed by multivariable meta regression. In the univariable analysis, study design (p=0.031), sampling year (p=0.034), sampling technique (p=0.018), sample size (p=0.012), and diagnostic methods (p=0.047) were statistically significant at $p < 0.05$ (**Table 4**). However, in the multivariable meta-regression, only two variables: sampling year and sample size, remained statistically significant, with coefficients of 0.324 (95% CI: 0.014–0.634) and 0.331 (95% CI: 0.064–0.598), respectively ($p < 0.05$). The final model explained 33.98% of the observed heterogeneity and demonstrated a significant Wald chi-square test ($\chi^2 = 11.56$, $p = 0.003$) (**Table 4**).

Table 4: Result of univariable and multivariable meta-regression model for detecting probable sources of heterogeneity

Variable's name	Univariable meta regression		Multivariable meta regression					
	Coefficient (95% CI)	p value	Coefficient (95% CI)	p value	Std. error	R^2	Wald χ^2	p value
Continent	0.181 (-0.044-0.406)	0.114	-	-	-	33.98%	11.59	0.003
Quality Score	0.374 (0.056-0.692)	0.021*	-	-	-			
Country	0.079 (-0.098-0.256)	0.381						
Disease Pattern	0.322 (-0.102-0.747)	0.137	-	-	-			
Study Design	0.465 (0.041-0.889)	0.031*	-	-	-			
Sampling Year	0.376 (0.029-0.722)	0.034*	0.324 (0.014-0.634)	0.041	0.158			
Study Duration	0.256 (-0.009-0.522)	0.058	-	-	-			
Sampling Technique	0.347 (0.059-0.634)	0.018*	-	-	-			
Sample Size	0.368 (0.082-0.653)	0.012*	0.331 (0.064-0.598)	0.015	0.136			
Detection Test	0.253 (0.003-0.502)	0.047*	-	-	-			

*Statistically significant

3.4. Publication Bias

To assess potential publication bias, a funnel plot analysis and Egger's test were applied. The funnel plot revealed a slight asymmetry in the distribution of effect sizes, suggesting possible publication bias (**Figure 5**). Egger's test, conducted under a random-effects model (REML), regressed the Freeman–Tukey transformed prevalence against its standard error and yielded an intercept (β_0) of 6.42 (SE = 2.673, z = 2.40, p = 0.0164) (**Figure 6**). This result indicates significant small-study effects (p < 0.05) and potential publication bias. However, the trim-and-fill analysis detected no imputed or missing studies, suggesting that the overall pooled prevalence estimates are robust and not substantially influenced by publication bias.

3.5. Sensitivity Analysis

For assessing the robustness of this meta-analysis, a leave-one-out sensitivity analysis was performed using a random-effects (REML) model. Each of the studies was excluded sequentially, and the pooled prevalence was recalculated to assess the influence of individual studies. **Figure 7** shows pooled estimates ranging from 28% (95% CI: 19–39%) to 33% (95% CI: 22–44%), compared with the overall pooled prevalence of 31.2 % (95% CI: 21.0–42.5%). Especially, excluding [8] yielded the lowest prevalence (28%), while omitting [43] produced the highest (33%). The consistent results, with all p-values (< 0.001) remaining significant, indicate that no single study biased the findings, confirming the reliability of the overall estimate despite high heterogeneity (I^2 = 99.43 %).

3.6. Potential Risk factors

Cattle over two years of age (OR = 1.47; 95% CI: 1.01–2.15; *P* = 0.047) had a significantly higher risk of infection compared to cattle aged one year or younger. Similarly, females (OR = 1.32; 95% CI: 1.06–1.65; *P* = 0.047) were more likely to be infected than males. Crossbred cattle (OR = 2.92; 95% CI: 1.41–6.05; *P* = 0.001) had a significantly higher infection rate compared to tropical breeds, and cattle reared under extensive management systems (OR = 1.63; 95% CI: 1.26–2.12; *P* = 0.000) were more likely to be infected than those under intensive rearing systems. Detailed results of the assessed risk factors are presented in **Table 5**.

Table 5: Risk factor analysis for the seroprevalence of LSD in cattle

Variable	Category	No. of study	Prevalence % (Infected/Total)	Odds Ratio (OR)		OR Heterogeneity		
				OR (95% CI)	p value	I^2	τ^2	p value
Age	Calf	13	23.1 (403/1818)	Ref	-	0.00	0.000	-
	Yearling		31.6 (464/2223)	1.58 (0.83 - 2.55)	0.055	83.17%	0.498	<0.001
	Adult		29.2 (920/3653)	1.47 (1.01 – 2.15)	0.047	78.36%	0.341	<0.001
Sex	Male	13	24.3 (722/2818)	Ref	0.011	00.00	0.000	-
	Female		30.5 (1091/5226)	1.32 (1.06 – 1.65)		61.74%	0.09	<0.001
Breed	Cross	10	40.5 (642/1693)	2.92 (1.41 – 6.05)	<0.001	89.99%	1.097	<0.001
	Temperate		56.3 (81/258)	2.47 (0.82 – 7.42)	0.113	59.69%	0.509	0.094
	Tropical		23.0 (376/2022)	Ref	-	0.00	0.000	-
Rearing system	Extensive	07	24.8 (329/1302)	1.63 (1.26 – 2.12)	0.000	0.03%	0.002	0.726
	Semi-intensive		19.4 (627/3797)	1.38 (0.92 – 2.08)	0.121	51.12%	0.102	0.064
	Intensive		19.1 (237/1013)	Ref	-	0.00	0.000	-

