

Prevalence, and Antimicrobial Resistance Profile of *Escherichia coli* O157:H7 Isolated from Human, Animal, and Environmental Samples in Ethiopia: A Systematic Review and Meta-Analysis

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Abstract

Background

Escherichia coli O157 is an important foodborne zoonotic pathogen with consequences for human and animal health and food safety. Its circulation at the human–animal–environment interface, together with antimicrobial resistance, makes it an important One Health concern. However, evidence on the burden and antimicrobial resistance of *E. coli* O157 across these interconnected sources in Ethiopia remains fragmented. This systematic review and meta-analysis aimed to estimate the pooled prevalence of *E. coli* O157 and characterize its antimicrobial resistance patterns from a One Health perspective.

Methods

PubMed, ScienceDirect, Scopus, Web of Science, and Google Scholar were searched for cross-sectional studies published between January 2015 and May 2025. Two groups of reviewers independently screened studies using predefined eligibility criteria. Study quality was assessed using the Joanna Briggs Institute tool. Pooled prevalence and antimicrobial resistance proportions were estimated using random-effects models. Heterogeneity and publication bias were assessed, and sensitivity analysis was performed.

Results

A total of 1,224 records were identified, of which 52 studies were included in the meta-analysis. The overall pooled prevalence of *E. coli* O157 was 4.65% (95% CI: 3.58–6.02%), with substantial heterogeneity across studies. Prevalence varied by sample source, ranging from 3.21% (95% CI: 2.08–4.96%) in environmental samples to 7.65% (95% CI: 3.80–15.42%) in human samples. Antimicrobial resistance also varied considerably across agents, with the highest resistance observed for erythromycin (89.65%; 95% CI: 66.31–97.45%) and the lowest for ciprofloxacin (8.44%; 95% CI: 4.42–15.52%).

Conclusion

E. coli O157 remains an important One Health concern in Ethiopia, with evidence of circulation across human, animal, and environmental sources and substantial variation in antimicrobial resistance. These findings underscore the need for integrated One Health surveillance, strengthened antimicrobial stewardship, and coordinated interventions across human health, animal production, food safety, and environmental sectors. This review was registered in PROSPERO (CRD420251163665) and received no external funding.

1. Introduction

Escherichia coli O157:H7 is the prototype serotype of Shiga toxin-producing *Escherichia coli* (STEC), also referred to as enterohemorrhagic *E. coli* (EHEC), and is one of the most important foodborne zoonotic pathogens worldwide [1, 2]. Unlike commensal *E. coli*, this serotype possesses potent virulence factors, including Shiga toxins, that can cause hemorrhagic colitis and life-threatening complications such as hemolytic uremic syndrome, particularly in children and other vulnerable populations [3, 4]. Foodborne STEC was responsible for an estimated 51.9 million illnesses, 20,500 deaths, and 1.24 million disability-adjusted life years (DALYs) globally in 2021[2], underscoring the continuing public health importance of *E. coli* O157:H7.

The epidemiology of *E. coli* O157:H7 is inherently linked to the human–animal–environment interface. Healthy ruminants, particularly cattle, are the primary reservoirs and shed the organism into the environment through feces, contaminating food, water, soil, and agricultural settings [5, 6]. Human infection occurs mainly through consumption of contaminated food or water or direct contact with infected animals or contaminated environments [7]. In Ethiopia, where livestock production, close human–animal contact, and the consumption of raw or undercooked animal products are common, these interconnected pathways provide favorable conditions for the persistence and transmission of *E. coli* O157:H7 [8, 9]. Accordingly, a One Health approach is not merely useful but a prerequisite for accurately characterizing the epidemiology, reservoirs, and antimicrobial resistance profile of *E. coli* O157:H7 in Ethiopia [10].

The emergence of antimicrobial-resistant *E. coli* O157:H7 adds another dimension to this public health challenge. Although antimicrobial therapy is generally avoided for uncomplicated STEC infections because some agents may increase Shiga toxin production and the risk of hemolytic uremic syndrome [11], resistant O157:H7 strains remain epidemiologically and clinically important. They may limit treatment options for invasive infections, serve as reservoirs of transferable resistance genes capable of horizontal spread to other bacterial pathogens, and reflect antimicrobial selection pressure across human, animal, and environmental sectors [12]. Reports of resistance to critically important antimicrobials, including fluoroquinolones, third-generation cephalosporins, and other commonly used agents, further emphasize the need for continued surveillance within a One Health framework [13].

In Ethiopia, numerous primary studies have reported the occurrence of *E. coli* O157 in humans, livestock, foods of animal origin, and environmental samples [9, 14, 15]. However, these findings remain fragmented, with considerable variation in reported prevalence, study populations, laboratory methods, and antimicrobial susceptibility profiles. A recent systematic review synthesized *E. coli* O157 across African countries, but its objective was to generate continental estimates rather than provide a comprehensive assessment of the epidemiology and antimicrobial resistance profile within Ethiopia [16]. Moreover, this syntheses have not comprehensively captured all available Ethiopian primary studies, limiting the representativeness and completeness of the current evidence. Another systematic review conducted in Ethiopia evaluated the prevalence and antimicrobial resistance of *E. coli* isolates but did not distinguish the O157 serotype and excluded environmental evidence, limiting its relevance to this clinically important zoonotic pathogen [17]. Therefore, to our knowledge, no systematic review has

specifically synthesized the prevalence and antimicrobial resistance profile of *E. coli* O157 across human, animal, and environmental sources in Ethiopia using a One Health framework.

Therefore, this systematic review and meta-analysis aims to estimate the pooled prevalence and antimicrobial resistance profile of *Escherichia coli* O157 isolated from human, animal, and environmental samples in Ethiopia. The findings will provide a comprehensive synthesis of the available evidence to support One Health surveillance, inform antimicrobial stewardship and food safety policies, and guide strategies for the prevention and control of *E. coli* O157 in Ethiopia.

2. Materials and methods

2.1. Search strategy

A comprehensive literature search was conducted using bibliographic and citation databases, including Google Scholar, PubMed, Web of Science, Scopus, and ScienceDirect, to identify pertinent articles. The search covered the period from October 8 2025, to December 18, 2025, to include up-to-date data and reflect current *E. coli* O157:H7 prevalence trends. The comprehensive search strategy used the condition (*E. coli* O157:H7), context (Ethiopia), and population (humans, animals and environment) (CoCoPop) research question mnemonic frameworks. The complete search strategy and associated keywords are presented in the supplementary material (Table S1). The search strategy was adapted to align with the specific requirements of each database. An example of the detailed search strategy used for Scopus and PubMed is provided in the supplementary material (Table S2). This study was reported according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines [18], which is provided in the supplementary material (Table S4). The protocol for this study was registered in PROSPERO (an international prospective register of systematic reviews) on October 08, 2025, with the registration number CRD420251163665.

2.2. Inclusion and exclusion criteria

All cross-sectional studies conducted in Ethiopia and published in English, including peer-reviewed publications were eligible for inclusion in this study. To ensure the incorporation of current and pertinent evidence on the prevalence of *E. coli* O157:H7 in Ethiopia, only studies conducted after 2015 were considered.

Research articles were excluded for one of the following reasons: (a) reporting the knowledge, attitudes, and practices of *E. coli* O157:H7 (qualitative studies); (b) articles with insufficient information or records with missing outcomes of interest; and (c) personal opinions, correspondence, letters to the editor, proceedings, and reviews.

2.3. Study selection and quality assessment

The quality of the included studies was assessed using the Joanna Briggs Institute's critical appraisal tool, which is designed to evaluate prevalence studies [19]. The tool has nine items, each measured with

four options: “yes,” “no,” “not applicable” and “unclear,” which assess study quality, including bias, confounding, the validity of exposure and outcome measurements, and the validity of analysis methods. The assessment of the included studies was conducted by two independent teams: Team A (SGE, BT, FBK, and EWA) and Team B (AW, DKA, JMK, and SKA). In this scoring framework, responses categorized as ‘yes’ received a score of 1, whereas responses of ‘no’ or ‘unclear’ (including cases where information was either absent or considered irrelevant) received 0 points. The total scores for each article were aggregated on a scale of 0–9. According to these scores, the articles were classified into three quality categories: good (7–9 points), medium (4–6 points), and low (0–3 points). Disagreements between the two reviewers were resolved through discussion. All studies included in this systematic review and meta-analysis demonstrated moderate to good methodological quality; therefore, none were excluded for an inadequate study quality (Table S5).

