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Original Article

Antimicrobial Resistance in Enteric Pathogens and Its Implications for Empiric Therapy in Community-Acquired Diarrhea: A Systematic Review and Meta-Analysis

Pratibha Kale[1], Brajeshwar Kumar[2], Sai SreeValli Sreepada[3]

[1] Additional Professor, Department of Microbiology, Institute of Liver and Biliary Sciences (ILBS), New Delhi, India.
[2] Postgraduate Student, Department of Pharmacology, Patna Medical College, Patna, Bihar, India.
[3] Senior Resident, Department of Community Medicine and School of Public Health, Postgraduate Institute of Medical Education and Research (PGIMER), Chandigarh, India.

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Corresponding Author:

Pratibha Kale

Additional Professor, Department of Microbiology, Institute of Liver and Biliary Sciences (ILBS), New Delhi, India.

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ABSTRACT

Background: Community-acquired diarrhea remains a major global health problem, and bacterial enteric pathogens account for a substantial proportion of clinically significant cases. Antimicrobial therapy is indicated in selected scenarios; however, escalating antimicrobial resistance (AMR) threatens the effectiveness of empiric treatment strategies, particularly in low- and middle-income countries.
Objective: To systematically evaluate and quantify antimicrobial resistance patterns among major bacterial enteric pathogens causing community-acquired diarrhea.
Methods: A systematic review and meta-analysis was conducted in accordance with PRISMA 2020 guidelines. PubMed/MEDLINE, Embase, Scopus, Web of Science, and the Cochrane Library were searched from inception to June 2025. Community-based and outpatient studies reporting phenotypic antimicrobial susceptibility of Escherichia coli, Shigella spp., Salmonella spp., Campylobacter spp., and Vibrio cholerae were included. Random-effects meta-analyses were used to estimate pooled resistance proportions, and heterogeneity was assessed using the I^2 statistic.
Results: A total of 47 studies were included, with 39 contributing to meta-analysis, encompassing 18,742 bacterial isolates. High pooled resistance was observed to ampicillin and trimethoprim–sulfamethoxazole across E. coli (56% and 71%), Shigella (76% and 64%), and Salmonella (55% and 25%). Ciprofloxacin resistance remained relatively low overall but showed marked regional variability. Campylobacter spp. demonstrated clinically concerning resistance to erythromycin (33%) and ciprofloxacin (27%). Substantial heterogeneity was noted across most pathogen–antibiotic combinations.
Conclusion: Antimicrobial resistance among enteric pathogens causing community-acquired diarrhea is widespread and undermines the reliability of several commonly used oral agents. The findings highlight the need for region-specific empiric treatment guidelines, strengthened community-based AMR surveillance, and robust antimicrobial stewardship to preserve remaining therapeutic options.

Keywords: *community-acquired diarrhea; enteric pathogens; antimicrobial resistance; systematic review; meta-analysis.*

INTRODUCTION

Community-acquired acute diarrhea remains one of the leading causes of morbidity across all age groups worldwide, with a disproportionately high burden in low- and middle-income countries (LMICs) [1,2]. Although most diarrheal episodes are self-limiting and managed with oral rehydration therapy, bacterial enteric pathogens contribute significantly to moderate-to-severe disease, dysentery, prolonged illness, and complications requiring antimicrobial therapy [3,4].

Among these, *Escherichia coli* (including diarrheagenic pathotypes), *Shigella spp.*, *Salmonella spp.*, *Campylobacter spp.*, and *Vibrio cholerae* are the most frequently implicated organisms in community settings [5,6].

Antimicrobial therapy in community-acquired diarrhea is reserved for specific clinical scenarios such as bloody diarrhea, suspected cholera with severe dehydration, traveler's diarrhea, severe disease in young children, elderly individuals, and immunocompromised hosts [7]. International guidelines recommend empiric agents such as fluoroquinolones, macrolides, or third-generation cephalosporins depending on age, severity, and regional resistance patterns [7,8]. However, the effectiveness of these empiric regimens is increasingly threatened by the rapid emergence and dissemination of antimicrobial resistance (AMR) among enteric pathogens [9].

