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Prevalence and antimicrobial resistance of *Salmonella spp.* in human, animal, and environmental reservoirs in Africa: A systematic review and meta-analysis

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Abstract

Background: *Salmonella* is a leading cause of foodborne and enteric infections worldwide, with increasing antimicrobial resistance (AMR) threatening human and animal health. In Africa, fragmented surveillance systems limit understanding of *Salmonella* epidemiology. This review synthesized evidence on the prevalence, serovar distribution, AMR, and One Health transmission dynamics of *Salmonella* spp. across Africa.

Methods: PubMed was searched following PRISMA 2020 guidelines. Of 109 records identified, 64 studies were included in the qualitative synthesis and 21 studies reporting prevalence in human stool samples were included in a random-effects meta-analysis. Study quality was assessed using Joanna Briggs Institute tools, and publication bias was evaluated using funnel plots and Egger's regression test.

Results: Most studies were of high quality (57/64). *Salmonella* spp. were reported in human, animal, food, and environmental reservoirs, supporting circulation at the human–animal–environment interface. The most frequently reported serovars were *S.* Typhimurium, *S.* Enteritidis, and *S.* Kentucky. Antimicrobial susceptibility data revealed widespread resistance to β-lactams, tetracyclines, sulfonamides, aminoglycosides, and fluoroquinolones. Common resistance determinants included *blaTEM, blaCTX-M, blaSHV, tet(A), tet(B), sul1, sul2, dfrA, aadA,* and *qnr*. Multidrug-resistant phenotypes were frequently associated with plasmids and class 1 integrons.

The pooled prevalence of human *Salmonella* infection was 6% (95% CI, 5–9%), with substantial heterogeneity (I^2=89.7%). No significant publication bias was detected.

Conclusions: Salmonellosis remains a major public health challenge in Africa. Shared serovars and resistance determinants across reservoirs highlight the need for integrated One Health surveillance, antimicrobial stewardship, and strengthened food safety systems.

Keywords: *Salmonella* spp.; salmonellosis; antimicrobial resistance; multidrug resistance; One Health; prevalence; Africa; systematic review; meta-analysis.

1. Introduction

Salmonella spp. are among the most important foodborne bacterial pathogens worldwide and are responsible for a substantial burden of gastrointestinal and invasive infections in humans. Among the numerous serovars of Salmonella enterica, Salmonella Typhimurium and Salmonella Enteritidis are frequently associated with disease outbreaks in both humans and animals (Ajmera & Shabbir, 2026; Oludairo et al., 2022). The burden of salmonellosis remains particularly high in low- and middle-income countries, where inadequate sanitation, limited access to clean water, and poor food safety practices facilitate pathogen transmission (Hugho et al., 2024).

The epidemiology of Salmonella is complex because transmission occurs through interconnected human, animal, and environmental reservoirs. Human infections are commonly acquired through contaminated food or water, direct contact with infected animals, or exposure to contaminated environments. Consequently, the One Health approach has become increasingly important for understanding the circulation of Salmonella across ecosystems. Recent studies have identified genetically related Salmonella strains in humans, livestock, and environmental samples, suggesting the existence of shared transmission pathways and common sources of infection (Akinyemi et al., 2023). In addition, contamination of water sources, fresh produce, and agricultural environments has been recognized as a significant route for the dissemination of Salmonella (Alio Sanda et al., 2017). Animal reservoirs play a critical role in maintaining and spreading Salmonella. Poultry, cattle, pigs, and other livestock species may carry the pathogen asymptomatically and contribute to environmental contamination through fecal shedding. Poor biosecurity measures and the use of animal manure in agriculture further increase opportunities for transmission between animals, the environment, and humans (Hailu et al., 2021). Studies conducted in African countries have reported the presence of Salmonella in food-producing animals, slaughterhouse environments, and wildlife, highlighting the widespread distribution of the pathogen across multiple reservoirs (Akoachere et al., 2009; Nelly et al., 2024). Moreover, the emergence and spread of antimicrobial-resistant Salmonella strains represent an additional challenge for public health. Although many cases of non-typhoidal salmonellosis are self-limiting, severe infections require antimicrobial treatment. However, increasing resistance to commonly used antibiotics, including beta-lactams, fluoroquinolones, and third-generation cephalosporins, threatens treatment effectiveness (Lamichhane et al., 2024; Stoycheva & Murdjeva, 2006). The misuse and overuse of antimicrobials in human medicine and animal production systems have been identified as major

drivers of resistance development, while mobile genetic elements facilitate the dissemination of resistance determinants among bacterial populations (Jibril et al., 2021; Petrin et al., 2023).

Despite growing evidence on the occurrence of Salmonella and its antimicrobial resistance patterns, available studies are often limited to specific reservoirs or geographical settings. Consequently, there remains a lack of integrated evidence describing the prevalence and antimicrobial resistance of Salmonella across human, animal, and environmental reservoirs in Africa. A comprehensive synthesis of available data is needed to better understand transmission dynamics, identify major resistance trends, and support the development of effective One Health surveillance and control strategies. Therefore, this systematic review aimed to synthesize evidence on the prevalence and antimicrobial resistance of *Salmonella spp.* in fecal and fecally contaminated samples collected from human, animal, and environmental reservoirs across Africa.

2. Methods

2.1 Study Design

This systematic review was conducted to synthesize evidence on the prevalence and antimicrobial resistance of *Salmonella* spp. isolated from fecal and fecally contaminated samples obtained from human, animal, and environmental reservoirs in Africa. The review was performed following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines.

2.2 Search Strategy

A comprehensive literature search was conducted in PubMed to identify relevant studies published between January 2015 and March 2026. The search strategy was developed based on the Population–Exposure–Outcome (PEO) framework and combined terms related to Salmonella spp., prevalence, antimicrobial resistance, fecal samples, and African countries. Keywords included "Salmonella", "Salmonella enterica", "prevalence", "occurrence", "epidemiology", "antimicrobial resistance", "antibiotic resistance", "feces", "stool", "manure", "humans", "animals", "livestock", "poultry", "environment", and "Africa". Search terms and Boolean operators were adapted according to the requirements of PubMed database. The complete search strategy and database-specific search strings are provided in Supplementary Table S1.

2.3 Eligibility Criteria

Studies were considered eligible if they: (i) were conducted in Africa; (ii) involved human, animal, or environmental samples contaminated with fecal material; (iii) reported data on the prevalence and/or antimicrobial resistance of *Salmonella* spp.; (iv) were observational studies, including cross-sectional, cohort, or surveillance studies; and (v) were published in English or French.

Studies were excluded if they did not involve fecal or fecally contaminated samples, lacked prevalence or antimicrobial resistance data, were review articles, editorials, opinion papers, experimental laboratory studies without epidemiological data, case reports, duplicate publications, or articles for which the full text was unavailable.

2.4 Study Selection

All records identified through the database searches were imported into Rayyan for reference management, duplicate removal, and screening (Ouzzani et al., 2016). Two independent reviewers screened titles and abstracts against the predefined eligibility criteria. Full texts of potentially relevant articles were subsequently assessed independently by the same reviewers to determine eligibility for inclusion. Any disagreements arising during the screening or study selection process were resolved through discussion. Where consensus could not be reached, a third reviewer was consulted to make the final decision. The study selection process was documented using a PRISMA flow diagram (Supplementary Figure S1).

2.5 Data Extraction

Data were extracted independently by two reviewers using a standardized data extraction form developed prior to the review. Extracted information included author and year of publication, country of study, study design, sample source, sample type, sample size, number of Salmonella isolates, identified species or serovars, prevalence estimates, antibiotics tested, antimicrobial resistance profiles, resistance rates, and laboratory methods used for pathogen detection and characterization. Any discrepancies in data extraction were resolved through discussion between the reviewers, and unresolved disagreements were adjudicated by a third reviewer.

2.6 Quality Assessment

The methodological quality and risk of bias of included studies were assessed independently by two reviewers using the Joanna Briggs Institute (JBI) Critical Appraisal Checklist for Analytical Cross-Sectional Studies. The checklist evaluates key methodological domains, including the definition of inclusion criteria, description of study participants and settings, validity and reliability of exposure and outcome measurements, identification and management of confounding factors, and appropriateness of statistical analyses. Any discrepancies in quality assessment were resolved through discussion between the reviewers. When consensus could not be reached, a third reviewer was consulted to adjudicate the final assessment. Although the JBI does not recommend calculating an overall quality score, studies were classified for descriptive purposes according to the proportion of criteria fulfilled: high quality (≥80% of criteria met), moderate quality (60–79%), and low quality (<60%).

2.7 Data Synthesis and Statistical Analysis

A narrative synthesis was conducted to summarize the characteristics of included studies, study settings, sample sources, *Salmonella* serovars, and antimicrobial resistance profiles across human, animal, and environmental reservoirs. Findings were summarized using descriptive tables and figures.

In addition, a meta-analysis was performed to estimate the pooled prevalence of *Salmonella* spp. in human fecal samples across eligible studies. Prevalence estimates and corresponding sample sizes were extracted from each study and combined using a random-effects model to account for expected methodological and geographical heterogeneity among studies. Pooled prevalence estimates were reported with 95% confidence intervals (95% CI). Statistical heterogeneity among

studies was assessed using Cochran's Q test and quantified using the I^2 statistic. Values of I^2 were interpreted as indicating low (<25%), moderate (25–75%), or substantial (>75%) heterogeneity. Forest plots were generated to visualize individual study prevalence estimates and pooled effect sizes. Where appropriate, subgroup analyses were conducted to explore potential sources of heterogeneity according to study characteristics, including geographic region, study population, and sample source. Publication bias was assessed using funnel plot inspection and Egger's regression test when sufficient studies were available.