2.4. Outcome variables and operational definitions

The primary outcome of this study was the pooled magnitude of *E. coli* O157:H7 (reported as proportion) in Ethiopia. Secondary outcomes included the pooled antimicrobial susceptibility pattern of *E. coli* O157:H7 isolates (reported as proportion).

2.5. Data extraction

Data were extracted independently by two research teams; Team A (SGE, BT, FBK, and EWA) and Team B (AW, DKA, JMK, and SKA) using a predefined extraction sheet in Microsoft Excel (version 16.54). The extracted data included the name of the first author, year of publication, region where the study was conducted, study subject, sample size, type of transport media, and prevalence of *E. coli* O157:H7. Additionally, the antimicrobial resistance profile of *E. coli* O157:H7 isolates was recorded for antibiotics that were analyzed by at least four authors, including Amikacin, Amoxicillin, Amoxicillin–clavulanic acid, Ampicillin, Cefotaxime, Cefoxitin, Ceftazidime, Ceftriaxone, Cephalothin, Chloramphenicol, Ciprofloxacin, Erythromycin, Gentamicin, Kanamycin, Nalidixic acid, Nitrofurantoin, Norfloxacin, Streptomycin, Tetracycline, Trimethoprim, and Trimethoprim–sulfamethoxazole.

2.6. Data management and Statistical analysis

Data analysis was conducted in R [20] using *meta* package [21]. Due to substantial heterogeneity observed across studies, with significant between-study variability indicated by the inconsistency index (I^2) of 95.5% [95% CI: 94.1%; 96.5%], a random effects meta-analysis model was used to calculate the overall pooled effect size. Prevalence was transformed to the Logit (PLO) Proportions to stabilize variances and better approximate the normality of the effect-size distribution. Between-study variance was estimated using the commonly used estimator called the DerSimonian-Laird (DL) approach [22]. Given small number of included studies, Hartung-Knapp-Sidik-Jonkman (HKSJ) adjustments were applied to improve confidence interval coverage and reduce type I error inflation [23, 24].

The pooled prevalence of *E. coli* O157:H7 among individuals was graphically synthesized using forest plot to display individual study estimates with 95% confidence intervals (CI). Between-study

heterogeneity was quantified using the Cochrane Q-test [25], and I^2 statistic (proportion of total variability due to heterogeneity rather than sampling error) [26].

Furthermore, subgroup, sensitivity, and meta-regression analyses were conducted to address the substantial heterogeneity observed in the pooled estimates. Subgroup analysis was conducted based on geographic region, study subjects or groups, and type of detection methods for the sample to explore the sources of variability. Leave one out sensitivity analysis was used to assess the reliability of the combined results by systematically removing each study one at a time. If the confidence interval of the excluded study did not include the overall effect size estimate, it was considered to have a significant impact on the results [27]. To further examine the cause of variability among studies, both univariable and multivariable meta-regression models were utilized for categories including sample size, publication year, type of transport media, and region of the study.

Finally, publication bias was assessed using Egger's regression test [28] as well as Begg's rank correlation test [29] to check the symmetry of funnel plots. A non-significant outcome in Egger's test and Begg's rank correlation test ($p > 0.05$) suggests no evidence of significant publication bias or small-study effects.

For the antimicrobial resistance analysis, only antibiotics that were tested in at least four independent studies were included in the susceptibility assessment to ensure sufficient data for pooling, and improve the precision and stability of the estimated resistance patterns.

3. Result

3.1. Literature search and eligible studies

A total of 1,224 articles were initially retrieved through electronic searches and manual screening of the reference lists. Approximately 841 articles were excluded because of duplication. After reviewing their titles and abstracts, 276 articles were excluded because of unrelated titles and abstract content. The full texts of 107 studies were evaluated for eligibility. Consequently, 55 articles were excluded for the following reasons: the outcome of interest was not reported, not *E. coli* O157:H7 strain, the studies were review articles, or they were qualitative studies. Finally, after the methodological quality assessment, 52 studies were included in this systematic review and meta-analysis (Fig. 1).

3.2. Characteristics of the included studies

A total of 34 studies conducted in Ethiopia met the eligibility criteria, providing 52 independent datasets because some studies reported separate prevalence estimates for human, animal, and environmental samples (Table 1). The studies were published between 2015 and 2025 and collectively included 15,475 samples. They covered seven administrative regions, with the largest contribution from Oromia ($n = 13$), followed by Addis Ababa ($n = 8$).

The included evidence represented all three components of the One Health interface. Animal studies focused on livestock and food-associated samples, human studies mainly involved stool specimens from patients, food handlers, and community participants, while environmental studies examined water, food, and food-contact surfaces. The full range of sample types and study characteristics is provided in Table 1.

Laboratory approaches for identifying *E. coli* O157 varied across studies, with latex agglutination, culture-based methods, and PCR being the main approaches used. Sampling methods also differed, although simple and systematic random sampling were commonly reported. Across the datasets, reported prevalence ranged from 0.00% in human stool samples from Addis Ababa [30] to 32.35% in animal rectal samples from SNNPR [31].

Table 1
Characteristics of included studies for the prevalence of *E. coli* O157:H7 in Ethiopia

Author Name	Publication years	Region	Sample source	Sample Size	Combined Prevalence (%)
Ababu, A., et al. [32]	2020	Oromia	Animals	210	5.24
Abdissa, R., et al.[30]	2017	Addis Ababa	Animals, Humans and Environment	2,482	0.64
Abebe, E., et al. [33]	2023	Amhara	Animals, and Environment	386	6.48
Abunna, F., et al.[34]	2023	Oromia	Animals, and Environment	352	3.97
Adugna, A., et al.[35]	2015	Amhara	Humans	422	13.98
Geresu, M. A. & Regassa, S.[36]	2021	Oromia	Animals, and Environment	192	2.08
Atnafie, B., et al.[14]	2017	SNNPR	Animals, and Environment	630	2.38
Ayalneh, S. T., et al.[13]	2024	Oromia	Humans	423	8.98
Ayenew, H. Y., et al.[37]	2021	Amhara	Environment	280	8.93
Ayichew, S., et al.[38]	2025	SNNPR	Animals, Humans and Environment	644	3.11
Beyi, A. F., et al. [39]	2017	Addis Ababa	Animals, and Environment	525	1.71
Chala, G., et al. [40]	2025	SNNPR	Environment	298	3.69
Dejene, H., et al.[41]	2022	Addis Ababa	Animals, and Environment	450	6.00
Disassa, N., et al.[42]	2017	Benishangul Gumz	Animals	380	2.89
Dulo, F., et al. [43]	2015	Somali	Animals, and Environment	235	2.55
Engda, T., et al. [44]	2023	Amhara	Animals, and Humans	1478	10.89
Fesseha, H., et al. [31]	2022	SNNPR	Animals	68	32.4

Author Name	Publication years	Region	Sample source	Sample Size	Combined Prevalence (%)
Fikadu, Y., et al. [45]	2023	Oromia	Animals, and Environment	516	2.71
Getaneh, D. K., et al. [15]	2021	Harari	Humans	365	15.34
Getie, M., et al. [46]	2019	Amhara	Humans	257	1.95
Gudisa, M. B., et al.[47]	2022	Oromia	Animals	262	1.53
Gugsa, G., et al. [48]	2022	Oromia	Animals	284	3.52
Gutema, F. D., et al.[49]	2021	Oromia	Humans, and Animals	583	5.32
Haile, A. F., et al.[50]	2022	Addis Ababa	Environment	384	3.65
Haile, A. F., et al.	2021	Addis Ababa	Environment	390	0.51
Haile, A. F., et al.	2017	Oromia	Animals	300	8.33
Mesele, F., et al.[51]	2023	Oromia	Animals, and Environment	408	4.65
Mogessie, H., et al.[52]	2024	Addis Ababa	Environment	206	13.59
Sebsibe, M. A. & Asfaw, E. T. [53]	2020	Oromia	Animals, and Environment	505	5.35
Shecho, M., et al.[54]	2017	Oromia	Animals	194	13.40
Tadese, N. D., et al[55]	2021	Oromia	Animals	197	9.14
Tarekegn, A. A., et al.[56]	2023	Amhara	Animals, and Environment	248	12.50
Tegegne, H., et al.[57]	2024	Addis Ababa	Animals, and Environment	499	5.21
Zeynudin, A., et al.[58]	2025	Addis Ababa	Environment	242	2.07