4. Discussion

This systematic review and meta-analysis provides a consolidated estimate of LSD seroprevalence in cattle across Asia and Africa over a 25-year period. The overall pooled seroprevalence was 31.2%, indicating a substantial serological burden in the included regions. The findings also showed marked variation by continent, disease setting, study design, sampling period, sample size, and diagnostic method, emphasizing that both epidemiological and methodological factors influence reported LSD prevalence.

A key outcome of this analysis was the higher pooled seroprevalence observed in Asia compared with Africa, suggesting either greater recent transmission intensity, differences in surveillance and sampling strategies, or variation in vaccination and control coverage across regions. In two independent studies, the pooled prevalence was 28.8% and 40.4% in Africa and Asia, respectively [48, 49]. The increased seroprevalence observed in Asian regions may be attributed to several factors, including the transboundary movement of infected cattle without adequate quarantine measures, hot and humid climatic conditions that favor vector proliferation, insufficient vaccination coverage and surveillance, limited farmer awareness, and inadequate financial and technical resources for disease control in developing countries [29, 34, 41, 43, 50]. Among the included studies, Ethiopia contributed the highest number of reports. The majority of studies employed a cross-sectional design, yielding a pooled prevalence of 18.3%, consistent with findings by Abebaw (2024). Pakistan (38.0%) showed the highest seroprevalence of LSD among the Asian countries, followed by India (27.1%) and Bangladesh (25.8%). These differences may reflect variations in vaccination coverage and disease surveillance, consistent with the findings of [37]. Most studies have associated LSD occurrence with endemic conditions, showing a comparatively lower pooled prevalence of 26.4% than that observed during outbreak situations [48]. Among study designs, longitudinal studies showed higher pooled prevalence, likely because repeated or extended sampling increases the probability of detecting infection [51]. Recent studies from 2021-2025 (34.8%) and occurred in less than 6 months (48.4%) showed high prevalence, as their increased climatic change, transboundary animal movement. Recent studies conducted between 2021 and 2025 (34.8%) and those with study durations of less than six months (48.4%) reported higher prevalence, likely reflecting the effects of increasing climatic variability and intensified transboundary animal movement. Studies that followed purposive sampling or small sample sizes often intentionally selected herds or districts known or suspected to be infected with LSD, which may have led to inflated pooled prevalence [49]. Additionally, the Ab-ELISA (Antibody detecting) being the most frequently applied and showed high prevalence estimates (36.1%), while SNT and IFAT were used less frequently. Since antibodies persist longer than viral DNA, samples collected after an outbreak tend to show higher ELISA positivity compared with other diagnostic assays [52]

The univariable meta-regression indicated that study design, sampling year, sampling technique, sample size, and detection test significantly contributed to heterogeneity, confirming earlier evidence that methodological differences strongly influence seroprevalence outcomes [52, 53]. In the multivariable model, sampling year and sample size remained significant, highlighting the impact of temporal shifts in disease dynamics and study precision [49].

Funnel plot asymmetry and Egger's test suggested possible small-study effects or publication bias. However, these findings should be interpreted cautiously because true epidemiological heterogeneity, geographic variation, and differences in diagnostic methods can also produce asymmetry. Leave-one-out sensitivity analysis showed that the pooled estimate remained within a narrow range, indicating that no single study disproportionately influenced the overall result [54]. Moreover, the minimal variation in pooled estimates (28–33%) compared with the overall prevalence indicates that no single study exerted undue influence on the summary effect. Consistent with [55], the leave-one-out approach confirmed the robustness of the estimate, supporting the reliability of the findings despite substantial heterogeneity.

Age-related differences in LSD prevalence were observed, with the highest prevalence in yearlings, followed by adults, and the lowest in calves. This pattern aligns with earlier reports [29, 42, 50] though some studies noted opposite trends [31, 56]. Higher prevalence in yearlings may reflect increased exposure to circulating viruses, poor nutrition, underdeveloped immunity, and suboptimal management. In adults, elevated prevalence may be associated with cumulative environmental exposure and waning maternally derived antibodies. Furthermore, the pooled prevalence of LSD was significantly higher in female cattle than in males. This may reflect longer retention of females for breeding and milk production, their predominance in herds, and physiological stress from reproduction and lactation[42, 43]. Though some studies found higher prevalence in younger male-dominated populations [29], while others noted no sex-based differences [50]. Crossbred cattle showed higher odds of LSD infection than tropical breeds, likely due to lower environmental adaptability, as reported in previous studies [42, 57]. Similarly, extensive rearing system increased infection risk, consistent with evidence that outside grazing elevates exposure to vectors responsible for LSD transmission [3]. These findings emphasize the need for risk-based control measures considering age, sex, breed, and management practices.

