One Health 20 (2025) 101090

Contents lists available at ScienceDirect

One Health

journal homepage: www.elsevier.com/locate/onehlt

Prevalence of ESBL-producing *Escherichia coli* in sub-Saharan Africa: A meta-analysis using a One Health approach

Morufat Oluwatosin Olaitan [a,*], Oluwatosin Qawiyy Orababa [b], Rukayya Bushola Shittu [c], Gift Maureen Obunukwu [d], Ayomikun Emmanuel Kade [b,e], Margaret Toluwalayo Arowolo [e], Adams Alabi Oyediran [d], Rildwan Alaba Yusuff [f]

[a] Department of Biology, Microbiology and Science Laboratory Technology, Nile University of Nigeria, Abuja, Nigeria
[b] School of Life Sciences, University of Warwick, Coventry, United Kingdom
[c] Department of Microbiology, Osun State University, Osogbo, Nigeria
[d] Department of Microbiology, University of Ibadan, Ibadan, Nigeria
[e] Department of Microbiology, University of Lagos, Akoka, Lagos, Nigeria
[f] Department of Microbiology, University of Ilorin, Nigeria

ARTICLE INFO

Keywords:
AMR
ESBL
E. coli
ESBL-Ec
One health
Public health
Sub-Saharan Africa

ABSTRACT

The rise in the prevalence of antimicrobial-resistant (AMR) pathogens globally has been a major concern, especially due to the increasing mortality associated with AMR. One of these pathogens –classified as a WHO priority pathogen– is extended-spectrum beta-lactamase (ESBL)-producing *Escherichia coli*. In this study, we aim to determine the prevalence of ESBL-producing *E. coli* in sub-Saharan Africa (SSA) as well as the genes responsible for its spread in the region. Based on the PRISMA guideline, we screened 6521 articles published between 2013 and 2023 from PubMed, AJOL, Google Scholar, Scopus, and Web of Science using pre-set eligibility criteria. The final meta-analysis included one hundred and ninety-six of these articles. In this study, we reported an overall ESBL-producing *E. coli* prevalence of 20.76 % in SSA. Subregion analysis showed that West Africa had the highest prevalence of 22.80 % while Southern Africa (13.76 %) has the lowest ESBL-producing *E. coli* prevalence in SSA. Among the countries in SSA, Burkina Faso (33.37 %) had the highest prevalence of ESBL-producing *E. coli*. Additionally, sample source subgroup analysis revealed animals as the highest source of ESBL-producing *E. coli* in SSA with a prevalence of 29.15 %. We also found that $bla_{\text{CTX-M-15}}$ is the most reported ESBL gene in *E. coli* in SSA. Our study shows a high prevalence of ESBL-producing *E. coli* in SSA countries, with animals significantly contributing to the spread of ESBL resistance in the region compared to humans, the environment and food. This study further emphasizes the importance of an interdisciplinary and intergovernmental approach to reducing AMR spread in SSA. Additionally, we implore policymakers to implement policies that will encourage responsible use of antimicrobials in both the clinic and agriculture to prevent the widespread of AMR genes.

1. Introduction

Antimicrobial resistance (AMR) has emerged as one of the most pressing global health challenges, ranking among the top ten threats to human well-being [1]. According to recent statistics, which found that about 8.9 million deaths happened owing to bacterial infections and 1.27 million deaths were attributable to AMR, with an additional estimated 4.95 million deaths attributed to its repercussions globally in 2019 alone [2,3]. Of particular concern is the rise of AMR associated with extended-spectrum beta-lactamase (ESBL)-producing bacteria, which has seen a surge in both hospital and community settings in recent years [4]. The proliferation of AMR is significantly fueled by the misuse of antibiotics in human medicine and animal husbandry, particularly in sub-Saharan African (SSA) regions [5]. Without intervention, projections suggest that in 5 years' time (2030), infections stemming from AMR will pose a substantial threat to the global economy, with low- and

* Corresponding author at: Department of Biology, Microbiology and Science Laboratory Technology, Nile University of Nigeria, Plot 681, Cadastral Zone C-OO, Research & Institution Area, Jabi Airport Bypass, Abuja, FCT 900001, Nigeria.
E-mail addresses: morufat.olaitan@nileuniversity.edu.ng, morufatoolaitan@gmail.com (M.O. Olaitan).

https://doi.org/10.1016/j.onehlt.2025.101090
Received 29 December 2024; Received in revised form 25 May 2025; Accepted 25 May 2025
Available online 2 June 2025

middle-income countries (LMIC), especially in SSA, bearing a disproportionate burden [6].

Furthermore, it is profusely clear that AMR in livestock is intricately linked to their presence in humans and environments [7]. It is projected that AMR would result in a significant number of deaths throughout the world [2], which would also lead to immense economic damages and a substantial decline in animal production worldwide [8]. Additionally, wastewater and sewage systems serve as major sources of environmental contamination in the region, acting as hotspots for the proliferation of resistant bacteria and the horizontal exchange of genetic determinants of resistance [9].

Among the Enterobacteriaceae, *Escherichia coli* is becoming a main storehouse of ESBL genes, which confer resistance to several β-lactam antibiotics including penicillin, aztreonam and most cephalosporins [10]. *E. coli* is a Gram-negative facultative anaerobe which assumes a noteworthy role as a bacterial commensal dwelling in the intestinal microbiota of varied animal species, comprising human beings. Within this association, *E. coli* upholds a harmonious coexistence with its hosts, naturally exhibiting a symbiotic relationship devoid of pathogenicity [11]. Nevertheless, it is noteworthy to mention that *E. coli* also emerges as a prominent etiological agent responsible for initiating a myriad of prevalent bacterial infections affecting both human and animal populations alike i.e. it is the most common cause of urinary tract infection (UTI), urosepsis, neonatal meningitis, septicemia, etc. in human [12], colibacillosis in poultry and mastitis in dairy cattle [13,14].

The World Health Organization's integrated global surveillance on ESBL-producing *E. coli*, utilizing a "One Health" approach, highlights the significant ecological role of ESBL-*E. coli* as a bioindicator for antimicrobial resistance in Gram-negative bacteria [15]. These bacteria exhibit resistance to most beta-lactam antibiotics, necessitating treatment with last-resort drugs like carbapenems or colistin. However, access to these drugs is limited in some settings [15]. The increased use of these antimicrobials has driven the emergence of carbapenem resistance against which current antibiotics are largely ineffective [16]. Moreover, *E. coli* is harbored in the intestinal tract of all animal species used for food production and this bacterium demonstrates great genetic versatility and adaptability to constantly changing environments, as well as acquires numerous mechanisms of antimicrobial resistance, such as enzymes encoded by plasmids [17].

In addition to *E. coli* generally being transmitted through the fecal–oral route, multidrug-resistant (MDR) forms of ESBL *E. coli* are transmissible through contact with humans, animals, the environment, as well as ingestion of contaminated food or water [10]. In fact, one study showed that 60 % of community-acquired ESBL *E. coli* were attributable to human-to-human transmission, whereas food accounted for about 20 % [18]. The intestinal carriage of ESBL *E. coli* is usually asymptomatic and persistent. However, many studies have shown the association of fecal carriage with ESBL *E. coli* infections [19]. Unlike infections with β-lactam-susceptible *E. coli*, ESBL *E. coli* infections have poor clinical outcomes [20]. For instance, the mortality rate of ESBL *E. coli* sepsis (60 %) is three times higher than for β-lactam susceptible strains (20 %) [21]. In SSA, studies have reported the carriage of ESBL-*E. coli* in the intestinal tracts of humans and animals, emphasizing that seven individuals without gastrointestinal symptoms can be carriers of ESBL [22]. Understanding the current status of this MDR bacterium is critical for developing effective methods for its control, including the prevention of its transmission and decolonization of carriers.

The rationale for focusing specifically on sub-Saharan Africa is implicit yet compelling. SSA bears the world's highest incidence of deaths attributable to antimicrobial resistance (AMR). A staggering estimate suggests that the region's AMR-related death rate surpasses 100 per 100,000 individuals in western SSA [2]. This alarming burden is exacerbated by limited access to diagnostic and microbiological testing in most SSA areas, resulting in a scarcity of empirical data on AMR [23].

SSA poses unique challenges for antimicrobial resistance surveillance and interventions due to a combination of factors. Limited laboratory capacity is a significant obstacle, as many SSA countries lack adequate equipment, infrastructure, and personnel to detect and confirm AMR. This limitation hinders the ability to monitor and track AMR trends, as evidenced by a study in Tanzania, which found that only 9 AMR sentinel sites were active and functional with few well-trained laboratory staffs [24]. Furthermore, data collection and reporting systems for AMR are often weak or non-existent in SSA countries [25]. This is particularly concerning, given the high burden of infectious diseases such as HIV, tuberculosis, and malaria, which are often treated with antibiotics [26]. The increased use of antibiotics can drive the development and spread of AMR, limiting access to quality medicines [27]. Additionally, a study in Kenya found that 37.7 % of antibiotics available in the market were of poor quality [28]. Poor infection prevention and control (IPC) practices, such as hand hygiene and proper use of personal protective equipment, are also inadequate in SSA healthcare settings [29]. A recent study found that about 30–60 % of healthcare workers do not practice proper hand hygiene [30]. These challenges underscore the need for targeted interventions to strengthen laboratory capacity, improve data collection and reporting, and enhance IPC practices in SSA countries.

Despite existing research on the prevalence of ESBL-producing *E. coli*, previous studies have primarily focused on a few countries, such as Burkina Faso, Gabon, Ghana and Tanzania, leaving a substantial void in our understanding of the situation in other SSA countries [31]. Moreover, these studies have been limited by inadequate sampling frames, relying on convenience sampling or small sample sizes, which may not accurately represent the broader population, leading to biased estimates of ESBL *E. coli* prevalence [25]. Additionally, insufficient data on antimicrobial use patterns in SSA has hindered our understanding of the critical factors driving the development and spread of ESBL *E. coli* [27].

Moreover, literature has revealed that *Enterobacterales*, including *E. coli*, exhibited high proportions of resistance to several antibiotics commonly recommended in clinical guidelines used in sub-Saharan Africa [23]. This study fills a critical knowledge gap by providing contemporary data on antibiotic resistance patterns in SSA, where such information is scarce. Specifically, we intend to address these gaps by providing a comprehensive systematic review and meta-analysis of ESBL-producing *E. coli* prevalence in SSA, using a robust One Health approach, shedding light on the effectiveness of current clinical guidelines and informing evidence-based antibiotic stewardship practices in the region.