3.3. Nasopharyngeal carriage rate

Across the 52 independent datasets, 15,195 samples were assessed, yielding 806 confirmed *E. coli* O157 isolates. The reported prevalence varied substantially across the included studies. The pooled prevalence of *E. coli* O157 in Ethiopia was 4.65% (95% CI: 3.58–6.02%). Considerable between-study heterogeneity was observed ($I^2 = 89.2\%$; $Q = 472.53$, $df = 51$, $p < 0.001$), with an estimated between-study variance of $\tau^2 = 0.6085$ ($\tau = 0.7801$). The pooled estimate therefore represents an overall national prevalence across diverse study settings and sample sources (Fig. 2).

3.4. Handling heterogeneity

Substantial heterogeneity was observed across the included studies. The Cochran's Q test indicated significant between-study variation ($Q = 472.53$, $df = 51$, $p < 0.001$), with an estimated between-study variance of $\tau^2 = 0.6085$ (95% CI: 0.4918–1.3023). The I^2 statistic was 89.2% (95% CI: 86.7–91.3%), indicating that most of the variability in the reported prevalence estimates reflected differences between studies rather than sampling error. Given this considerable heterogeneity, the pooled prevalence was estimated using a random-effects model.

3.4.1. Subgroup analysis

To further explore the observed heterogeneity, pre-specified subgroup analyses were performed based on epidemiologically and methodologically relevant study characteristics. The subgroup analyses showed that the pooled prevalence of *E. coli* O157 varied significantly by geographic region, sample source, and laboratory detection method (Table 2). Regional differences were significant ($p = 0.0102$), with the highest pooled prevalence observed in Amhara. Prevalence also differed by sample source ($p = 0.0365$), being highest in human samples, and by laboratory detection method ($p = 0.0148$), with the highest estimate observed among studies using culture on Sorbitol MacConkey agar.

Substantial heterogeneity remained within most subgroups ($I^2 = 39.9\%$ – 94.5%), suggesting that geographic region, sample source, and detection method accounted for only part of the observed variability. The remaining heterogeneity may reflect other differences in study populations, sampling procedures, epidemiological settings, or laboratory practices.

Table 2

Subgroup analysis of the pooled prevalence of *E. coli* O157:H7 in Ethiopia according to region, sample source, and detection method.

Variables	Categories	Included datasets (k)	Pooled prevalence (95% CI)	Heterogeneity (I^2)	P-value
Region	Oromia	19	0.0507 (0.0379–0.0678)	73.0%	0.0102
	Addis Ababa	13	0.0267 (0.0132–0.0540)	90.9%	
	Amhara	9	0.0922 (0.0549–0.1547)	82.0%	
	SNNPR	7	0.0377 (0.0133–0.1071)	94.5%	
Sample source	Animal	24	0.0536 (0.0373–0.0770)	91.2%	0.0365
	Human	8	0.0765 (0.0380–0.1542)	85.7%	
	Environment	20	0.0321 (0.0208–0.0496)	82.3%	
Detection method	LAT	41	0.0508 (0.0379–0.0682)	90.3%	0.0148
	Culture on SMA	3	0.0769 (0.0312–0.1899)	39.9%	
	PCR	6	0.0277 (0.0133–0.0575)	52.8%	

SMA (Sorbitol MacConkey agar), PCR (Polymerase chain reaction), LAT (Latex agglutination test)

The forest plot shows a significantly higher pooled prevalence of *E. coli* O157 in human samples (7.65%; 95% CI: 3.80–15.42%) than in animal samples (5.36%; 95% CI: 3.73–7.70%; $p = 0.0365$). Substantial heterogeneity was observed in both groups ($I^2 = 85.7\%$ and 91.2% , respectively) (Fig. 3).

3.4.2. Sensitivity analysis

A leave-one-out analysis was performed to assess how each study influenced the overall effect size estimate. The meta-analysis produced a pooled effect size of 0.046 (4.60%), which aligned with the confidence intervals of every individual study included in the analysis. Sensitivity testing further confirmed the stability of these findings, as removing any single study from the analysis did not meaningfully change the overall prevalence estimate (Fig. 4). Thus, the meta-analysis results including all the studies added in this study was reliable.

3.5. Meta-regression models

To explore potential sources of between-study heterogeneity, mixed-effects meta-regression models were fitted using study region, sample size, publication year, sample source, and detection method as potential moderators (Table 3). In the univariable analyses, study region explained the largest proportion of heterogeneity ($R^2 = 25.74\%$), followed by detection method, sample source, sample size, and publication year. In the multivariable model, the effect estimates remained significantly higher for Amhara and SNNPR compared with the reference region. Environmental samples had a significantly lower effect estimate than animal samples, whereas the difference between human and animal sources was not significant. Publication year, sample size, and detection method were not significantly associated with the effect size after adjustment.

Table 3

Univariable and multivariable meta-regression analysis results of *E. coli* O157:H7 in humans, animals and environment in Ethiopia

Moderators	Category	Univariable R ² (%)	Univariable coefficient (95% CI)	Multivariable R ² (%)	Multivariable coefficient (95% CI)
Region	Amhara	25.74	1.12 (0.32, 1.92)**	60.73	0.86 (0.09, 1.62) **
	Benishangul		−0.01 (− 1.87, 1.85)		−0.34 (− 2.02, 1.35)
	Harari		1.80 (0.04, 3.56)*		1.37 (− 0.27, 3.02)
	Oromia		0.51 (− 0.18, 1.20)		0.15 (− 0.52, 0.81)
	SNNPR		0.39 (− 0.50, 1.29)		1.30 (0.10, 2.49) **
	Somali		−0.17 (− 1.85, 1.50)		−0.41 (− 2.14, 1.32)
Sample size	Continuous	7.69	−0.0007 (− 0.0016, 0.0002)		−0.0008 (− 0.0016, 0.00)
Publication year	Continuous	3.12	0.06 (− 0.03, 0.16)		0.05 (− 0.06, 0.16)
Source	Animal	10.76	Reference		Reference
	Environment		−0.57 (− 1.15, 0.02)	−0.59 (− 1.14, − 0.03) **	
	Human		0.17 (− 0.61, 0.95)	−0.12 (− 0.88, 0.64)	
Detection method	Culture on SMA	11.78	1.09 (− 0.68, 2.85)		1.44 (− 0.66, 3.54)
	LAT		0.85 (− 0.56, 2.26)		1.67 (− 0.06, 3.39)
	PCR		0.08 (− 1.52, 1.69)		0.22 (− 1.41, 1.85)
Full model	Region + publication year + source + detection method + sample size				
**=Significant variables or categories, R ² = Coefficient of determination					

3.5. Publication bias

Visual inspection of the funnel plot indicated asymmetry in the distribution of effect estimates across the included studies (Fig. 5). The Egger's regression test showed significant funnel-plot asymmetry ($t = -6.57$, $df = 50$, $p < 0.0001$), with a bias estimate of -4.31 ($SE = 0.66$). Similarly, Begg's rank correlation test showed significant asymmetry ($z = -4.43$, $p < 0.0001$). Both tests therefore indicated significant funnel-plot asymmetry and small-study effects. These findings indicate funnel-plot asymmetry but do not distinguish publication bias from other potential sources of asymmetry, including between-study heterogeneity, methodological differences, and variation in effect sizes.