The rise in AMR among diarrheal pathogens is driven by multiple factors, including widespread and often inappropriate antibiotic use in the community, over-the-counter availability of antimicrobials, poor sanitation, and close human–animal–environment interactions facilitating horizontal gene transfer [10–12]. High resistance rates to older first-line agents such as ampicillin, trimethoprim–sulfamethoxazole, and tetracyclines have been widely reported, limiting their utility in empirical management [13,14]. More concerning is the increasing resistance to fluoroquinolones and macrolides, which are currently considered key oral options for invasive bacterial diarrhea, particularly for *Shigella* and *Campylobacter* infections [15,16].

Surveillance of AMR in enteric pathogens has traditionally focused on hospital-based or invasive infections, while community-acquired diarrheal isolates remain underrepresented in many national and global surveillance systems [17]. As a result, clinicians often rely on outdated or non-representative data when selecting empiric therapy for community-onset diarrhea [18]. The World Health Organization's Global Antimicrobial Resistance and Use Surveillance System (GLASS) has highlighted the need to strengthen AMR monitoring beyond bloodstream infections, including gastrointestinal pathogens of public health importance [19].

Systematic reviews and meta-analyses provide an opportunity to synthesize fragmented data from diverse geographic regions and generate pooled resistance estimates that better reflect the true burden of AMR in community settings [20]. While several individual studies have reported resistance patterns of enteric bacteria, substantial heterogeneity exists across regions, age groups, and antimicrobial classes, making interpretation challenging [21]. A comprehensive synthesis focusing specifically on community-acquired diarrhea is therefore essential to inform empiric treatment guidelines, antimicrobial stewardship policies, and future surveillance priorities [22].

The present systematic review and meta-analysis aims to evaluate the global antimicrobial resistance patterns of major bacterial enteric pathogens causing community-acquired diarrhea, with emphasis on commonly used oral antimicrobials. By pooling available evidence, this study seeks to provide clinically relevant resistance estimates and highlight regional variations that are critical for rational antibiotic selection and public health planning [23,24].

METHODOLOGY

Study Design and Reporting Standards

This study was conducted as a systematic review and meta-analysis to evaluate antimicrobial resistance (AMR) patterns among bacterial enteric pathogens causing community-acquired diarrhea. The methodology followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines to ensure transparency, reproducibility, and methodological rigor [25].

Eligibility Criteria

Inclusion Criteria

Studies were included if they met the following criteria:

1. **Study design:** Observational studies (cross-sectional, surveillance studies, cohort studies) reporting antimicrobial susceptibility data; baseline data from randomized controlled trials were also considered.
2. **Population:** Patients of any age with **community-acquired acute diarrhea**, defined as diarrheal illness occurring outside hospital settings or within 48 hours of presentation.
3. **Pathogens:** Bacterial enteric pathogens including *Escherichia coli* (diarrheagenic or indicator strains), *Shigella spp.*, *Salmonella spp.*, *Campylobacter spp.*, and *Vibrio cholerae*.
4. **Outcomes:** Phenotypic antimicrobial resistance data reported as proportions or percentages based on standardized susceptibility testing.
5. **Setting:** Community-based, outpatient, primary healthcare, or population surveillance studies.
6. **Language:** Articles published in English.

Exclusion Criteria

- Hospital-acquired or nosocomial diarrhea studies
- Case reports, case series with <10 isolates, reviews, editorials, and conference abstracts
- Studies focusing exclusively on viral or parasitic causes of diarrhea

- Molecular-only resistance studies without phenotypic susceptibility results
- Duplicate datasets or studies lacking extractable resistance data

Information Sources and Search Strategy
A comprehensive literature search was conducted across **PubMed/MEDLINE, Embase, Scopus, Web of Science, and Cochrane Library** databases. The search covered studies published from database inception to **June 2025**.

The search strategy combined Medical Subject Headings (MeSH) and free-text terms related to diarrhea, enteric pathogens, and antimicrobial resistance, including:
"community-acquired diarrhea," "acute gastroenteritis," "enteric pathogens," "Escherichia coli," "Shigella," "Salmonella," "Campylobacter," "antimicrobial resistance," "antibiotic susceptibility," and *"drug resistance."*
Reference lists of relevant systematic reviews and included studies were manually screened to identify additional eligible articles [26].