Lumpy skin disease has significant economic implications, including reduced milk yield, loss of draught power due to lameness, reproductive disorders such as abortion and infertility, as well as costs associated with treatment and vector control [25, 58]. Despite the intent to present a global overview of LSD, no seroprevalence data were available from continents other than Africa and Asia, preventing estimation beyond these regions. Additionally, this review excluded non-English publications, unpublished data, editorials, methodological papers, experimental trials, and case reports to ensure consistency and reliability. Although age is a key determinant of LSD infection, limited studies provided age-specific information; therefore, subgroup analyses were restricted to broad categories – "calf," "young," and "adult." Substantial heterogeneity among models indicates that unmeasured or unreported factors may have influenced the pooled estimates. Furthermore, evidence of publication bias was identified, as suggested by the funnel plot and the relationship between effect sizes and standard errors. These limitations indicate that the pooled estimate should be interpreted as a regional summary rather than a precise global estimate. Nevertheless, the study provides an evidence base for prioritizing harmonized serological surveillance, standardized reporting, and targeted vaccination strategies in high-risk cattle populations.

5. Conclusions

This meta-analysis showed that LSD seroprevalence in cattle remains substantial across Asia and Africa, with an overall pooled estimate of 31.2%. Higher seropositivity was associated with Asian studies, outbreak settings, smaller sample sizes, adult and female cattle, crossbred animals, and extensive management systems. These findings support the need for risk-based surveillance, standardized diagnostic reporting, and targeted vaccination programs, particularly in regions with active transmission or transboundary animal movement. Future studies should use harmonized study designs and reporting frameworks to improve comparability and generate more reliable estimates of LSD burden.

List of abbreviations

LSD	Lumpy Skin Disease
LSDV	Lumpy Skin Disease Virus
VNT	Virus Neutralization Test
ELISA	Enzyme Linked Immuno-Sorbent Assay
PRISMA	Preferred Reporting Items for Systematic Reviews and Meta-Analyses
IFAT	Indirect Fluorescent Antibody Test
SNT	Serum Neutralization Test

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

All authors have reviewed and approved the final version of the manuscript and consent to its publication.

Availability of data and materials

All data generated or analyzed during this study are included in this published article and in its

supplementary information files.

File name	Description
Supplementary Tables S1-S2, Microsoft Word file	Table S1: The inclusion and exclusion criteria set for article screening. Table S2: The checklist of the quality assessment criteria that has been followed to score the eligible manuscripts.
Supplementary Table S3, Microsoft Excel file	Details of the excluded manuscripts with reasons for exclusion

Competing interests

The authors declare no conflicts of interest.

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Authors' contributions

MJHR, SNT, MMH, FA:planning, data collection, data compilation, validation, quality assessment, data visualization, writing – original draft; **TAN, AAF, MA**:data curation, data visualization, quality assessment, writing – review and editing; **MJHR, MAH, TMR**:conceptualization, supervision, formal analysis, writing – review and editing.