A trim-and-fill analysis was conducted to examine the effect of funnel-plot asymmetry on the pooled estimate. The analysis imputed 21 potentially missing studies, increasing the total number of studies from 52 to 73 (Fig. 6). Following imputation, the random-effects model produced an adjusted pooled prevalence of *E. coli* O157 of 8.30% (95% CI: 6.05–11.27%). Heterogeneity remained high after imputation ($I^2 = 91.1\%$; $\tau^2 = 0.94$; $Q = 812.25$, $df = 72$, $p < 0.0001$).

3.6. Antimicrobial resistance profile

Antimicrobial susceptibility data were reported for 21 antimicrobial agents (Table 4). The Pooled resistance estimates varied across antimicrobial agents. The highest resistance was reported for erythromycin (89.65%; 95% CI: 66.31–97.45), ampicillin (82.59%; 95% CI: 66.23–91.98), and amoxicillin (76.38%; 95% CI: 39.52–94.12). Resistance was also relatively high for cefoxitin (62.69%; 95% CI: 14.90–94.16), tetracycline (39.63%; 95% CI: 23.58–58.27), streptomycin (35.90%; 95% CI: 22.11–58.29), and amoxicillin–clavulanic acid (33.49%; 95% CI: 18.47–60.73). Estimates for the remaining agents ranged from 8.44% for ciprofloxacin (95% CI: 4.42–15.52) to 27.58% for trimethoprim–sulfamethoxazole (95% CI: 14.89–45.31), except for trimethoprim (26.92%; 95% CI: 5.32–100.00) and nitrofurantoin (20.02%; 95% CI: 1.45–100.00), both of which had wide confidence intervals.

Between-study heterogeneity varied across antimicrobial agents, with I^2 ranging from 40.8% for ceftriaxone to 92.1% for cephalothin. The highest heterogeneity was observed for cephalothin ($I^2 = 92.1\%$), erythromycin (83.5%), streptomycin (84.1%), kanamycin (83.3%), tetracycline (81.5%), and amoxicillin–clavulanic acid (90.0%). Lower heterogeneity was observed for ceftriaxone (40.8%), amikacin (50.0%), and cefotaxime (50.5%) (Table 4).

Table 4

Pooled antimicrobial resistance rate of *E. coli* O157:H7 in humans, animals and environment in Ethiopia

Type of antimicrobial	Group of antimicrobial agents	No. of studies	No. of <i>E. coli</i> O157 isolates	Pooled resistance (%) (95% CI)	I ² (%) (p-value)
Amikacin	Aminoglycosides	6	157	18.46 (7.56–38.55)	50.0 (0.0751)
Amoxicillin	Penicillins	7	132	76.38 (39.52–94.12)	78.6 (< 0.0001)
Amoxicillin–clavulanic acid	β-lactam/β-lactamase inhibitor	10	406	33.49 (18.47–60.73)	90.0 (< 0.0001)
Ampicillin	Penicillins	17	372	82.59 (66.23–91.98)	71.9 (< 0.0001)
Cefotaxime	Third-generation cephalosporins	7	119	11.47 (4.57–28.79)	50.5 (0.0593)
Cefoxitin	Cephameycins	6	97	62.69 (14.90–94.16)	76.0 (0.0009)
Ceftazidime	Third-generation cephalosporins	8	294	17.38 (5.12–45.06)	79.4 (< 0.0001)
Ceftriaxone	Third-generation cephalosporins	10	356	14.30 (8.25–23.64)	40.8 (0.0857)
Cephalothin	First-generation cephalosporins	6	134	14.86 (4.02–54.99)	92.1 (< 0.0001)
Chloramphenicol	Phenicol	20	562	9.12 (5.80–14.05)	52.7 (0.0031)
Ciprofloxacin	Fluoroquinolones	21	592	8.44 (4.42–15.52)	68.5 (< 0.0001)
Erythromycin	Macrolides	7	140	89.65 (66.31–97.45)	83.5 (< 0.0001)
Gentamicin	Aminoglycosides	21	575	10.54 (6.12–17.56)	71.3 (< 0.0001)
Kanamycin	Aminoglycosides	10	200	14.11 (5.16–38.60)	83.3 (< 0.0001)
Nalidixic acid	Quinolones	13	248	15.12 (7.71–29.68)	67.1 (0.0003)
Nitrofurantoin	Nitrofurans	4	68	20.02 (1.45–100.00)	69.9 (0.0189)

Type of antimicrobial	Group of antimicrobial agents	No. of studies	No. of <i>E. coli</i> O157 isolates	Pooled resistance (%) (95% CI)	I ² (%) (p-value)
Norfloxacin	Fluoroquinolones	6	275	17.37 (5.69–53.07)	87.2 (< 0.0001)
Streptomycin	Aminoglycosides	13	270	35.90 (22.11–58.29)	84.1 (< 0.0001)
Tetracycline	Tetracyclines	25	675	39.63 (23.58–58.27)	81.5 (< 0.0001)
Trimethoprim	Folic acid metabolism inhibitors	4	84	26.92 (5.32–100.00)	88.3 (< 0.0001)
Trimethoprim–sulfamethoxazole	Folic acid metabolism inhibitors	17	522	27.58 (14.89–45.31)	77.7 (< 0.0001)

3.8. Trends of *E. coli* O157:H7 prevalence over time

Meta-regression showed no significant temporal trend in antimicrobial resistance ($\beta = 0.0634$, 95% CI: -0.0318 – 0.1585 ; $p = 0.1872$). Although the estimated slope was positive, the confidence interval included zero, indicating no clear increase or decrease in resistance over time. Substantial residual heterogeneity remained ($I^2 = 90.52\%$; $p < 0.0001$), while publication year explained only 3.12% of the observed heterogeneity (Fig. 7).

4. Discussion

From a One Health perspective, *Escherichia coli* O157 is an important foodborne zoonotic pathogen because it can move across the animal–food–environment interface and subsequently affect human health. The present systematic review and meta-analysis brought together evidence on its prevalence and antimicrobial resistance in Ethiopia and showed substantial variation across study settings and sample sources. The findings also indicate considerable resistance to several tested antimicrobial agents, underscoring the dual importance of pathogen control and antimicrobial stewardship. Taken together, the evidence suggests that *E. coli* O157 remains a relevant food-safety and One Health concern in Ethiopia and supports integrated surveillance spanning livestock, food, environmental, and human health sectors.

The overall pooled prevalence of *E. coli* O157 was 4.65% (95% CI: 3.58–6.02%). This estimate is broadly consistent with previous evidence from Ethiopia, including a national meta-analysis of foods of animal origin that reported a pooled prevalence of approximately 4% [59]. The slightly higher estimate in the present review may reflect differences in the evidence base, including the broader range of sample sources, geographical coverage, and diagnostic approaches represented in the included studies. The

persistence of *E. coli* O157 across these settings indicates an ongoing food-safety concern and highlights the need for prevention measures that address contamination throughout the animal–food–environment continuum.

Prevalence differed significantly by sample source, with the highest pooled estimate observed in human samples (7.65%; 95% CI: 3.80–15.42%), followed by animal samples (5.36%; 95% CI: 3.73–7.70%) and environmental samples (3.21%; 95% CI: 2.08–4.96%). The higher estimate among human samples may reflect exposure to contaminated food, water, animals, or other environmental sources, although the available evidence does not allow the direction of transmission to be established. Substantial heterogeneity persisted within all three source groups ($I^2 = 85.7\%$, 91.2% , and 82.3% for human, animal, and environmental samples, respectively), indicating that sample source alone does not explain the observed differences. Nevertheless, the detection of *E. coli* O157 across all three One Health compartments reinforces the interconnected nature of potential transmission pathways and the value of coordinated surveillance and prevention [60].

