EPIDEMIOLOGICAL SURVEILLANCE AND BURDEN OF ZOONOTIC DISEASES IN AFRICA: A SYSTEMATIC AND META-ANALYSIS REVIEW

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ABSTRACT

Introduction Emerging zoonotic diseases (EZDs) are a growing global public health concern, driven by complex human-animal environment interactions (Hossain et al., 2025). Understanding their epidemiology and regional disparities is essential for effective prevention and control. This study aimed to assess the current burden of zoonotic diseases in Africa and evaluate the effectiveness of surveillance systems in their detection and management. **Methods**: A systematic review and meta-analysis were conducted on studies published between 2007 and 2024, using PRISMA guidelines to ensure transparency and quality. A total of 52 studies were included, focusing on prevalence, case fatality rates (CFRs), and risk factors for zoonotic diseases across the continent. **Results:** it substantial variability in zoonotic disease prevalence, ranging from 0.86 (95% CI: 0.58–1.76) in Cameroon to 0.01 (95% CI: –0.00 to 0.02) in Central Africa, with high heterogeneity ($I^2 = 99.06\%$). Meta-regression revealed that attack rate was a significant predictor of effect size (coefficient = 1.00; $p < 0.001$), fully explaining between-study variance ($R^2 = 100\%$). The pooled CFR was estimated at 26% (95% CI: 12–40%), with regional variations from 72% in the Democratic Republic of Congo to 0% in Mozambique, Mauritania, and Ethiopia-Namibia. Although evidence of publication bias was found, sensitivity analysis confirmed robustness. **Conclusion:** zoonotic diseases remain a substantial health burden in Africa, shaped by disparities in surveillance systems, healthcare access, and socioeconomic conditions. Effective control requires stronger One Health coordination, integrated veterinary human surveillance, enhanced laboratory capacity, adoption of advanced detection technologies, and community engagement.

Keywords: Zoonotic diseases, emerging infectious diseases, outbreaks, Africa, systematic review, meta-analysis

INTRODUCTION

The spread of infectious diseases is a significant global problem. Emerging zoonotic diseases (EZDs) pose a growing threat to public health, driven by complex interactions among humans, animals, and the environment (Hossain et al., 2025). Zoonoses are infectious illnesses transmitted between people and animals, caused by bacteria, viruses, parasites, and fungi, and affect individuals of all ages (Elsohaby & Villa, 2023; Behravesh, 2016; Kelly et al., 2017). They are classified by etiology into bacterial (anthrax, brucellosis), viral (rabies, Ebola, avian influenza), parasitic (ringworm), rickettsial (Q fever), and protozoal zoonoses, among others (Sharma, Dhasmana & Arora, 2023). The recent SARS CoV 2 pandemic highlights the pandemic potential of emerging infections and the need for stronger preparedness (Chakraborty & Maity, 2020).

Low and middle income countries (LMICs) are particularly vulnerable due to weak health systems and reliance on livestock for livelihoods (Grace & Alonso, 2023). High income countries have reduced or eradicated several zoonoses through costly interventions, leaving LMICs bearing the heaviest burden. Endemic zoonotic diseases affecting marginalized populations receive less attention and funding than emerging ones that threaten global economies (Cleaveland et al., 2017; Eichler, Ernst & Muller, 2018). This imbalance is evident in Africa, where emerging diseases like Ebola attract more investment than endemic infections such as brucellosis, anthrax, and rabies (Grace & Alonso, 2023; WHO, 2022).

Zoonotic surveillance involves collecting, analyzing, and sharing data on diseases transmitted between animals and humans. Approximately 75% of emerging infectious diseases and over 60% of known infections are zoonotic (WHO, 2020). Surveillance enables early outbreak detection, disease trend tracking, and development of preventive strategies. Close human–animal contact, biodiversity, and ecological disruption make Africa especially prone to zoonotic spillover. Diseases such as Ebola and Marburg frequently originate from wildlife reservoirs (Muvunyi et al., 2025). Zoonoses and animal-origin diseases account for more than 25% of disability adjusted life years (DALYs) lost to infections in Sub Saharan Africa, compared to less than 1% in high income regions (Sing, 2023).

Between 2001 and 2022, zoonotic outbreaks comprised 33% of all public health emergencies (PHEs) in Sub Saharan Africa, with a 63% increase in outbreaks from 2012 to 2022. About 70% of these were attributed to Ebola virus disease (WHO, 2022). Exposure to livestock pathogens continues to cause substantial morbidity and mortality (Rodarte et al., 2023). Thirteen key zoonoses account for 2.4 billion human cases and 2.2 million deaths annually, particularly in Ethiopia, Nigeria, Tanzania, and India (Borah et al., 2025).

Research on zoonoses has advanced understanding of transmission, diagnosis, and control. For example, studies on HIV have informed treatment and prevention through antiretroviral therapy (Hardy, 2023; AIDS Professional Group, Society of Infectious Diseases of the Chinese Medical Association, 2024). Disease emergence is driven by environmental, biological, economic, and social factors (Emerging Pandemics: Connections with Environment and Climate Change, 2023). Lower latitudes are hotspots for zoonotic emergence (Salkeld, Hopkins & Hayman, 2024). Therefore, the aim of this study was to assess the current burden of zoonotic diseases and evaluate the effectiveness of epidemiological surveillance systems in detecting and managing these diseases across Africa. Specifically, the review synthesizes literature, examines the strengths and weaknesses of existing surveillance approaches, and identifies opportunities for strengthening One Health–based surveillance and response mechanisms on the continent.

METHODS

The PRISMA checklist requirements were adhered to (Page et al., 2020). The internationally accepted procedures for conducting systematic reviews are outlined in these guidelines. A systematic search was first conducted using specific keywords in the target databases to obtain abstracts of publications that were suitable for the study. Following the abstracts' screening according to eligibility requirements, the full papers for the remaining reports were identified and carefully examined to ascertain whether or not they met the inclusion criteria. Until the qualifying reports were found for data extraction and analysis, the reasons for exclusion were indicated at every stage.

Research Question

The research question for this study was: “What is the current burden (incidence rate, prevalence, or case fatality rate), and effectiveness of epidemiological surveillance systems in detecting and managing zoonotic diseases in Africa?”

Search Strategy and Data Source

A systematic review of peer-reviewed and grey literature from 2007 to 2024 was conducted in accordance with PRISMA 2019 guidelines (Page et al., 2020). The review examined the burden of zoonotic diseases and the effectiveness of epidemiological surveillance systems in Africa.

Eligibility criteria were guided by the PICOS framework (Population, Intervention, Comparison, Outcome, Setting) developed by the Joanna Briggs Institute (2014). The population included individuals and communities in Africa, with interventions focusing on integrated disease surveillance systems encompassing core, support, and attribute functions. Outcomes assessed were the burden of zoonotic diseases and surveillance system performance.

A comprehensive search was undertaken across five databases: Africa Journals Online (AJOL), PubMed, Google Scholar, Science Direct, and Cochrane Library. Search terms included 'zoonotic', 'outbreak', 'emerging', 'reservoir', and 'Africa', applied to titles and abstracts. Boolean operators (AND/OR) were used to refine and combine keywords, such as: (Burden OR prevalence OR "case fatality rate") AND (Effectiveness OR "reporting timeliness" OR "outbreak detection") AND ("epidemiological surveillance" OR "integrated disease surveillance") AND ("zoonotic diseases" OR zoonoses OR "emerging infectious diseases") AND (Africa OR "Sub-Saharan Africa").