To the best of our knowledge, there is currently no study reporting the overall prevalence of ESBL-producing *E. coli* in SSA. Additionally, the prevalence of this antibiotic-resistant strain in each of the subregions in SSA is not clear, as well as the predominant genes in the region. This study therefore aims to determine the overall prevalence of ESBL-producing *E. coli* in SSA as well as its subregions. We also aim to identify the prevalent ESBL genes in *E. coli* in different parts of SSA.

2. Methods

2.1. Search protocol and selection criteria

This systematic review and meta-analysis adhered to the Preferred Reporting Items for Systematic Reviews and Meta-Analysis (PRISMA) 2020 guidelines [32]. A comprehensive literature search was conducted by four investigators (MO Olaitan, RB Shittu, OQ Orababa, and GM Obunukwu) using a combination of keywords ("ESBL", "Extended-spectrum beta-lactamase", "resistance", "*E. coli*", "*Escherichia coli*", "sub-Saharan Africa", "SSA") across five databases: PubMed, African Journal Online, Google Scholar, Scopus, and Web of Science. Specifically, keywords including "ESBL" AND "producing" AND ("*Escherichia coli*" OR "*E. coli*") AND ("sub" AND "Saharan" AND "Africa") OR "sub Saharan Africa"), which were aligned with relevant Medical Subject Headings (MeSH) terms in PubMed were utilized. The search results were

subsequently filtered by year, no language restrictions were applied at this stage. To be included in the review, studies had to be published between January 2013 and December 2023 and present data on extended-spectrum beta-lactam resistance on *E. coli* in sub-Saharan Africa. We excluded review articles, systematic reviews, meta-analyses, abstract-only publications, studies without English translations, and studies that did not report on ESBL-*E. coli* or lacked specific data on it. The literature search was completed in December 2023. To minimize selection bias, the quality of the studies was evaluated using the Joanna Briggs Institute (JBI) Critical Appraisal Checklist for prevalence data studies [33]. The checklist consists of 9 questions, which were assessed based on JBI guidelines, with answers categorized as 'yes', 'no', 'unclear', or 'not applicable'. Only studies that received a 'yes' response to all questions were included in the analysis.

2.2. Data extraction and critical appraisal

A data extraction table was created by MO Olaitan to capture key information from the articles, including the first author's name, publication year, study type, country, subregion, sample source, size, and ESBL-*E. coli* details (notably, the number of *E. coli* isolates, the number of ESBL-*E. coli*, the AST method employed, and the ESBL gene detected). Six investigators (RB Shittu, OQ Orababa, GM Obunukwu, AA Oyediran, and RA Yusuff) independently selected eligible articles and extracted the data. All discrepancies were reviewed and resolved through discussions with MO Olaitan, and OQ Orababa when necessary. For quality assurance, MO Olaitan verified all the extracted data with OQ Orababa's assistance for accuracy and consistency. In cases where the number of positive *E. coli* isolates exceeded the sample size due to culturing, it was recorded as 100 % for meta-analysis purposes only. The study quality was assessed based on the methods used to characterize extended-spectrum beta-lactam strains. Studies using only phenotypic methods (e.g., disc diffusion, broth microdilution, automated antimicrobial susceptibility testing such as NMIC-203 card, Etest, VITEK, Mindray TDR 300B) were considered low quality; those using only genotypic/molecular methods were medium quality; and those employing both phenotypic and molecular methods were high quality.

2.3. Meta-analysis and statistical inference

The extracted data were compiled in Excel, scrutinized for duplicate entries, and vetted for eligibility criteria accuracy. Statistical analysis was conducted using R progamming language in RStudio version 4.4.1 (R Core Team 2024). Pooled prevalence was determined with a random effect model (to account for heterogeneity between the studies), while I^2 and Cochran Q statistics were used to assess heterogeneity across studies. In particular, due to anticipated between-study heterogeneity stemming from sample size and study settings, a random-effects model was employed [34]. To understand the root of heterogeneity, we performed subgroup analyses based on four pre-specified factors: subregion (East, West, South and Central Africa), sample source (human, animal, environment, and food-related data), publication year (2013–2016, 2017–2019, and 2020–2023), and country (limited to countries with more than two eligible studies). Heterogeneity (I^2) levels were categorized as low (25 %), moderate (50 %), and high (> 75 %) based on I^2 values. Statistical significance was denoted as $p < 0.05$. Potential publication bias was determined by funnel plots. The sub-Saharan Africa map of eligible studies was generated using R's naturalearth and ggplot2 packages. MO Olaitan performed all the analyses.

3. Results

3.1. Search and screening outcome

The search yielded 6521 potentially relevant articles from five electronic databases: PubMed, African Journal Online, Google Scholar, Scopus, and Web of Science. After initial screening, 4363 articles were excluded, leaving 2158. Following title and abstract screening, 1501 more were eliminated. The remaining 657 articles were assessed for eligibility, resulting in the exclusion of 384 and the removal of 77 duplicates. Ultimately, 196 studies met the criteria and were included in the systematic review and meta-analysis (Fig. 1).

3.2. Overview of included studies

This systematic review identified 196 eligible studies from 27 sub-Saharan African nations, with the majority coming from East Africa (85) and West Africa (80) (Fig. 2A). Two studies spanned multiple regions.

The majority of studies were published in 2022 (34) and 2023 (32), with a significant increase in recent years (2020–2023: 115 studies, 58.67 %) compared to earlier periods combined (2013–2016: 41 studies; 2017–2019: 40 studies) even though the earlier period is nearly double the length of the later period (Fig. 2B).

Country-specific analysis revealed that Nigeria led with 35 studies, followed by Ethiopia (25), Ghana (24), Tanzania (21), and Uganda (14) (Fig. 3A). Two studies were conducted in multiple countries.

Most studies focused on human samples (146), with fewer examining animal (25), environmental (18), and food (7) samples (Fig. 2C).

The quality of studies varied, with 108 (55.1 %) using both phenotypic and molecular methods (high quality), 82 (41.84 %) using only phenotypic methods (low quality), and 6 (3.06 %) using only molecular methods (medium quality) (Fig. 2D).

The studies analyzed a total of 107,719 samples, yielding 18,527 ESBL producers from 31,112 *E. coli* isolates in SSA, indicating that almost two-thirds (60 %) of identified *E. coli* isolates produce ESBL

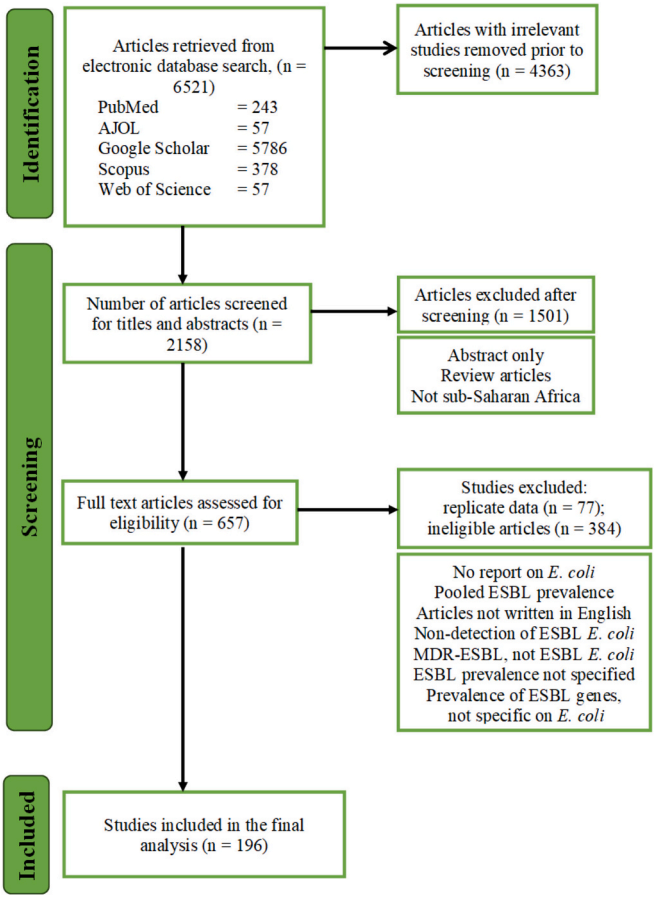

Fig. 1. Selection of studies following the PRISMA flowchart protocol.