In this study, the highest pooled resistance among *E. coli* isolates was observed for ampicillin (82.59%; 95% CI: 66.23–91.98%), followed by erythromycin (89.65%; 95% CI: 66.31–97.45%), whereas lower resistance was observed for chloramphenicol (9.12%; 95% CI: 5.80–14.05%), ciprofloxacin (8.44%; 95% CI: 4.42–15.52%), and ceftriaxone (14.30%; 95% CI: 8.25–23.64%). This findings is consistent with previous reports on antibacterial resistance of *E. coli* in Ethiopia [61]. The high resistance observed to several commonly used antimicrobials may reflect sustained antimicrobial exposure and selective pressure, particularly where antibiotics are widely accessible and frequently used in human and veterinary settings. In contrast, the comparatively lower resistance to chloramphenicol, ciprofloxacin, and ceftriaxone may partly reflect differences in antimicrobial use, prescribing practices, and availability. However, these interpretations should be considered cautiously because resistance patterns can also vary according to bacterial source, study population, geographic setting, and laboratory testing practices.

The high level of ampicillin resistance is of particular concern because ampicillin and related β -lactam antibiotics have historically been widely used for the treatment of bacterial infections. Continued exposure to these agents can favour the selection and dissemination of resistant *E. coli* strains, particularly through acquisition and spread of resistance determinants [62]. The substantial resistance observed for erythromycin should also be interpreted in relation to the intrinsic resistance characteristics of *E. coli*, as these agents are primarily active against Gram-positive organisms and have limited clinical utility against Gram-negative *E. coli* [63]. Therefore, the high pooled resistance estimates for these agents may not necessarily indicate the same therapeutic implications as resistance to antibiotics routinely used for the treatment of *E. coli* infections.

The comparatively lower pooled resistance observed for ciprofloxacin and ceftriaxone is consistent with findings from an Ethiopian clinical study in which *E. coli* showed high resistance to erythromycin, amoxicillin, and tetracycline but substantially greater susceptibility to ciprofloxacin [64]. This pattern may reflect differences in antimicrobial exposure, prescribing practices, healthcare setting, and the

distribution of resistance mechanisms across study populations; however, the available evidence does not establish that lower use of ciprofloxacin or ceftriaxone caused the lower pooled resistance. In particular, ceftriaxone prescribing has also been reported to be frequently inappropriate in an Ethiopian referral hospital, so reduced resistance should not automatically be attributed to limited ceftriaxone exposure [65].

The findings have several implications for food safety and One Health surveillance in Ethiopia. The combination of *E. coli* O157:H7 occurrence and substantial antimicrobial resistance highlights the need to strengthen surveillance across the animal–food–human interface, consistent with international guidance on integrated One Health surveillance of antimicrobial resistance and antimicrobial use [66]. Control efforts should extend beyond clinical settings and include hygienic milk production, safe handling of animal-derived foods, water and environmental sanitation, and responsible antimicrobial use. Evidence from the Ethiopian dairy supply chain has documented *E. coli* O157:H7 contamination in raw milk, water, and milker-hand samples, as well as multidrug-resistant isolates, indicating that interventions should be implemented from dairy farms through consumption rather than at a single control point [41]. This interpretation is also consistent with a review of the Ethiopian dairy sector that identified *E. coli* O157:H7 in raw cow milk and called for improved hygiene and production practices across the supply chain [67].

Several limitations should be considered when interpreting these findings. First, substantial heterogeneity was observed across the included studies for both prevalence and antimicrobial resistance estimates. Second, the studies differed in sample sources, geographic settings, laboratory detection methods, antimicrobial panels, and study periods, which limits direct comparability. These differences may partly explain the variability in the pooled estimates and warrant caution when generalizing individual subgroup findings.

5. Conclusion

This systematic review and meta-analysis indicates that *E. coli* O157 remains an important foodborne zoonotic pathogen in Ethiopia, with evidence of its occurrence across human, animal, and environmental sources. The observed antimicrobial resistance, particularly the high resistance to erythromycin and ampicillin, further emphasizes the importance of antimicrobial stewardship and continued resistance surveillance. A coordinated One Health approach is needed to address the pathogen and its associated resistance across interconnected transmission pathways. Strengthening surveillance across human, animal, food, and environmental sectors, improving food and water hygiene, promoting evidence-based antimicrobial use, and guiding treatment through antimicrobial susceptibility testing could help reduce the transmission and further emergence of antimicrobial-resistant *E. coli* in Ethiopia.

Abbreviations

AMR

Antimicrobial resistance

E. coli O157

Escherichia coli O157:H7

OR

Odds ratio

CI

Confidence interval

PRISMA

Preferred Reporting Items for Systematic Review and Meta-Analysis

SNNPR

Southern Nations, Nationalities, and Peoples' Region

WHO

World Health Organization

Declarations

Ethics approval and consent to participate: Not applicable

Consent for publication: Not applicable

Availability of data and materials: All data set are included in the manuscript or as supplementary files.

Competing interests: The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Figures

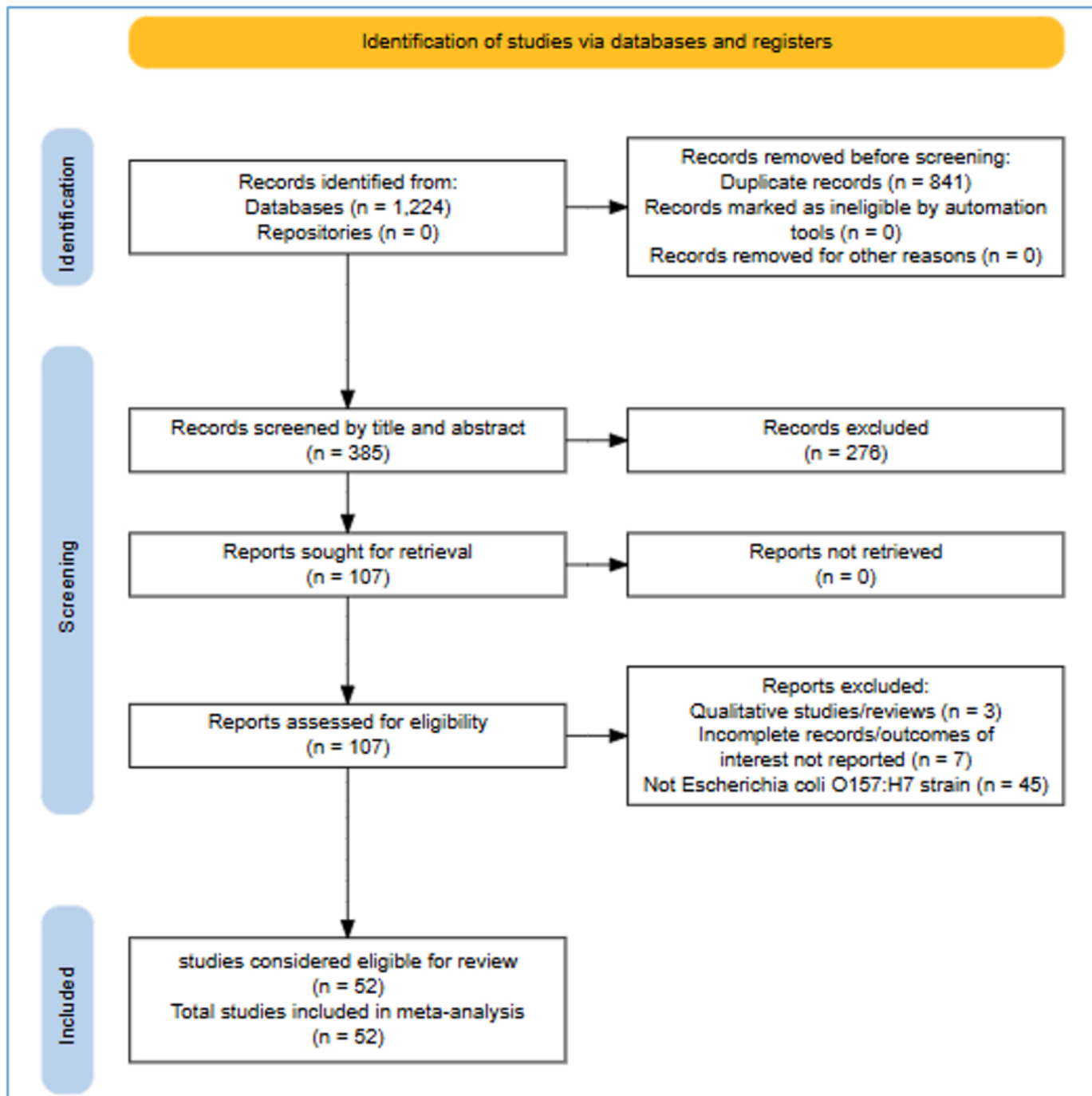


Figure 1

PRISMA flow diagram for study selection (identification, screening, eligibility assessment, and inclusion of studies) in the systematic review and meta-analysis