2.7 Outcome Measures

The primary outcome was the prevalence of *Salmonella* spp. in fecal and fecally contaminated samples collected from human, animal, and environmental reservoirs. For the quantitative synthesis, the primary outcome was the pooled prevalence of *Salmonella* spp. in human fecal samples. Secondary outcomes included antimicrobial resistance rates to major antibiotic classes, prevalence of multidrug-resistant (MDR) *Salmonella* isolates, distribution of resistance-associated serovars, and reported risk factors associated with the occurrence and spread of antimicrobial-resistant *Salmonella*.

3. Results

3.1 Study Selection

The literature search identified 109 records from PubMed using the predefined search strategy (Supplementary Table S1). No duplicate records were identified, and no studies were removed through automation tools or other exclusion procedures. Consequently, all 109 records were retained for title and abstract screening. Following the screening process, 25 records were excluded because they did not meet the eligibility criteria. The full texts of 84 potentially relevant articles were sought for retrieval; however, 13 reports could not be obtained. As a result, 71 full-text articles were assessed for eligibility. Of these, seven studies were excluded, including four studies with an ineligible population, one study reporting an ineligible outcome, one study with an inappropriate study design, and one study that did not correspond to the study types specified in the eligibility criteria. Ultimately, 64 studies met all inclusion criteria and were included in the qualitative synthesis. Among these, 21 studies reporting prevalence data from human samples provided sufficient information for inclusion in the quantitative synthesis and meta-analysis (Supplementary Figure S1). Quality assessment using the JBI Critical Appraisal Checklist showed that 57 of the 64 included studies were of high quality and 7 were of moderate quality, with no studies classified as low quality (Supplementary Table S2). Overall, the included studies presented a low risk of bias, although some methodological limitations related to sample size justification, response rates, and participant recruitment were identified.

3.2 Geographic Distribution of Included Studies

The 64 studies included in this review were conducted across 14 African countries, with a marked geographical concentration in Eastern Africa (Figure 1; Supplementary Table S2). Ethiopia

contributed the largest number of studies (n = 18), accounting for more than one-quarter of all included publications, followed by South Africa (n = 10) and Kenya (n = 8). Additional studies were conducted in Uganda (n = 4), Ghana (n = 4), Tanzania (n = 3), Nigeria (n = 3), and Cameroon (n = 3). Fewer studies originated from Egypt (n = 2), Burkina Faso (n = 2), and Mozambique (n = 2), while Côte d'Ivoire, Libya, and Chad were each represented by a single study. Two investigations were multicountry studies involving several African countries, including Kenya, Mali, The Gambia, Ghana, and Tanzania (Supplementary Table S2).

When grouped by African subregions, East Africa was the most represented region, contributing 35 of the 64 included studies (54.7%). Southern Africa, represented exclusively by studies from South Africa, accounted for 10 studies (15.6%). West and Central Africa collectively contributed 14 studies (21.9%), whereas North Africa was represented by only three studies from Egypt and Libya (4.7%). The remaining two studies (3.1%) were conducted across multiple African countries. This uneven geographical distribution highlights the predominance of research efforts in Eastern Africa and the relative scarcity of data from North, Central, and parts of West Africa.

The observed distribution likely reflects differences in research capacity, surveillance infrastructure, and publication output across the continent. Countries such as Ethiopia, Kenya, and South Africa have established veterinary, public health, and food safety research programs that have generated substantial evidence on *Salmonella* occurrence and antimicrobial resistance. In contrast, large regions of Africa remain underrepresented, limiting the ability to fully characterize the continental epidemiology of *Salmonella* and its resistance patterns. Consequently, the findings of this review should be interpreted in the context of this geographical imbalance, which may influence estimates of prevalence and antimicrobial resistance at the continental scale.

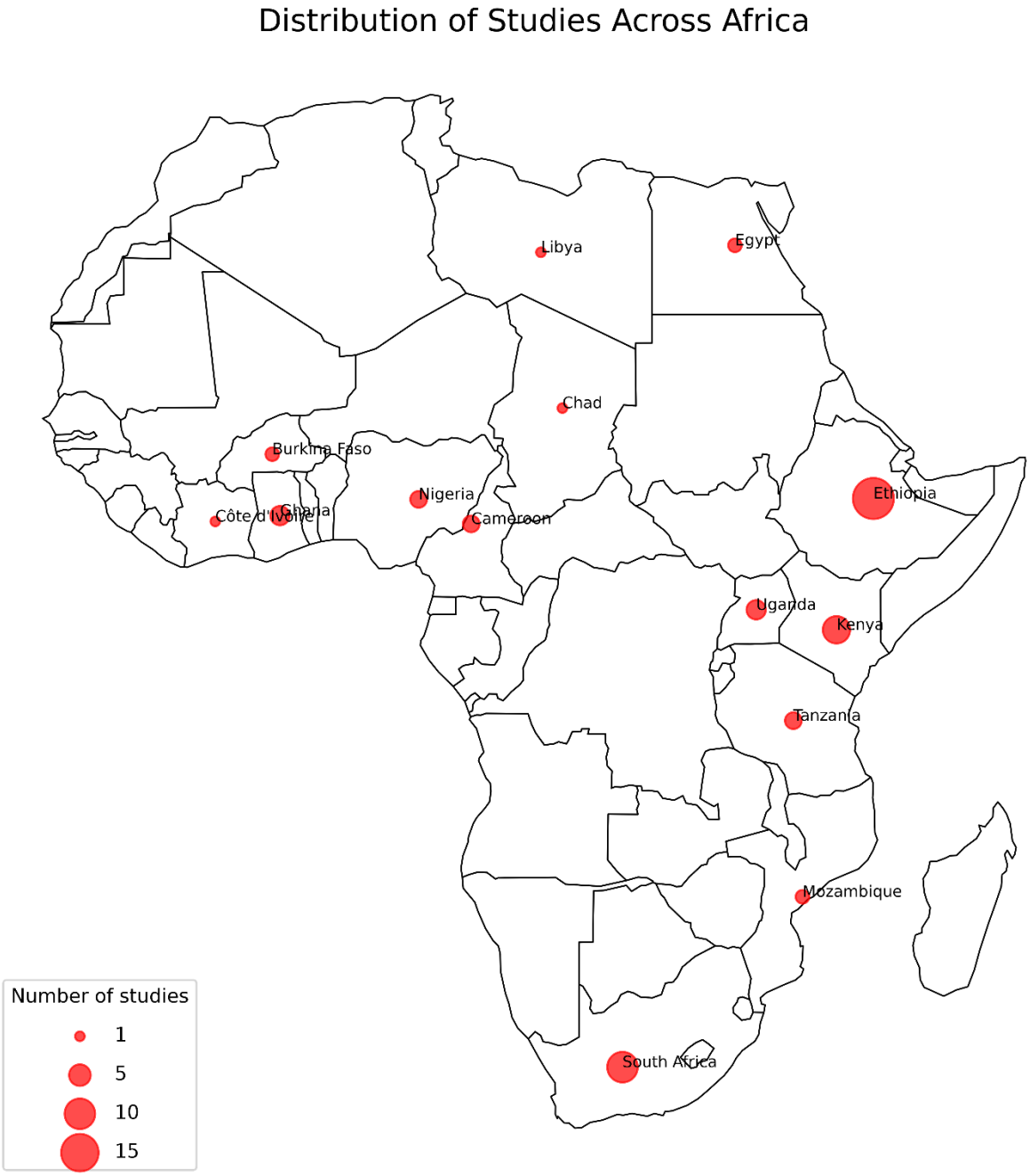

Figure 1. Geographic distribution of studies included in the systematic review across African countries.

3.3 Distribution of Sample Sources

3.3.1 Human-Derived Samples

Human-derived samples constituted the most frequently investigated source of *Salmonella* in the reviewed literature, with 22 studies focusing exclusively on human populations (Table1; Supplementary Table S2). Most of these investigations analyzed stool specimens collected from

patients presenting with diarrhea, gastroenteritis, or suspected enteric fever, although several studies also included asymptomatic individuals and food handlers (Akinola et al., 2019; Assoumy et al., 2021). A smaller number of studies incorporated blood samples alongside stool specimens to investigate invasive salmonellosis and bloodstream infections. The predominance of stool-based investigations reflects the importance of fecal shedding in the diagnosis and surveillance of both typhoidal and non-typhoidal *Salmonella* infections.

The reliance on human fecal samples was particularly evident in studies conducted in healthcare facilities, where culture-based detection of *Salmonella* was primarily used to assess disease burden and antimicrobial resistance profiles among symptomatic individuals.

Table 1. Distribution of sample sources and sample types among included studies.

Source category	Number of studies	Main sample types
Human	22	Stool, blood
Animal	20	Feces, cloacal swabs, milk, carcasses
Environmental	3	Water, wastewater, soil, vegetables
Human + Animal	4	Stool, feces
Animal + Environment	9	Feces, feed, water, litter
Human + Animal + Environment	6	Mixed One Health sampling

3.3.2 Animal-Derived Samples

Twenty studies investigated *Salmonella* occurrence exclusively in animal reservoirs, making animals the second most represented source category in the review (Table1; Supplementary Table S2). Poultry was the most commonly studied animal reservoir, with numerous investigations targeting broiler, layer, indigenous chicken, and commercial poultry production systems (Abayneh et al., 2023; Aga et al., 2025). Samples collected from poultry frequently included cloacal swabs, fecal droppings, litter, feed, carcasses, and drinking water.

In addition to poultry, several studies focused on cattle and other livestock species, including sheep, goats, buffaloes, dogs, and cats. Common sample types included feces, rectal swabs, milk, and nasal swabs. The extensive representation of livestock reflects their recognized role as important reservoirs of zoonotic *Salmonella* and their potential contribution to foodborne transmission and environmental contamination.

3.3.3 Environmental Samples

Environmental reservoirs were comparatively underrepresented, with only three studies focusing exclusively on environmental sources. These investigations analyzed a diverse range of samples,

including wastewater, drinking water, soil, manure, vegetables, sewage, and slaughterhouse environments (Table1; Supplementary Table S2). Environmental surveillance studies aimed to evaluate the persistence and dissemination of *Salmonella* outside host populations and to identify potential pathways linking human and animal contamination sources.

