Section: Miscellaneous

Original Research Article

PROSPECTIVE STUDY OF ENTERIC PATHOGENS CAUSING ACUTE DIARRHEA IN THE COMMUNITY AND THEIR ANTIMICROBIAL SUSCEPTIBILITY PROFILES

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ABSTRACT

Background: Acute diarrhea remains a major cause of morbidity in the community and contributes significantly to outpatient visits and hospital admissions. The etiological spectrum is diverse, and increasing antimicrobial resistance among enteric bacteria complicates empirical treatment. Local surveillance of enteric pathogens and their antimicrobial susceptibility profiles is essential to guide rational therapy and strengthen antimicrobial stewardship at tertiary care centers. The aim is to determine the spectrum of enteric bacterial pathogens causing acute diarrhea among community-presenting patients and to evaluate their antimicrobial susceptibility profiles, including multidrug resistance (MDR) and ESBL production.

Materials and Methods: A prospective, hospital-based observational study was conducted at a tertiary care hospital. A total of 125 consecutive patients presenting from the community with acute diarrhea (≥3 loose stools/24 hours) were enrolled. Fresh stool specimens were collected and processed using standard microbiological methods for isolation and identification of enteric bacterial pathogens. Antimicrobial susceptibility testing was performed by Kirby–Bauer disk diffusion on Mueller–Hinton agar and interpreted as per CLSI recommendations. MDR was defined as non-susceptibility to at least one agent in three or more antimicrobial classes; ESBL production among Enterobacterales was assessed using phenotypic methods where indicated.

Results: Among 125 patients, the most affected age group was 16–45 years (44.80%), with male predominance (57.60%). Vomiting (59.20%), abdominal pain (54.40%) and fever (48.80%) were common; blood/mucus in stool was present in 23.20%, and severe dehydration in 14.40%. Enteric bacterial pathogens were isolated in 79 cases (63.20%). Diarrheagenic Escherichia coli was the most frequent isolate (27.20%), followed by Salmonella spp. (14.40%), Shigella spp. (9.60%), Vibrio cholerae (7.20%) and Campylobacter spp. (4.80%). Fever ($p = 0.003$), blood/mucus in stool ($p < 0.001$) and dehydration ($p = 0.01$) were significantly associated with bacterial positivity. High resistance was observed to ampicillin and nalidixic acid, while amikacin and carbapenems showed high susceptibility. MDR and ESBL production among Enterobacterales were 40.63% and 28.13%, respectively.

Conclusion: Bacterial pathogens accounted for nearly two-thirds of community acute diarrhea cases, with diarrheagenic E. coli predominating. Significant resistance to commonly used antibiotics and substantial MDR/ESBL rates highlight the need for routine stool culture with

susceptibility testing and strengthened antimicrobial stewardship to guide empirical therapy.
Keywords: Acute diarrhea; Enteric pathogens; Antimicrobial susceptibility; Multidrug resistance; ESBL.