Manual searches of reference lists from relevant papers supplemented the database search, ensuring comprehensive coverage of literature on zoonotic disease surveillance in Africa.

Criteria for including Studies in the Review

If the PICOS format did not fit the research question, the question was divided into separate concepts and categorized under each heading.

Table 1: The PICOS model for defining the eligibility of studies for the primary research question

Pico Criteria	Details
Population	Individuals and communities in Africa
Intervention	Epidemiological surveillance systems
Comparison	Not Applicable
Outcome measure	Burden of Zoonotic diseases and Effectiveness of the surveillance system
Setting	African countries

Definition of Terms

The percentage of a study population that was reported to have the zoonotic illness during a particular study is known as the Attack Rate. This is determined by dividing the number of disease cases that are reported by the total population under study, and then expressing the result per1000.

The percentage of zoonotic disease-infected humans that die is known as the case fatality rate, or CFR. It is stated per 1000 and is computed by dividing the number of recorded deaths by the total number of infected cases. The effectiveness of the surveillance system is determined by sensitivity in that the proportion of actual zoonotic disease/events is correctly detected by the system.

Study Selection

There were two stages to the research selection procedure. Initially, a screening of the received materials titles was conducted. Secondly, studies that did not answer the research topic or were duplicates were removed. All studies that satisfied the requirements for both abstract and full-text screening were uploaded and screened using EndNote X9 software.

Inclusion and Exclusion Criteria

The study considered quantitative reports from African countries (including case reports and series) that were published from January 2007 to 2024, and that provided empirical data on the prevalence of zoonotic diseases in humans with verified proof of animal origin. Where available, World Health Organisation (WHO) outbreak statistics were also taken from published literature. The manuscript eliminated or excluded studies that had reported infections solely in animals with no resultant human cases, due to the fact that the goal was to find zoonotic illnesses that are likely to impact the overall human population. The study excluded articles that were published but not written in the English language. The study also excluded opinion papers and viewpoints, systematic reviews, commentaries, and mathematical modelling research papers.

Data extraction

The evaluation of reports for quality was strict enough to allow reports that included some information on the topic at hand to be included, since the aim of this analysis was to be comprehensive and as wide as possible in documenting zoonotic outbreaks in Africa from the year 2007. After conducting abstract screening, the two authors chose which studies qualified for inclusion. To decide whether to accept or reject the study in the event of disagreements, the viewpoint of another author was sought. Afterwards, pertinent raw data were taken from the included studies and entered into Microsoft Excel spreadsheets.

Attack rates of the zoonotic diseases were calculated using the primary variables of interest, which comprised the number of zoonotic infection cases mentioned in the paper, initially among humans and perhaps among the animals under study. In order to calculate Case fatality rates, the reports also provided the available mortality statistics among infected human patients. The year and region of the study, the study context (whether or not an outbreak was underway), and the known animal reservoirs for the causative virus were additional variables of interest.

Data Synthesis and Analysis

Using the appropriate statistical methods, a meta-analysis was conducted to determine pooled prevalence rates and the associated 95% CIs. The heterogeneity of the included studies was assessed using statistical methods such as the I-squared statistic and the chi-squared test. If considerable heterogeneity was observed, a random-effects model was used for the meta-analysis; if not, a fixed-effects model was used.

To investigate potential sources of variability and evaluate the robustness of the findings, subgroup analysis and sensitivity analyses were carried out, where necessary. If there were enough studies available, publication bias was evaluated using graphical techniques like funnel plots and statistical tests like Egger's test.The results of the meta-analysis, including pooled prevalence rates and 95% CI, were described throughout the whole manuscript. The Epidemiological Surveillance and Burden of Zoonotic Diseases in Africa was also thoroughly reviewed using narrative summaries of the findings from several studies.

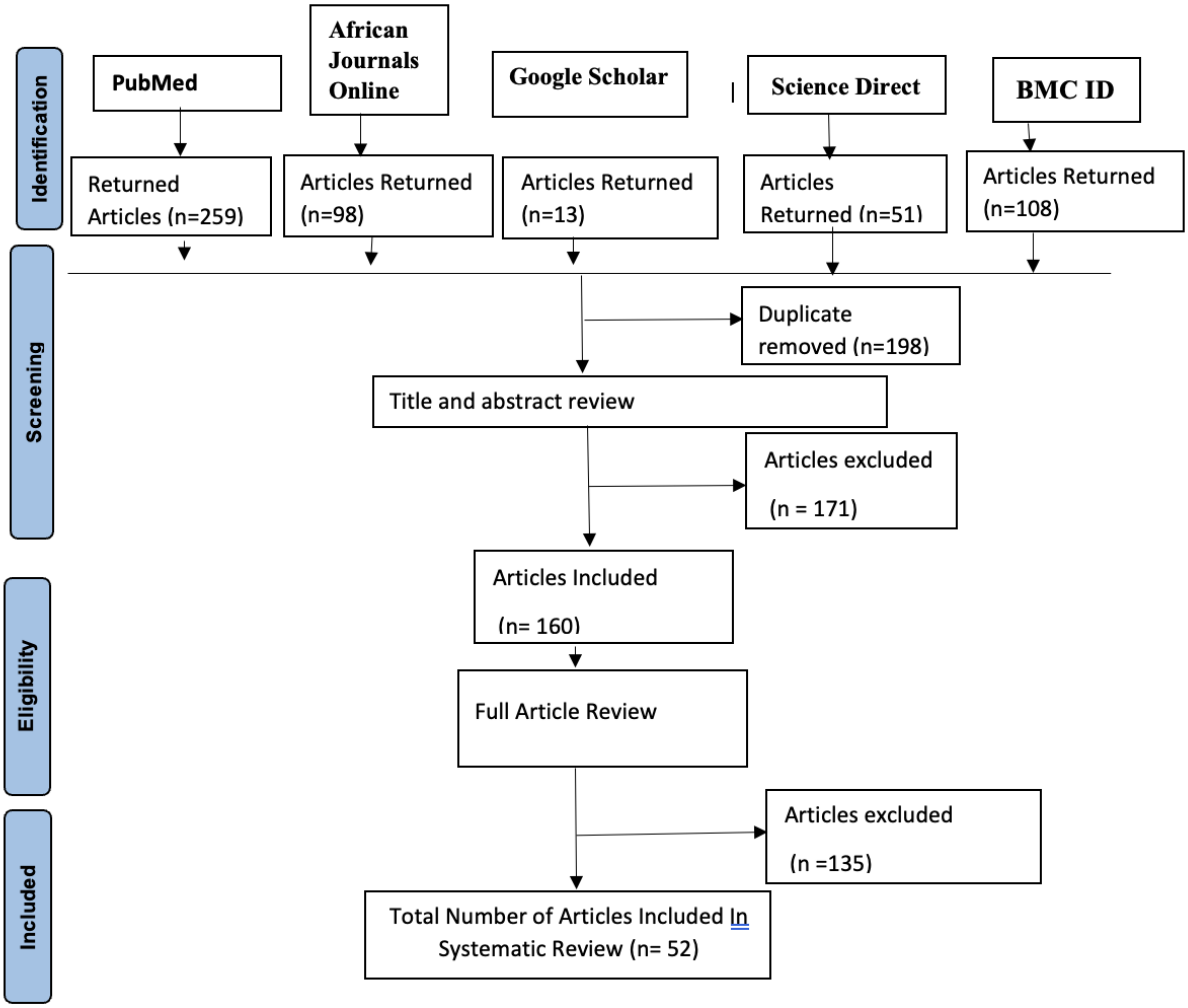

Figure 1: PRISMA Flow Diagram

RESULTS

The literature search (both databases and manual) resulted in 526 abstracts. Upon screening, 52 studies were included for analysis.