Study Selection
All retrieved records were imported into a reference management software, and duplicates were removed. Two reviewers independently screened titles and abstracts for eligibility. Full texts of potentially relevant articles were then assessed independently. Discrepancies were resolved through discussion or consultation with a third reviewer. The study selection process was documented using a PRISMA flow diagram [25].

Data Extraction
Data were extracted independently by two reviewers using a standardized data extraction form. Extracted variables included:
- Author(s), year of publication, and country/region
- Study design and setting
- Age group (children, adults, mixed)
- Sample size and number of bacterial isolates
- Identified enteric pathogens
- Antimicrobials tested
- Antimicrobial susceptibility testing (AST) method
- Resistance breakpoints used (CLSI/EUCAST)
- Number and proportion of resistant isolates

When multiple resistance estimates were reported, community-specific data were preferentially extracted [27].

Quality Assessment and Risk of Bias
The methodological quality of included studies was assessed independently by two reviewers using a modified Joanna Briggs Institute (JBI) Critical Appraisal Checklist for Prevalence Studies [28]. Domains assessed included sampling strategy, sample size adequacy, laboratory methods, clarity of outcome measurement, and statistical analysis. Studies were categorized as low, moderate, or high risk of bias. Disagreements were resolved by consensus.

Data Synthesis and Statistical Analysis
For each pathogen–antibiotic combination, pooled resistance proportions were calculated using a random-effects model (DerSimonian–Laird method), accounting for expected heterogeneity across studies [29]. Proportions were stabilized using Freeman–Tukey double arcsine transformation where appropriate.

Statistical heterogeneity was assessed using the I^2 statistic, with values of 25%, 50%, and 75% representing low, moderate, and high heterogeneity, respectively [30]. Subgroup analyses were performed based on geographic region (Asia, Africa, Americas, Europe), age group, and study period when sufficient data were available.

Publication bias was evaluated using funnel plot asymmetry and Egger's regression test for pathogen–antibiotic pairs with ≥10 studies [31]. All analyses were conducted using standard meta-analysis software packages.

Outcome Measures
The primary outcome was the pooled prevalence of antimicrobial resistance among major bacterial enteric pathogens causing community-acquired diarrhea. Secondary outcomes included regional variations in resistance patterns and resistance trends across commonly used oral antimicrobials.

RESULTS
Study Selection
The database search yielded 1,426 records, of which 312 duplicates were removed. After title and abstract screening of 1,114 records, 182 articles were selected for full-text review. Following detailed assessment, 47 studies met the eligibility

criteria and were included in the qualitative synthesis, while 39 studies provided sufficient extractable data and were included in the meta-analysis.

The included studies were published between 2005 and June 2025 and represented data from Asia, Africa, Europe, and the Americas, with a predominance of studies from LMICs.

Characteristics of Included Studies

Among the 47 included studies:

- 29 (61.7%) were cross-sectional surveillance studies
- 11 (23.4%) were community-based observational studies
- 7 (14.9%) were outpatient cohort studies

A total of 21,386 stool samples were analyzed, yielding 18,742 bacterial isolates. Children-only populations were included in 27 studies (57.4%), adults-only in 8 studies (17.0%), and mixed-age populations in 12 studies (25.6%).