Despite their limited number, these studies highlighted the capacity of environmental matrices to serve as reservoirs and transmission vehicles for *Salmonella*, particularly in settings characterized by inadequate sanitation and waste management practices.

3.3.4 Integrated One Health Investigations

Nineteen studies adopted a multisectoral approach by simultaneously investigating two or more interconnected reservoirs. Among these, six studies examined human, animal, and environmental sources concurrently, while four studies investigated both human and animal reservoirs, and nine studies combined animal and environmental sampling (Table 1; Supplementary Table S2). Sample types collected in these investigations included stool, feces, wastewater, environmental swabs, poultry droppings, livestock feces, drinking water, feed, vegetables, and slaughterhouse samples.

These integrated studies provided valuable insights into the circulation of *Salmonella* across the human–animal–environment interface and generated evidence supporting the One Health paradigm. By investigating multiple reservoirs within the same epidemiological context, they enabled comparisons of prevalence patterns, serovar distribution, and antimicrobial resistance profiles across interconnected transmission pathways. Such studies remain relatively limited in Africa but represent an increasingly important approach for understanding the ecology and dissemination of antimicrobial-resistant *Salmonella*.

3.4 Methods Used for the Detection and Identification of *Salmonella* spp.

3.4.1 Culture-Based Isolation and Biochemical Identification

The 64 studies included in this review employed a wide range of laboratory approaches for the detection and confirmation of *Salmonella* spp., although conventional culture-based methods remained the cornerstone of diagnosis across all countries and sample types. Most studies followed internationally recognized isolation workflows involving pre-enrichment in buffered peptone water, selective enrichment in Rappaport–Vassiliadis or selenite broth, and subsequent plating on selective media such as Xylose Lysine Deoxycholate (XLD), MacConkey, Brilliant Green, or Salmonella–Shigella agars (Abayneh et al., 2023; Aga et al., 2025; Amare et al., 2024; Tosisa et al., 2020). These approaches were applied across human, animal, food, and environmental samples, highlighting the continued reliance on classical microbiological methods for routine surveillance in African settings.

Following isolation, confirmation of presumptive *Salmonella* colonies was frequently achieved through biochemical characterization. Thirteen studies explicitly reported the use of biochemical identification tests, including Triple Sugar Iron (TSI), citrate utilization, urease, indole, methyl red, and Voges–Proskauer assays (Abda et al., 2021; Assoumy et al., 2021; Usmael et al., 2022). Some investigations further employed commercial identification systems such as API strips and

VITEK 2 to improve species-level identification and standardization of laboratory procedures (Amsalu et al., 2021; Assoumy et al., 2021).

3.4.2 Molecular and Genomic Approaches for *Salmonella* Characterization

Molecular methods were increasingly incorporated into diagnostic workflows. Polymerase chain reaction (PCR) was reported in 35 of the 64 studies and was commonly used either to confirm culture-positive isolates or to detect specific virulence markers such as the *invA* gene, a highly conserved target among *Salmonella* spp. (Akinola et al., 2019; Tabo et al., 2015; Tosisa et al., 2020). Several studies combined conventional culture with PCR-based confirmation, reflecting a trend toward improving diagnostic specificity and sensitivity (Abdalhamed et al., 2021; Afema et al., 2016).

Serotyping remained an important epidemiological tool and was reported in 22 studies. This approach enabled the identification of clinically and epidemiologically relevant serovars and facilitated comparisons across human, animal, and environmental reservoirs (Abayneh et al., 2023; Amsalu et al., 2021; Andoh et al., 2016). In addition, some investigations employed advanced molecular epidemiological techniques, including pulsed-field gel electrophoresis (PFGE), multiple-locus variable-number tandem-repeat analysis (MLVA), and DNA sequencing to characterize genetic relationships among isolates and investigate potential transmission pathways within a One Health framework (Afema et al., 2016; Andoh et al., 2016).

Recent studies increasingly adopted whole-genome sequencing (WGS), which was reported in eight investigations. WGS provided high-resolution characterization of isolates, enabling simultaneous assessment of serotype, virulence determinants, phylogenetic relationships, and antimicrobial resistance genes (Sunmonu et al., 2025; Thye et al., 2025). The growing use of genomic approaches reflects the gradual transition from conventional phenotypic methods toward more comprehensive molecular surveillance strategies, particularly in studies aiming to investigate transmission dynamics across interconnected human, animal, and environmental reservoirs.

3.5 Antimicrobial Susceptibility Testing and Detection of Resistance Determinants

3.5.1 Phenotypic Antimicrobial Susceptibility Testing

Assessment of antimicrobial resistance was largely based on phenotypic susceptibility testing. Disk diffusion methods were the predominant approach, being reported in 55 of the 64 included studies. Most investigators performed susceptibility testing according to the Clinical and Laboratory Standards Institute (CLSI) guidelines, while a smaller number followed European Committee on Antimicrobial Susceptibility Testing (EUCAST) or Comité de l'Antibiogramme de la Société Française de Microbiologie (CA-SFM) recommendations (Aga et al., 2025; Amsalu et al., 2021; Assoumy et al., 2021). The Kirby–Bauer disk diffusion method was explicitly reported in 36 studies and represented the most commonly used technique for evaluating resistance to clinically important antibiotic classes, including β-lactams, fluoroquinolones, tetracyclines, aminoglycosides, and sulfonamides (Abayneh et al., 2023; Amare et al., 2024; Tosisa et al., 2020).

Although phenotypic methods dominated the literature, several studies complemented disk diffusion testing with minimum inhibitory concentration (MIC) determination. Twelve studies reported MIC-based approaches, either alone or in combination with disk diffusion assays (Abdalhamed et al., 2021; Andoh et al., 2016; Ssemakadde et al., 2025; Taviani et al., 2022). Broth microdilution, considered the reference method for antimicrobial susceptibility testing, was reported in a limited number of recent studies and was frequently associated with genomic investigations of antimicrobial resistance (Thye et al., 2025).

3.5.2 Molecular Detection of Antimicrobial Resistance Determinants

Beyond phenotypic resistance testing, molecular approaches were increasingly used to investigate the genetic basis of antimicrobial resistance. PCR-based detection of resistance genes was employed in several studies, particularly those investigating multidrug-resistant isolates or extended-spectrum β-lactamase (ESBL)-producing *Salmonella* strains (Abdalhamed et al., 2021; Tigabie et al., 2023). These studies targeted genes associated with resistance to β-lactams, tetracyclines, sulfonamides, aminoglycosides, and fluoroquinolones, providing insights into the mechanisms underlying observed resistance phenotypes.

3.5.3 Whole-Genome Sequencing for Resistance Surveillance

Whole-genome sequencing further expanded the capacity for antimicrobial resistance surveillance. Recent studies used WGS to identify acquired resistance genes, chromosomal mutations, and mobile genetic elements associated with multidrug resistance (Sunmonu et al., 2025; Thye et al., 2025). Compared with conventional susceptibility testing, genomic approaches offered a more comprehensive understanding of resistance determinants and facilitated the investigation of resistance transmission across human, animal, and environmental interfaces. Collectively, these findings indicate a progressive shift from solely phenotypic characterization toward integrated phenotypic and genomic surveillance of antimicrobial-resistant *Salmonella* in Africa.

3.6 Distribution of *Salmonella* Species and Serovars

The distribution of *Salmonella* species and serovars reported across the included studies revealed considerable diversity among human, animal, and environmental reservoirs in Africa. Serotyping was performed in 22 of the 64 included studies, allowing the identification of epidemiologically important serovars and facilitating comparisons across reservoirs (Supplementary Table S2). Overall, non-typhoidal *Salmonella enterica* serovars predominated, with *Salmonella Typhimurium* and *Salmonella Enteritidis* being the most frequently reported serovars across multiple countries and sample sources. These serovars are recognized globally as major causes of foodborne disease and invasive salmonellosis in both humans and animals (Ajmera & Shabbir, 2026; Oludairo et al., 2022).

3.6.1 Predominant Serovars Identified

Human-derived studies consistently reported the occurrence of *S. Typhimurium* and *S. Enteritidis*, particularly among patients presenting with diarrhea, gastroenteritis, bloodstream infections, or suspected enteric fever (Akinola et al., 2019; Andoh et al., 2016; Assoumy et al., 2021; Tigabie et al., 2023; Usmael et al., 2022). In addition to these dominant serovars, several investigations

identified *S. Typhi*, *S. Paratyphi*, *S. Newport*, *S. Virchow*, *S. Kentucky*, and *S. Infantis*, highlighting the heterogeneous nature of *Salmonella* populations circulating in human communities across the continent (Afema et al., 2016; Ball et al., 2019; Ssemakadde et al., 2025; Taviani et al., 2022).

Animal reservoirs exhibited the greatest diversity of serovars. Poultry-associated studies frequently reported *S. Enteritidis* and *S. Typhimurium* in broilers, layers, indigenous chickens, and commercial poultry farms (Abayneh et al., 2023; Aga et al., 2025; Eguale et al., 2015, 2016). Other serovars commonly identified in poultry included *S. Kentucky*, *S. Infantis*, *S. Hadar*, *S. Heidelberg*, *S. Saintpaul*, *S. Newport*, and *S. Anatum* (Amsalu et al., 2021; Cuco et al., 2024; Dlamini et al., 2024; Sunmonu et al., 2025). The frequent detection of *S. Kentucky* is particularly noteworthy because this serovar has increasingly been associated with multidrug resistance and international dissemination through poultry production and trade networks (Jibril et al., 2021; Petrin et al., 2023).