INTRODUCTION

Acute diarrhea remains one of the most frequent syndromic reasons for seeking healthcare in the community and at tertiary-care hospitals, spanning all age groups and clinical severities. It is classically defined as the passage of three or more loose or watery stools in 24 hours, and the most immediate life-threatening complication is dehydration, particularly in children, older adults, and individuals with limited physiological reserve. Despite being largely preventable and treatable, diarrhoeal illness continues to contribute substantially to morbidity, healthcare utilization, lost productivity, and avoidable deaths, especially where safe water, sanitation, and hygiene (WASH) are suboptimal.[1] From a global perspective, diarrhoeal disease continues to exert a major health burden. The World Health Organization emphasizes that diarrhoeal illness is preventable and treatable, yet still causes large numbers of childhood deaths each year and contributes to malnutrition and repeated illness cycles in vulnerable populations. Global transmission is closely linked to contaminated food and water, person-to-person spread in settings of poor hygiene, and inequities in access to safe drinking water and sanitation. These factors often overlap in community environments and are further amplified during seasonal surges, local outbreaks, and population movement.[2] Recent global estimates reinforce that, although progress has occurred, diarrhoeal diseases remain a leading cause of health loss across ages. The Global Burden of Disease Study 2021 systematic analysis reported that diarrhoeal diseases caused an estimated 1.17 million deaths in 2021 and were associated with ~59.0 million DALYs worldwide, highlighting that substantial burden persists beyond under-five populations as well. The same analysis underscores that risk factors such as unsafe water and poor sanitation continue to drive disease burden in older children and adults, which is directly relevant to community-acquired diarrhea presenting to tertiary-care facilities.[3] Children remain disproportionately affected by diarrhoeal disease, and real-world treatment gaps persist. UNICEF's diarrhoea profile notes that diarrhoea accounted for approximately 9% of global under-five deaths in 2021, translating to roughly 444,000 child deaths annually, despite the existence of low-cost and effective therapies such as oral rehydration. This persistent mortality—alongside ongoing underuse of recommended interventions in many settings—emphasizes the continued need to strengthen prevention and early case management while simultaneously improving etiological diagnosis and rational antimicrobial use.[4] The etiological spectrum of acute diarrhea includes viruses (e.g., rotavirus, norovirus), bacteria (e.g., diarrheagenic Escherichia coli, Shigella, Salmonella, Vibrio cholerae, Campylobacter), and parasites, with the relative contribution shaped by host age, exposures, sanitation, seasonality, and local outbreaks. In routine clinical practice, diarrhea is frequently managed syndromically, and stool cultures may be underutilized outside of severe illness, dysentery, suspected outbreaks, prolonged disease, or high-risk hosts. Consequently, many facilities lack robust local data that link community presentations to the actual distribution of enteric bacteria and their resistance patterns—data that are crucial for selecting appropriate empirical therapy when antibiotics are indicated. The need for improved detection and surveillance is strengthened by evidence that modern multiplex molecular panels can increase diagnostic yield and identify gaps missed by conventional approaches, thereby supporting more timely clinical decisions and public health action.[5] Antimicrobial therapy in acute diarrhea requires careful stewardship because most episodes are self-limiting or viral, and unnecessary antibiotics can promote resistance, increase costs, and risk adverse events. Nevertheless, antibiotics may be indicated in defined scenarios such as suspected invasive bacterial diarrhea, dysentery, cholera with severe dehydration, enteric fever, or high-risk hosts. In many settings, however, antibiotics are still prescribed excessively and empirically. A hospital-based evaluation of antibiotic utilization for acute diarrheal diseases reported very high antibiotic exposure (over four-fifths of patients receiving antibiotics), illustrating how frequently antimicrobials are used even when only a minority of cases are likely invasive in nature. Such patterns emphasize the importance of local pathogen surveillance and antimicrobial susceptibility profiling to support rational prescribing. The urgency of local antimicrobial susceptibility data is further heightened by global trends in antimicrobial resistance (AMR), including resistance relevant to gastrointestinal infections. The WHO Global antibiotic resistance surveillance report 2025 highlights AMR as a growing threat and describes analyses drawing on millions of bacteriologically confirmed infections, including gastrointestinal infections, supporting the premise that resistance surveillance must include enteric pathogens. For clinicians managing community acute diarrhea, AMR translates into reduced effectiveness of commonly used oral agents, increasing reliance on broader-spectrum drugs, and greater risk of treatment failure in invasive disease. Therefore, developing facility-specific antibiograms

for enteric bacteria is both a clinical and stewardship priority.[6]

MATERIALS AND METHODS

A prospective, hospital-based observational study was conducted at a tertiary care hospital to evaluate enteric pathogens responsible for acute diarrhea among community-presenting patients and to determine their antimicrobial susceptibility profiles. The study was planned to generate local epidemiological and resistance data to guide empirical therapy and support antimicrobial stewardship practices in routine clinical care. A total of 125 consecutive patients presenting to outpatient services and/or admitted from the community with acute diarrhea were enrolled. Acute diarrhea was defined as the passage of ≥3 loose or watery stools within 24 hours with a symptom duration consistent with an acute episode. Patients were included if they provided a fresh stool sample and consented to participate (or assent/guardian consent where applicable). Patients were excluded if diarrhea was clearly attributable to non-infectious causes (e.g., inflammatory bowel disease flare, malabsorption syndromes), if stool sample quantity was inadequate or improperly collected, or if the patient had received systemic antibiotics shortly before sample collection (documented and considered for exclusion as per protocol). Demographic and clinical details were recorded using a structured proforma at enrollment.