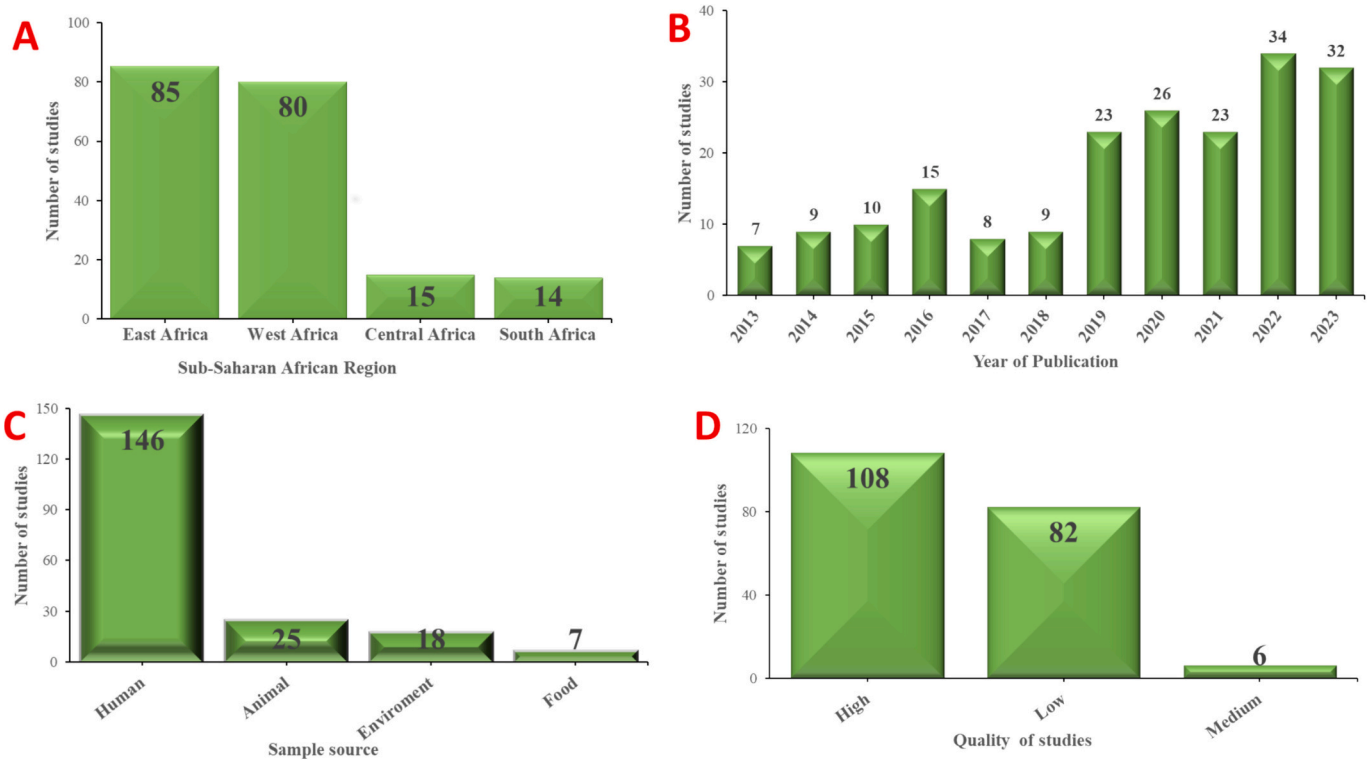

Fig. 2. Distribution of Included Studies. (A) Regional Distribution in sub-Saharan Africa: number of studies by region. Note: Two studies spanned multiple regions, affecting total count. (B) Publication Year: number of studies by year. (C) Sample Source: type of sample source. (D) Identification Method. Low: Phenotype only (41.84 %); Medium: Molecular only (3.06 %); High: Phenotype and molecular (55.10 %).

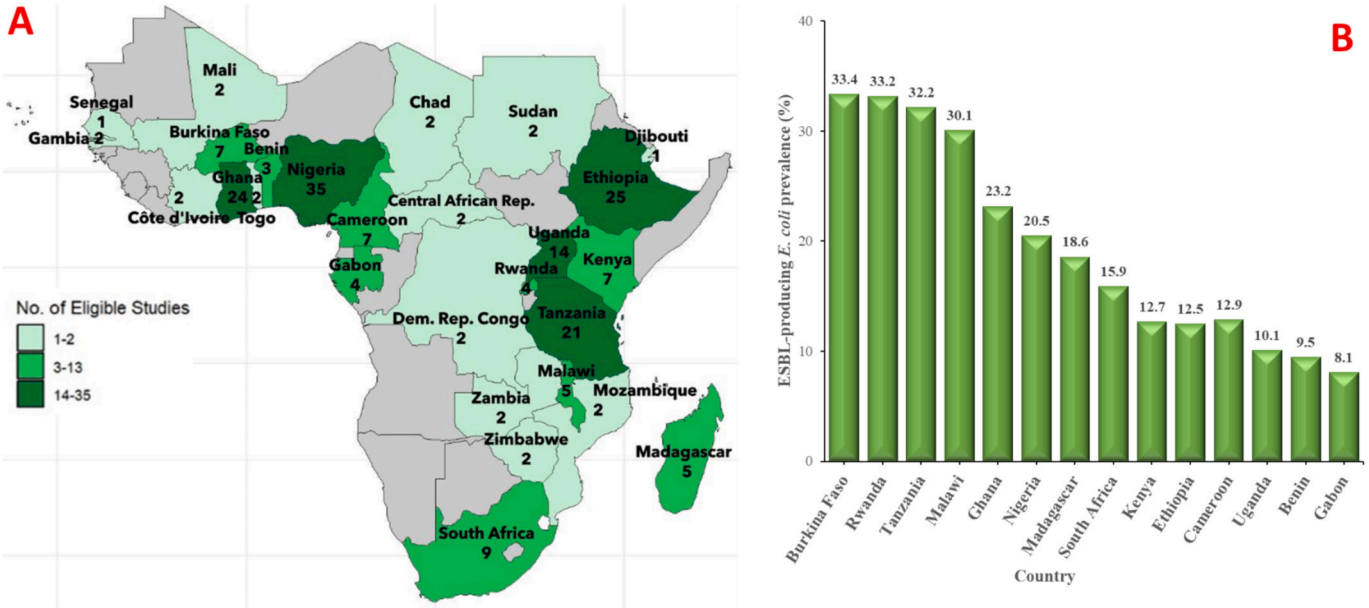

Fig. 3. Geographical Distribution and Prevalence of ESBL-producing *E. coli* in sub-Saharan Africa. (A) Map of sub-Saharan Africa: countries with eligible studies. (B) Country-specific Prevalence of ESBL-producing *E. coli*: estimated prevalence rates.

(Table 1). The characteristics of the 196 eligible studies are presented in the Supplementary Table 1.

3.3. Meta-analysis of the burden of ESBL-producing E. coli in SSA

A meta-analysis of ESBL-producing *E. coli* in sub-Saharan Africa revealed a pooled prevalence of 20.76 % (95 %-CI: 17.56–24.15, $p = 0$) with significant heterogeneity ($I^2 = 99.2$ %; $Q = 24{,}495.39$) (Fig. 4).

Regional analysis showed varying prevalence rates, with West Africa having the highest rate (22.80 %; 95 %-CI: 17.88–28.11, $p = 0$), followed by East Africa (20.82 %; 95 %-CI: 15.71–26.43, $p = 0$), Central Africa (19.82 %; 95 %-CI: 9.43–32.78, $p < 0.01$), and Southern Africa (13.76 %; 95 %-CI: 6.48–23.13, $p = 0$). Significant heterogeneity was observed across all regions (Table 1).

Table 1
Proportion of ESBL-producing *E. coli* in sub-Saharan Africa (SSA) across subgroup analyses by region, year of publication and sample source.

Subgroup analyses	Total sample size (N)	Total ESBL-*E. coli* (n)	Prevalence (%)	95 % CI	Q	I^2 (%)	*p*-value	*p*-value between study groups
Geographical region								
East	29,680	5441	20.82	15.7–26.4	6948.09	98.8	0	0.08
West	36,771	10,689	22.80	17.9–28.1	6567.44	98.8	0	
South	36,323	1704	13.76	6.5–23.1	1554.23	99.2	0	
Central	4221	663	19.82	9.4–32.8	493.23	97.2	<0.01	
Multiples	724	30	4.87	0.0–17.5	27.24	96.3		
Publication period								
2013–2016	11,942	1344	14.42	10.5–18.8	1498.72	97.3	<0.01	0.02
2017–2019	38,197	2444	24.19	16.2–33.2	3601.70	98.9	0	
2020–2023	57,580	14,739	22.10	17.6–26.9	11,955.74	99	0	
Sample Source								
Food	1370	159	14.02	4.8–26.9	203.73	97.1	<0.01	0.34
Animal	8269	1903	29.15	16.8–43.3	2010.24	98.8	0	
Human	94,033	15,883	20.23	16.7–24	21,439	99.3	0	
Environment	4047	582	17.14	9.4–26.6	615.01	97.2	<0.01	
Overall								
Total sample size	107,719	18,527	20.76	17.6–24.2	24,495.39	99.2	0	**Country**: <0.0001
Total *E. coli* isolates	31,112							

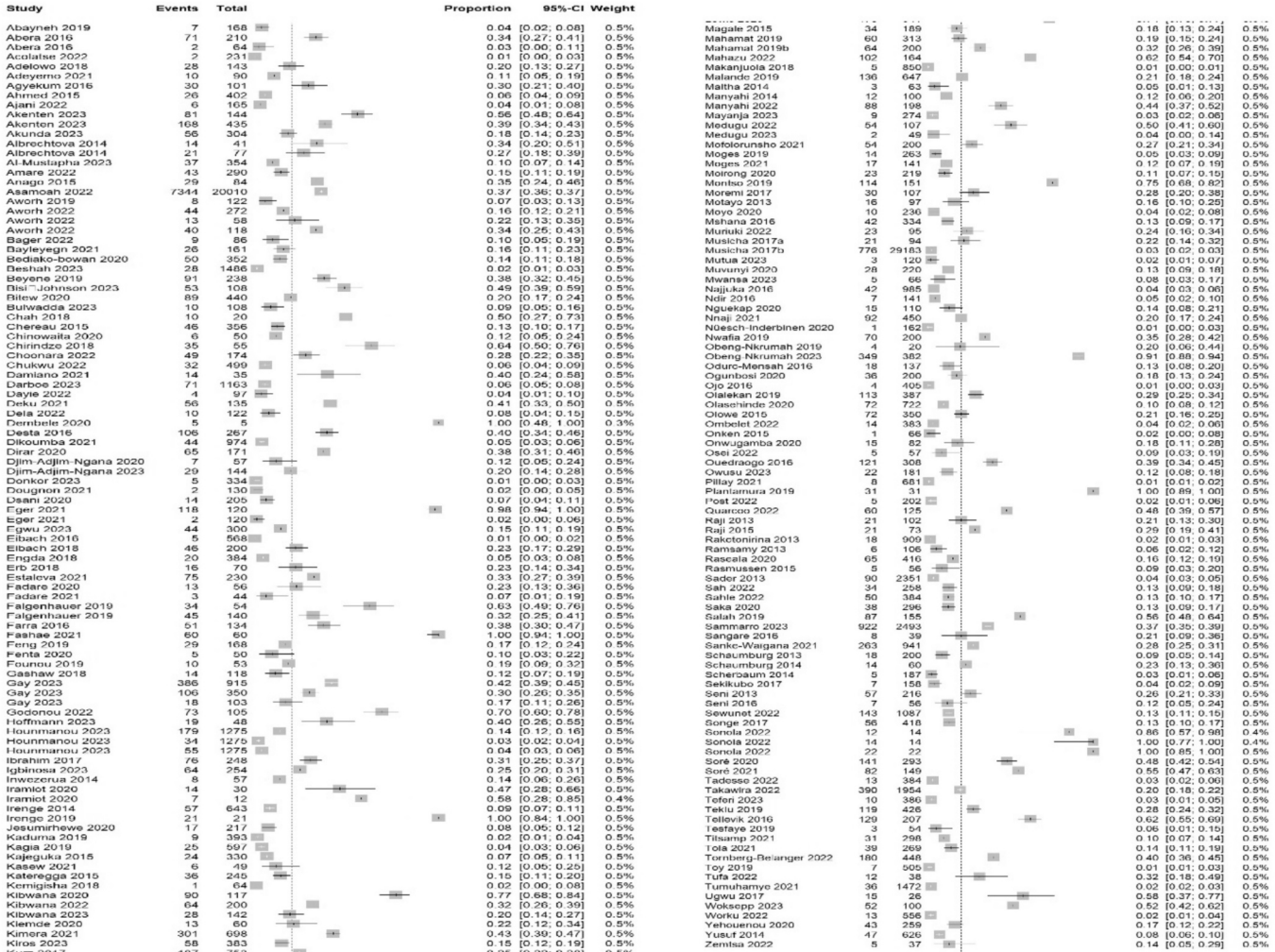

Fig. 4. (A) Forest Plot of Pooled Prevalence of ESBL-producing *E. coli* in sub-Saharan Africa. (B) Forest Plot of Subgroup Analysis of ESBL-producing *E. coli* in sub-Saharan Africa by Year of Publication.