Table 2: Summary characteristics of some zoonotic diseases by author, number of human and Animals infections reported, human deaths, and risk factors.

s/n	Authors	Zoonotic disease/ Pathogen (Countries)	Studies conducted in Outbreak Settings	Total Number of Human Infections reported	Total Number of Human Deaths Reported	Total Number of Animal Infections	Animal Reservoirs identified	Identified Risk Factors
1	Chota et al. 2016	Brucellosis (Tanzania, Kenya)	Yes	1140	0	2232	cattle and Goats	Consumption of contaminated animal products
2	Faye et al. 2016	Leishmaniasis (Senegal)	No	315	73	57	Dogs	Bites and Scratches
3	van der Westhuizen et al. 2023	brucellosis and M. bovis (South Africa)	No	90	0	90	Cattle	Consumption of Contaminated Animal Products
4	Nessan & Robert et al. 2024	Anthrax, leishmania, Rabies, bovine brucellosis (Burkina Faso)	No	1840	0	0	Cattle, dogs rodents	Contact with infected animals or products, Bites and scratches
5	Edia-Asuke et al. 2015	Cysticercosis (Nigeria)	No	300	43	0	Pigs	Data not reported
6	Yinka-Ogunleye et al. 2018	Mpox (Nigeria)	Yes	42	1	0	Humans	Data not reported
7	Ramadan et al. 2022	RVF (South Sudan)	No	6	4	6	Humans	Data not reported
8	Naidoo et al. 2020	Leptospirosis (South Africa)	No	2	1	8	Rodents	Data not reported
9	Rolanda et al. 2021	Streptobacillus (South Africa)	No	0	0	54	Rats	bites or scratches, ingestion of contaminat

								ed food or water
10	Peninah et al. 2015	Anthrax, RVF, rabies, Q-fever, dengue fever, and brucellosis. (Kenya)	No	291	0	291	cattle, goats, Dogs,	bites, contaminated food
11	Bachirou et al. 2015	RVF (West Africa)	No	1132	40	191	cattle, goats, mosquitoes	
12	El Zowalaty et al. 2022	Influenza A (Cameroon, South Africa)	No	89	59	64	Poultry, Pigs	Not documented
13	Muadica et al. 2020	Enterocytozoon (Mozambique)	No	301	27	0	Cattle, Pigs, Goats	
14	Hikufe et al. 2019	Rabies (Ethiopia, Namibia)	No	3316013	2293	1907	Dogs, Cats	Bites, Scratches
15	Teklu et al. 2017	Rabies (Ethiopia)	No	2180	1363	0	Dogs	Bites, Scratches
16	Simpson et al. 2018	Leptospirosis (South Africa)	No	138	19	0	Not documented	Not documented
17	Faye et al.2007	RVF (Mauritania)	No	98	25	0	Not documented	Data not reported
18	Besombes et al. 2023	Mpox (Central Africa Republic)	yes	25	1	0	Humans	Data not reported
19	Julius et al. 2018	brucellosis (Cameroon)	No	15	0	35	Cattle	Data not reported
20	Tsegay et al. 2017	brucellosis (Ethiopia)	No	7	0	0	Data not reported	Data not reported
21	Djuicy et al. 2024	Mpox (Cameroon)	No	29	0	0	Humans	Data not reported
22	Prince-David et al. 2016	Streptococcus Suis (Togo)	No	1	0	0	Data not reported	Data not reported
23	Lukambagire et al. 2015	human fascioliasis (Tanzania)	No	305	0	0	Human	Data not reported
24	Kabuga & Zowalaty., 2019	Mpox (Nigeria)	Yes	115	7	0	Humans	Data not reported
25	Koundouno et al. 2022	Marburg (Guinea)	Yes	1	1	0	Humans	Data not reported
26	Genzebu et al.2018	Ethiopia	No	0	0	1	Cattle	Data not reported
27	Lukman et al. 2013	Lassa fever (Nigeria)	yes	0	0	877	Data not reported	Data not reported

28	Mhlanga et al. 2024	Bartonella (South Africa)	No	0	0	31	Data not reported	Data not reported
29	Jobbins et al. 2014	Leptospirosis (Botswana)	no	0	0	18	Banded mongoose (Mungos mungo), Selous' mongoose	Data not reported
30	Vlahakis et al. 2018	Anaplasmosis (Anaplasma platys) (Zambia)	No	0	0	27	Dogs	Data not reported
31	Chipwaza et al. 2015	Leptospirosis, brucellosis (Tanzania)	No	26	0	0	Humans	Data not reported
32	Hang'omb e et al. 2012	Anthrax (Zambia)	No	17	0	0	Humans hippopotamu ses	Data not reported
33	Forrester et al. 2017	Plague (Yersinia pestis) (Uganda)	yes	78	0	0	Data not reported	Data not reported
34	Njeru et al.2016	Brucellosis (Kenya)	No	146	0	0	Humans	Data not reported
35	Njeru et al.2016	Q fever (Kenya)	No	204	0	0	Humans	Data not reported
36	Elhelw et al. 2014	Lyme borreliosis/Borr elia burgdorferi (Egypt)	No	15	0	24	Cattle, dogs, humans	Data not reported
37	Lagadec et al. 2012	Leptospira spp (Madagascar)	No	0	0	25	Bats	Data not reported
38	Komba et al.2015	Campylobacter (Tanzania)	No	136	0	0	Humans	Data not reported
39	Sa'idu et al. 2015	Bovine tuberculosis (Nigeria)	No	0	0	120	Cattle	Data not reported
40	Okeke et al. 2014	Bovine tuberculosis (Nigeria)	No	0	0	36	Cattle	Data not reported
41	Erume et al. 2016	Brucellosis (Uganda)	No	0	0	3	Pigs	Data not reported
42	Bouley et al. 2012	Brucellosis (Tanzania)	No	16	0	0	Humans	Data not reported
43	Kanouté et al. 2017	Brucellosis, Q Fever (Côte d'Ivoire)	No	5	0	29	Livestock and humans	Data not reported
44	Samir et al. 2015	Leptospirosis (Egypt)	No	0	0	241	Rats, dogs, cows, buffaloes, sheep, horses, donkeys and	Data not reported

							camels, humans and water sources	
45	Tebug et al. 2014	Brucellosis and bovine tuberculosis (bTB) (Malawi)	No	0	0	23	Cattle	Data not reported
46	Dietrich et al. 2014	Leptospira (Madagascar)	No	0	0	44	Rodents and livestock	Data not reported
47	Njeru et al. 2017	Tularaemia (Kenya)	No	98	0	0	Humans	Data not reported
48	Eguale et al. 2016	Salmonellosis (Ethiopia)	No	0	0	30	Dairy cattle	Data not reported
49	Jemberu et al. 2013	Rabies (Ethiopia)	No	83	0	0	Humans	Data not reported
50	Yibrah & Damtie. 2015	Rabies (Ethiopia)	No	40	0	0	Humans	Data not reported
51	Yizengaw et al. 2018	Rabies (Ethiopia)	No	206	0	0	Humans	Data not reported
52	Beyene Mourits & Hogeveen. 2017	Rabies (Ethiopia)	No	83	0	0	Humans	Data not reported
Total				3325628	3957	6464		

Prevalence of Zoonotic diseases in Africa

The meta-analysis combined data from several studies across African countries, with results summarised in Figure 2. Substantial variability in effect sizes was observed across countries. Cameroon showed a high effect size of 0.86 (95% CI: 0.58–1.76; $p < 0.001$), while Ethiopia reported a lower but significant value of 0.12 (95% CI: 0.01–0.24). In contrast, the Central Africa cluster had an insignificant effect size of 0.01 (95% CI: –0.00 to 0.02; $p = 0.156$), reflecting the diverse epidemiological profiles of zoonotic diseases across the continent.