Eligible patients underwent a standardized clinical evaluation at presentation. Clinical variables captured included age, sex, residence (urban/rural), socioeconomic indicators (as available in records), history of unsafe water intake or outside food consumption, recent travel, contact history with similar illness, and comorbidities (e.g., diabetes, chronic kidney disease, chronic liver disease, immunosuppression). Symptom profile included frequency of stools/day, duration of diarrhea at presentation, presence of fever, vomiting, abdominal pain/cramps, tenesmus, visible blood or mucus in stool, and signs of dehydration. Dehydration severity was assessed clinically (general condition, thirst, sunken eyes, skin pinch, urine output, pulse and blood pressure) and categorized for analysis. Prior medication exposure (especially antibiotics, antidiarrheals, proton pump inhibitors) was documented, and baseline vital parameters were recorded.

Methodology

A single fresh stool specimen (or rectal swab where stool could not be obtained) was collected from each patient in a wide-mouthed sterile, leak-proof container following standard aseptic precautions. Patients/attendants were instructed to avoid contamination with urine or disinfectants. Samples were transported promptly to the microbiology laboratory in appropriate conditions; when immediate processing was not feasible, specimens were maintained under recommended cold-chain conditions. Gross appearance (watery, loose, formed; presence of blood/mucus) was noted at receipt, and each specimen was assigned a unique laboratory identifier.

Laboratory processing and identification of enteric pathogens

All stool samples underwent direct microscopic examination and culture-based processing for enteric bacterial pathogens following standard microbiology protocols. A saline and iodine wet mount was prepared where indicated to assess fecal leukocytes, red blood cells, and to screen for parasitic elements; additional concentration methods were employed when clinically warranted. For bacterial isolation, specimens were inoculated onto appropriate selective and differential media such as MacConkey agar and XLD/SS agar, with enrichment in selective broths (e.g., selenite F or alkaline peptone water) as required for suspected pathogens. Plates were incubated aerobically at 35–37°C and examined for typical colony morphology. Suspected isolates were identified using Gram staining and a standard panel of biochemical tests (e.g., oxidase, catalase, TSI, indole, citrate, urease, motility) and confirmed with serological methods where applicable (e.g., slide agglutination for Salmonella/Shigella). Identification was finalized after correlating colony characteristics, biochemical reactions, and confirmatory tests. If institutional protocol supported it, additional confirmation using automated identification systems was performed, and results were cross-verified with conventional methods. Quality assurance procedures were followed throughout, and control strains were used as per laboratory policy to validate media and reagents.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing (AST) was performed on all clinically significant bacterial isolates using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar, and results were interpreted according to current Clinical and Laboratory Standards Institute (CLSI) recommendations followed by the laboratory. A standardized inoculum (0.5 McFarland) was prepared from a pure culture, lawn-cultured on Mueller–Hinton agar, and antibiotic discs were applied with appropriate spacing. Plates were incubated at 35–37°C for the recommended duration, and zone diameters were measured in millimeters. The antibiotic panel for Gram-negative enteric isolates included agents commonly used for diarrheal disease and invasive enteric infections, such as ampicillin, amoxicillin–clavulanate, ciprofloxacin, nalidixic acid, azithromycin (where applicable), ceftriaxone/cefotaxime, ceftazidime, cefixime, trimethoprim–sulfamethoxazole, gentamicin, amikacin, and carbapenems (imipenem/meropenem) when clinically indicated or for suspected multidrug-resistant isolates. For

suspected Vibrio spp., appropriate media and interpretive considerations were applied and a relevant AST panel was used as per protocol. Multidrug resistance (MDR) was defined as non-susceptibility to at least one agent in three or more antimicrobial classes. Screening for extended-spectrum β-lactamase (ESBL) production among Enterobacterales was performed when indicated using phenotypic confirmatory tests (e.g., combination disc method), and results were reported accordingly. Internal quality control was maintained using reference strains (e.g., Escherichia coli ATCC 25922, Pseudomonas aeruginosa ATCC 27853, Staphylococcus aureus ATCC 25923) as applicable.

All demographic, clinical, and laboratory variables were entered into a structured database with coded identifiers. Primary outcome measures included the prevalence of specific enteric bacterial pathogens among community acute diarrhea cases and the antimicrobial susceptibility profile of each isolate. Secondary measures included associations between pathogen detection and clinical features (e.g., fever, dehydration, blood/mucus in stool), and distribution of resistance patterns including MDR and ESBL rates where detected.