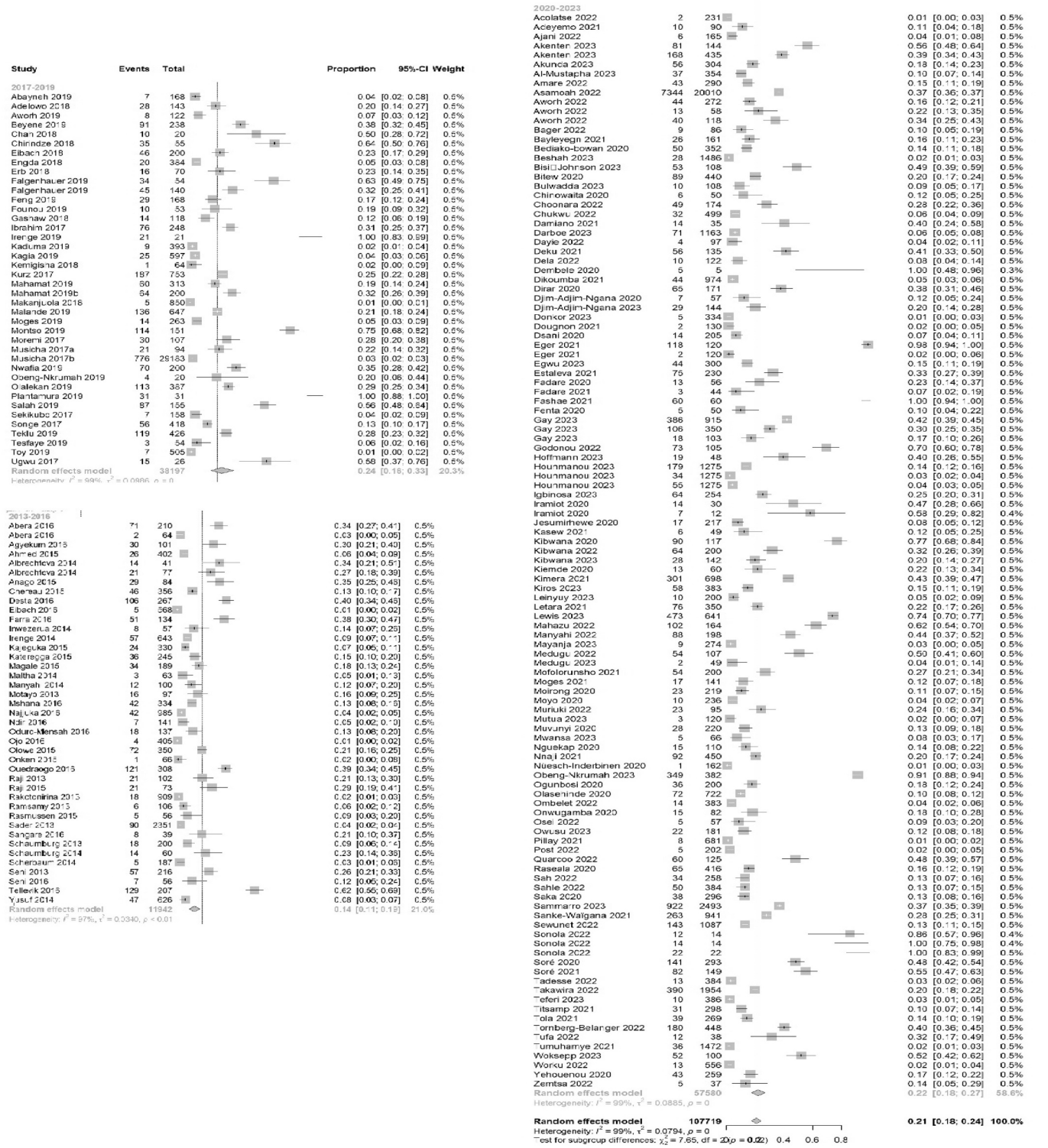

Fig. 4. (*continued*).

Temporal analysis revealed that the highest prevalence was found in 2017–2019 (24.19 %, $p = 0$), followed by 2020–2023 (22.10 %, $p = 0$), and 2013–2016 (14.42 %, $p < 0.01$) (Table 1). Fig. 4B shows the forest plot of subgroup analysis of ESBL-producing *E. coli* based on year of publication.

Country-specific analysis identified Burkina Faso, Rwanda, Tanzania, and Malawi as the top four countries with the highest burden of ESBL-producing *E. coli*, with prevalence rates ranging from 30.1 % to 33.37 %. Other countries, including Ghana, Nigeria, Madagascar, and South Africa, had moderately prevalence rates ranging from 15.88 % to 23.2 % (Fig. 3B).

Notably, animal samples had the highest burden of ESBL-producing *E. coli* (29.15 %, $p = 0$), followed by human, environmental, and food samples, with prevalence rates of 20.23 %, $p = 0$; 17.14 %, $p < 0.01$; and 14.02 %, $p < 0.01$ respectively (Table 1). Detailed forest plots of these subgroup analyses can be found in the Supplementary data file.

Statistical significance testing between study groups revealed notable differences (Table 1). Specifically, the *p*-values for year of publication ($p = 0.02$), country ($p < 0.0001$), subregion ($p = 0.08$), and sample source ($p = 0.34$) indicate that year of publication and country are significant sources of heterogeneity. In contrast, sample source does not contribute significantly to heterogeneity. These findings suggest that year of publication and country may have substantially influenced study outcomes. Subregions may have had a moderate impact, whereas sample source appears to have had no significant effect on study outcomes.

3.4. Prevalence of ESBL genes in SSA

We found that of the 196 eligible studies included in the meta-analysis, 114 (58.2 %) of them employed genomic tests to identify ESBL-producing *E. coli* and its genes (Fig. 2D). The most abundant ESBL genes found in the studies under analysis are ***bla*$_{\text{CTX-M}}$** (*bla*$_{\text{CTX-M-15}}$, *bla*$_{\text{CTX-M-1}}$, *bla*$_{\text{CTX-M-14}}$, *bla*$_{\text{CTX-M-55}}$, *bla*$_{\text{CTX-M-825}}$, *bla*$_{\text{CTX-M-9}}$, *bla*$_{\text{CTX-M-914}}$, *bla*$_{\text{CTX-M-2}}$, *bla*$_{\text{CTX-M-12}}$, *bla*$_{\text{CTX-M-27}}$, *bla*$_{\text{CTX-M-127}}$, *bla*$_{\text{CTX-M-55}}$, *bla*$_{\text{CTX-M-102}}$, *bla*$_{\text{CTX-M-103}}$, *bla*$_{\text{CTX-M-3}}$, *bla*$_{\text{CTX-M-101}}$, *bla*$_{\text{CTX-M-28}}$, *bla*$_{\text{CTX-M-8}}$, *bla*$_{\text{CTX-M-32}}$, *bla*$_{\text{CTX-M-79}}$); ***bla*$_{\text{TEM}}$** (*bla*$_{\text{TEM-1}}$, *bla*$_{\text{TEM-104}}$, *bla*$_{\text{TEM-4}}$, *bla*$_{\text{TEM-24}}$, *bla*$_{\text{TEM-135}}$, *bla*$_{\text{TEM-169}}$, *bla*$_{\text{TEM-190}}$, *bla*$_{\text{TEM-2}}$, *bla*$_{\text{TEM-6}}$); ***bla*$_{\text{SHV}}$** (*bla*$_{\text{SHV-73}}$, *bla*$_{\text{SHV-12}}$, *bla*$_{\text{SHV-28}}$, *bla*$_{\text{SHV-31}}$); and ***bla*$_{\text{OXA}}$** (*bla*$_{\text{OXA-1}}$, *bla*$_{\text{OXA-48}}$). A few other genes occur very rarely (*bla*$_{\text{CMY-2}}$, *bla*$_{\text{DHA}}$, *bla*$_{\text{PER}}$, and *bla*$_{\text{GES}}$). Of these genes, *bla*$_{\text{CTX-M-15}}$ was the most frequently reported in the majority of the evaluated studies. All sample types, notably human, animal, environmental, and food sources, harbored the *bla*$_{\text{CTX-M}}$, *bla*$_{\text{SHV}}$, and *bla*$_{\text{TEM}}$ ESBL genes. However, *bla*$_{\text{OXA}}$ and *bla*$_{\text{CMY}}$ genes were detected in all sample types except for food samples, where they were notably absent.

4. Discussion

The general spread and global prevalence of Extended Spectrum Beta-Lactamase (ESBL)-producing *Escherichia coli* remain a critical health concern as it confers resistance to antibiotics with beta-lactam rings, which thus increases treatment complexity. Beta-lactam antibiotics account for about 65 % of antibiotics administered through injections yearly in the United States [35], and resistance to this drug is of immense consequence. It is not surprising that WHO Bacterial Priority Pathogen List (WHO BPPL) elevated third-generation cephalosporin-resistant *E. coli* and carbapenem-resistant *E. coli* in their recent update of organisms needing urgent therapeutic development [36]. In this study, we shed light on the epidemiology of Extended Spectrum Beta-Lactamase (ESBL)-producing *Escherichia coli* across various subregions and populations in sub-Saharan Africa.

We revealed an overall pooled prevalence of ESBL-producing *E. coli* in sub-Saharan Africa to be 20.76 % [95 % CI: 17.56–24.15]. A similar study in South America by Bastidas-Caldes et al. [37] revealed a lower pooled prevalence (17.2 %) of ESBL-producing *E. coli* using the One health approach that encompasses samples from humans, animals and environments. The disparity observed in the prevalence might be due to differences in sample size, types, study period, and even geographical characteristics (including temperatures, location, humidity), among others. Although, our prevalence closely matched the report of Islam et al. [38], it is important to stress that their study only captured a country in Asia.