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Figures

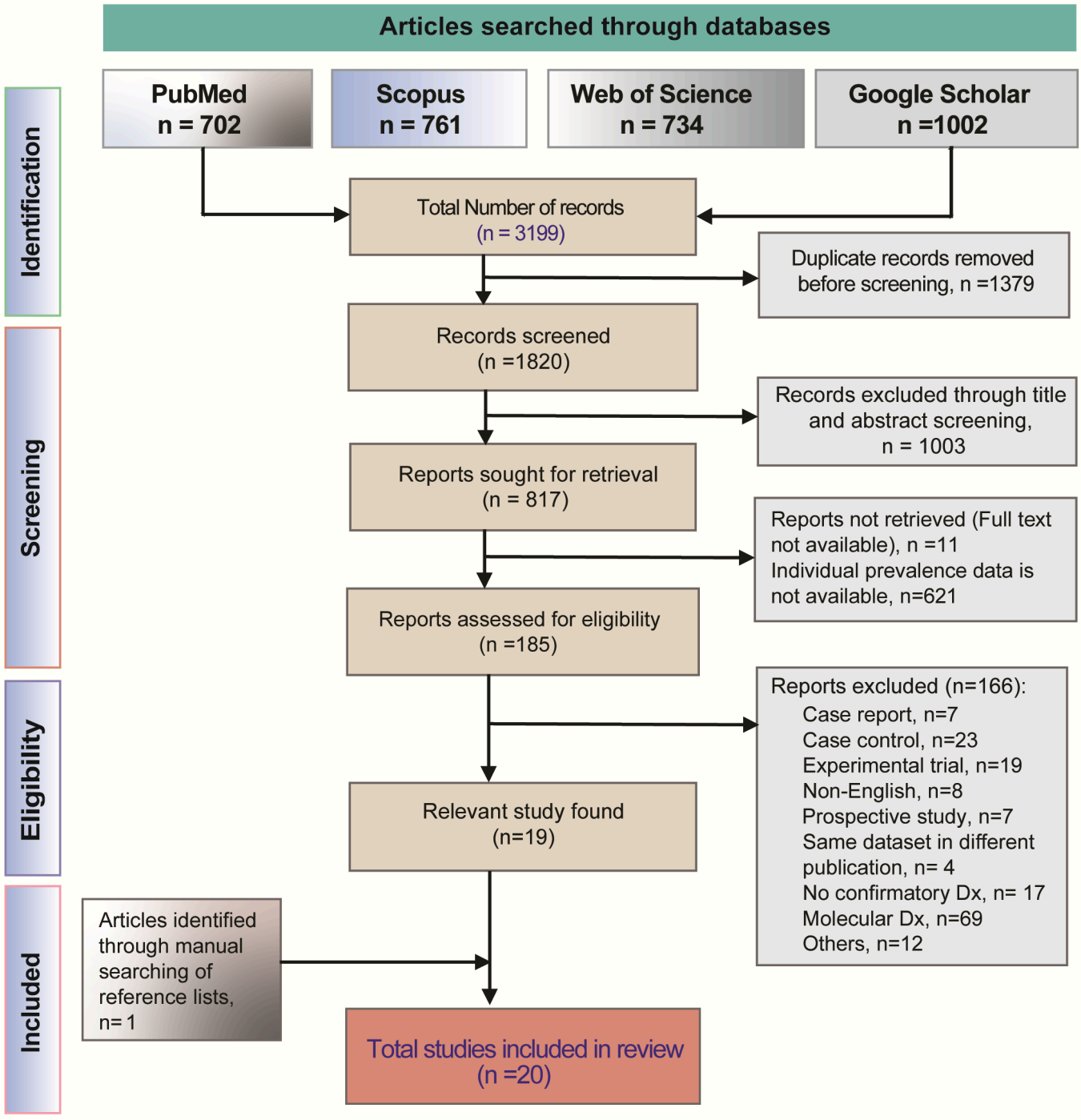


Figure 1

Flow diagram of the selection of eligible studies for inclusion in the meta-analysis on LSD based on PRISMA 2020 Guideline.