Statistical analysis: Data were analyzed using SPSS version 25.0 (IBM Corp., USA). Continuous variables were summarized as mean ± standard deviation or median with interquartile range depending on distribution, while categorical variables were expressed as frequencies and percentages. Associations between categorical variables were assessed using Chi-square test or Fisher's exact test as appropriate, and comparisons of continuous variables were performed using Student's t-test or Mann–Whitney U test based on normality. A p-value <0.05 was considered statistically significant. Where relevant, odds ratios with 95% confidence intervals were calculated to measure the strength of association between clinical predictors and pathogen positivity or resistance outcomes.

RESULTS

The present prospective study included a total of 125 patients presenting with acute diarrhea from the community.

Demographic and clinical characteristics [Table 1]

The age distribution of patients showed that the majority belonged to the 16–45 years age group (44.80%), followed by children aged ≤15 years (30.40%) and patients older than 45 years (24.80%). This indicates that acute diarrheal illness predominantly affected the young and economically productive age group. Males constituted a higher proportion of cases (57.60%) compared to females (42.40%). Slightly more patients were from urban areas (55.20%) than rural areas (44.80%), reflecting greater healthcare access or reporting from urban settings. Regarding clinical presentation, vomiting was the most common symptom, observed in 59.20% of patients, followed by abdominal pain or cramps in 54.40% and fever in 48.80%. Blood or mucus in stool, suggestive of invasive diarrhea, was present in 23.20% of cases. Assessment of dehydration status revealed that 44.00% of patients had some degree of dehydration, while severe dehydration was noted in 14.40%, highlighting the clinical severity and need for prompt management in a substantial proportion of patients.

Distribution of enteric bacterial pathogens [Table 2]

Enteric bacterial pathogens were isolated from 79 out of 125 stool samples, yielding an overall bacterial positivity rate of 63.20%. Diarrheagenic Escherichia coli was the most frequently isolated pathogen, accounting for 27.20% of cases, followed by Salmonella spp. (14.40%) and Shigella spp. (9.60%). Vibrio cholerae was isolated in 7.20% of patients, while Campylobacter spp. constituted 4.80% of isolates. No bacterial pathogen could be isolated in 36.80% of samples, possibly due to viral or parasitic etiologies, prior antibiotic exposure, or low organism load.

Association between clinical features and pathogen positivity [Table 3]

A statistically significant association was observed between certain clinical features and bacterial pathogen positivity. Among patients presenting with fever, 67.21% were pathogen-positive compared to 59.38% among those without fever, and this difference was statistically significant ($p = 0.003$). The presence of blood or mucus in stool showed a strong association with bacterial isolation, with 86.21% of such cases being pathogen-positive compared to 56.25% in those without blood or mucus, a difference that was highly significant ($p < 0.001$). Similarly, patients with dehydration (any degree) demonstrated significantly higher pathogen positivity (71.23%) than those without dehydration (51.92%), with a p value of 0.01.

Antimicrobial susceptibility patterns in relation to pathogen type [Table 4]

Antimicrobial susceptibility testing revealed considerable variation in resistance patterns among different enteric pathogens. High resistance to ampicillin was observed across all organisms, particularly in E. coli (76.47%) and Campylobacter spp. (100.00%), with the difference across pathogens being statistically significant ($p = 0.02$). Resistance to amoxicillin–clavulanate was also high, especially among E. coli (64.71%) and Campylobacter spp. (100.00%), showing significant inter-organism variation ($p = 0.01$).

Fluoroquinolone resistance was notable, particularly among Campylobacter spp., which showed 83.33% resistance to ciprofloxacin, compared to lower resistance rates in Salmonella spp. and Vibrio cholerae. This difference was statistically significant ($p = 0.03$). Nalidixic acid resistance was widespread,

especially in E. coli (70.59%) and Shigella spp. (66.67%), with a significant p value of 0.04.

Third-generation cephalosporins such as ceftriaxone and ceftazidime showed relatively better activity, although resistance was still observed, particularly among E. coli. However, the differences in susceptibility across pathogens for these antibiotics did not reach statistical significance. Trimethoprim–sulfamethoxazole showed moderate to high resistance across organisms, with statistically significant variation (p = 0.04).