Regional variations in the prevalence of ESBL-producing *E. coli* also emerged as a significant finding of this study. The subregion analysis showed that the highest prevalence was observed in West Africa (22.80 %), with the lowest observed in Southern Africa (13.76 %). The high prevalence in West Africa is concerning and warrants further investigation into potential drivers. The low prevalence in Southern Africa can be linked to the low number of studies (14) on ESBL-producing *E. coli* from this region, thus necessitating more surveillance. However, the relatively low number of studies from Central Africa is not surprising as this region ranks low in socioeconomic indexes, which invariably impact their ability to perform research. Reports by Mahamat et al. [39], who assessed the prevalence of extended-spectrum β-lactamase- and carbapenemase-producing Enterobacteriaceae in humans, animals, and the environment in West and Central Africa showed that the prevalence varies from 11 % to 72 % across different countries and settings. Despite having the largest population and number of studies (85) in this review, East Africa's prevalence (20.82 %) was lower than that of West Africa, however, higher than the overall prevalence in SSA. A variation in the distribution of ESBL-producing *E. coli* was also reported in the different subregions in Europe [40]. This variation between subregions reflects the complex interplay of factors influencing antimicrobial resistance which could include differences in antibiotic use patterns, healthcare practices, and surveillance systems. This underscores the need for tailored approaches to combat ESBL-producing *E. coli* in different geographical contexts.

We observed that in countries within the sub-Saharan Africa region – those that reported at least more than two eligible studies – the prevalence of ESBL-producing *E. coli* ranges from 8.06 % to 33.37 % which is similar to the range of 5.8 % to 40.2 % reported by the Surveillance Atlas of Infectious Diseases in Europe [41]. Mahamat et al. [39] reported a range of 11 % to 72 % for ESBL-producing Enterobacteriaceae (ESBL-PE) prevalence which encompasses ESBL-producing *E. coli* and *Klebsiella pneumoniae* across different countries and settings in Central and West Africa. Identifying countries with the highest burden of ESBL-producing *E. coli* (Burkina Faso, Rwanda, Tanzania, and Malawi) in this study is crucial to inform rapid intervention in mitigating the spread of these resistant pathogens. Notably, there was a significant difference in the number of studies emanating from these countries, which could have influenced the total prevalence reported in our study.

This study also observed an increase in publications from 2019 to 2023, corresponding with an increase in reported prevalence. The consistent increase across different populations and regions underscores the growing threat of ESBL-producing *E. coli* worldwide and emphasizes the urgent need for continued surveillance and intervention strategies. This trend aligns with the global upward trend reported by Bezabih et al. [42], suggesting that the rise of ESBL-producing *E. coli* is a widespread phenomenon not limited to specific regions or populations.

Majority of the studies focused on humans within the context of infectious disease and antimicrobial resistance, and we observed a human prevalence of 20.23 % in SSA. This is not surprising as one of six people either healthy or sick worldwide is believed to harbour this organism [42]. This is generally higher than the prevalence in Europe where the highest EU/EEA population-weighted mean resistance percentage for ESBL producing-*E. coli* is 13.8 % in healthcare settings [43] but lower than in South-East Asia, which has 35.1 % and 32.9 % prevalence in both community and healthcare settings [42]. Also, report from some selected Asian countries shows an average increased carriage of ESBL-producing *E. coli* by 17.7 % both in hospital and community settings [44]. However, our prevalence closely aligns with the prevalence reported in the Eastern Mediterranean and the global prevalence reported by Bezabih et al. [42], who found that 21.1 % of inpatients in healthcare settings and 17.6 % of healthy individuals in the community worldwide carried ESBL-producing *E. coli*. This concordance suggests that the SSA region may not significantly deviate from world trends, given the region's unique challenges with poverty, education, antibiotics stewardship, and dearth of healthcare infrastructure. However, it is essential to note that our prevalence was broader, encompassing different countries and settings, which may mask localized hotspots of higher prevalence.

A significant strength of our study is adopting a One Health approach, encompassing data from studies on human, animal, environmental, and even food samples. This comprehensive strategy offers a broader ecological perspective, which could provide an in-depth view into potential sources and the complex interplay of these sources in the propagation of this resistant pathogen within sub-Saharan Africa. The highest prevalence of ESBL-producing *E. coli* in animal samples (29.15 % [95 % CI: 16.78–43.27]) raises important questions about the potential role of animals in the transmission and spread of this resistant

bacterium. Several studies have reported the presence of ESBL-producing *E. coli* in animals in Europe such as in the Netherlands [45], Switzerland [46], and France [47], Asia such as China [48], South Korea [49], in America such as Chile [50] and United States [51] as well as in Africa such as Egypt [52].

A study in Ecuador [37] showed that domesticated animals possess ESBL-producing *E. coli* strains. They also reported the simultaneous presence of these strains in both animal and human populations, demonstrating a potential animal-to-human or human-to-animal route of transmission. Even though some of the studies (55 %) utilized molecular techniques using either PCR, genotypic assay, or whole-genome sequencing in identifying the ESBL-producing *E. coli* obtained from different sources, the route of transmission was not established. A potential source of this resistant pathogen could be through their feeds and the fact that third-generation cephalosporin, ceftiofur, is widely approved for treating early mortality infections in early old turkeys and chicks [53]. Although the practice of using antimicrobials as growth promoters has been legislatively phased out by the United States, Canada, and the European Union, there is still no enforced legislation on this in most countries in sub-Saharan Africa.

Even though the prevalence in food is the least (14.02 % [95 % CI: 4.75–26.94]), this is still a source of concern from a food safety perspective. The presence of ESBL-producing *E. coli* has been reported in several studies on various food items across different regions in the world, including milk samples in India [54], dairy products in Mexico [55] and Turkey [56], meats from Portugal [57], and cattle, swine, poultry, and vegetables in Germany [58]. In 2022, European Food Safety reported that about 61 % of samples from broiler meat and 71.15 % of samples from turkey meat were presumptively positive for ESBL-/AmpC-/CP-producing *E. coli* [43]. The presence of this organism in food necessitates implementing measures that increase vigilance and food policies that mitigate the risk of the spread of ESBL-producing *E. coli* transmission through food in sub-Saharan Africa. The prevalence of food observed in our review is lower than 39 % reported in Bangladesh [38], though the latter only caters to a country.

The environment also remains a key contributor to the spread of ESBL-producing *E. coli* with a prevalence of 17.14 % in sub-Saharan Africa. Recent reports in the region have shown that surface water is a major hotspot for the dissemination of ESBL-producing *E. coli* due to poor adherence to proper water safety practices and indiscriminate disposal of pollutants into water bodies [59]. Similar detection in surface water and wastewater has been reported in the Netherlands [60], Switzerland [61], Malaysia [62], New Zealand [63], and Brazil [64]. Furthermore, a recent investigation examining the contribution of drinking water sources to the environmental dissemination of antibiotic-resistant *Escherichia coli* in Africa revealed widespread fecal contamination of these water sources with *E. coli* strains exhibiting both antibiotic resistance phenotype and genotype [65].

We also identified several genes involved in beta-lactamase production in *E. coli* from studies in SSA. A proportion (58.2 %) of the articles in sub-Saharan Africa utilized either molecular tools or in combination with phenotypic methods with increased specificity and sensitivity to unravel the genes coding for the beta-lactamase production, but there is still need for a comprehensive approach to ESBL detection and characterization in sub-Saharan Africa. The primary gene driving this resistance in these studies is the bla_{CTX} gene. This is consistent with reports from China [66], Portugal [67], Romania [68], the Netherlands [69], and the United States of America [70]. The $bla_{\text{CTX-M-15}}$ variants predominate and were found across the different sources, which is consistent with Houkes et al. [71] report of $bla_{\text{CTX-M}}$ genes contributing to 85 % ESBL resistance in *Enterobacteriaceae* in the Netherlands [71]. This consistency across different populations and regions emphasizes the global significance of $bla_{\text{CTX-M}}$ in ESBL-producing *E. coli* and suggests potential targets for intervention strategies.

We also observed the presence of the bla_{TEM}, and bla_{SHV} genes in various articles, which is consistent with reports from Spain [72], where genes coding for $bla_{\text{SHV-12}}$, $bla_{\text{CTX-M-1}}$, $bla_{\text{CTX-M-32}}$, and $bla_{\text{TEM-52}}$ enzymes were reported in chicken meat. A study in Germany also reported the presence of the $bla_{\text{SHV-12}}$ gene on an IncHI2 plasmid which also harbored the $bla_{\text{VIM-1}}$ gene from ESBL-producing *E. coli* isolated from livestock and derivative products [73]. Although the bla_{PER} gene was reported by one study in sub-Saharan Africa, this is such a rarity as the gene is often associated with *Acinetobacter* and *Citrobacter* [74]. Similarly, the bla_{GES} gene are often found in *Klebsiella* spp. and *Enterobacter* spp. [75]. The presence of $bla_{\text{CTX-M-15}}$, bla_{TEM}, and bla_{SHV} genes in ESBL-producing *E. coli* throughout the sample types (human, animal, environment, and food) highlights the importance of the one health approach in understanding the prevalence of AMR and in mitigating strategies to curb its spread.

It is worth noting that the present systematic review and meta-analysis may be subject to several limitations. Firstly, publication bias may have influenced the results, as studies with significant or favourable findings are more likely to be published than those with null or unfavourable results. Although we attempted to mitigate this bias by searching multiple databases and included all available eligible studies, some relevant studies may still have been missed. While the present systematic review only included English-language publications, it is worth noting that the majority of studies on ESBL-producing *E. coli* in sub-Saharan Africa are indeed published in English. A preliminary search revealed that English-language publications dominated the literature, with very few studies published in other languages. Given the prevalence of English-language publications in this field, the language restriction is unlikely to have introduced significant bias into the review. Nevertheless, the possibility that some relevant non-English studies may have been excluded cannot be entirely ruled out.

Sample size variability across studies may have contributed to heterogeneity in the meta-analysis. The included studies had varying sample sizes, which may have affected the precision of the estimates. To address these limitations, researchers should strive to conduct well-powered studies with adequate sample sizes to ensure reliable estimates and minimize heterogeneity. The significant heterogeneity observed in this meta-analysis might be due to the uneven distribution of studies across different countries and the methodology variations, which could potentially impact the generalizability of our findings.