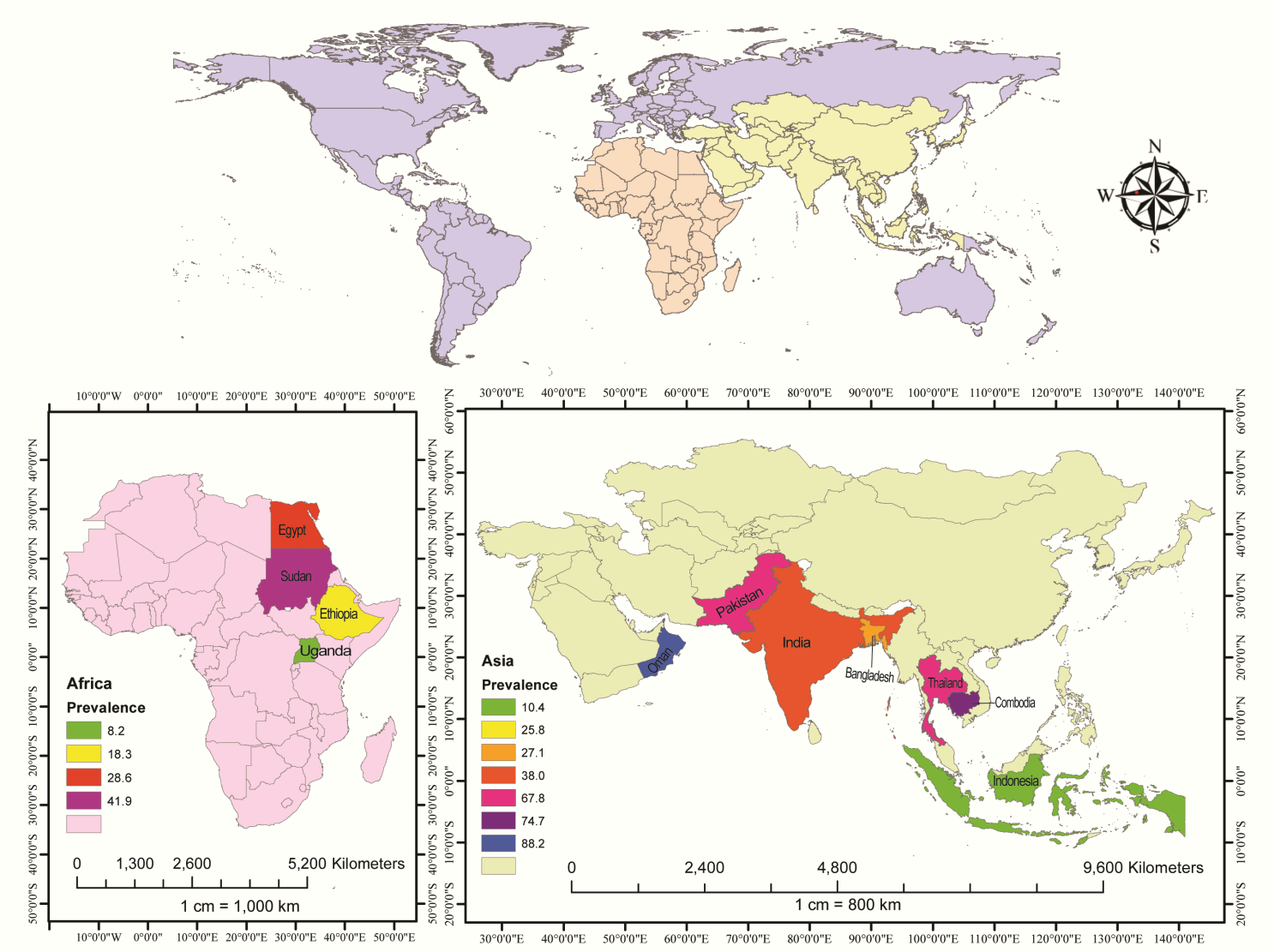


Figure 2

Spatial distribution of estimated seroprevalence of LSDV across Asia and Africa during 2000-2025. The map was produced using ArcMap v.10.8 (Esri, Redlands, CA, USA).

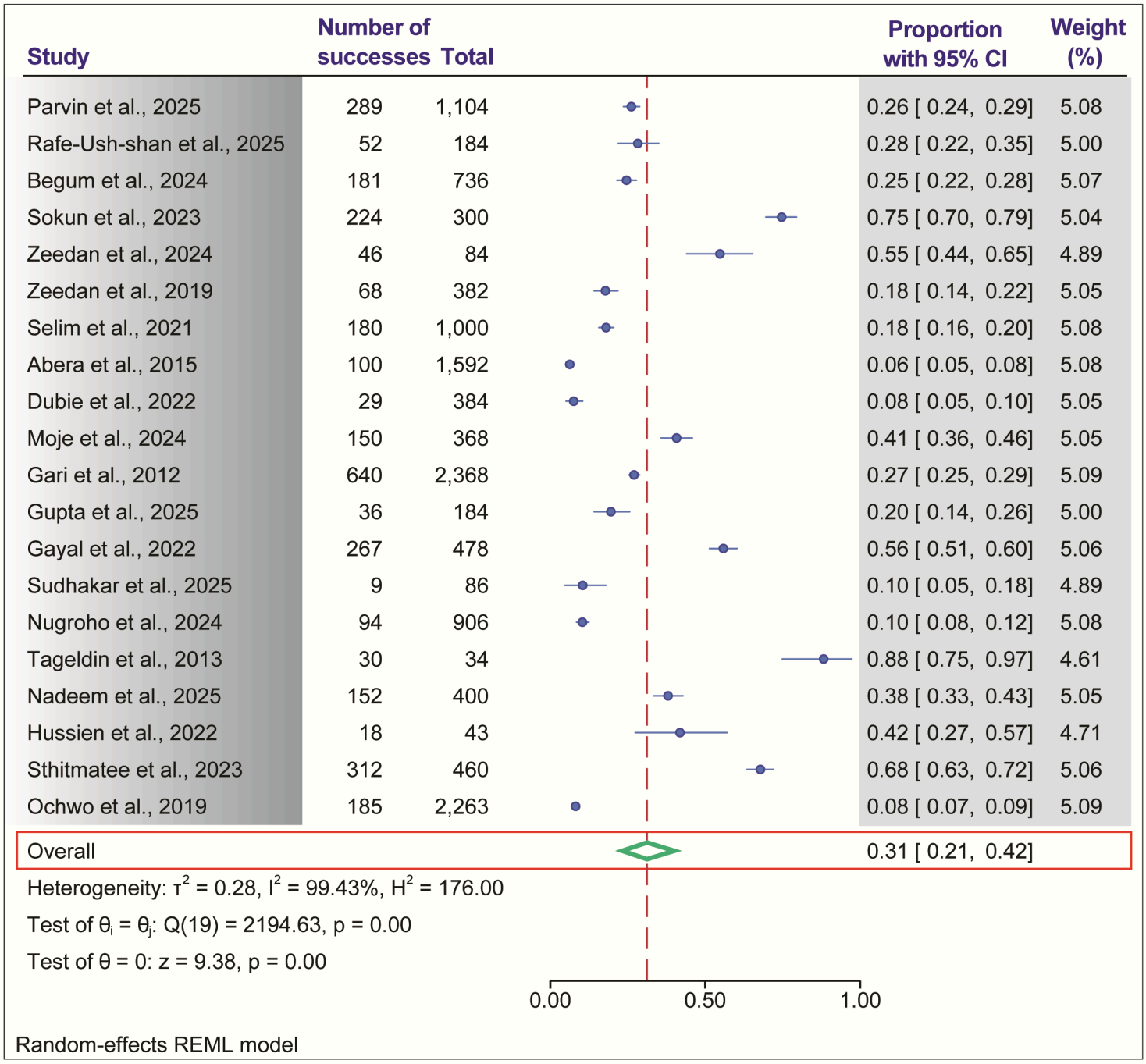


Figure 3

Forest plot illustrating the seroprevalence of lumpy skin disease (LSD) in cattle across Asia and Africa (2000–2025), with individual study estimates and pooled prevalence calculated using a random-effects model.