At the author level, significant variability was also evident. For instance, Beyene, Mourits and Hogeveen (2017) reported an effect size of 0.30 (95% CI: 0.24–0.35), whereas Chota et al. (2016) found –0.83 (95% CI: –1.01 to –0.64). Group difference tests confirmed statistically significant variation, with $Q = 6330.41$ ($p < 0.001$) among clusters and $Q = 9168.82$ ($p < 0.001$) among authors.

Heterogeneity measures further supported this variation ($\tau^2 = 0.05$, $I^2 = 99.06\%$, $H^2 = 2243.73$), indicating very high inconsistency across studies and validating the application of a random-effects model.

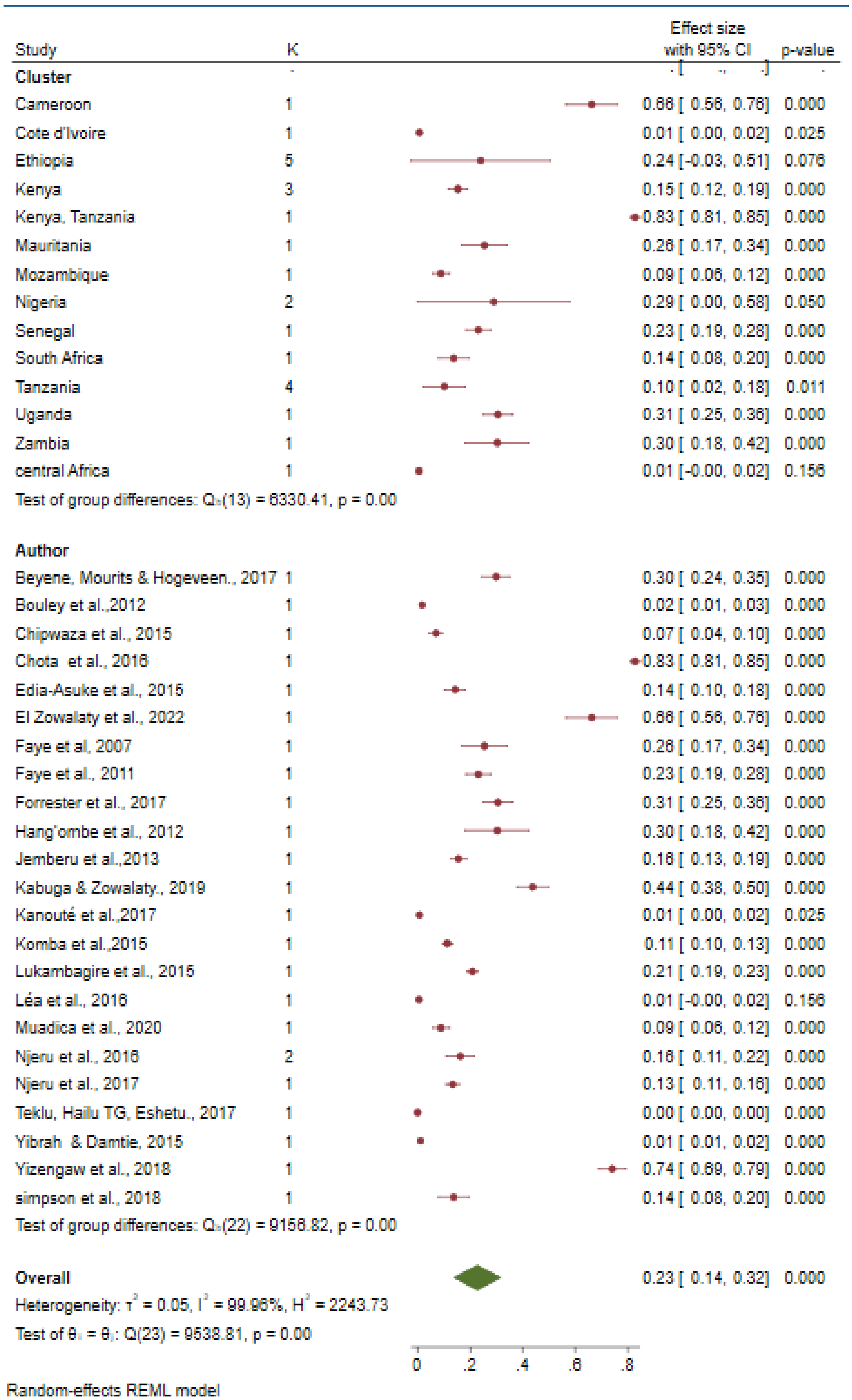

Figure 2: Metal analysis of zoonotic diseases prevalence in Africa.

Meta-Analysis Regression

A random effects meta regression was performed using the attack rate (AR) as a covariate to assess its influence on effect size across 24 studies. The REML estimation method showed AR as a significant predictor (coefficient = 1.00; 95% CI: 0.9799 to 1.0201; $p < 0.001$), indicating a strong positive association. The Wald chi square test was highly significant ($\chi^2(1) = 9538.61$, $p < 0.001$), confirming AR's contribution to effect size variance.

The model explained all between study variance ($R^2 = 100.00\%$), suggesting that AR fully accounted for heterogeneity. Residual variance was negligible ($tau^2 = 2.9e\text{-}10$, $I^2 = 0.00\%$, $H^2 = 1.00$), and the residual heterogeneity test ($Q_{res}(22) = 0.00$; $p = 1.000$) showed no remaining unexplained variation.

Although AR emerged as a strong epidemiological predictor, its apparent explanatory power may be overstated. The single covariate design cannot account for confounding factors such as diagnostic methods, case definitions, reporting quality, ecological factors, and health system capacity. The model's complete explanatory outcome may reflect overfitting or covariance with unmeasured determinants rather than true causation.