Livestock studies involving cattle, sheep, goats, buffaloes, and companion animals similarly identified a broad range of serovars, including *S. Typhimurium*, *S. Dublin*, *S. Newport*, and *S. Enteritidis* (Afema et al., 2016; Andoh et al., 2016; Hailu et al., 2021; Nelly et al., 2024; Taviani et al., 2022). The occurrence of these serovars in food-producing animals reinforces their importance as reservoirs of zoonotic salmonellae and highlights their potential contribution to contamination along the food production chain.

Although environmental investigations were relatively limited, the studies available demonstrated the presence of serovars commonly reported in human and animal populations. Wastewater, surface water, vegetables, soil, and slaughterhouse environments were found to harbor *S. Typhimurium*, *S. Enteritidis*, *S. Kentucky*, and other non-typhoidal serovars (Afema et al., 2016; Alio Sanda et al., 2017; Cuco et al., 2024; Sunmonu et al., 2025). These findings suggest that environmental matrices may act as reservoirs and transmission vehicles, facilitating the persistence and dissemination of *Salmonella* within communities and agricultural systems.

3.6.2 Serovar Distribution Across Reservoirs

Comparison of serovar distribution across reservoirs revealed substantial overlap between human, animal, and environmental sources. *S. Typhimurium* and *S. Enteritidis* were repeatedly detected in all three reservoirs and represented the most geographically widespread serovars reported in the reviewed studies (Afema et al., 2016; Akinola et al., 2019; Andoh et al., 2016; Assoumy et al., 2021; Cuco et al., 2024; Dlamini et al., 2024; Hailu et al., 2021; Sunmonu et al., 2025; Tosisa et al., 2020; Usmael et al., 2022). Their recurrent detection across diverse ecological niches underscores their adaptability and their importance as major zoonotic pathogens in Africa.

Poultry emerged as a particularly important reservoir for *S. Enteritidis*, whereas *S. Typhimurium* exhibited a broader ecological distribution encompassing poultry, cattle, companion animals, humans, and environmental samples (Abayneh et al., 2023; Aga et al., 2025; Amsalu et al., 2021; Eguale et al., 2015, 2016; Nelly et al., 2024). Similarly, *S. Kentucky* was frequently reported in poultry and environmental samples and was occasionally identified among human isolates,

suggesting possible transmission through contaminated food products and environmental exposure pathways (Amsalu et al., 2021; Cuco et al., 2024; Dlamini et al., 2024; Tigabie et al., 2023).

Evidence from integrated One Health studies further supported the circulation of shared serovars among interconnected reservoirs. Investigations simultaneously sampling humans, animals, and environmental matrices frequently reported overlapping serovar profiles and, in some cases, genetically related isolates, indicating potential transmission between reservoirs (Afema et al., 2016; Akinyemi et al., 2023; Andoh et al., 2016; Sunmonu et al., 2025; Thye et al., 2025). These findings reinforce the growing recognition that salmonellosis is maintained through complex interactions occurring at the human–animal–environment interface.

3.7 Antimicrobial Resistance Profiles of *Salmonella* Isolates

3.7.1 Overview of Antimicrobial Resistance Patterns

Antimicrobial susceptibility testing was reported in 55 of the 64 studies included in this review and revealed widespread resistance among *Salmonella* isolates recovered from human, animal, and environmental reservoirs across Africa. Resistance profiles varied considerably according to geographic location, reservoir type, serovar composition, and antimicrobial exposure history. Nevertheless, a consistent pattern of resistance to commonly used first-line antibiotics was observed throughout the continent (Afema et al., 2016; Akinola et al., 2019; Amsalu et al., 2021; Andoh et al., 2016; Assoumy et al., 2021; Eguale et al., 2015, 2016; Hlashwayo et al., 2023; Mengistu et al., 2025; Ofori et al., 2023).

High resistance rates were particularly common among isolates recovered from poultry, livestock, and food-animal production systems, where antimicrobial exposure is often more intensive. Several studies reported resistance levels exceeding 50% for one or more antimicrobial classes, while multidrug resistance (MDR) was frequently documented in both human and animal isolates (Abayneh et al., 2023; Abda et al., 2021; Cuco et al., 2024; Dlamini et al., 2024; Kasiano et al., 2024; Muturi et al., 2024; Sunmonu et al., 2025). Particularly concerning was the recurrent identification of MDR phenotypes among *S. Typhimurium*, *S. Enteritidis*, and *S. Kentucky*, serovars that were also among the most widely distributed across reservoirs.

3.7.2 Resistance to β-Lactam Antibiotics

Resistance to β-lactam antibiotics was among the most frequently reported antimicrobial resistance phenotypes. High resistance rates to ampicillin and amoxicillin were observed in isolates from poultry, cattle, humans, and environmental samples across multiple African countries (Abda et al., 2021; Abdalhamed et al., 2021; Amsalu et al., 2021; Hailu et al., 2021; Kasumba et al., 2023; Kavai et al., 2024). In some studies, resistance to ampicillin reached 100%, indicating extensive selective pressure associated with the long-term use of β-lactams in both human and veterinary settings (Abda et al., 2021; Abdalhamed et al., 2021).

Resistance to extended-spectrum cephalosporins and the emergence of extended-spectrum β-lactamase (ESBL)-producing isolates were also increasingly reported (Cuco et al., 2024; Kavulavu et al., 2025; Ramatla et al., 2024; Tigabie et al., 2023). Several studies identified ESBL-associated

genes, including blaTEM, blaSHV, blaCTX-M, and blaOXA, among isolates recovered from livestock, poultry, food products, and environmental samples (Abdalhamed et al., 2021; Cuco et al., 2024; Hailu et al., 2021; Langata et al., 2019; Ramatla et al., 2022, 2024; Sunmonu et al., 2025). More recently, carbapenemase-associated genes such as blaVIM, blaKPC, and blaOXA-48 have also been detected, raising concerns regarding the emergence of resistance to critically important last-resort antibiotics (Kavulavu et al., 2025).

3.7.3 Resistance to Tetracyclines

Tetracycline resistance was consistently among the highest resistance phenotypes reported across the reviewed studies. High resistance levels were documented in poultry, livestock, environmental, and human isolates, often exceeding 50% and occasionally reaching 100% (Abayneh et al., 2023; Abda et al., 2021; Eguale et al., 2015, 2016; Hailu et al., 2021; Yirsa & Tigistu, 2025). This widespread resistance likely reflects the extensive use of tetracyclines in animal production systems throughout Africa.

Molecular investigations identified several tetracycline resistance determinants, including tet(A), tet(B), tet(C), tet(K), and tetQ (Cuco et al., 2024; Dlamini et al., 2024; Fashae et al., 2018; Gorham et al., 2017; Hailu et al., 2024; Iwu et al., 2016; Mthembu et al., 2019; Ramatla et al., 2024; Raufu et al., 2021; Sunmonu et al., 2025; Thye et al., 2025).

3.7.4 Resistance to Sulfonamides and Trimethoprim

Resistance to sulfonamides and trimethoprim-sulfamethoxazole was commonly reported among both human and animal isolates (Afema et al., 2016; Akinola et al., 2019; Andoh et al., 2016; Odoch et al., 2017; Ofori et al., 2023; Usmael et al., 2022). These antimicrobials have historically been widely used in both clinical and veterinary settings, contributing to sustained selective pressure.

Genotypic analyses revealed a high prevalence of sul1, sul2, and dfrA resistance determinants, including dfrA7 and dfrA15, among multidrug-resistant isolates (Dlamini et al., 2024; Gharieb et al., 2015; Hailu et al., 2024; Kavai et al., 2025; Mthembu et al., 2019; Muturi et al., 2024; Ramatla et al., 2024; Raufu et al., 2021; Thye et al., 2025).

3.7.5 Resistance to Aminoglycosides

Resistance to aminoglycosides such as streptomycin and gentamicin was reported in numerous studies involving poultry, livestock, and human isolates (Afema et al., 2016; Akinola et al., 2019; Andoh et al., 2016; Odoch et al., 2017; Ofori et al., 2023; Usmael et al., 2022). Although resistance levels were generally lower than those observed for tetracyclines and β-lactams, aminoglycoside resistance remains widespread.

The principal resistance determinants identified included aadA2, aadA7, aadA, aac(3)-Id, aph(6)-Id, aph(3"), and strA/strB genes (Fashae et al., 2018; Gharieb et al., 2015; Hailu et al., 2024; Iwu et al., 2016; Muturi et al., 2024; Ramatla et al., 2024; Raufu et al., 2021). These genes were frequently associated with integrons and plasmids, facilitating their dissemination among bacterial populations.

3.7.6 Resistance to Fluoroquinolones

Fluoroquinolones remain critically important for the treatment of invasive salmonellosis; however, reduced susceptibility and resistance have increasingly been reported across Africa (Ball et al., 2019; Karama et al., 2026; Sunmonu et al., 2025; Tabo et al., 2015). Although resistance rates generally remained lower than those observed for β-lactams and tetracyclines, several studies documented resistance to ciprofloxacin and nalidixic acid.

Molecular investigations identified plasmid-mediated quinolone resistance genes such as qnrB, qnrB19, qnrD1, and qnrS1, as well as chromosomal mutations in the gyrA gene (Ball et al., 2019; Karama et al., 2026; Kavai et al., 2025; Muturi et al., 2024; Sunmonu et al., 2025; Tabo et al., 2015; Thye et al., 2025).

3.7.7 Multidrug Resistance and Mobile Genetic Elements

Multidrug resistance was one of the most important findings emerging from this review. MDR phenotypes, defined as resistance to three or more antimicrobial classes, were reported in human, animal, food, and environmental isolates across numerous countries (Abayneh et al., 2023; Abda et al., 2021; Amsalu et al., 2021; Cuco et al., 2024; Dlamini et al., 2024; Kasiano et al., 2024; Ndima Etouke et al., 2024; Sunmonu et al., 2025). Some studies reported MDR prevalence exceeding 40–90%, particularly among poultry-associated isolates.