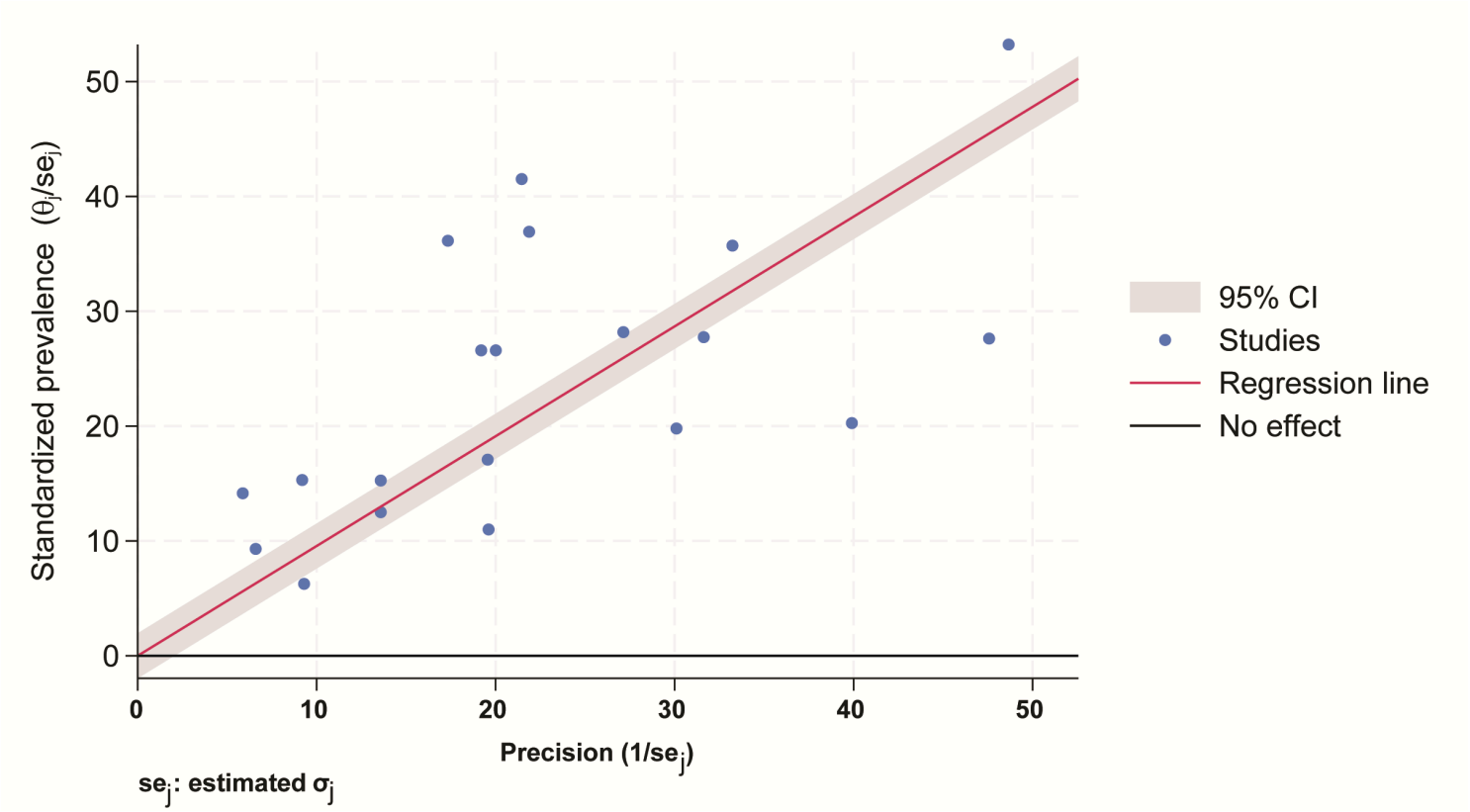


Figure 4

Galbraith (radial) plot assessing between-study heterogeneity. Each point represents an individual study plotted as standardized prevalence (θ𝑗 / SE𝑗) against study precision (1 / SE𝑗). The central horizontal line denotes the no-effect value, while the diagonal lines indicate the 95% confidence limits.