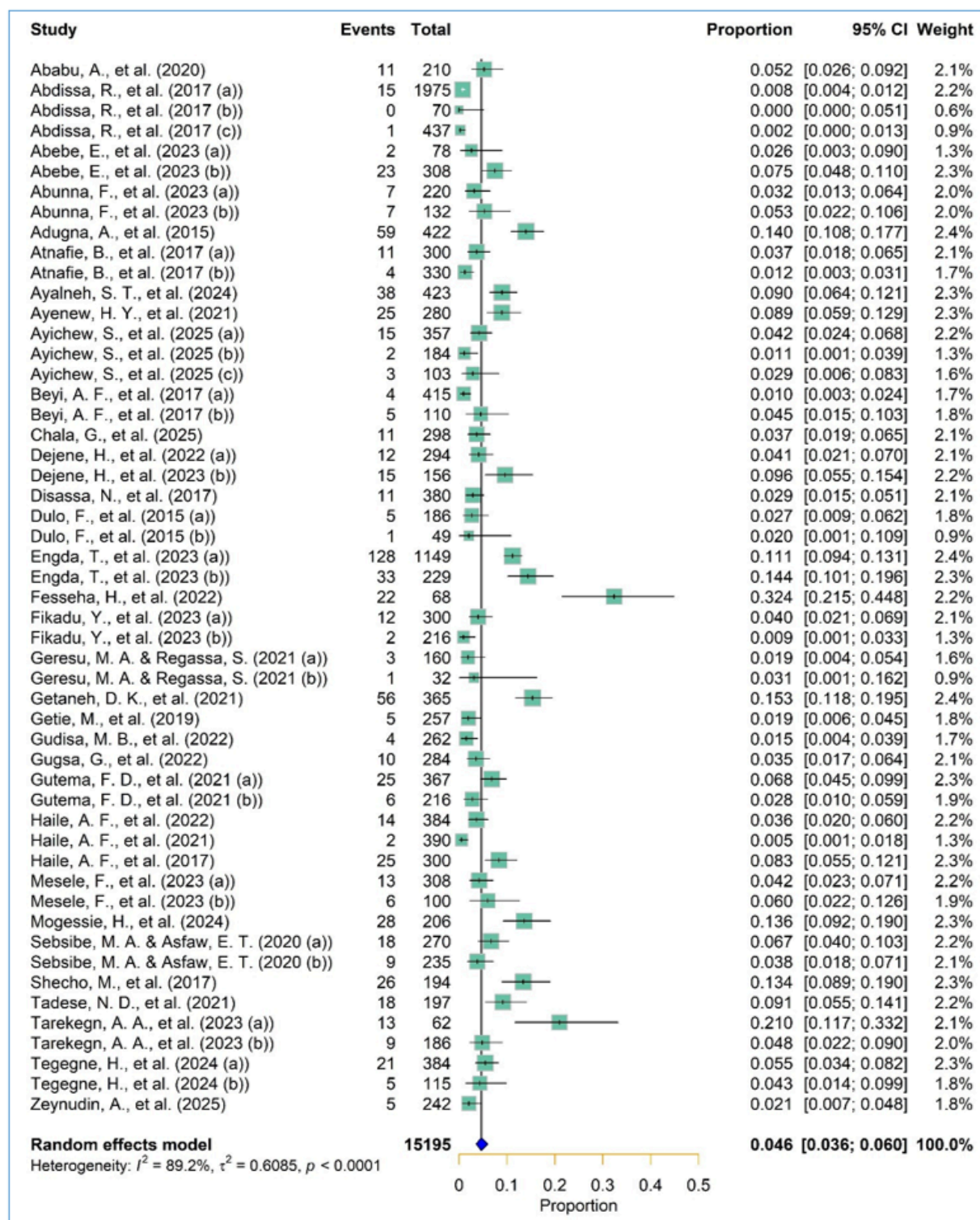


Figure 2

Forest plot for pooled prevalence of *E. coli* O157:H7 in humans, animals and environment in Ethiopia

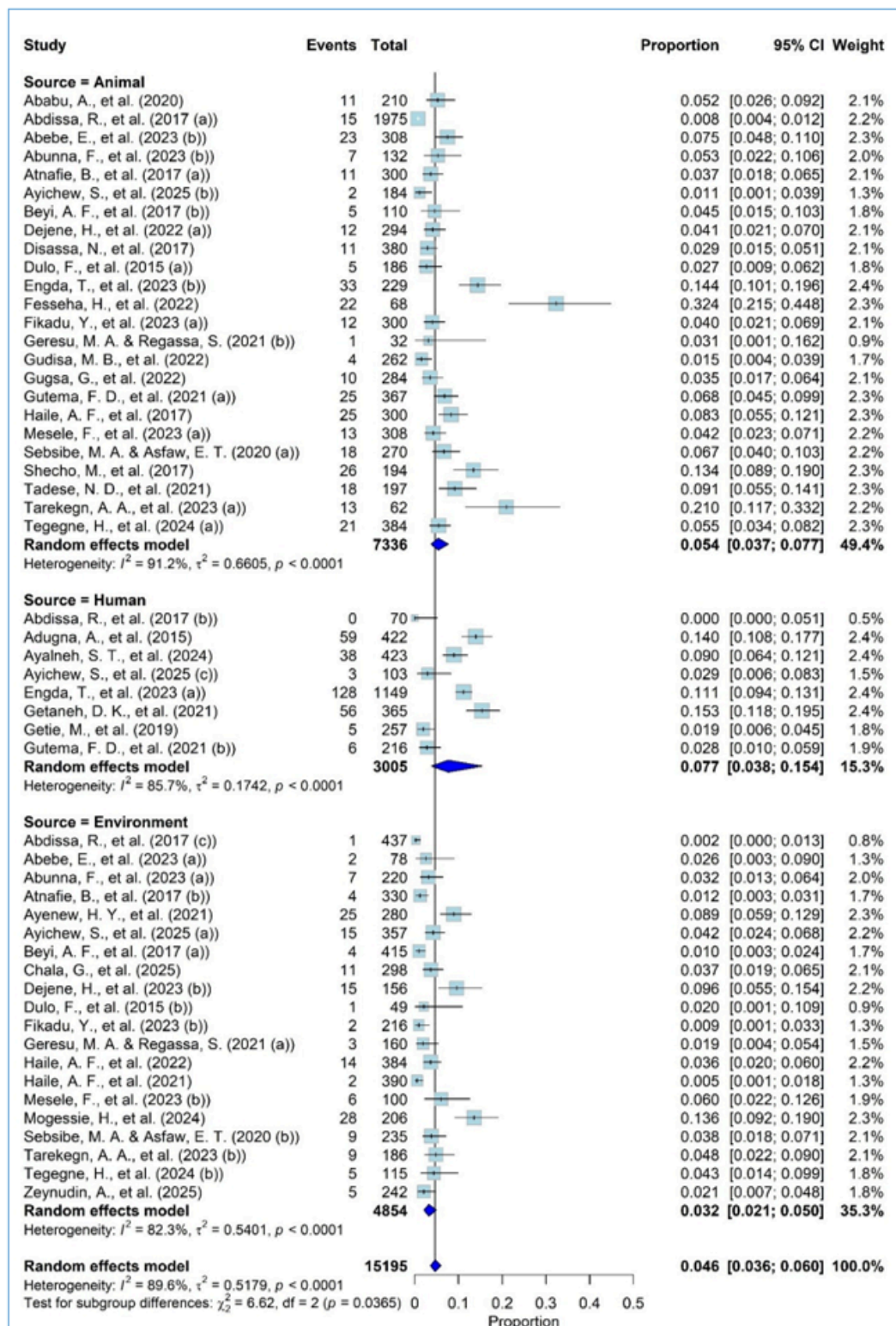


Figure 3

Forest plot for subgroup analysis using sample source (animals, humans and environment)