Further research should explore sources of heterogeneity related to study design, diagnostic tools, sampling frames, and population characteristics such as pastoralist versus peri urban communities. Regional ecological conditions including livestock movement, seasonality, and biodiversity also shape transmission dynamics. Without accounting for these, AR may be attributed excessive explanatory weight

```
. meta regress AR

  Effect-size label: Effect size
        Effect size: AR
          Std. err.: _meta_se

Random-effects meta-regression                     Number of obs  =        24
Method: REML                                       Residual heterogeneity:
                                                               tau2 = 2.9e-10
                                                             I2 (%) =    0.00
                                                                 H2 =    1.00
                                                      R-squared (%) =  100.00
                                                   Wald chi2(1)   =   9538.61
                                                   Prob > chi2    =    0.0000

------------------------------------------------------------------------------
    _meta_es | Coefficient  Std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
          AR |          1    .010239    97.67   0.000     .9799319    1.020068
       _cons |  -1.08e-19   .0000232    -0.00   1.000    -.0000455    .0000455
------------------------------------------------------------------------------
Test of residual homogeneity: Q_res = chi2(22) = -0.00   Prob > Q_res = 1.0000
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Figure 3: Meta-analysis regression of zoonotic disease prevalence in Africa

Subgroup of the zoonotic diseases prevalence in Africa

The pooled human case fatality rates (CFRs) for zoonotic diseases across multiple African countries are summarized in Figure 4. This meta-analysis combined data from 15 studies, grouped by author and region, to estimate the mortality burden of zoonotic infections. The overall pooled CFR was 26% (95% CI: 12% to 40%), indicating that approximately one in four infected individuals die from these diseases in Africa. A random effects model accounted for between-study variability, revealing substantial heterogeneity (I^2 = 99.82%), which reflects considerable differences in mortality outcomes across settings.

At the individual study level, CFRs varied widely. The highest rate was 72% (Ierory et al., 2007), whereas Hikufe et al. (2019) and Kabuga and Zowalaty (2019) reported 0%. Other elevated rates included 66% (El Zowalaty et al., 2022), 63% (Teklu et al., 2017), and 67% (Ramadan et al., 2022). Lower CFRs were observed in studies such as Bachirou et al. (2015) and Besombes et al. (2023), both at 4%. Geographically, the Democratic Republic of the Congo recorded the highest CFR (72%), followed by South Sudan (67%) and the Cameroon–South Africa cluster (66%). Ethiopia reported 63%, while Ethiopia–Namibia, Mauritania, and Mozambique recorded 0%. These differences between regional clusters were statistically significant (Q = 4676.26, $p < 0.001$).

Interpreting the pooled CFR requires consideration of confounding factors including diagnostic capacity, case definitions, completeness of reporting, and access to healthcare. Outbreak-specific studies may report higher CFRs due to overwhelmed health systems, while underreporting of mild or asymptomatic cases can inflate fatality estimates. The observed high heterogeneity ($I^2 = 99.82\%$) indicates that the pooled estimate should be seen as a general trend rather than a precise measure of mortality risk.

Variation across studies likely reflects differences in study design, diagnostic methods, population demographics, and healthcare infrastructure. Disparities between urban and rural areas, conflict conditions, and differences in epidemic response also contribute to inconsistent outcomes. Without accounting for these contextual factors, variation in CFRs could be mistakenly attributed solely to pathogen characteristics or regional effects.

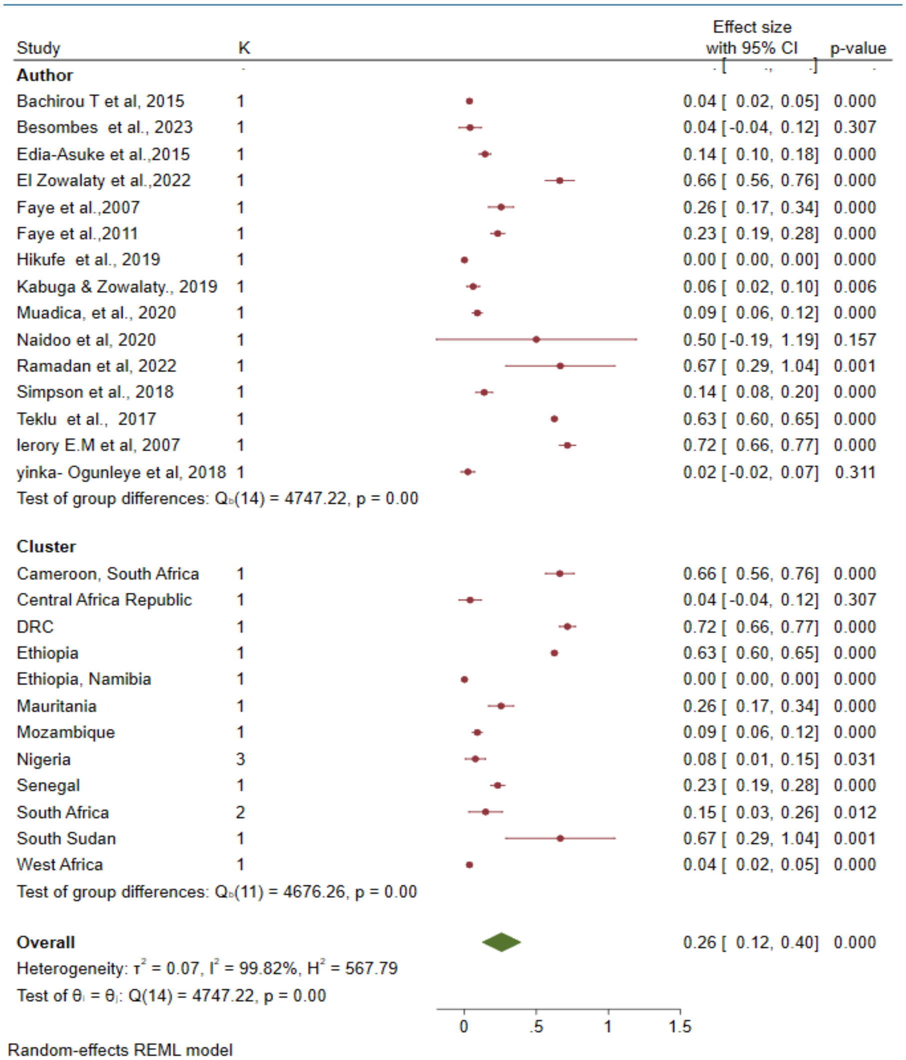

Figure 4: Subgroup metal analysis of zoonotic diseases prevalence in Africa by human case fertility rate

Publication Bias

The funnel plot illustrates the distribution of studies in a meta-analysis on human-infecting zoonotic diseases across Africa, used to assess potential publication bias and variation in effect sizes. The x-axis shows effect size (prevalence of infections) and the y-axis shows standard error, with larger studies appearing at the top. Ideally, the plot should form a symmetrical inverted funnel around the pooled estimate.

The observed plot shows asymmetry, with more studies on the right reporting higher effect sizes and fewer on the left with lower or near-zero estimates, suggesting possible publication bias. Studies outside the pseudo 95% confidence limits indicate heterogeneity, likely due to differences in study populations, methods, settings, or surveillance quality across the continent.

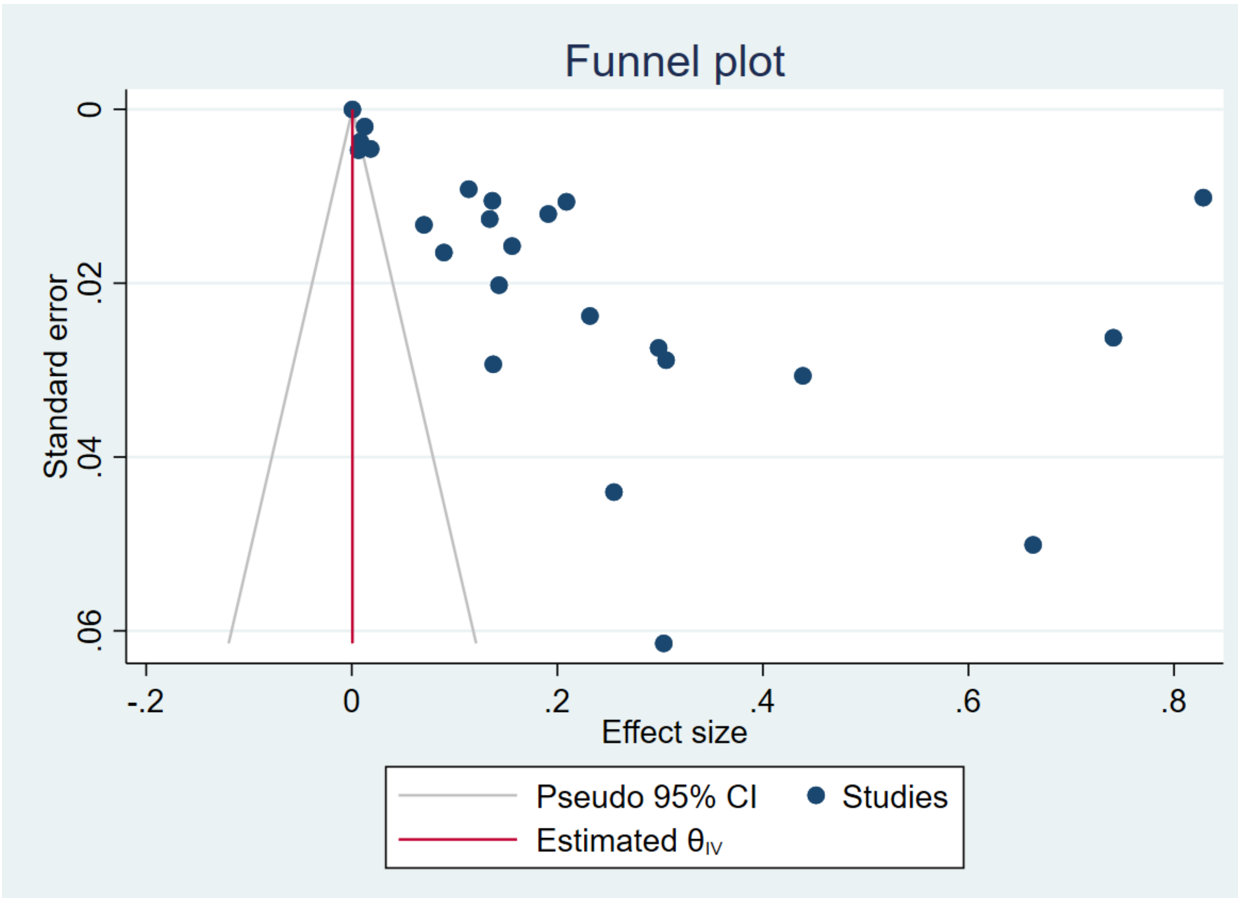

Figure 5: Funnel plot of zoonotic disease prevalence in Africa

Sensitivity Analysis

A leave-one-out sensitivity analysis was conducted to assess the robustness of the pooled prevalence estimates. Each study was sequentially omitted, and the effect size recalculated using a random effects REML model.

The results showed minimal variation, with prevalence estimates ranging from 0.20 (95% CI 0.12–0.28) to 0.24 (95% CI 0.14–0.33) and p-values remaining <0.001. No single study significantly influenced the summary estimate, as indicated by overlapping confidence intervals.