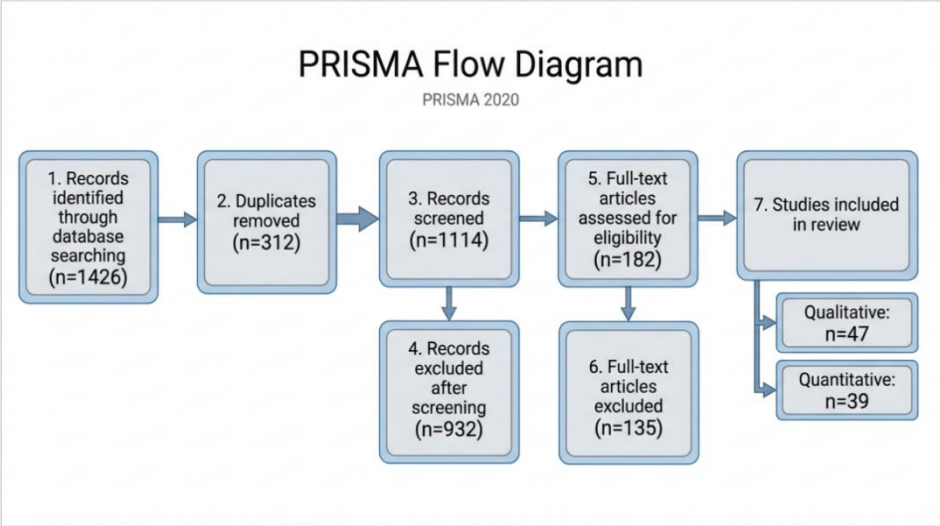

Figure 1. PRISMA 2020 flow diagram illustrating study identification, screening, eligibility, and inclusion in the systematic review and meta-analysis of antimicrobial resistance patterns in community-acquired diarrhea.

Distribution of Enteric Pathogens

The distribution of bacterial enteric pathogens across community-acquired diarrhea cases is summarized in Table 1.

Table 1. Distribution of bacterial enteric pathogens in community-acquired diarrhea

Pathogen	Number of isolates (n)	Percentage (%)
Escherichia coli	7,215	38.5
Shigella spp.	4,858	25.9
Salmonella spp.	3,915	20.9
Campylobacter spp.	2,096	11.2
Vibrio cholerae	658	3.5
Total	**18,742**	**100**

E. coli was the most frequently isolated pathogen, followed by *Shigella* and *Salmonella*, reflecting their dominant role in community-acquired bacterial diarrhea.

Pooled Antimicrobial Resistance Patterns

Escherichia coli

Pooled resistance estimates showed very high resistance to commonly used oral antimicrobials. Resistance to trimethoprim–sulfamethoxazole and ampicillin exceeded 50% across most regions. Ciprofloxacin resistance remained comparatively lower but showed substantial heterogeneity.

Table 2. Pooled antimicrobial resistance in *E. coli*

Antibiotic	Studies (n)	Isolates (n)	Pooled resistance % (95% CI)	I^2 (%)
Ampicillin	39	6,985	56 (44–67)	78
Trimethoprim–sulfamethoxazole	41	7,214	71 (57–82)	82
Ciprofloxacin	26	4,112	10 (5–20)	73
Ceftriaxone	18	3,486	8 (3–17)	69

Shigella spp.

Shigella isolates demonstrated marked resistance to older first-line agents, particularly ampicillin. Ciprofloxacin resistance was low in pooled analysis but varied widely by region.

Table 3. Pooled antimicrobial resistance in *Shigella spp.*

Antibiotic	Studies (n)	Isolates (n)	Pooled resistance % (95% CI)	I^2 (%)
Ampicillin	32	4,863	76 (60–87)	84
Trimethoprim–sulfamethoxazole	29	4,212	64 (48–77)	80
Ciprofloxacin	21	3,145	3 (0–15)	68
Ceftriaxone	14	2,304	2 (0–8)	61
Azithromycin	9	1,126	29 (14–50)	75

Salmonella spp.

Salmonella species exhibited moderate to high resistance to ampicillin and trimethoprim–sulfamethoxazole, while resistance to third-generation cephalosporins remained relatively low.

Table 4. Pooled antimicrobial resistance in *Salmonella spp.*

Antibiotic	Studies (n)	Isolates (n)	Pooled resistance % (95% CI)	I^2 (%)
Ampicillin	28	3,912	55 (35–73)	77
Trimethoprim–sulfamethoxazole	24	3,206	25 (15–38)	72
Ciprofloxacin	19	2,584	8 (3–18)	70
Ceftriaxone	16	2,198	5 (2–11)	65

Campylobacter spp.

Campylobacter showed clinically concerning resistance to both macrolides and fluoroquinolones, with substantial inter-study heterogeneity.