The spread of MDR was frequently associated with mobile genetic elements, including plasmids and class 1 integrons carrying multiple resistance determinants (Gharieb et al., 2015; Igbinosa, 2015; Langata et al., 2019; Ramatla et al., 2022). Whole-genome sequencing studies further demonstrated the co-occurrence of β-lactam, tetracycline, sulfonamide, aminoglycoside, and quinolone resistance genes within individual isolates, providing evidence for the accumulation and dissemination of resistance determinants across interconnected human, animal, and environmental reservoirs (Karama et al., 2026; Muturi et al., 2024; Sunmonu et al., 2025; Thye et al., 2025).

3.8 Overall Prevalence of *Salmonella* spp. in Humans Across Africa

A meta-analysis of 21 studies investigating the prevalence of Salmonella spp. in human stool samples across Africa revealed substantial geographic variation in infection rates (Figure 2). The majority of studies originated from the East African region, particularly Ethiopia and Kenya, where prevalence estimates ranged from as low as 1.2% among food handlers in Gondar, Ethiopia (Getie et al., 2019) to 11.5% in Kenya (Kavulavu et al., 2025). Most Ethiopian studies reported prevalence estimates between approximately 3% and 9%, while Kenyan studies ranged from 2.0% to 11.5%. Ghanaian studies showed particularly contrasting results, with prevalence estimates of 3.8% and 14.8% (Sam et al., 2024; Sunmonu et al., 2025). The highest prevalence estimates were observed in the Southern African region, represented by studies from Tanzania, where prevalence ranged from 8.3% in Morogoro (Cuco et al., 2024) to 16.5% (Ngogo et al., 2020). In West Africa, prevalence estimates varied considerably, ranging from 4.0% to 8.7% in Burkina Faso (Héma et al., 2025; Karama et al., 2026) and from 7.6% to 14.1% in Nigeria (Fashae et al., 2018; Ohanu et al., 2019). The only study from Central Africa, conducted in Chad, reported a prevalence of 9.3% (Tabo et al.,

2015), while the sole study from North Africa, conducted in Egypt, reported a prevalence of 4.0% (Gharieb et al., 2015).

Using a random-effects model, the pooled prevalence of *Salmonella* spp. in human populations across the included studies was estimated at approximately 6% (95% CI: 5–9%), indicating that *Salmonella* remains a significant enteric pathogen in African settings. However, considerable between-study heterogeneity was observed ($I^2 = 89.7\%$, $p < 0.0001$), suggesting that prevalence estimates were strongly influenced by differences in study populations, geographic settings, diagnostic approaches, sanitation conditions, and local epidemiological contexts. The subgroup analysis by country and location (Supplementary Figure S2) confirmed that location explained part of this heterogeneity, with some sites exhibiting substantially higher prevalence than others.

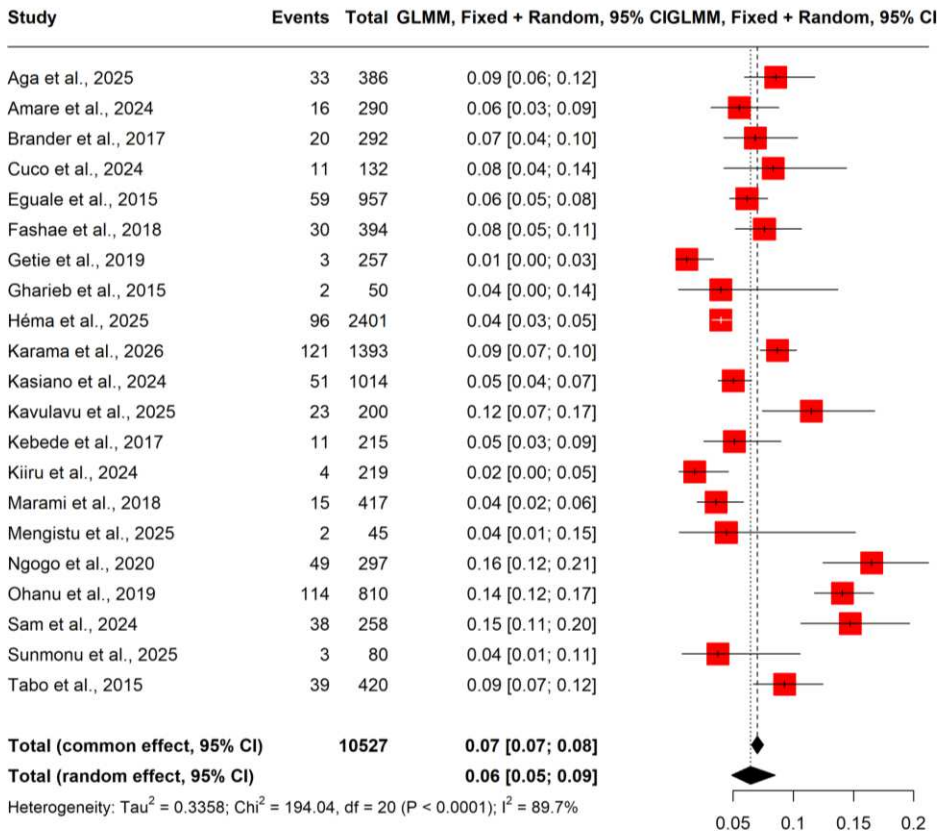

Figure 2. Forest plot showing study-specific and pooled prevalence estimates (random-effects model) of Salmonella spp. across 21 studies.

Assessment of publication bias using the funnel plot (Figure 3) suggested no significant small-study effects. The Egger's regression test was not statistically significant ($t = -1.30$, $df = 19$, $p = 0.2093$), indicating that the pooled prevalence estimate is unlikely to be substantially influenced by publication bias. Although slight asymmetry was visually apparent in the funnel plot, the statistical evidence did not support the presence of systematic reporting bias among the included studies.

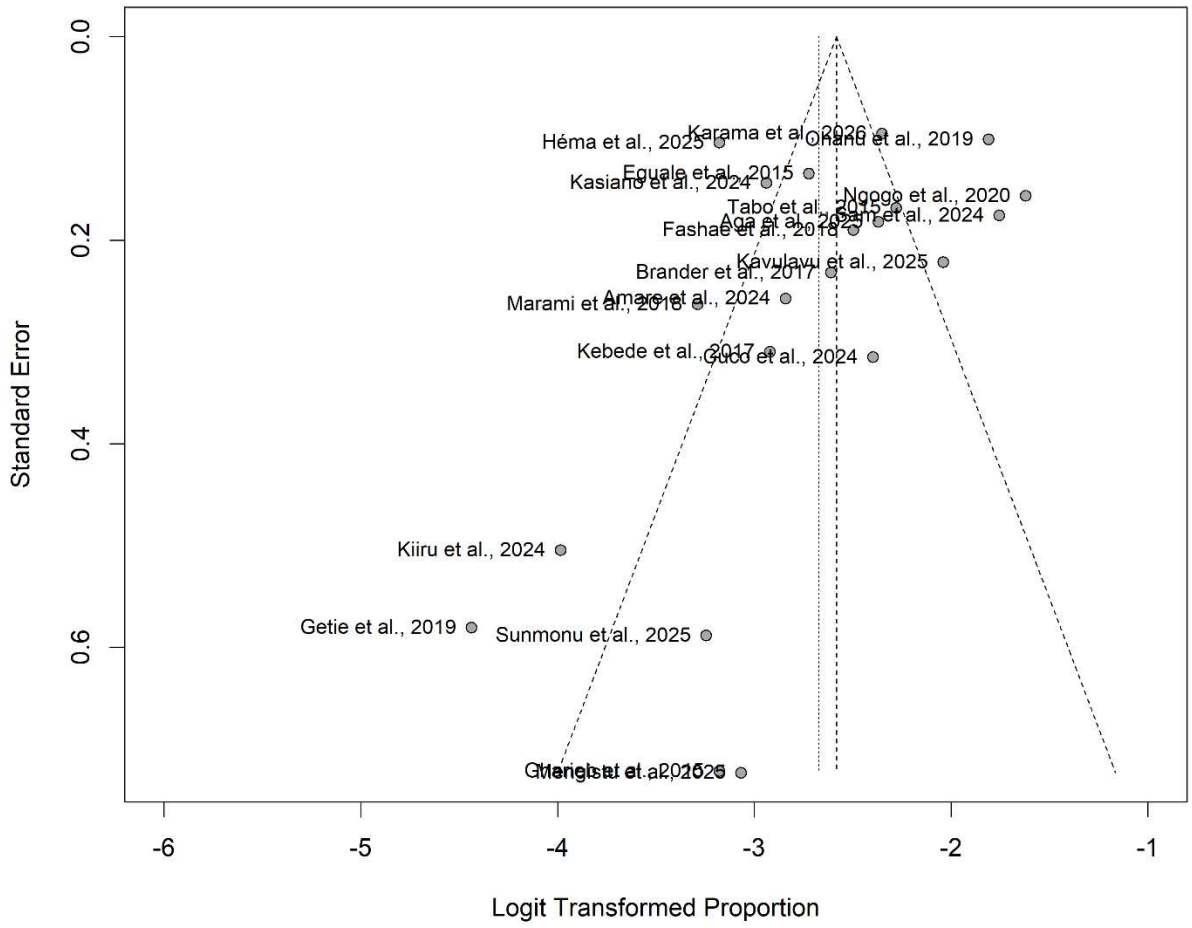

Figure 3. Funnel plot assessing publication bias across included studies

4. Discussion

4.1 Burden of Human Salmonellosis in Africa

This systematic review and meta-analysis provides a comprehensive synthesis of the prevalence of *Salmonella* spp. among human populations across Africa and demonstrates that salmonellosis remains a substantial public health concern on the continent. The pooled prevalence estimate of approximately 6% indicates that nearly one in sixteen individuals included in the analyzed studies carried *Salmonella*, highlighting the continued importance of this pathogen as a cause of enteric disease. This finding aligns with global reports identifying *Salmonella* as one of the leading causes of foodborne bacterial infections worldwide and a major contributor to diarrheal disease burden, particularly in low- and middle-income countries (Ajmera & Shabbir, 2026; WHO, 2015, 2018).