Aminoglycosides demonstrated good efficacy overall. Gentamicin susceptibility ranged from 76.47% in E. coli to 83.33% in Salmonella and Shigella spp., while amikacin showed high susceptibility across most pathogens, exceeding 88% in all except Campylobacter spp., with significant inter-pathogen differences (p = 0.03). Carbapenems exhibited excellent activity against nearly all isolates, with susceptibility rates approaching 100% in Enterobacterales, and the observed differences were statistically significant (p = 0.01).

Multidrug resistance and ESBL production [Table 5]

Among the 64 Enterobacterales isolates, multidrug resistance was detected in 26 isolates, corresponding to an MDR prevalence of 40.63%. Extended-spectrum β-lactamase (ESBL) production was identified in 18 isolates (28.13%).

Table 1: Demographic and clinical characteristics of patients with acute diarrhea (N = 125)

Variable	Number (n)	Percentage (%)
Age group (years)		
≤15	38	30.40
16–45	56	44.80
>45	31	24.80
Sex		
Male	72	57.60
Female	53	42.40
Residence		
Urban	69	55.20
Rural	56	44.80
Clinical features		
Fever	61	48.80
Vomiting	74	59.20
Abdominal pain/cramps	68	54.40
Blood/mucus in stool	29	23.20
Dehydration status		
No dehydration	52	41.60
Some dehydration	55	44.00
Severe dehydration	18	14.40

Table 2: Distribution of enteric bacterial pathogens isolated from stool samples (N = 125)

Pathogen isolated	Number (n)	Percentage (%)
Escherichia coli (diarrheagenic)	34	27.20
Salmonella spp.	18	14.40
Shigella spp.	12	9.60
Vibrio cholerae	9	7.20
Campylobacter spp.	6	4.80
No bacterial pathogen isolated	46	36.80

Table 3: Association between selected clinical features and bacterial pathogen positivity (N = 125)

Clinical feature	Pathogen positive n (%)	Pathogen negative n (%)	p value
Fever			
Present (n = 61)	41 (67.21)	20 (32.79)	0.003
Absent (n = 64)	38 (59.38)	26 (40.62)	
Blood/mucus in stool			
Present (n = 29)	25 (86.21)	4 (13.79)	<0.001
Absent (n = 96)	54 (56.25)	42 (43.75)	
Dehydration (any)			
Present (n = 73)	52 (71.23)	21 (28.77)	0.01
Absent (n = 52)	27 (51.92)	25 (48.08)	

Chi-square test; p < 0.05 considered statistically significant.

Table 4: Antimicrobial susceptibility pattern of enteric bacterial isolates in relation to pathogen type (N = 79)

Antibiotic	E. coli (n=34) S/R n (%)	Salmonella spp. (n=18) S/R n (%)	Shigella spp. (n=12) S/R n (%)	V. cholerae (n=9) S/R n (%)	Campylobacter spp. (n=6) S/R n (%)	p value
Ampicillin	8 / 26 (23.53 / 76.47)	6 / 12 (33.33 / 66.67)	3 / 9 (25.00 / 75.00)	5 / 4 (55.56 / 44.44)	0 / 6 (0.00 / 100.00)	0.02
Amoxicillin–clavulanate	12 / 22 (35.29 / 64.71)	8 / 10 (44.44 / 55.56)	5 / 7 (41.67 / 58.33)	6 / 3 (66.67 / 33.33)	0 / 6 (0.00 / 100.00)	0.01