These findings confirm that the pooled prevalence is stable and robust, supporting the reliability of the meta-analytic conclusions on zoonotic diseases in Africa

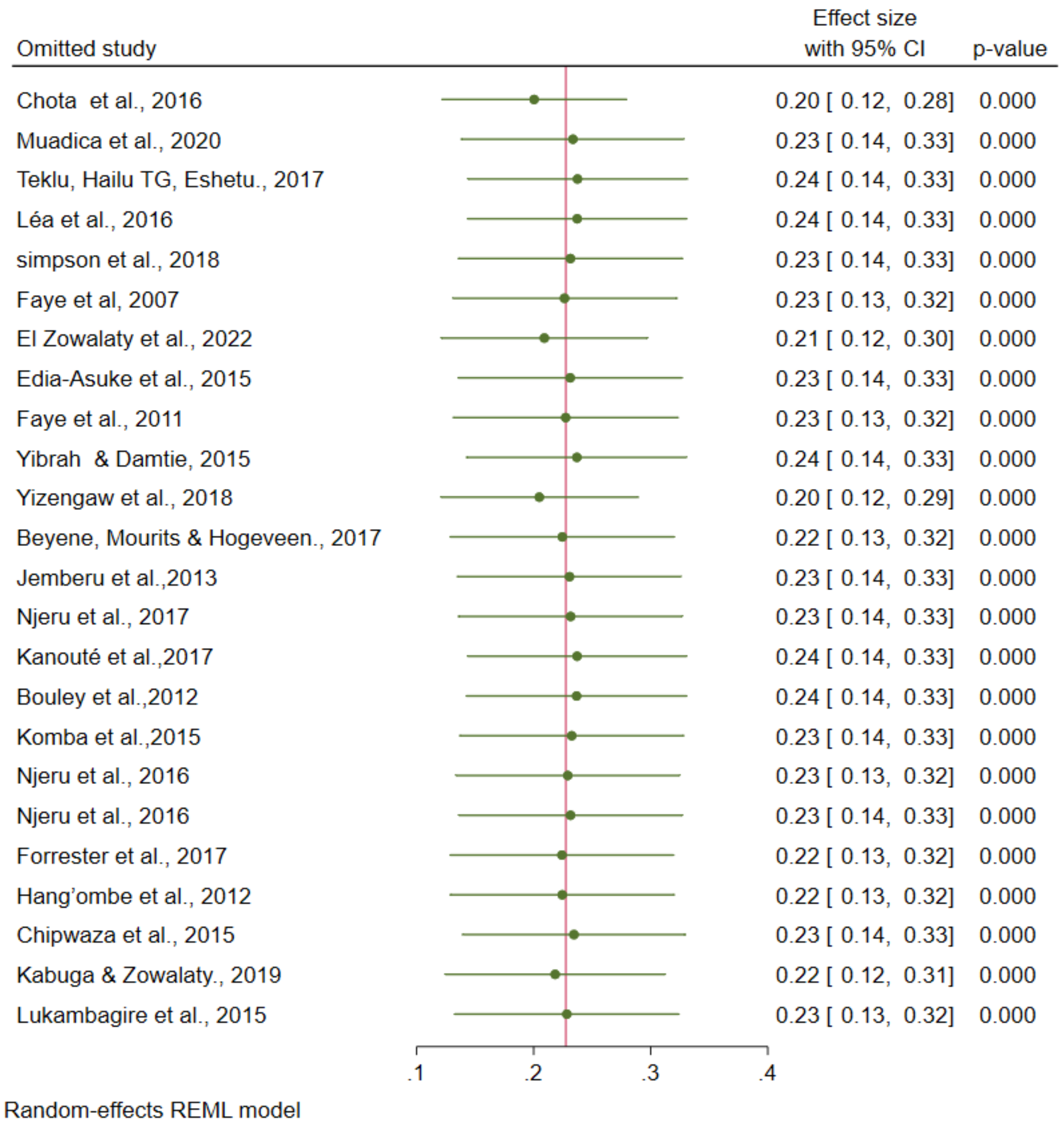

Figure 6: Leave-one-out- sensitivity analysis

DISCUSSION

The meta-analysis demonstrated substantial variability in zoonotic disease prevalence, ranging from 0.86 (95% CI: 0.58–1.76) in Cameroon to 0.01 (95% CI: –0.00 to 0.02) in Central Africa, with high heterogeneity ($I^2 = 99.06\%$). Meta-regression showed that attack rate was a significant predictor of effect size (coefficient = 1.00; $p < 0.001$), fully accounting for between-study variance ($R^2 = 100\%$). The pooled CFR was estimated at 26% (95% CI: 12–40%), with regional CFRs varying from 72% in DRC to 0% in Mozambique, Mauritania, and Ethiopia-Namibia. These findings are consistent with Evidence of publication bias was identified, though sensitivity analysis confirmed the robustness of the findings. Zoonotic diseases remain a significant health burden in Africa, influenced by disparities in surveillance systems, healthcare access, and socioeconomic factors. Strengthened One Health approaches, enhanced surveillance capacity, innovative technology, and community engagement are critical for effective disease control and mitigation.

6.1 Prevalence of Zoonotic Diseases in Africa

The meta-analysis revealed significant variation in zoonotic disease impact across African countries. Cameroon showed the highest effect (0.86), Ethiopia a smaller yet significant effect (0.12), and Central Africa a negligible effect (0.01). Heterogeneity was extreme ($\tau^2 = 0.05$, $I^2 = 99.06\%$, $H^2 = 2243.73$), confirming the appropriateness of a random-effects model. The pooled prevalence was 23% (95% CI: 14–32%), suggesting that about one in four individuals may be exposed or infected. This aligns with findings by Djibril et al. (2025), Grace et al. (2017), and Qiu et al. (2023), who reported similar burdens linked to close human–animal interaction, occupational exposure, and weak health systems.

Regional disparities were evident in the study. Cameroon's high prevalence corresponds with frequent Rift Valley fever, brucellosis, and anthrax outbreaks in pastoral areas (Peninah et al., 2015; Bachirou et al., 2015). In contrast, Ethiopia's lower rate reflects better veterinary and vaccination coverage (Beyene et al., 2017), while Central Africa's minimal prevalence likely stems from poor surveillance and underreporting (Choffnes et al., 2010; Tambo et al., 2016).

Differences among authors, such as positive effects in Beyene et al. (2017) and negative in Chota et al. (2016), highlight methodological and contextual diversity (Anyangu et al., 2010). Overall, the high heterogeneity underscores the influence of ecological, cultural, and livestock factors (Hasler et al., 2014; Daszak et al., 2020) and emphasizes the need for integrated One Health approaches that strengthen surveillance, coordination, and response across human, animal, and environmental sectors (Rabinowitz et al., 2013; FAO, 2020).

Meta-Analysis Regression of Prevalence of Zoonotic Diseases in Africa

The meta-regression showed a strong, statistically significant relationship between attack rate (AR) and zoonotic disease prevalence across the 24 studies. The coefficient of 1.00 (95% CI: 0.9799–1.0201; $p < 0.001$) indicated a near-perfect linear relationship, with prevalence rising proportionally with AR. The high Wald chi-square confirmed the robustness of this association.

AR explained all between-study variance ($R^2 = 100\%$), suggesting it is the dominant determinant of zoonotic disease prevalence in Africa. These results align with previous findings: Grace et al. (2017) noted higher ARs in communities with intense human–animal interactions, while Kock et al. (2015) linked elevated ARs to areas with close contact among humans, livestock, and wildlife. Beyene et al. (2017) observed seasonal livestock movements influenced brucellosis AR in Ethiopia, and Tambo et al. (2016) associated AR differences with ecological and socioeconomic vulnerabilities. Globally, Daszak et al. (2020) and Jones et al. (2008) recognized AR as a key predictor of emerging infectious diseases, often intensified by deforestation, biodiversity loss, and land-use changes.

The near-total explanation of heterogeneity supports the One Health perspective (Rabinowitz et al., 2013; Mackenzie & Jeggo, 2019), highlighting the importance of integrating AR into human–animal–environment assessments. Standardized measurement and reporting of AR is crucial for improving zoonotic surveillance and risk assessment (FAO, 2020; Okello et al., 2011).

In conclusion, AR is a strong predictor of zoonotic disease prevalence in Africa, reflecting high-risk ecological and social systems where transmission is most likely

Subgroup Metal Analysis of Zoonotic diseases prevalence in Africa by Human Case fertility Rate

The subgroup meta-analysis revealed considerable variability in zoonotic disease case fatality rates (CFRs) across Africa, reflecting the continent's diverse epidemiological and health system contexts. The pooled CFR was 26% (95% CI: 12%–40%), meaning roughly one in four infected individuals die from zoonotic diseases. This finding aligns with Oyono et al. (2022), who reported a 31.1% CFR for yellow fever virus, and Qiu et al. (2023), who linked high fatality risks to environmental factors, animal trade, and weak biosecurity systems.