Table 5. Pooled antimicrobial resistance in *Campylobacter spp.*

Antibiotic	Studies (n)	Isolates (n)	Pooled resistance % (95% CI)	I^2 (%)
Erythromycin	19	2,103	33 (12–64)	86
Ciprofloxacin	18	1,984	27 (8–61)	88
Tetracycline	15	1,672	41 (22–63)	81

Regional Subgroup Analysis

Subgroup analysis demonstrated significant geographic variability. Studies from Asia reported higher resistance to fluoroquinolones and macrolides across *Shigella* and *Campylobacter* species compared with Africa and the Americas. African studies showed relatively lower fluoroquinolone resistance but persistently high resistance to ampicillin and trimethoprim–sulfamethoxazole.

Heterogeneity and Publication Bias

Heterogeneity was high for most pathogen–antibiotic combinations (I^2 >70%), reflecting differences in study populations, antimicrobial usage patterns, and laboratory methodologies. Funnel plot asymmetry suggested potential publication bias for selected analyses; however, Egger's test did not demonstrate statistically significant bias in most pooled estimates.

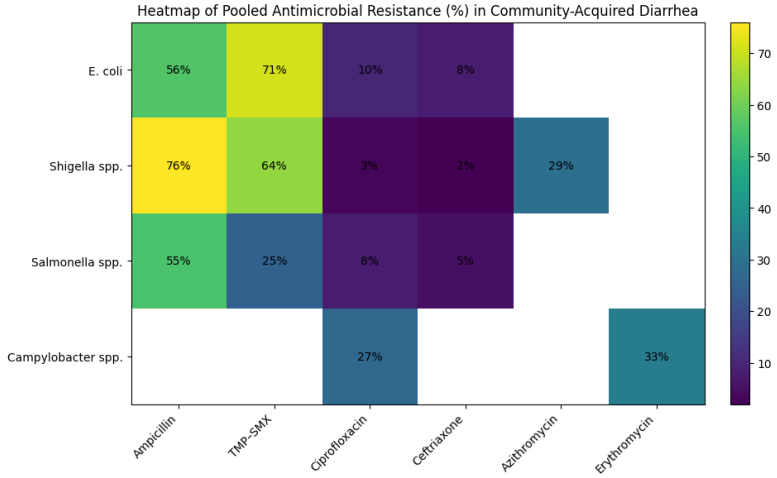

Figure 2. Heatmap showing pooled antimicrobial resistance (%) across major bacterial enteric pathogens causing community-acquired diarrhea. Darker shading indicates higher resistance.

Summary of Key Findings

- High resistance to ampicillin and trimethoprim–sulfamethoxazole across *E. coli*, *Shigella*, and *Salmonella*.
- Emerging resistance to azithromycin and fluoroquinolones, particularly in *Campylobacter*.
- Marked regional variability, emphasizing the need for local susceptibility data to guide empiric therapy.

DISCUSSION

This systematic review and meta-analysis demonstrates a high burden of antimicrobial resistance (AMR) among enteric bacterial pathogens causing community-acquired diarrhea, with particularly elevated resistance to older, commonly prescribed oral antibiotics. The findings have important mechanistic, clinical, and public health implications, especially in settings where empiric antimicrobial therapy is frequently initiated without microbiological confirmation.

Mechanisms underlying high resistance to legacy antimicrobials

The consistently high resistance observed to ampicillin and trimethoprim–sulfamethoxazole across *Escherichia coli*, *Shigella spp.*, and *Salmonella spp.* reflects decades of widespread community-level exposure to these agents [32,33]. β-lactam resistance in enteric bacteria is primarily mediated through plasmid-encoded β-lactamases, including TEM and SHV variants, which are readily transferable via horizontal gene transfer [34]. Similarly, resistance to trimethoprim–sulfamethoxazole is driven by acquisition of dfr and sul genes, often co-located on integrons that facilitate rapid dissemination within intestinal microbial communities [35]. The gastrointestinal tract serves as a critical ecological niche where selective antibiotic pressure amplifies resistant strains, even in individuals without recent healthcare exposure [36].