In spite of these limitations, this review represents the most comprehensive synthesis of ESBL-producing *E. coli* in sub-Saharan Africa to date, incorporating data from human, animal, and environment, as well as food-related data spanning 27 countries from different regions and subgroups. By employing robust statistical methods, we generated pooled estimates that provide a nuanced understanding of this critical public health pathogen.

Addressing the issue of ESBL-producing *E. coli* in sub-Saharan Africa requires concerted efforts across different sectors in the region. Given the pooled prevalence of 20.76 % in sub-Saharan Africa, there is a need to establish a regional surveillance system that incorporates standardized protocols throughout the subregions. Our analysis revealed that the disparity in the number and quality of research in different countries could be attributed to capacity and infrastructural deficits in some of the regions. Thus, there is a need to ensure uniformity in surveillance through the establishment of reference laboratories equipped with molecular capacity across the region. This would strengthen monitoring in Central and Southern Africa, where information on ESBL-producing *E. coli* is currently limited. All data from these subregions can be channeled into a central database that can inform healthcare policies across the whole region, which can strengthen antibiotics stewardship. This centralized database can strengthen regional collaboration, and the advancement of technology, especially artificial intelligence (AI), can offer the unique advantage of real-time monitoring that can hasten policymaking throughout the region. Also, there is a need for capacity building through healthcare worker training, public awareness campaigns, and community-based education programs.

To reduce the prevalence in animals, strict legislation needs to be

implemented to phase out the use of antimicrobials as growth promoters within the region, with governments providing subsidized alternatives to farmers. Despite lower prevalence in food, there is still a need to tighten food safety measures through compulsory molecular surveillance of ESBL-producing *E. coli* in foods and HACCP implementation.

5. Conclusion

Resistance to extended-spectrum beta-lactam antibiotics greatly threatens the sustainable use of beta-lactams in the clinic. Our study indicates that, while the overall prevalence of ESBL-producing *E. coli* in SSA and its subregions is lower than previously reported in certain other WHO regions, including Asia, some SSA countries exhibit relatively high prevalence rates. Consequently, there is a need for the implementation of country-tailored measures and policies aimed at mitigating the dissemination of these multidrug-resistant pathogens in SSA.

Although our study estimated the highest prevalence of ESBL-producing *E. coli* in animals within SSA, the comparatively high prevalence observed in both humans and the environment is alarming. This further emphasizes the necessity of a One Health approach in curbing the spread of AMR in the region. Strict measures and policies should be put in place to curtail or completely eradicate the use of antimicrobials used in human medicine for agriculture. Programs for antimicrobial stewardship should also be put in place to encourage the appropriate use of antibiotics in the environment and in clinical settings, as well as to lessen the burden on currently available therapeutically relevant antibiotics.

We implore policymakers in the region to create and implement action plans that involve all stakeholders from human, animal, and environmental health as well as food safety to mitigate the effect of the spread of AMR pathogens and associated mortality. Additionally, action plans that will improve hygiene, strengthen healthcare systems, and improve the standard of living in the region, which may indirectly reduce the spread of AMR, must be taken. SSA governments must increase their investments in surveillance research, research facilities, and rapid diagnostic techniques for prompt understanding of AMR status in the region regularly and implement measures to curb its spread. Furthermore, there is a need for a strong collaboration between governments of sub-Saharan African countries as well as subregional organizations like ECOWAS to reduce AMR prevalence and spread in the region. This partnership will further enhance active surveillance, research, and data sharing among government agencies and nations to understand AMR prevalence and halt its spread.

Finally, AMR is a complex problem that requires a multifaceted strategy to reduce the estimated mortality that will accompany a post-antibiotic era. Hence, building strong health systems, fostering cooperation between governments and key stakeholders, and improving surveillance, diagnostic, and research facilities are measures that will mitigate the spread of AMR and provide a sustainable future for infection therapy.

Data sharing

All dataset generated and analyzed in this study are included within the article and/or its Supplementary data file.

CRediT authorship contribution statement

Morufat Oluwatosin Olaitan: Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Oluwatosin Qawiyy Orababa:** Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Software, Resources, Methodology, Investigation, Data curation. **Rukayya Bushola Shittu:** Methodology, Investigation, Data curation. **Gift Maureen Obunukwu:** Methodology, Investigation, Data curation. **Ayomikun Emmanuel Kade:** Writing – original draft, Visualization, Methodology. **Margaret Toluwalayo Arowolo:** Writing – original draft, Methodology. **Adams Alabi Oyediran:** Methodology, Investigation. **Rildwan Alaba Yusuff:** Methodology, Investigation.

Declaration of competing interest

The authors declare no competing interests.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.onehlt.2025.101090.

Data availability

All data used are available within the manuscript or/and its Supplementary data file

References

[1] World Health Organisation (WHO), Global Antimicrobial Resistance and Use Surveillance System (GLASS) Report, WHO, 2020. http://www.who.int/glass/resources/publications/early-implementation-report-2020/en/ (accessed 26 July 2024).
[2] C.J.L. Murray, K.S. Ikuta, F. Sharara, L. Swetschinski, G. Robles Aguilar, A. Gray, et al., Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis, Lancet 399 (10325) (2022) 629–655, https://doi.org/10.1016/S0140-6736(21)02724-0.
[3] M. Naghavi, S.E. Vollset, K.S. Ikuta, L.R. Swetschinski, A.P. Gray, E.E. Wool, et al., Global burden of bacterial antimicrobial resistance 1990–2021: a systematic analysis with forecasts to 2050, Lancet 404 (2024) 1199–1226, https://doi.org/10.1016/S0140-6736(24)01867-1.
[4] O.G. Onduru, R.S. Mkakosya, S. Aboud, S.F. Rumisha, Genetic determinants of resistance among ESBL-producing Enterobacteriaceae in community and hospital settings in east, central, and southern Africa: a systematic review and meta-analysis of prevalence, Can. J. Infect. Dis. Med. Microbiol. 5153237 (2021), https://doi.org/10.1155/2021/5153237.
[5] P. Moyo, E. Moyo, D. Mangoya, M. Mhango, T. Mashe, M. Imran, et al., Prevention of antimicrobial resistance in sub-Saharan Africa: what has worked? What still needs to be done? J. Infect. Public Health 16 (2023) 632–639, https://doi.org/10.1016/j.jiph.2023.02.020.
[6] M. Sammaro, B. Rowlingson, D. Cocker, K. Chidziwisano, S.T. Jacob, H. Kajumbula, et al., Risk factors, temporal dependence, and seasonality of human extended-spectrum β-lactamases-producing *Escherichia coli* and *Klebsiella pneumoniae* colonization in Malawi: a longitudinal model-based approach, Clin. Infect. Dis. 77 (2023) 1–8, https://doi.org/10.1093/cid/ciad117.
[7] M. Tawyabur, M.S. Islam, M.A. Sobur, M.J. Hossain, M.M. Mahmud, S. Paul, et al., Isolation and characterization of multidrug-resistant *Escherichia coli* and *Salmonella* spp. from healthy and diseased turkeys, Antibiotics 9 (11) (2020) 770, https://doi.org/10.3390/antibiotics9110770.
[8] M. Talukder, M.S. Islam, S. Ievy, M.A. Sobur, F.M. Ballah, M. Najibullah, et al., Detection of multidrug-resistant *Salmonella* spp. from healthy and diseased broilers having potential public health significance, J. Adv. Biotechnol. Exp. Ther. 4 (2) (2021) 248–255, https://doi.org/10.5455/JABET.2021.D125.
[9] A. Karkman, T.T. Do, F. Walsh, M.P.J. Virta, Antibiotic-resistance genes in wastewater, Trends Microbiol. 26 (2018) 220–228, https://doi.org/10.1016/j.tim.2017.09.005.
[10] Y.M. Bezabih, W. Sabiiti, E. Alamneh, A. Bezabih, G.M. Peterson, W.M. Bezabhe, A. Roujeinikova, The global prevalence and trend of human intestinal carriage of ESBL-producing *Escherichia coli* in the community, J. Antimicrob. Chemother. 76 (1) (2021) 22–29, https://doi.org/10.1093/jac/dkaa399.
[11] L.F. Ribeiro, N.M. Nespolo, G.A.M. Rossi, J.M. Fairbrother, Exploring extended-spectrum beta-lactamase (ESBL)-producing *Escherichia coli* in food-producing animals and animal-derived foods, Pathogens 13 (2024) 346–357, https://doi.org/10.3390/pathogens13040346.
[12] N.M. Dreger, S. Degener, P. Ahmad-Nejad, G. Wobker, S. Roth, Urosepsis—etiology, diagnosis, and treatment, Dtsch. Arztebl. Int. 112 (2015) 837–847, https://doi.org/10.3238/arztebl.2015.0837.
[13] S. Levy, M.S. Islam, M.A. Sobur, M. Talukder, M.B. Rahman, M.F.R. Khan, M. T. Rahman, Molecular detection of avian pathogenic *Escherichia coli* (APEC) for the first time in layer farms in Bangladesh and their antibiotic resistance patterns, Microorganisms 8 (7) (2020) 1021–1036, https://doi.org/10.3390/microorganisms8071021.
[14] M.S. Islam, M.M.H. Nayeem, M.A. Sobur, S. Ievy, M.A. Islam, S. Rahman, et al., Virulence determinants and multidrug resistance of *Escherichia coli* isolated from migratory birds, Antibiotics (Basel) 10 (2) (2021) 190–203, https://doi.org/10.3390/antibiotics10020190.