CFRs varied markedly between studies, from 72% (Ierory et al., 2007) to 0% (Hikufe et al., 2019; Kabuga & Zowalaty, 2019), consistent with Tambo et al. (2016) and Grace et al. (2017), who found that mortality outcomes depend on pathogen virulence, outbreak preparedness, and healthcare access. Regionally, the highest CFRs occurred in the Democratic Republic of Congo (72%), South Sudan (67%), and the Cameroon–South Africa cluster (66%), areas prone to Ebola, anthrax, and Rift Valley fever outbreaks (Tamfum et al., 2012; El Zowalaty et al., 2022). Conversely, Ethiopia–Namibia, Mauritania, and Mozambique recorded 0%, likely due to stronger veterinary systems or underreporting (Bachirou et al., 2015; Besombes et al., 2023).

The high heterogeneity underscores the influence of healthcare deficiencies, delayed detection, and political instability (Häsler et al., 2014). Strengthened One Health approaches integrating veterinary, environmental, and public health systems remain vital to reduce fatality risks, especially in high-burden regions such as DRC, South Sudan, and Cameroon (Rabinowitz et al., 2013; FAO, 2020)

Publication Bias

The funnel plot analysis offered insights into the reliability of pooled zoonotic disease prevalence estimates across Africa. Ideally, an unbiased distribution forms a symmetrical inverted funnel around the pooled effect (Sterne et al., 2011). However, the observed asymmetry, with more studies on the right (higher prevalence) and fewer on the left (lower prevalence), suggests potential publication bias. This indicates that studies reporting higher zoonotic burdens are more likely to be published, while low or null findings may remain unpublished a reflection of the "file drawer problem" (Dwan et al., 2008; Song et al., 2010).

Such bias is likely intensified in Africa by limited research funding, weak surveillance, and restricted publication access (Choffnes et al., 2010; Tambo et al., 2016). Comparable asymmetry has been observed in meta-analyses of hepatitis B (Bigna & Noubiap, 2019) and malaria (Adesina et al., 2020). The presence of studies outside the pseudo 95% confidence limits and very high heterogeneity ($I^2 > 99\%$) reflect diverse diagnostics, populations, and surveillance capacities (Grace et al., 2017; Okello et al., 2011).

Trim-and-fill analysis suggested up to 29 missing studies on the plot's left side, implying underrepresentation of low-prevalence data. From 521 screened studies, 52 met inclusion criteria, indicating selective reporting may have inflated pooled estimates. These findings emphasize the need for balanced reporting and open publication of both high and low prevalence studies to improve accuracy and support stronger One Health policies across Africa

Sensitivity Analysis

The leave-one-out sensitivity analysis provided strong evidence for the stability and robustness of the pooled prevalence estimate of zoonotic diseases in Africa. Sequential omission of each study, followed by recalculation under a random-effects REML model, yielded consistent pooled prevalence estimates ranging narrowly from 20% (95% CI: 12%–28%) to 24% (95% CI: 14%–33%), with all p-values remaining highly significant ($p < 0.001$). This minimal variation indicates that no single study disproportionately influenced the overall outcome, confirming that the pooled estimate is not driven by outlier results.

These findings align with Borenstein et al. (2009), who highlight sensitivity analysis as essential for assessing meta-analytic reliability. The absence of highly influential studies strengthens confidence in the conclusion that zoonotic diseases constitute a significant public health burden across Africa. Similar stability has been reported in other infectious disease meta-analyses, such as Noubiap et al. (2019) on diabetes mellitus and Adesina et al. (2020) on malaria, both of which demonstrated consistent estimates across sensitivity iterations implying true epidemiological variation rather than methodological artefacts.

The robustness observed also validates the application of the random-effects model, which accommodates genuine variability among studies due to ecological, demographic, and methodological differences (DerSimonian & Laird, 1986; Higgins et al., 2003). Given the high heterogeneity observed ($I^2 > 99\%$), this approach was particularly appropriate. Although broader structural limitations such as publication bias and surveillance variability persist, the leave-one-out analysis confirms that these factors do not materially alter the main conclusion.

This analysis reinforces that the pooled prevalence estimate reliably reflects the available data and provides a sound foundation for prioritizing resource allocation, surveillance strengthening, and One Health policy responses to zoonotic diseases across Africa.

Broader Global Context

Zoonotic diseases are an increasing global health concern, as high-profile outbreaks such as COVID-19, Ebola, MERS, and avian and swine influenza show how pathogens at the human–animal interface can spread rapidly, disrupting health systems and economies (Daszak et al., 2020; Jones et al., 2008). These events highlight shared drivers of emergence including environmental disruption, wildlife trade, urbanization, and globalization.

Africa faces unique challenges due to its rich biodiversity, expanding human–wildlife interactions, endemic poverty, weak health infrastructure, limited laboratories, inadequate veterinary services, and fragmented surveillance (Kock et al., 2015; Grace et al., 2017; Tambo et al., 2016). These factors increase vulnerability to both endemic diseases such as brucellosis, anthrax, rabies, and Rift Valley fever and novel pathogens.