The observed prevalence is particularly concerning considering that the included studies were conducted in diverse populations, including symptomatic patients, food handlers, community

residents, and asymptomatic carriers. The detection of *Salmonella* among apparently healthy individuals suggests the existence of important human reservoirs that may facilitate sustained community transmission. Similar observations have been reported in Kenya and Burkina Faso, where asymptomatic carriage was identified as a potential driver of transmission and persistence within communities (Karama et al., 2026; Kavai et al., 2025). Such carriers may contribute to environmental contamination and foodborne dissemination, especially in settings characterized by inadequate sanitation and limited access to safe water.

The substantial heterogeneity observed among studies (I^2 = 89.7%) further indicates that the epidemiology of salmonellosis is highly context-dependent across Africa. This variability likely reflects differences in environmental conditions, socioeconomic status, healthcare access, food production systems, diagnostic capacity, and exposure to contaminated food and water sources. Previous investigations have demonstrated strong associations between poor sanitation infrastructure, inadequate hygiene practices, contaminated water supplies, and increased risk of *Salmonella* infection (Gorham et al., 2017; Hugho et al., 2024). Consequently, the burden of salmonellosis should not be viewed as uniformly distributed across Africa but rather as a disease influenced by local ecological and socioeconomic factors.

4.2 Geographic Heterogeneity and Regional Differences

One of the most notable findings of this study was the marked geographic heterogeneity in prevalence estimates across African regions. The highest prevalence values were reported in Tanzania, Ghana, and Nigeria, whereas lower prevalence estimates were observed in several Ethiopian study sites. These differences may reflect variations in environmental exposure, food handling practices, water quality, urbanization, healthcare infrastructure, and surveillance capacity.

The elevated prevalence observed in Tanzania is consistent with recent evidence identifying *Salmonella* as a significant contributor to gastrointestinal infections in both children and adults. Studies from Tanzania have highlighted several risk factors associated with infection, including unsafe drinking water, inadequate sanitation, household crowding, and close contact with domestic animals (Cuco et al., 2024; Hugho et al., 2024). Similarly, studies from Nigeria and Ghana have documented widespread circulation of *Salmonella* across human, livestock, and environmental reservoirs, suggesting that transmission frequently occurs at the human–animal–environment interface (Akinyemi et al., 2023; Ofori et al., 2023; Sunmonu et al., 2025).

The variability observed within countries was equally striking. Ethiopia, for example, contributed the largest number of studies yet displayed prevalence estimates ranging from approximately 1% to 9%. Such intra-country variation suggests that local determinants, including sanitation practices, food safety standards, population density, and healthcare-seeking behavior, may exert a stronger influence on disease occurrence than national-level characteristics alone. This observation reinforces the importance of subnational surveillance systems capable of identifying local hotspots of transmission and informing targeted interventions.

Importantly, the subgroup analysis demonstrated that geographic location accounted for a substantial proportion of the observed heterogeneity. The clustering of higher prevalence estimates

in specific localities suggests the existence of transmission hotspots that may be driven by environmental contamination, intensive livestock production, or deficiencies in water and sanitation infrastructure. Similar geographic clustering has been reported in foodborne disease surveillance systems in Asia and other regions, where localized environmental and socioeconomic conditions strongly influence salmonellosis incidence (Wang et al., 2025).

4.3 Evidence Supporting a One Health Transmission Cycle

Beyond the human burden identified in this review, increasing evidence suggests that *Salmonella* transmission in Africa is maintained through interconnected human, animal, food, and environmental reservoirs. Numerous studies included in the broader review detected *Salmonella* in poultry, cattle, pigs, vegetables, irrigation water, and farm environments, supporting the concept of a complex One Health transmission network.

Recent genomic investigations have strengthened this hypothesis. Whole-genome sequencing studies from Nigeria demonstrated close genetic relationships between isolates recovered from humans, animals, and environmental sources, indicating ongoing cross-sector transmission (Akinyemi et al., 2023). Similar findings have been reported in Ghana, where genomic analyses identified related *Salmonella enterica* strains circulating among cattle, beef products, and humans (Sunmonu et al., 2025). Environmental contamination of vegetables and irrigation systems has also been documented in Niger and Ethiopia, providing additional opportunities for foodborne exposure (Alio Sanda et al., 2017; Hailu et al., 2024).

Collectively, these findings suggest that effective control of salmonellosis in Africa cannot rely solely on clinical interventions. Rather, integrated One Health strategies involving human health, veterinary services, food safety authorities, and environmental management sectors will be required to reduce transmission and limit the emergence of antimicrobial-resistant strains.

5. Conclusion

This systematic review and meta-analysis highlights the substantial burden of *Salmonella* spp. across Africa, with a pooled prevalence of approximately 6% in human populations and considerable geographic variability between regions and countries. The findings underscore the widespread circulation of *Salmonella* in diverse epidemiological settings and reveal important differences in disease occurrence that are likely driven by local environmental, socioeconomic, and sanitation-related factors.

The review also demonstrates the growing challenge posed by antimicrobial-resistant and multidrug-resistant *Salmonella* strains across human, animal, food, and environmental reservoirs. Evidence from phenotypic and genomic studies supports the role of interconnected transmission pathways, emphasizing the importance of a One Health approach to surveillance and control.

Overall, these findings reinforce the need for strengthened food safety measures, improved water and sanitation infrastructure, enhanced antimicrobial stewardship, and integrated surveillance systems to mitigate the burden of salmonellosis and limit the spread of antimicrobial resistance across Africa.

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Supplementary Material

Supplementary Table S1. Search Strategy

Concept	Search Terms Used
Pathogen	"Salmonella"[Mesh] OR "Salmonella spp" OR "Salmonella enterica"
Epidemiological Outcome	prevalence OR occurrence OR epidemiology
Antimicrobial Resistance	"antimicrobial resistance" OR "antibiotic resistance"
Sample Type	feces OR fecal OR stool OR manure
Reservoir/Population	humans OR animals OR livestock OR poultry OR cattle OR pigs OR swine OR environment OR water OR soil
Geographical Scope (Africa)	"Africa"[Mesh] OR Africa OR "Sub-Saharan Africa" OR "North Africa" OR Algeria OR Angola OR Benin OR Botswana OR "Burkina Faso" OR Burundi OR Cameroon OR "Cape Verde" OR "Central African Republic" OR Chad OR Comoros OR Congo OR "Democratic Republic of the Congo" OR Djibouti OR Egypt OR "Equatorial Guinea" OR Eritrea OR Eswatini OR Ethiopia OR Gabon OR Gambia OR Ghana OR Guinea OR "Guinea-Bissau" OR "Ivory Coast" OR "Côte d'Ivoire" OR Kenya OR Lesotho OR Liberia OR Libya OR Madagascar OR Malawi OR Mali OR Mauritania OR Mauritius OR Morocco OR Mozambique OR Namibia OR Niger OR Nigeria OR Rwanda OR "Sao Tome and Principe" OR Senegal OR Seychelles OR "Sierra Leone" OR Somalia OR "South Africa" OR "South Sudan" OR Sudan OR Tanzania OR Togo OR Tunisia OR Uganda OR Zambia OR Zimbabwe

Supplementary Table S2. Characteristics of Included Studies

N	Reference	Location	Study population	Type of sample	Study design	Technique used	ATB resistance methods	Prevalence of Salmonella spp. in Human (%)
1	Abayneh et al., 2023	Ethiopia (Arba Minch)	Poultry (chicken breeding farms)	Cloacal swabs, feces	Cross-sectional	Culture, serotyping	Kirby-Bauer disk diffusion	
2	Abda et al., 2021	Ethiopia (Kafa zone)	Poultry (semi-intensive farms)	Cloacal/fecal swabs	Cross-sectional	Culture, biochemical tests	Kirby-Bauer disk diffusion	
3	Abdalhamed et al., 2021	Egypt	Livestock (cattle, sheep, goats, buffaloes)	Feces, milk, nasal swabs	Cross-sectional + experimental	Culture, PCR, MIC	Disk diffusion + PCR gene detection	
4	Afema et al., 2016	Uganda (Kampala)	Human, livestock, environment	Wastewater, slaughterhouse, feces, water	Cross-sectional (One Health)	Culture, PCR, MLVA, PFGE	Disk diffusion + agar dilution	
5	Aga et al., 2025	Ethiopia (Addis Ababa & surrounding towns)	Human, food animals, environment	Stool, meat, wastewater, swabs, chicken droppings	Cross-sectional	Culture, biochemical tests	Kirby-Bauer disk diffusion (CLSI)	8.6
6	Akinola et al., 2019	South Africa (North West)	Poultry (broilers, layers, indigenous)	Fecal swabs	Cross-sectional	Culture, PCR (invA, 16S), sequencing	Kirby-Bauer disk diffusion	