[15] World Health Organization. WHO Integrated Global Surveillance on ESBL-Producing *E. coli* Using a "One Health" Approach: Implementation and Opportunities. World health Organization. https://www.who.int/publications/i/item/9789240021402#:~:text=WHO%20and%20the%20Advisory%20Group92-4-002140-2, 2021 (accessed 13th February 2025).
[16] M.T. Arowolo, O.Q. Orababa, M.O. Olaitan, B.V. Osibeluwo, U.U. Essiet, et al., Prevalence of carbapenem resistance in *Acinetobacter baumannii* and *Pseudomonas aeruginosa* in sub-Saharan Africa: a systematic review and meta-analysis, PLoS ONE 18 (2023) e0287762, https://doi.org/10.1371/journal.pone.0287762.
[17] S. Ramos, V. Silva, M.L.E. Dapkevicius, M. Caniça, M.T. Tejedor-Junco, G. Igrejas, P. Poeta, *Escherichia coli* as commensal and pathogenic bacteria among food-producing animals: health implications of extended-spectrum β-lactamase (ESBL) production, Animals (Basel) 10 (2020) 2239–2254, https://doi.org/10.3390/ani10122239.
[18] L. Mughini-Gras, A. Dorado-García, E. van Duijkeren, G. van den Bunt, C. M. Dierikx, M.J.M. Bonten, et al., Attributable sources of community-acquired carriage of *Escherichia coli* containing β-lactam antibiotic resistance genes: a population-based modelling study, Lancet Planet Health 3 (2019) e357–e369, https://doi.org/10.1016/S2542-5196(19)30130-5.
[19] H. Bar-Yoseph, K. Hussein, E. Braun, M. Paul, Natural history and decolonization strategies for ESBL/carbapenem-resistant Enterobacteriaceae carriage: systematic review and meta-analysis, J. Antimicrob. Chemother. 71 (2016) 2729–2739. https://academic.oup.com/jac/article/71/10/2729/2388093?login=false.
[20] E. Ruppe, B. Lixandru, R. Cojocaru, C. Buke, E. Paramythiotou, C. Angebault, et al., Relative fecal abundance of extended-spectrum-β-lactamase-producing *Escherichia coli* strains and their occurrence in urinary tract infections in women, Antimicrob. Agents Chemother. 57 (2013) 4512–4517, https://doi.org/10.1128/aac.00238-13.
[21] M. Melzer, I. Petersen, Mortality following bacteremic infection caused by extended spectrum β-lactamase (ESBL) producing *E. coli* compared to non-ESBL producing *E. coli*, J. Inf. Secur. 55 (2007) 254–259, https://doi.org/10.1016/j.jinf.2007.04.007.
[22] B. Sapkota, S.K. Yadav, G. Dhungana, S. Ansari, S.K. Mishra, Intestinal carriage of extended-spectrum β-lactamase- (ESBL-) possessing *Escherichia coli* and Klebsiella species among Nepalese health science and non-health science students, Can. J. Infect. Dis. Med. Microbiol. 4767429 (2021), https://doi.org/10.1155/2021/4767429.
[23] M. Kowalski, B.M. Obama, G. Catho, J.E. Dewez, A. Merglen, M. Ruef, Antimicrobial resistance in enterobacterales infections among children in sub-Saharan Africa: a systematic review and meta-analysis, Lancet 70 (2024), https://doi.org/10.1016/j.eclinm.2024.102512.
[24] N. Camara, N. Moremi, J. Mghamba, E. Eliakimu, E. Shumba, P. Ondoa, B. Egyir, Surveillance of antimicrobial resistance in human health in Tanzania: 2016-2021, Afr. J. Lab. Med. 22 (12) (2023) 2053, https://doi.org/10.4102/ajlm.v12i1.2053.
[25] O.J. Okolie, U. Igwe, S.U. Ismail, U.L. Ighodalo, E.C. Adukwu, Systematic review of surveillance systems for AMR in Africa, J. Antimicrob. Chemother. 23 (78) (2022) 31–51, https://doi.org/10.1093/jac/dkac342.
[26] WHO, Tuberculosis, HIV, Malaria & Neglected Tropical Diseases, Strengthening Collaboration to Prevent and Manage Antimicrobial Resistance, World health Organization, 2019. https://iris.who.int/handle/10665/311689 (accessed 18 June 2024).
[27] M.A. Salam, M.Y. Al-Amin, M.T. Salam, J.S. Pawar, N. Akhter, A.A. Rabaan, M.A. A. Alqumber, Antimicrobial resistance: a growing serious threat for global public health, Healthcare (Basel) 5 (11) (2023) 1946, https://doi.org/10.3390/healthcare11131946.
[28] L.C. Koech, B.N. Irungu, M.M. Ng'ang'a, J.M. Ondicho, L.K. Keter, Quality and brands of amoxicillin formulations in Nairobi, Kenya, Biomed. Res. Int. 12 (2020) 7091278, https://doi.org/10.1155/2020/7091278.
[29] H. Lowe, S. Woodd, I.L. Lange, S. Janjanin, J. Barnet, W. Graham, Challenges and opportunities for infection prevention and control in hospitals in conflict-affected settings: a qualitative study, Confl. Heal. 15 (2021) 94, https://doi.org/10.1186/s13031-021-00428-8.
[30] A. Singh, T.G. Barnard, Health science students' perceptions of hand hygiene education and practice in a south African university: introducing the university hand hygiene improvement model, Healthcare (Basel) 15 (11) (2023) 2553, https://doi.org/10.3390/healthcare11182553.
[31] R.M. Moirongo, E. Lorenz, N.E. Ntinginya, D. Dekker, J. Fernandes, J. Held, et al., Regional variation of extended-spectrum beta-lactamase (ESBL)-producing enterobacterales, fluoroquinolone-resistant *Salmonella enterica* and methicillin-resistant *Staphylococcus aureus* among febrile patients in sub-Saharan Africa, Front. Microbiol. 25 (11) (2020), https://doi.org/10.3389/fmicb.2020.567235.
[32] M.J. Page, J.E. McKenzie, P.M. Bossuyt, et al., The PRISMA 2020 statement: an updated guideline for reporting systematic reviews, BMJ 372 (2021) 71, https://doi.org/10.1136/bmj.n71.
[33] Z. Munn, S. Moola, K. Lisy, D. Riitano, C. Tufanaru, Methodological guidance for systematic reviews of observational epidemiological studies reporting prevalence and incidence data, Int. J. Evid. Based Heal. 13 (3) (2015) 147–153, https://doi.org/10.1097/XEB.0000000000000054.
[34] L.M. Spineli, N. Pandis, Meta-analysis: random-effects model, Am. J. Orthod. Dentofacial Orthop. 157 (2) (2020) 280–282, https://doi.org/10.1016/j.ajodo.2019.10.007.
[35] B. Thakuria, K. Lahon, The beta-lactam antibiotics as an empirical therapy in a developing country: an update on their current status and recommendations to counter the resistance against them, J. Clin. Diagn. Res. 7 (6) (2013) 1207–1214, https://doi.org/10.7860/JCDR/2013/5239.3052.
[36] T. Jesudason, WHO publishes updated list of bacterial priority pathogens, Lancet Microbe 5 (9) (2024) 100940, https://doi.org/10.1016/j.lanmic.2024.07.003.
[37] C. Bastidas-Caldes, D. Romero-Alvarez, V. Valdez-Velez, R.D. Morales, A. Montalvo-Hernandez, C. Gomes-Dias, M. Calvopina, Extended-spectrum beta-lactamases producing *Escherichia coli* in South America: a systematic review with a one health perspective, Infect. Drug Resist. 15 (2022) 5759–5779, https://doi.org/10.2147/IDR.S371845.
[38] M.S. Islam, A.T. Rahman, J. Hassan, M.T. Rahman, Extended-spectrum beta-lactamase in *Escherichia coli* isolated from humans, animals, and environments in Bangladesh: a one health perspective systematic review and meta-analysis, One Health 16 (2023) 100526, https://doi.org/10.1016/j.onehlt.2023.100526.
[39] O.O. Mahamat, M. Kempf, M. Lounnas, A. Tidjani, M. Hide, J.A. Benavides, S. Godreuil, Epidemiology and prevalence of extended-spectrum β-lactamase-and carbapenemase-producing enterobacteriaceae in humans, animals, and the environment in west and Central Africa, Int. J. Antimicrob. Agents 57 (1) (2021) 106203, https://doi.org/10.1016/j.ijantimicag.2020.106203.
[40] World Health Organization, Antimicrobial Resistance Surveillance in Europe 2022–2020 Data, WHO, 2022.
[41] European Centre for Disease Prevention and Control, Surveillance Atlas of Infectious Diseases. https://www.ecdc.europa.eu/en/surveillance-atlas-infectious-diseases, 2021. (Accessed 21 October 2024).
[42] Y.M. Bezabih, A. Bezabih, M. Dion, E. Batard, S. Teka, A. Obole, et al., Comparison of the global prevalence and trend of human intestinal carriage of ESBL-producing *Escherichia coli* between healthcare and community settings: a systematic review and meta-analysis, JAC-Antimicrob. Resist. 4 (3) (2022) dlac048, https://doi.org/10.1093/jacamr/dlac048.
[43] European Food Safety Authority (EFSA), European Centre for Disease Prevention and Control (ECDC), the European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2021–2022, EFSA J. 22 (2) (2024) e8583, https://doi.org/10.2903/j.efsa.2024.8583.
[44] S.R. Singh, A.K.J. Teo, K. Prem, R.T.H. Ong, E.A. Ashley, H.R. Van Doorn, et al., Epidemiology of extended-spectrum beta-lactamase and carbapenemase-producing Enterobacterales in the greater Mekong subregion: a systematic-review and meta-analysis of risk factors associated with extended-spectrum beta-lactamase and carbapenemase isolation, Front. Microbiol. 12 (2021) 695027, https://doi.org/10.3389/fmicb.2021.695027.
[45] M.S. Brouwer, A. Zandbergen Van Essen, A. Kant, M. Rapallini, F. Harders, A. Bossers, K.T. Veldman, Implementation of WGS analysis of ESBL-producing *Escherichia coli* within EU AMR monitoring in livestock and meat, J. Antimicrob. Chemother. 78 (7) (2023) 1701–1704, https://doi.org/10.1093/jac/dkad158.
[46] A.L. Zogg, K. Zurfluh, S. Schmitt, M. Nüesch-Inderbinen, R. Stephan, Antimicrobial resistance, multilocus sequence types and virulence profiles of ESBL-producing and non-ESBL-producing uropathogenic *Escherichia coli* isolated from cats and dogs in Switzerland, Vet. Microbiol. 216 (2018) 79–84, https://doi.org/10.1016/j.vetmic.2018.02.011.
[47] L.C. Melo, M. Haenni, E. Saras, L. Cerdeira, Q. Moura, H.-J. Boulouis, J.-Y. Madec, Genomic characterisation of a multidrug-resistant TEM-52b extended-spectrum β-lactamase-positive *Escherichia coli* ST219 isolated from a cat in France, J. Glob. Antimicrob. Resist. 18 (2019) 223–224, https://doi.org/10.1016/j.jgar.2019.07.012.
[48] Y. Chen, Z. Liu, Y. Zhang, Z. Zhang, L. Lei, Z. Xia, Increasing prevalence of ESBL-producing multidrug resistance *Escherichia coli* from diseased pets in Beijing, China from 2012 to 2017, Front. Microbiol. 10 (2019) 2852, https://doi.org/10.3389/fmicb.2019.02852.
[49] J. Li, Z. Bi, S. Ma, B. Chen, C. Cai, J. He, J. Wang, et al., Inter-host transmission of carbapenemase-producing *Escherichia coli* among humans and backyard animals, Environ. Health Perspect. 127 (10) (2019) 107009, https://doi.org/10.1289/ehp5251.
[50] J.A. Benavides, M. Salgado-Caxito, A. Opazo-Capurro, P. Gonzalez Munoz, A. Piñeiro, M.O. Medina, et al., ESBL-producing *Escherichia coli* carrying CTX-M genes circulating among livestock, dogs, and wild mammals in small-scale farms of Central Chile, Antibiotics 10 (5) (2021) 510, https://doi.org/10.3390/antibiotics10050510.
[51] T.E. LeCuyer, B.A. Byrne, J.B. Daniels, D.V. Diaz-Campos, G.K. Hammac, C. B. Miller, Population structure and antimicrobial resistance of canine uropathogenic *Escherichia coli*, J. Clin. Microbiol. 56 (9) (2018) 10–1128, https://doi.org/10.1128/JCM.00788-18.
[52] M.A. Nossair, F.A. Abd El Baqy, M.S. Rizk, H. Elaadli, A.M. Mansour, A.H.A. El-Aziz, et al., Prevalence and molecular characterization of extended-spectrum β-lactamases and AmpC β-lactamase-producing Enterobacteriaceae among human, cattle, and poultry, Pathogens 11 (8) (2022) 852, https://doi.org/10.3390/pathogens11080852.
[53] R.S. Singer, N.F. Schrag, I. Ricke, M.D. Apley, On-farm antimicrobial usage in commercial Turkey production in the United States, 2013–2021, Front. Vet. Sci. 10 (2023) 1158943, https://doi.org/10.3389/fvets.2023.1158943.
[54] K. Batabyal, A. Banerjee, S. Pal, S. Dey, S.N. Joardar, I. Samanta, et al., Detection, characterization, and antibiogram of extended-spectrum beta-lactamase *Escherichia coli* isolated from bovine milk samples in West Bengal, India, Vet. World 11 (10) (2018) 1423, https://doi.org/10.14202/vetworld.2018.1423-1427.
[55] P.D. Loeza-Lara, R.I. Medina-Estrada, Á.E. Bravo-Monzón, R. Jiménez-Mejía, Frequency and characteristics of ESBL-producing *Escherichia coli* isolated from Mexican fresh cheese, Food Sci. Technol. 43 (2023) e108222, https://doi.org/10.1590/fst.108222.
[56] A. Gücükoğlu, T. Uyanik, Ö. Çadirci, E. Uğurtay, S. Kanat, A. Bölükbaş, Determination of extended spectrum β-lactamase-producing enterobacteriaceae in raw water buffalo milk and dairy products by conventional multiplex and real-time