Ciprofloxacin	18 / 16 (52.94 / 47.06)	12 / 6 (66.67 / 33.33)	7 / 5 (58.33 / 41.67)	6 / 3 (66.67 / 33.33)	1 / 5 (16.67 / 83.33)	0.03
Nalidixic acid	10 / 24 (29.41 / 70.59)	7 / 11 (38.89 / 61.11)	4 / 8 (33.33 / 66.67)	6 / 3 (66.67 / 33.33)	2 / 4 (33.33 / 66.67)	0.04
Ceftriaxone	20 / 14 (58.82 / 41.18)	14 / 4 (77.78 / 22.22)	8 / 4 (66.67 / 33.33)	7 / 2 (77.78 / 22.22)	3 / 3 (50.00 / 50.00)	0.08
Ceftazidime	19 / 15 (55.88 / 44.12)	13 / 5 (72.22 / 27.78)	9 / 3 (75.00 / 25.00)	6 / 3 (66.67 / 33.33)	2 / 4 (33.33 / 66.67)	0.06
Trimethoprim–sulfamethoxazole	13 / 21 (38.24 / 61.76)	9 / 9 (50.00 / 50.00)	6 / 6 (50.00 / 50.00)	5 / 4 (55.56 / 44.44)	1 / 5 (16.67 / 83.33)	0.04
Gentamicin	26 / 8 (76.47 / 23.53)	15 / 3 (83.33 / 16.67)	10 / 2 (83.33 / 16.67)	7 / 2 (77.78 / 22.22)	3 / 3 (50.00 / 50.00)	0.11
Amikacin	30 / 4 (88.24 / 11.76)	17 / 1 (94.44 / 5.56)	11 / 1 (91.67 / 8.33)	8 / 1 (88.89 / 11.11)	3 / 3 (50.00 / 50.00)	0.03
Carbapenems	33 / 1 (97.06 / 2.94)	18 / 0 (100.00 / 0.00)	12 / 0 (100.00 / 0.00)	9 / 0 (100.00 / 0.00)	4 / 2 (66.67 / 33.33)	0.01

S – Sensitive, R – Resistant

p values calculated using Chi-square test or Fisher's exact test where applicable; $p < 0.05$ considered statistically significant.

Table 5: Multidrug resistance (MDR) and ESBL production among Enterobacterales isolates (n = 64)

Resistance pattern	Number (n)	Percentage (%)
MDR isolates	26	40.63
Non-MDR isolates	38	59.37
ESBL producers	18	28.13
Non-ESBL producers	46	71.87

DISCUSSION

In the present study, acute diarrhea was seen predominantly in the young and economically productive age group, with 44.80% (56/125) of cases in 16–45 years and a male predominance of 57.60% (72/125). Clinically, vomiting (59.20%), abdominal pain/cramps (54.40%), and fever (48.80%) were common, while blood/mucus was present in 23.20% and severe dehydration in 14.40%. A comparable adult hospital-based profile was reported by Joseph et al. (2016), where males constituted 53.6% of cases and fever (~43.4%) was frequent, supporting that acute infectious diarrhea commonly presents with systemic and gastrointestinal symptoms, though our cohort had a higher proportion of vomiting (59.20% vs ~24.6%), possibly reflecting differences in case mix and community referral patterns.[7] The overall bacterial isolation rate in this study was 63.20% (79/125), indicating that a substantial proportion of community acute diarrhea in our setting is bacterial, while 36.80% had no bacterial pathogen isolated—suggesting viral/parasitic etiologies, low organism load, or prior unrecorded antimicrobial exposure. In contrast, large multicountry pediatric surveillance such as Kotloff et al. (2013) demonstrated that the dominant etiologies and attributable burden vary greatly by age and geography, with major contributions from non-bacterial pathogens in children alongside key bacterial agents like Shigella and ETEC, emphasizing that pathogen distribution in mixed-age community presenters (as in our cohort) may differ from under-five–focused datasets.8 Among bacterial positives in our study, diarrheagenic E. coli accounted for 43.04% (34/79) of isolates (27.20% of total cases), followed by Salmonella 22.78% (18/79), Shigella 15.19% (12/79), V. cholerae 11.39% (9/79), and Campylobacter 7.59% (6/79). A pediatric central India stool-culture study by Rajput & Waghmare (2019) reported a lower culture positivity (50.66%) with E. coli predominance (44.2% among positives), and smaller proportions of Salmonella (6.7%) and Shigella (11.6%), showing that while E. coli predominance is consistent, overall positivity and organism mix can vary by age group, diagnostic scope, and local epidemiology.[9] Similar organism predominance has been observed in other Indian tertiary-care observations. Rathaur et al. (2014), in an acute childhood diarrhea cohort, reported E. coli as the predominant isolate (44.2%), followed by Shigella (28.2%) and Salmonella (13.6%), reinforcing that diarrheagenic E. coli often remains the leading bacterial enteropathogen across Indian settings, while relative proportions of invasive pathogens (e.g., Shigella) can shift based on population (children vs mixed ages), hygiene exposures, and outbreak dynamics.[10] In our analysis of clinical predictors, fever ($p=0.003$), blood/mucus in stool ($p<0.001$), and dehydration ($p=0.01$) were significantly associated with bacterial pathogen positivity—particularly notable for dysenteric presentation where 86.21% were pathogen-positive. This aligns with the recognized clinicopathological pattern of invasive bacterial diarrhea, and Indian epidemiology reviews such as Taneja et al. (2016) emphasize that shigellosis classically presents with blood/mucus and fever and that such syndromic cues remain valuable for triage and early management where rapid diagnostics are limited.[11]