The meta-analysis highlights the importance of integrated One Health approaches, which promote collaboration across human, animal, and environmental sectors to enhance surveillance, early warning, and coordinated response systems (Rabinowitz et al., 2013; Mackenzie & Jeggo, 2019; FAO, 2020). In line with this, international organizations stress the need to build capacity in low- and middle-income countries, where the risk of zoonotic spillover is greatest (FAO, 2020; WHO, 2022)

The COVID-19 pandemic accelerated efforts to enhance health system resilience. These findings highlight the variability in Africa's capacity to detect and respond to zoonotic threats, reinforcing the need for coordinated, well-resourced One Health systems to improve outbreak preparedness.

Implications for Epidemiological Surveillance

Strengthening epidemiological surveillance remains central to managing zoonotic diseases. Integrated systems that link human, animal, and environmental health data are vital for early detection and timely response. Given the uneven capacity across African countries, resource mobilization and sustained capacity building are critical priorities.

Emerging technologies such as mobile health (mHealth) tools, geographic information systems (GIS), and other digital platforms offer innovative opportunities to enhance data collection, analysis, and reporting in resource-limited settings. Moreover, community-based surveillance initiatives that empower local populations to identify and report unusual health events can complement formal surveillance structures, improving coverage and responsiveness across diverse settings

6.9 Public Health Implications

For many African nations, implementing One Health strategies remains a public health priority. Namibia launched its Tripartite One Health National Strategy (2024–2028) in collaboration with the FAO and WHO, while Zambia's One Health Strategic Plan (2023) focuses on zoonotic disease prioritization, joint outbreak response, and a multisectoral technical working group (Africa CDC, 2024; One Health Observatory, 2023). These efforts illustrate the integration of environmental, animal, and human health systems.

Strengthening surveillance is critical. Rapid diagnostics, data sharing, and community-based or wildlife monitoring improve early detection, yet gaps remain, as shown in West Africa (Springer, 2025). Innovative approaches, such as Ethiopia's community-based system in Adadle, demonstrate that remote outbreak detection is feasible (CABI, 2023).

Short-term actions should include forming multisectoral working groups, developing national strategies, and enhancing laboratory capacity. Investments in molecular diagnostics, genomic sequencing, workforce training, and risk communication can yield immediate benefits, as highlighted by leptospirosis surveillance gaps in Sub-Saharan Africa (2014–2022). Medium-term priorities involve expanding integrated data platforms and strengthening human resources, while long-term goals focus on continental coordination and standardizing cross-border surveillance. The African Union and partners advocate harmonized One Health strategies to improve preparedness, close data gaps, and reduce the risk of uncontrolled zoonotic disease transmission (One Health Outlook, 2023).

Limitations of the Study

A key limitation of this study was the limited number of recently published research articles on certain zoonotic diseases in Africa, which constrained the depth of analysis on emerging trends. In addition, the demographic characteristics and methodological approaches of the included studies varied considerably, making it difficult to draw firm and consistent conclusions. The analysis was further affected by regional data gaps, with some areas of the continent being underrepresented in the available literature. This uneven distribution of evidence may have skewed the pooled estimates, as findings from regions with stronger surveillance systems and more active research outputs were more likely to dominate the results. Finally, since most of the included studies were cross-sectional in design, there was a substantial risk of bias, which may limit the robustness and generalizability of the overall findings.

CONCLUSION

This systematic review and meta-analysis provide strong evidence on the burden, prevalence, and fatality of zoonotic diseases across Africa. With a pooled prevalence of 23% and a case fatality rate of 26%, zoonotic infections remain major contributors to morbidity and mortality. The high heterogeneity observed reflects the interaction of ecological, socioeconomic, and health system factors influencing disease transmission. High-burden countries such as Cameroon, Kenya, Tanzania, and the Democratic Republic of the Congo face elevated risks due to close human–animal contact, occupational exposure, and limited diagnostic capacity. In contrast, lower prevalence in Mozambique and Central Africa may reflect both reduced transmission and underreporting linked to weak surveillance.

These findings emphasize Africa's continued vulnerability to endemic and emerging zoonoses, driven by poverty, biodiversity, and changing land use. Strengthened One Health approaches that enhance surveillance, diagnostics, and cross-border coordination are critical. Sustainable control will require political commitment, equitable policies, and investment in resilient, locally adaptive health systems.

Conflicts of Interest

The authors declare no conflicts of interest.

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