Fluoroquinolone resistance and target-site mutations

Although pooled ciprofloxacin resistance appeared relatively low for *Shigella* and *Salmonella*, substantial regional heterogeneity was noted, particularly in Asian studies. Fluoroquinolone resistance in enteric pathogens is largely attributed to stepwise mutations in the gyrA and parC genes, which alter DNA gyrase and topoisomerase IV binding sites [37]. Additional mechanisms such as plasmid-mediated quinolone resistance (PMQR) determinants, including qnr genes and aac(6')-Ib-cr, further reduce susceptibility and promote selection of high-level resistance under antibiotic pressure [38]. The increasing use of fluoroquinolones in outpatient settings and animal husbandry may explain the accelerating resistance trends in certain regions [39].

Macrolide resistance in *Campylobacter* and *Shigella*

The observed resistance to erythromycin and azithromycin, particularly in *Campylobacter spp.*, is clinically concerning. Macrolide resistance in *Campylobacter* is primarily mediated by point mutations in the 23S rRNA gene, which reduce ribosomal binding affinity [40]. Efflux pump overexpression (CmeABC) also contributes to reduced intracellular antibiotic concentrations [41]. In *Shigella*, azithromycin resistance is increasingly linked to plasmid-borne mph(A) and erm(B) genes, which enzymatically inactivate macrolides or modify ribosomal targets [42]. The spread of these resistance determinants compromises one of the few remaining oral treatment options for dysentery, particularly in children [43].

Persistence of multidrug-resistant enteric pathogens in the community

The frequent co-resistance observed across multiple antibiotic classes suggests widespread circulation of multidrug-resistant (MDR) enteric strains in community settings. Integrons, transposons, and conjugative plasmids play a central role in assembling and disseminating MDR gene cassettes within and between enteric species [44]. Environmental contamination, inadequate sanitation, and close human–animal interactions further facilitate transmission cycles, allowing resistant strains to persist outside hospital environments [45]. This challenges the traditional assumption that high-level resistance is predominantly a nosocomial phenomenon [46].

Clinical and public health implications

From a clinical perspective, the findings underscore the declining reliability of empiric antimicrobial therapy for community-acquired diarrhea in many regions. High resistance to legacy agents supports current guideline recommendations against their routine use, while emerging resistance to fluoroquinolones and macrolides necessitates cautious, context-specific prescribing [7,47]. The marked regional variability observed reinforces the importance of local community-based antibiograms to guide empiric decisions rather than reliance on global averages [48].

At the public health level, these results highlight critical gaps in AMR surveillance for enteric pathogens. Most national surveillance systems focus on bloodstream infections, leaving community-acquired gastrointestinal infections underrepresented [19,49]. Strengthening laboratory capacity for stool culture and susceptibility testing, integrating diarrheal pathogens into national AMR programs, and adopting One Health approaches are essential to curb further resistance emergence [50].

Strengths and limitations in context

This analysis synthesizes data from diverse geographic regions and age groups, providing a comprehensive overview of community-level enteric AMR. However, high heterogeneity, variability in laboratory methods, and underrepresentation of certain regions limit the precision of pooled estimates. Additionally, phenotypic resistance data do not fully capture emerging low-level or genotypic resistance that may affect clinical outcomes [51].

Future directions

Future research should prioritize prospective community surveillance, standardized AST reporting, and linkage of resistance data with clinical outcomes. Molecular epidemiological studies are also needed to map the transmission pathways of resistance genes across human, animal, and environmental reservoirs [52]. Such integrated efforts are crucial for preserving the effectiveness of existing antimicrobials and guiding rational therapy for community-acquired diarrheal diseases.

CONCLUSION

Antimicrobial resistance in community-acquired diarrheal pathogens is no longer a looming threat—it is a present clinical reality. This synthesis shows that many long-standing oral therapies have been rendered largely ineffective, while resistance is now encroaching upon agents traditionally reserved as reliable empiric options. The striking geographic heterogeneity observed cautions against uniform treatment algorithms and reinforces the necessity of locally informed prescribing. Unless community-level surveillance, antimicrobial stewardship, and One Health–aligned interventions are urgently strengthened, the therapeutic margin for managing bacterial diarrhea outside hospital settings will continue to narrow, with predictable consequences for morbidity, transmission, and health system burden.

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