PCR, Int. Dairy J. 140 (2023) 105581, https://doi.org/10.1016/j.idairyj.2022.105581.
[57] L. Clemente, C. Leão, L. Moura, T. Albuquerque, A. Amaro, Prevalence and characterization of ESBL/AmpC producing *Escherichia coli* from fresh meat in Portugal, Antibiotics 10 (11) (2021) 1333, https://doi.org/10.3390/antibiotics10111333.
[58] A. Kaesbohrer, K. Bakran-Lebl, A. Irrgang, J. Fischer, P. Kämpf, A. Schiffmann, et al., Diversity in prevalence and characteristics of ESBL/pAmpC producing *E. coli* in food in Germany, Vet. Microbiol. 233 (2019) 52–60, https://doi.org/10.1016/j.vetmic.2019.03.025.
[59] A. Beshiru, N.A. Isokpehi, I.H. Igbinosa, O. Akinnibosun, A.G. Ogofure, E. O. Igbinosa, Extended-spectrum beta-lactamase (ESBL)-and non-ESBL producing *Escherichia coli* surveillance in surface water sources in Edo state, Nigeria: a public health concern, Sci. Rep. 14 (1) (2024) 21658, https://doi.org/10.1038/s41598-024-72993-w.
[60] L. Crettels, N. Burlion, A. Habets, B. Taminiau, G. Daube, E. Delrée, et al., Exploring the presence, genomic traits, and pathogenic potential of extended spectrum β-lactamase *Escherichia coli* in freshwater, wastewater, and hospital effluents, J. Appl. Microbiol. lxae144 (2024), https://doi.org/10.1093/jambio/lxae144.
[61] A. Müller, R. Stephan, M. Nüesch-Inderbinen, Distribution of virulence factors in ESBL-producing *Escherichia coli* isolated from the environment, livestock, food and humans, Sci. Total Environ. 541 (2016) 667–672, https://doi.org/10.1016/j.scitotenv.2015.09.135.
[62] S. Tissera, S.M. Lee, Isolation of extended spectrum β-lactamase (ESBL) producing bacteria from urban surface waters in Malaysia, Malays. J. Med. Sci. 20 (3) (2013) 14–22. https://pubmed.ncbi.nlm.nih.gov/23966820/.
[63] H.A. Gray, P.J. Biggs, A.C. Midwinter, L.E. Rogers, A. Fayaz, R.N. Akhter, S. A. Burgess, Genomic epidemiology of extended-spectrum beta-lactamase-producing *Escherichia coli* from humans and a river in Aotearoa New Zealand, Microb. Genom. 11 (1) (2025) 001341, https://doi.org/10.1099/mgen.0.001341.
[64] R. Requena-Castro, M.G. Aguilera-Arreola, A.V. Martínez-Vázquez, W.L. Cruz-Pulido, G. Rivera, V. Bocanegra-García, Antimicrobial resistance, virulence genes, and ESBL (extended Spectrum Beta-lactamase) production analysis in *E. coli* strains from the Rio Grande/Rio Bravo River in Tamaulipas, Mexico, Braz. J. Microniol. (2024) 1–9, https://doi.org/10.1007/s42770-024-01376-0.
[65] A.G. Rabiu, A.J. Marcus, M.O. Olaitan, O.I. Falodun, Systematic review and Meta-analyses of the role of drinking water sources in the environmental dissemination of antibiotic-resistant *Escherichia coli* in Africa, Int. J. Environ. Health Res. 34 (1) (2024) 1–15, https://doi.org/10.1080/09603123.2024.2320934.
[66] Y.L. Zhang, F.Y. Huang, L.L. Gan, X. Yu, D.J. Cai, J. Fang, et al., High prevalence of Bla(CTX-M) and Bla(SHV) among ESBL-producing *E. coli* isolates from beef cattle in China's Sichuan-Chongqing circle, Sci. Rep. 11 (1) (2021) 13725, https://doi.org/10.1038/s41598-021-93201-z.
[67] I. Carvalho, J.A. Carvalho, S. Martínez-Álvarez, M. Sadi, R. Capita, C. Alonso-Calleja, et al., Characterization of ESBL-producing *Escherichia coli* and *Klebsiella pneumoniae* isolated from clinical samples in a northern Portuguese hospital: predominance of CTX-M-15 and high genetic diversity, Microorganisms 9 (9) (2021), https://doi.org/10.3390/microorganisms9091914.
[68] A.E. Ghenea, O.M. Zlatian, O.M. Cristea, A. Ungureanu, R.R. Mititelu, A. T. Balasoiu, et al., TEM, CTX-M, SHV genes in ESBL-producing *Escherichia coli* and *Klebsiella pneumoniae* isolated from clinical samples in a county clinical emergency hospital Romania-predominance of CTX-M-15, Antibiotics (Basel) 11 (4) (2022), https://doi.org/10.3390/antibiotics11040503.
[69] I. Willemsen, S. Oome, C. Verhulst, A. Pettersson, K. Verduin, J. Kluytmans, Trends in extended spectrum beta-lactamase (ESBL) producing enterobacteriaceae and ESBL genes in a Dutch teaching hospital, measured in 5 yearly point prevalence surveys (2010-2014), PLoS ONE 10 (11) (2015) e0141765, https://doi.org/10.1371/journal.pone.0141765.
[70] P.D. Tamma, T.T. Smith, A. Adebayo, S.M. Karaba, E. Jacobs, T. Wakefield, et al., Prevalence of Bla(CTX-M) genes in gram-negative bloodstream isolates across 66 hospitals in the United States, J. Clin. Microbiol. 59 (6) (2021), https://doi.org/10.1128/JCM.00127-21.
[71] K.M.G. Houkes, V. Weterings, W. van den Bijllaardt, M. Tinga, P.G.H. Mulder, et al., One decade of point-prevalence surveys for carriage of extended-spectrum beta-lactamase-producing Enterobacterales: whole genome sequencing-based prevalence and genetic characterization in a large Dutch teaching hospital from 2013 to 2022, Antimicrob. Resist. Infect. Control 13 (1) (2024) 102, https://doi.org/10.1186/s13756-024-01460-y.
[72] S. Martínez-Álvarez, U. Höfle, P. Châtre, C.A. Alonso, M.Á. Asencio-Egea, P. François, et al., One health bottom-up analysis of the dissemination pathways concerning critical priority carbapenemase- and ESBL-producing enterobacterales from storks and beyond, J. Antimicrob. Chemother. dkae371 (2024), https://doi.org/10.1093/jac/dkae371.
[73] N. Pauly, J.A. Hammerl, S. Schwarz, M. Grobbel, D. Meemken, B. Malorny, et al., Co-occurrence of the blaVIM-1 and blaSHV-12 genes on an IncHI2 plasmid of an *Escherichia coli* isolate recovered from German livestock, J. Antimicrob. Chemother. 76 (2) (2021) 531–533, https://doi.org/10.1093/jac/dkaa436.
[74] M. Ruggiero, K.M. Papp-Wallace, F. Brunetti, M.D. Barnes, R.A. Bonomo, G. Gutkind, et al., Structural insights into the inhibition of the extended-spectrum β-lactamase PER-2 by avibactam, Antimicrob. Agents Chemother. 63 (9) (2019) 10–1128, https://doi.org/10.1128/aac.00487-19.
[75] S. Takizawa, E. Soga, W. Hayashi, K. Sakaguchi, S. Koide, M. Tanabe, et al., Genomic landscape of Bla(GES-5)- and Bla(GES-24)-harboring gram-negative bacteria from hospital wastewater: emergence of class 3 integron-associated Bla (GES-24) genes, J. Glob. Antimicrob. Resist. 31 (2022) 196–206, https://doi.org/10.1016/j.jgar.2022.09.005.