7	Amare et al., 2024	Ethiopia (Gondar)	Human (food handlers)	Stool	Cross-sectional	Culture, biochemical tests	Kirby-Bauer disk diffusion	5.5
8	Amsalu et al., 2021	Ethiopia (Bahir Dar)	Human (suspected enteric fever patients)	Blood + stool	Hospital cross-sectional	Culture, VITEK, serotyping	Kirby-Bauer disk diffusion (CLSI)	
9	Andoh et al., 2016	Ghana (Accra & Kumasi)	Poultry farms	Feces, dust, feed, water, carcasses	Cross-sectional	Culture, serotyping, PFGE	Disk diffusion + MIC	
10	Assoumy et al., 2021	Côte d'Ivoire (Abidjan, Agnibilékrou)	Poultry farms	Fecal samples	Cross-sectional	Culture, biochemical tests, API	Disk diffusion (CA-SFM/EUCAST)	
11	Ball et al., 2018	Uganda (Wakiso)	Cattle (dairy farms)	Environmental fecal samples	Cross-sectional (multi-season)	Culture, PCR, WGS	Broth microdilution (MIC)	
12	Beyene et al., 2024	Ethiopia (Northwest)	Human, dairy animals, environment	Stool, milk, feces, swabs, sewage	Cross-sectional	Culture, MALDI-TOF, PCR	Kirby-Bauer disk diffusion	
13	Brander et al., 2017	Kenya	Human (children with diarrhea)	Stool	Cross-sectional hospital-based	Culture, PCR, MIC (MicroScan)	Automated MIC testing	6.8
14	Cuco et al., 2024	Tanzania (Morogoro)	Human (adults & children)	Stool	Cross-sectional	Culture, PCR, sequencing	Kirby-Bauer disk diffusion	8.3
15	Dlamini et al., 2024	South Africa	Poultry (broiler, layer, indigenous)	Cloacal swabs	Cross-sectional	Culture, PCR	Kirby-Bauer disk diffusion	

16	Eguale et al., 2015	Ethiopia (Addis Ababa)	Human (diarrheic + GI patients)	Stool	Cross-sectional	Culture, serotyping, PCR	Kirby-Bauer disk diffusion (18 antibiotics)	6.2
17	Eguale et al., 2016	Ethiopia (Addis Ababa & Oromia)	Dairy cattle	Feces	Cross-sectional	Culture, serotyping, PCR	Kirby-Bauer disk diffusion (18 antibiotics)	
18	Eguale et al., 2018	Ethiopia (Addis Ababa & Oromia)	Poultry farms	Fecal droppings	Cross-sectional	Culture, PCR, serotyping	Kirby-Bauer disk diffusion	
19	Elnageh et al., 2021	Libya (Tripoli)	Animal (cats, dogs)	Fecal samples	Cross-sectional	Culture, serotyping	Disk diffusion, MIC	
20	Fashae et al., 2018	Nigeria	Humans (diarrhoeic + healthy) & cattle	Feces	Cross-sectional + WGS	Culture, serotyping, WGS	Disk diffusion (CLSI) + genomic analysis	7.3
21	Getie et al., 2019	Ethiopia (Gondar)	Human (food handlers)	Stool	Cross-sectional	Culture, biochemical tests	Kirby-Bauer disk diffusion	1.2
22	Gharieb et al., 2015	Egypt	Human (diarrheic patients) + Poultry meat	Stool, poultry meat	Cross-sectional	Culture, PCR, serotyping	Disk diffusion	4
23	Gorham et al., 2017	Cameroon	Environment (water systems + households)	Drinking water	Cross-sectional + molecular	qPCR (microbial source tracking)	Molecular detection of AMR gene (tetQ)	
24	Hailu et al., 2024	Ethiopia (Addis Ababa)	Environment + cattle + vegetables	Soil, manure, vegetables, feces	Cross-sectional	Culture, PCR	Disk diffusion	

25	Héma et al., 2025	Burkina Faso	Human (children)	Stool	Cross-sectional	Culture, PCR	Disk diffusion	4
26	Hlashwayo et al., 2023	Mozambique (Maputo)	Human (diarrheic patients, HIV±)	Stool	Cross-sectional	Culture, serotyping	Kirby-Bauer disk diffusion	
27	Igbinosa et al., 2014	South Africa (Eastern Cape)	Cattle + goats	Feces	Cross-sectional	Culture, PCR	Disk diffusion + PCR gene detection	
28	Iwu et al., 2016	South Africa (Eastern Cape)	Swine (pigs)	Fecal samples	Cross-sectional	Culture, PCR (serogrouping)	Kirby-Bauer disk diffusion	
29	Karama et al., 2026	Burkina Faso (Nanoro)	Humans (asymptomatic) + Poultry	Stool + cloacal/cecal samples	Cross-sectional	Culture, API, WGS	Disk diffusion (CLSI)	8.7
30	Kasiano et al., 2024	Kenya (Mukuru informal settlement)	Human (symptomatic + carriers)	Stool, blood	Cross-sectional	Culture, serotyping, PCR	Kirby-Bauer disk diffusion	5
31	Kasumba et al., 2023	Kenya, Mali, Gambia	Human (children <5 yrs)	Stool	Case-control (VIDA cohort)	Culture, qPCR	Disk diffusion (CLSI)	
32	Kavai et al., 2024	Kenya (informal settlements, Nairobi)	Humans (children ≤16 y, symptomatic + asymptomatic)	Stool	Case-control (archived isolates)	Culture, serotyping, PCR	Kirby-Bauer disk diffusion	
33	Kavai et al., 2025	Kenya (Nairobi)	Human (cases & carriers)	Blood, stool	Longitudinal cohort	Culture, WGS	Kirby-Bauer disk diffusion	
34	Kavulavu et al., 2025	Kenya (Kisii)	Human, Animal, Environment	Stool, water, animal feces, soil	Cross-sectional	Culture, PCR	Kirby-Bauer disk diffusion	11.5

35	Kebede et al., 2017	Ethiopia (Hawassa)	Human (HIV patients)	Stool	Cross-sectional	Culture, biochemical tests, serotyping	Kirby-Bauer disk diffusion	5.1
36	Kiiru et al., 2024	Kenya (Mukuru informal settlement)	Human (children ≤5 years)	Stool	Cross-sectional	Culture, VITEK, PCR	MIC (VITEK AST)	2
37	Langata et al., 2019	Kenya (Nairobi)	Poultry environment	Chicken droppings	Cross-sectional	Culture, PCR, genotyping	Disk diffusion + molecular gene detection	
38	Madoroba et al., 2016	South Africa (Vhembe district)	Cattle, slaughter environment	Hides, carcasses, intestinal contents, feces	Cross-sectional	Culture, PCR (invA), serotyping	Kirby-Bauer disk diffusion	
39	Manyi-Loh et al., 2023	South Africa	Environment (pig manure biodigester)	Pig manure + sawdust	Experimental / longitudinal	Culture, API biochemical ID	Kirby-Bauer disk diffusion (14 antibiotics)	
40	Marami et al., 2018	Ethiopia (Haramaya)	Human (asymptomatic food handlers)	Stool	Cross-sectional	Culture, biochemical tests	Kirby-Bauer disk diffusion	3.6
41	Mengistu et al., 2025	Ethiopia (Bahir Dar)	Human, Poultry, Environment	Stool, cloacal swabs, boot swabs, feed, water	Cross-sectional	Culture, PCR, serotyping	Kirby-Bauer disk diffusion	4.4
42	Mthembu et al., 2019	South Africa	Livestock (multi-species)	Feces, environment	Cross-sectional	Culture, PCR	Disk diffusion + molecular detection	

43	Muturi et al., 2024	Kenya (Nairobi)	Human (patients & carriers)	Stool, blood	Longitudinal cohort	Culture, WGS	Kirby-Bauer disk diffusion	
44	Mwambene et al., 2025	Tanzania (Dar es Salaam)	Poultry	Fecal droppings	Cross-sectional	Culture, PCR, sequencing	Kirby-Bauer disk diffusion	
45	Ndima Etouke et al., 2024	Cameroon	Human	Stool	Cross-sectional	Culture, biochemical tests	Kirby-Bauer disk diffusion	
46	Ngogang et al., 2021	Cameroon (Yaoundé)	Poultry environment	Chicken litter manure	Cross-sectional	Culture, microbroth, CLSI	Disk diffusion + MIC	
47	Ngogo et al., 2020	Tanzania (Njombe)	Human (GI patients)	Stool	Cross-sectional	Culture, biochemical tests, serotyping	Kirby-Bauer disk diffusion (CLSI)	16.5
48	Odoch et al., 2017	Uganda	Poultry (layer farms)	Fecal pooled samples	Cross-sectional	Culture, serotyping	Kirby-Bauer disk diffusion	
49	Ofori et al., 2023	Ghana (Ashanti region)	Environment (farm systems)	Soil, dust, poultry feces	Cross-sectional	Culture, VITEK, serotyping	Disk diffusion (EUCAST)	
50	Ohanu et al., 2019	Nigeria (Enugu)	Human (febrile patients)	Blood, stool, urine	Prospective case-control	Culture, Widal test, serotyping	Disk diffusion (CLSI)	14.1
51	Ramatla et al., 2022	South Africa	Poultry + rats (farm interface)	Fecal samples	Cross-sectional (molecular)	PCR, sequencing	Disk diffusion + gene detection	
52	Ramatla et al., 2024	South Africa	Poultry (broiler chickens)	Fecal samples	Laboratory / cross-sectional	Culture, PCR, sequencing	Disk diffusion	

53	Raseala et al., 2020	South Africa	Environment (soil, manure, water)	Soil, manure, irrigation water, freshwater	Cross-sectional (One Health genomic)	Culture, PCR, sequencing	Molecular ARG detection	
54	Raufu et al., 2021	Nigeria (Ilorin)	Swine (pig farms)	Fecal samples	Cross-sectional + WGS	Culture, serotyping, MLST, WGS	Disk diffusion + genomic AMR analysis	
55	Sam et al., 2024	Ghana (Southern regions)	Human (suspected typhoid patients)	Blood, stool	Cross-sectional	Culture, PCR, Typhidot RDT	Kirby-Bauer disk diffusion	14.8
56	Ssemakadde et al., 2025	Uganda (Wakiso)	Poultry	Cloacal & fecal swabs	Cross-sectional	Culture, PCR, MIC	Kirby-Bauer + MIC	
57	Sunmonu et al., 2025	Ghana (Tamale)	Human, cattle, beef	Stool, cattle blood, beef	Cross-sectional	Culture, WGS	Genomic AMR detection	3.8
58	Tabo et al., 2015	Chad (N'Djamena hospitals)	Human (diarrheic patients)	Stool	Cross-sectional	Culture, serotyping, PCR	Kirby-Bauer disk diffusion	9.3
59	Taviani et al., 2022	Mozambique (Moamba)	Water supply system (environment)	Raw, treated, tap water	Cross-sectional	Culture, PCR	MIC + disk diffusion	
60	Thye et al., 2025	Ghana & Tanzania	Human, livestock, environment	Blood, stool, feces, dust, soil	Cross-sectional (multi-site One Health)	Culture, WGS	Broth microdilution + WGS	
61	Tigabie et al., 2023	Ethiopia (Gondar)	Poultry (farms)	Chicken droppings	Cross-sectional	Culture, biochemical, ESBL test	Kirby-Bauer + ESBL confirmatory	