Antimicrobial susceptibility in our isolates showed high resistance to older first-line agents, with ampicillin resistance of 76.47% in E. coli, 66.67% in Salmonella, 75.00% in Shigella, and 100.00% in

Campylobacter, reflecting substantial loss of utility of ampicillin/amoxicillin-based therapy for empirical coverage. For cholera, our V. cholerae isolates retained 66.67% ciprofloxacin susceptibility but showed important resistance signals (33.33% resistant), supporting cautious use of fluoroquinolones. This concern is consistent with Khan et al. (2015) who demonstrated diminished ciprofloxacin susceptibility in V. cholerae O1 and highlighted nalidixic-acid testing as a useful screening approach for reduced ciprofloxacin susceptibility—relevant to our observed nalidixic acid resistance patterns and the need for evidence-based agent selection during suspected cholera presentations.[12] Fluoroquinolone resistance in our dataset was most striking for Campylobacter (ciprofloxacin resistance 83.33%), while E. coli and Shigella also showed notable ciprofloxacin resistance (47.06% and 41.67%, respectively). This magnitude is consistent with global high quinolone resistance described by Schiaffino et al. (2019), who reported ciprofloxacin resistance of 77.4% in C. jejuni and 79.8% in non-C. jejuni isolates, underscoring that fluoroquinolones are increasingly unreliable for empiric treatment when Campylobacter is a plausible cause, and macrolide-based strategies may be more appropriate in selected settings.[13] Third-generation cephalosporins in our study showed moderate-to-good activity but with meaningful resistance—e.g., ceftriaxone resistance in E. coli was 41.18%, and ceftazidime resistance 44.12%. In contrast, carbapenems showed near-universal susceptibility among Enterobacterales in our cohort (e.g., 97.06% in E. coli; 100% in Salmonella and Shigella), though Campylobacter susceptibility was lower (66.67%). Pediatric Indian data from Moharana et al. (2019) reported that >50% of isolates were resistant to ciprofloxacin and ceftriaxone, and documented even imipenem resistance (2.4%) in their setting, highlighting that escalation pressure and resistance can emerge even to last-resort agents—supporting strict stewardship and reserving carbapenems for clearly indicated severe or complicated infections.[14] Finally, resistance burden in our Enterobacterales was substantial: MDR was 40.63% (26/64) and ESBL production 28.13% (18/64), explaining the reduced performance of beta-lactams and some cephalosporins and emphasizing the importance of local antibiograms. Comparable concerns are reported in molecular Indian surveillance: Mandal et al. (2017) found ESBL production in 37.6% of diarrheagenic E. coli isolates (DEC) among diarrheal children and noted very high resistance of ESBL isolates to ceftriaxone (98.1%) while maintaining high susceptibility to amikacin (>96%), which mirrors our observation of strong amikacin activity overall (≥88% in most pathogens) and supports aminoglycosides (when clinically appropriate) and targeted therapy guided by culture/AST.[15]

CONCLUSION

This prospective study among 125 community-presenting acute diarrhea cases demonstrated a high bacterial isolation rate (63.20%), with diarrheagenic E. coli as the predominant pathogen, followed by Salmonella and Shigella. Fever, blood/mucus in stool, and dehydration were significant clinical predictors of bacterial etiology. Antimicrobial susceptibility results showed high resistance to commonly used agents such as ampicillin and nalidixic acid, while aminoglycosides and carbapenems retained good activity. The presence of MDR (40.63%) and ESBL production (28.13%) among Enterobacterales highlights the need for routine stool culture with AST and strict antimicrobial stewardship to guide empirical therapy and limit resistance.

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