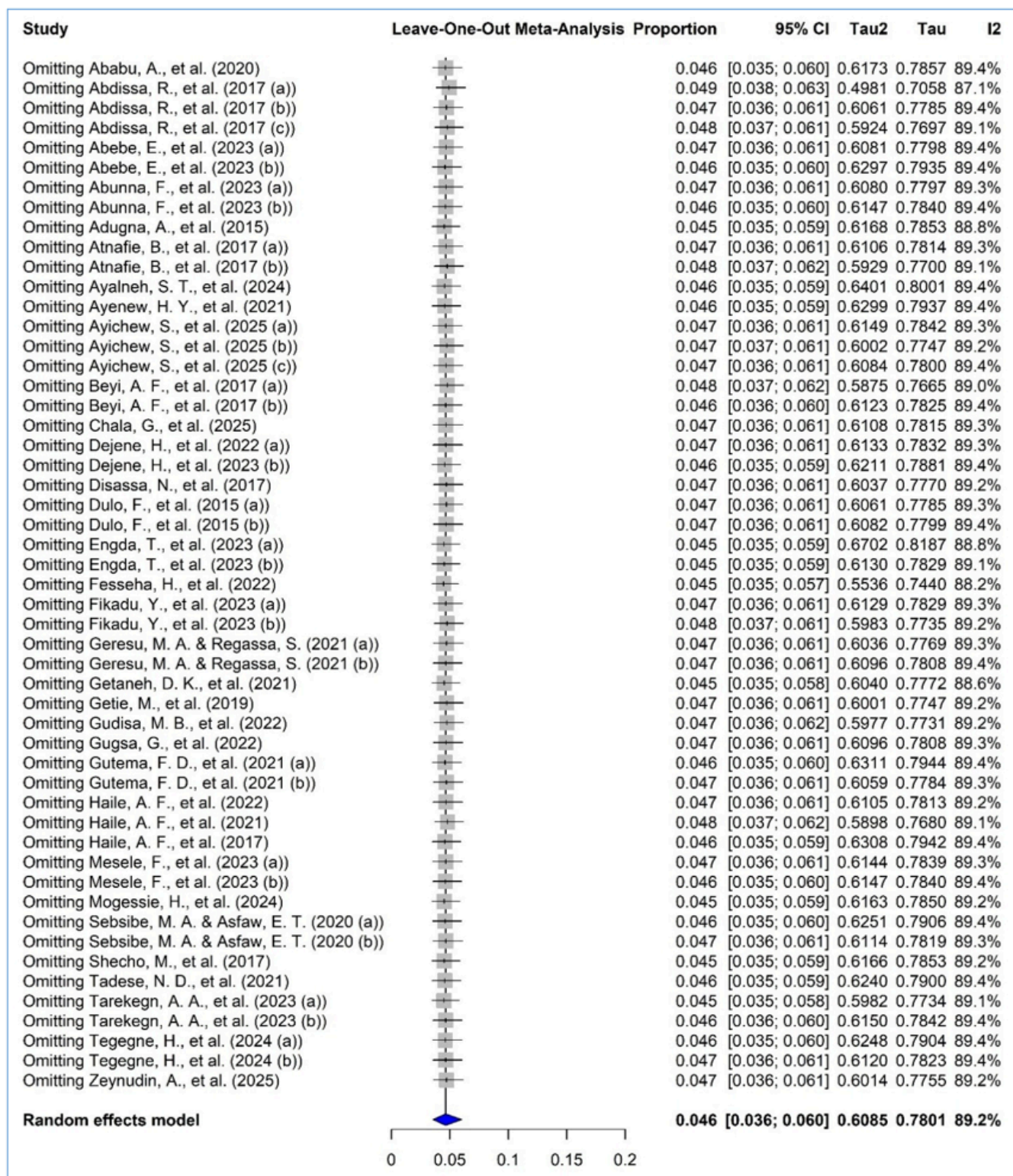


Figure 4

Sensitivity analysis of prevalence of *E. coli* O157:H7 in humans, animals and environment in Ethiopia

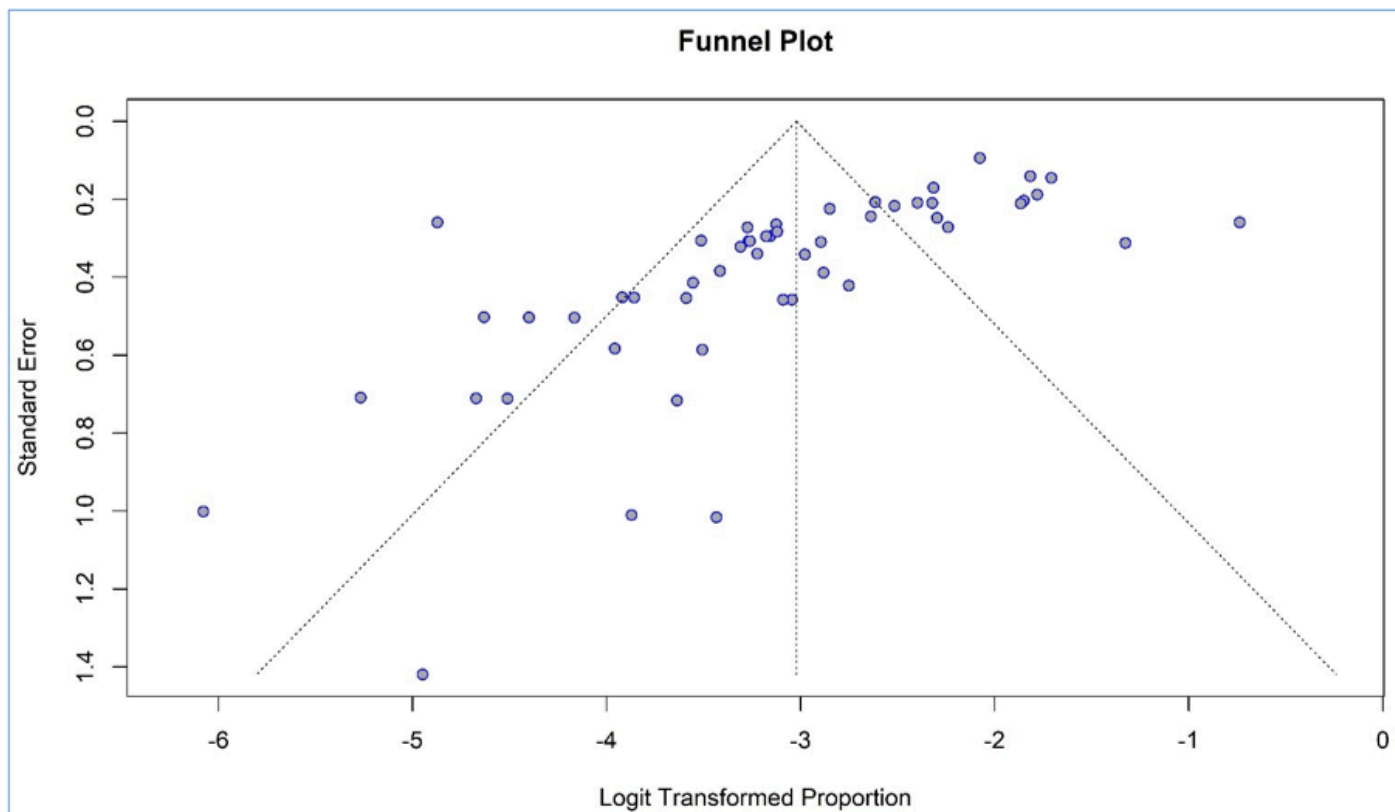


Figure 5

Funnel plot of the pooled *E. coli* O157:H7 in humans, animals and environment in Ethiopia