62	Tosisa et al., 2020	Ethiopia (Ambo)	Human (children <5 years)	Stool	Cross-sectional	Culture, PCR, serotyping	Kirby-Bauer disk diffusion
63	Usmael et al., 2022	Ethiopia (Harar)	Animal (dogs)	Rectal swabs	Cross-sectional	Culture, biochemical tests	Kirby-Bauer disk diffusion
64	Yirsa & Tigistu, 2025	Ethiopia (Gondar)	Cattle	Feces, bulk milk	Cross-sectional	Culture, biochemical tests	Kirby-Bauer disk diffusion

Supplementary Table S3. Quality Assessment Results

N	Reference	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Overall appraisal
1	Abayneh et al., 2023	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
2	Abda et al., 2021	Yes	Yes	Unclear	Yes	Yes	Unclear	Yes	No	Yes	Moderate
3	Abdalhamed et al., 2021	Yes	Yes	Unclear	Yes	Yes	Yes	Yes	NA	Yes	High
4	Afema et al., 2016	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
5	Aga et al., 2025	Yes	Unclear	Yes	Yes	Yes	Yes	Unclear	NA	Yes	Moderate
6	Akinola et al., 2019	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
7	Amare et al., 2024	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
8	Amsalu et al., 2021	Yes	Yes	No	Yes	Yes	Unclear	Yes	Unclear	Unclear	Moderate
9	Andoh et al., 2016	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
10	Assoumy et al., 2021	Yes	Yes	No	Yes	Yes	Unclear	Yes	Unclear	Unclear	Moderate
11	Ball et al., 2018	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
12	Beyene et al., 2024	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	High
13	Brander et al., 2017	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
14	Cuco et al., 2024	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	High
15	Dlamini et al., 2024	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	High
16	Eguale et al., 2015	Yes	Yes	yes	yes	yes	Unclear	yes	yes	Yes	High
17	Eguale et al., 2016	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
18	Eguale et al., 2018	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
19	Elnageh et al., 2021	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
20	Fashae et al., 2018	Yes	Yes	Yes	Yes	No	Yes	Yes	NA	Yes	High
21	Getie et al., 2019	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
22	Gharieb et al., 2015	Yes	Yes	No	Yes	No	Unclear	Yes	Unclear	Yes	Moderate
23	Gorham et al., 2017	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Moderate	High
24	Hailu et al., 2024	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
25	Héma et al., 2025	Yes	Unclear	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
26	Hlashwayo et al., 2023	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
27	Igbinosa et al., 2014	YES	YES	Unclear	YES	YES	Unclear	YES	YES	YES	High
28	Iwu et al., 2016	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High

29	Karama et al., 2026	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	High
30	Kasiano et al., 2024	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
31	Kasumba et al., 2023	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
32	Kavai et al., 2024	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	High
33	Kavai et al., 2025	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
34	Kavulavu et al., 2025	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
35	Kebede et al., 2017	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
36	Kiiru et al., 2024	Yes	Yes	Unclear	Yes	Yes	Yes	Yes	NA	Yes	High
37	Langata et al., 2019	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
38	Madoroba et al., 2016	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
39	Manyi-Loh et al., 2023	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
40	Marami et al., 2018	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
41	Mengistu et al., 2025	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
42	Mthembu et al., 2019	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
43	Muturi et al., 2024	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
44	Mwambene et al., 2025	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	High
45	Ndima Etouke et al., 2024	Yes	Yes	Yes	Unclear	Yes	Yes	Yes	Unclear	Yes	High
46	Ngogang et al., 2021	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
47	Ngogo et al., 2020	Yes	Yes	Yes	Unclear	Yes	Unclear	Yes	Unclear	Yes	Moderate
48	Odoch et al., 2017	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
49	Ofori et al., 2023	Yes	Yes	Unclear	Yes	Yes	Yes	Yes	NA	Yes	High
50	Ohanu et al., 2019	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	Unclear	Yes	High
51	Ramatla et al., 2022	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	High
52	Ramatla et al., 2024	Yes	Yes	Unclear	Yes	Unclear	Yes	Yes	NA	Yes	Moderate
53	Raseala et al., 2020	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
54	Raufu et al., 2021	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
55	Sam et al., 2024	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	High
56	Ssemakadde et al., 2025	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High

57	Sunmonu et al., 2025	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
58	Tabo et al., 2015	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
59	Taviani et al., 2022	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
60	Thye et al., 2025	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
61	Tigabie et al., 2023	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	Yes	High
62	Tosisa et al., 2020	Yes	Yes	Unclear	Yes	Yes	Yes	Yes	Unclear	Yes	High
63	Usmael et al., 2022	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High
64	Yirsa & Tigistu, 2025	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	High

Q1: Were the study subjects and setting described in detail?

Q2: Were valid methods used for the identification of the condition?

Q3: Were study participants recruited in an appropriate way?

Q4: Was the condition measured in a standard, reliable way for all participants?

Q5: Was there appropriate statistical analysis?

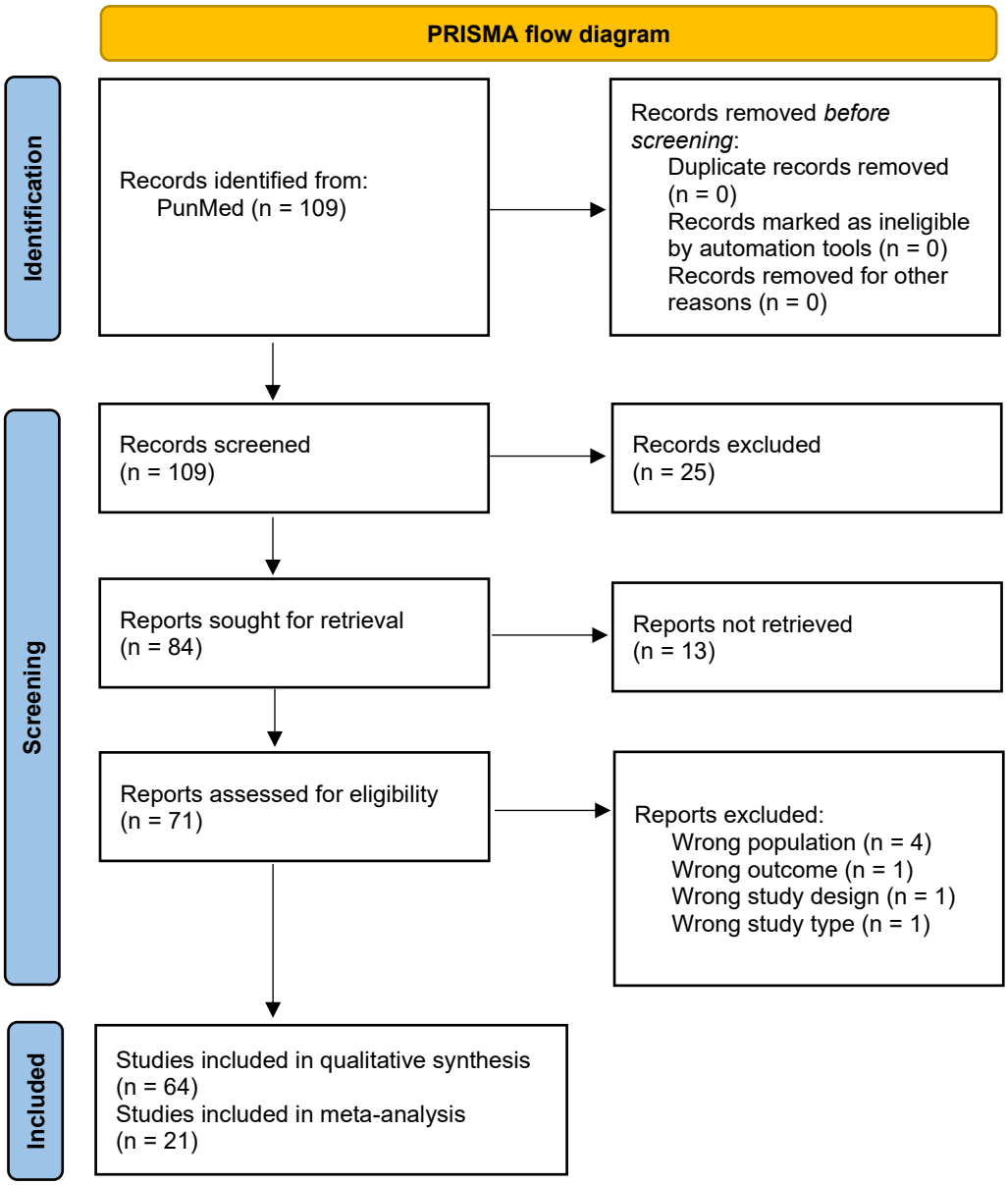
Q6: Was the sample frame appropriate to address the target population?

Q7: Was data analysis conducted with sufficient coverage of the identified sample?

Q8: Was the response rate adequate, and if not, was the low response rate managed appropriately?

Q9: Was the sample size adequate?

Supplementary Figure S1. PRISMA Flow Diagram



Supplementary Figure S2. Subgroup analysis by country and location