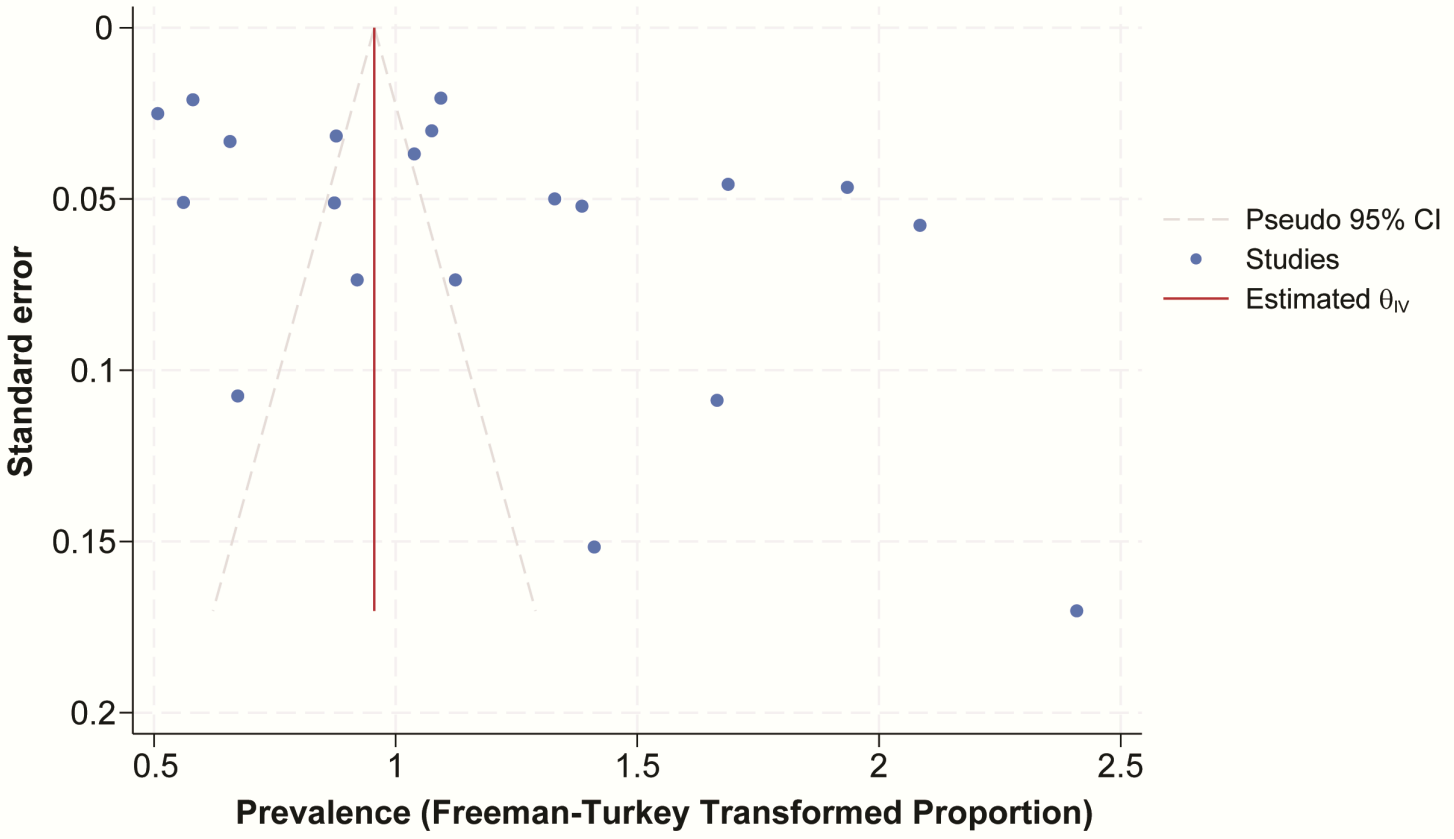


Figure 5

Funnel plot with pseudo 95 % confidence interval limits for the examination of publication bias of the seroprevalence estimates for LSDV infection. The plot displays the relationship between the study-specific standard error and the Freeman–Tukey transformed seroprevalence estimates. Each point represents an individual study included in the meta-analysis.