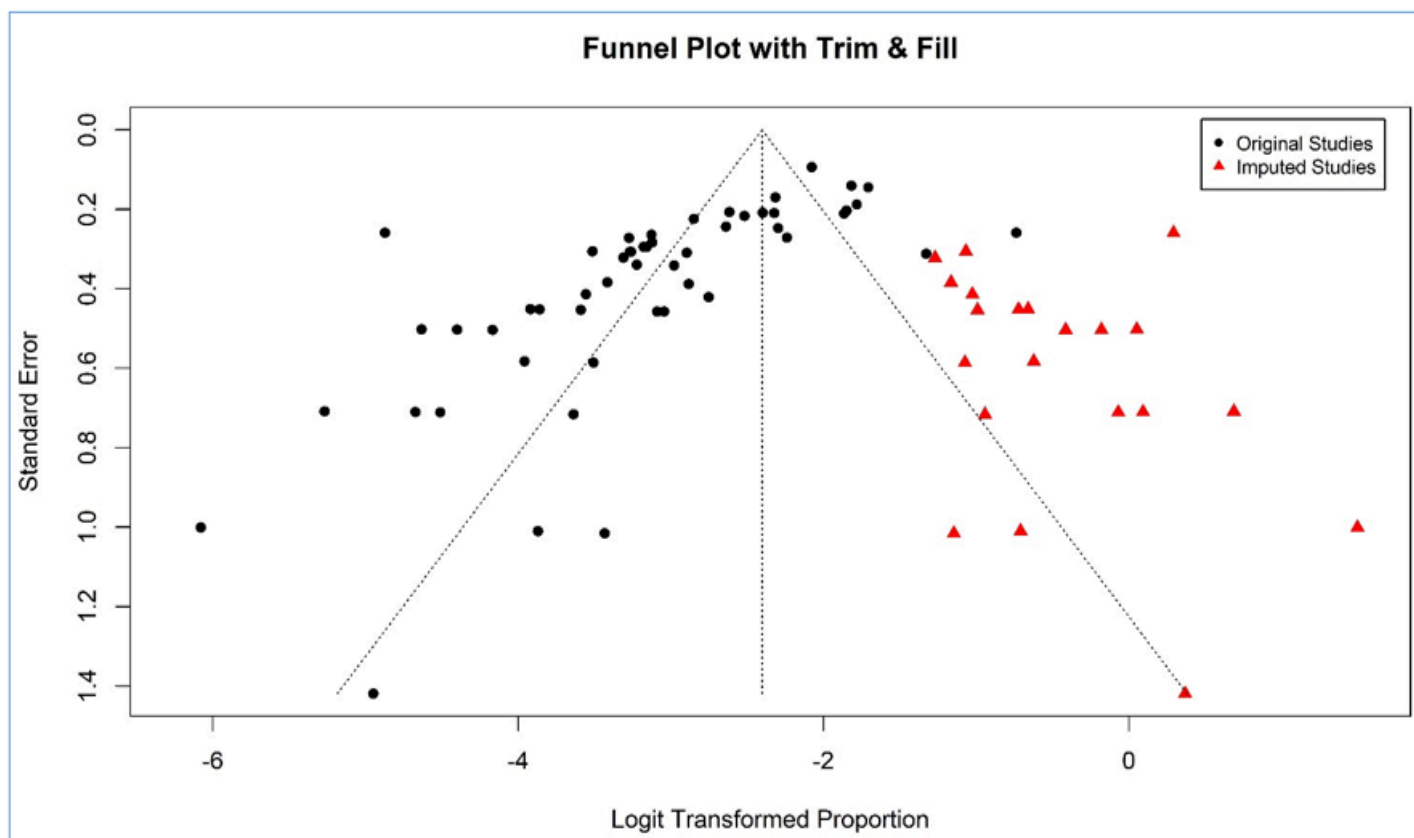


Figure 6

Trim and fill analysis by imputing imaginary studies

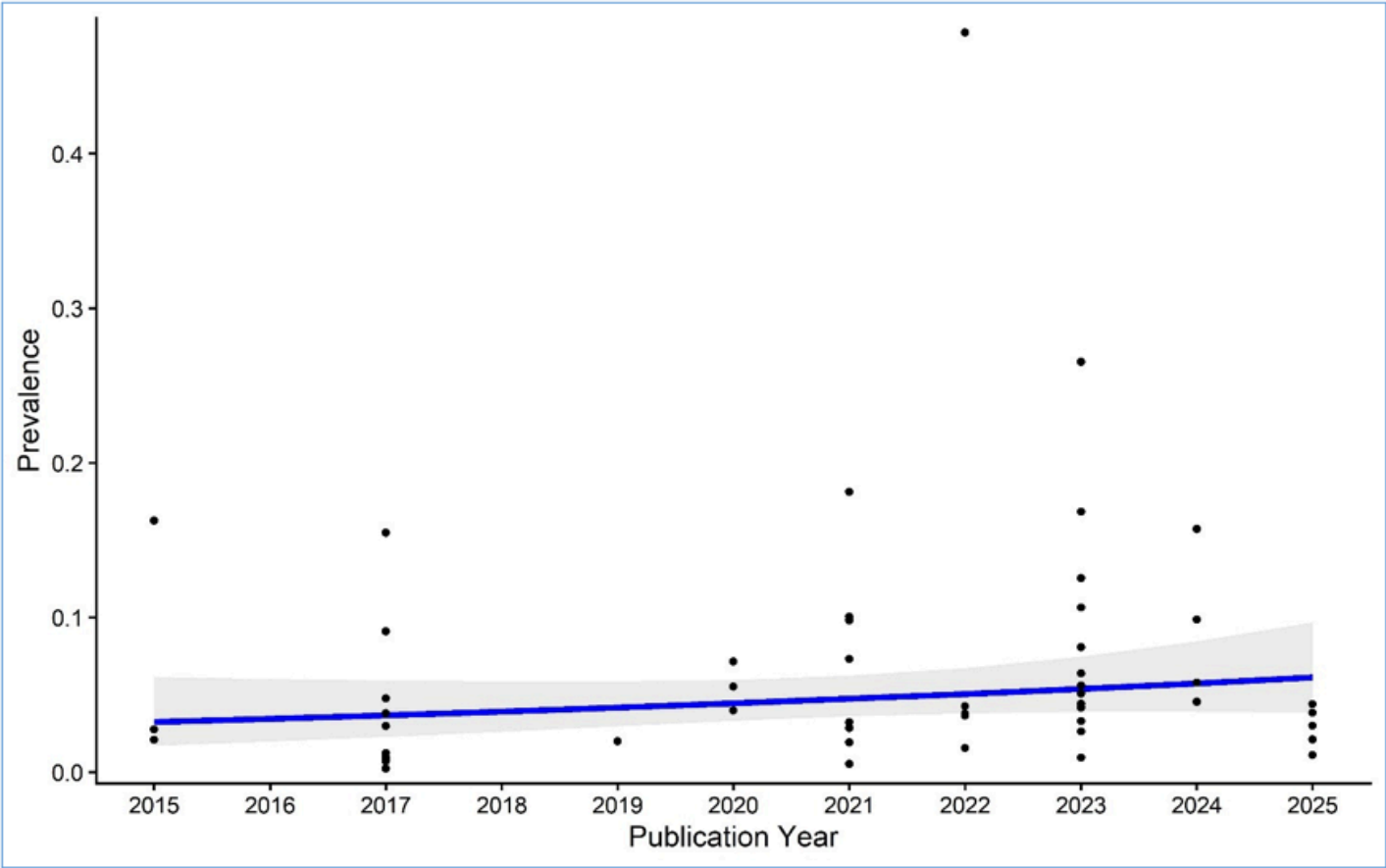


Figure 7

Trends in *E. coli* O157:H7 prevalence predicted based on existing studies over time (2015–2025).

Supplementary Files

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

- [SupportingInformation.docx](#)