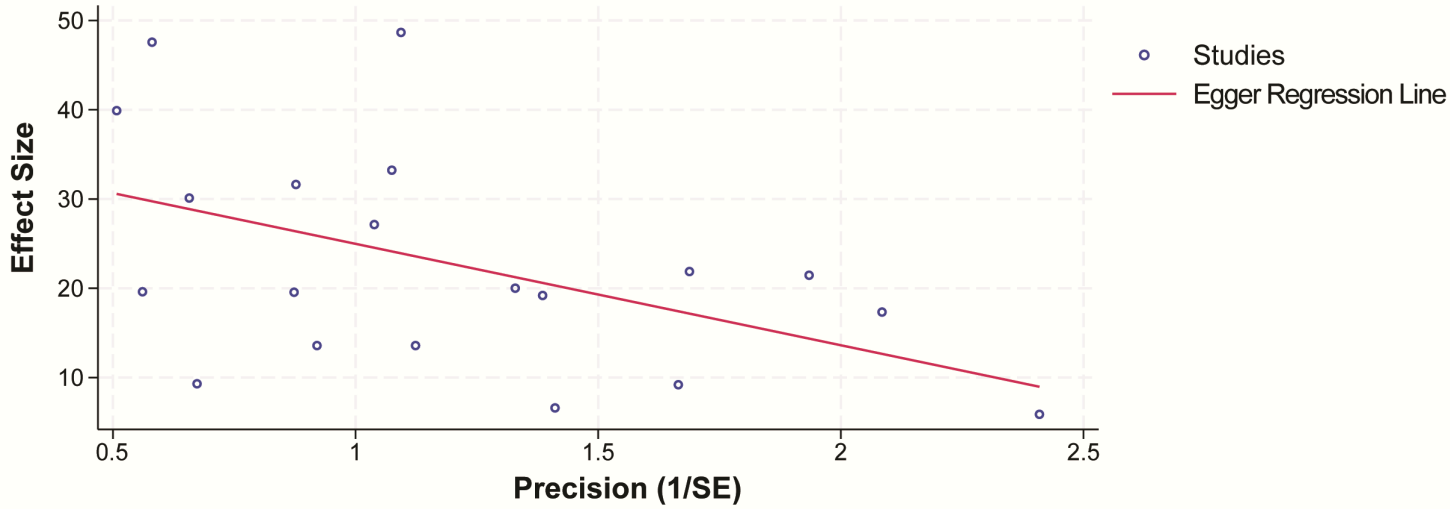


Figure 6

Egger's test for publication bias of Lumpy Skin Disease (LSD) seroprevalence. The relationship between study precision (1/SE) and effect size to assess potential small-study effects is plotted. Each point represents an individual seroprevalence study included in the meta-analysis. The fitted Egger regression line is shown to evaluate funnel plot asymmetry.

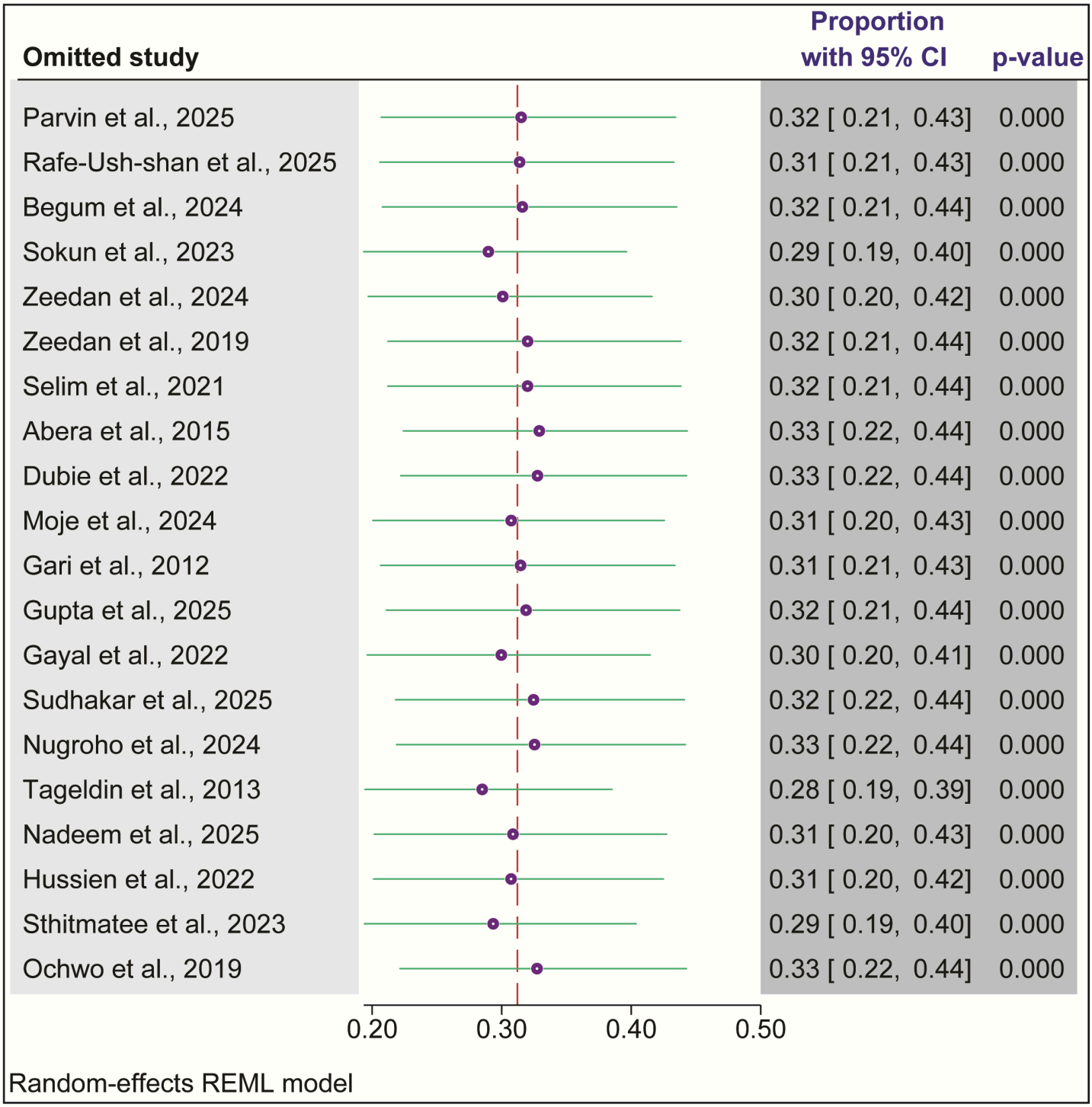


Figure 7

Sensitivity analysis of the seroprevalence estimates for LSDV infection across Asia and Africa during 2000-2025. A leave-one-out sensitivity analysis demonstrating the influence of each included study on the overall pooled seroprevalence estimate. For each iteration, one study was omitted from the random-effects REML model, and the resulting seroprevalence proportion with corresponding 95% confidence interval (CI) is shown.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- Supplementary.zip