RESEARCH ARTICLE

Antimicrobial Resistance Profiling of Shiga Toxin-Producing *Escherichia coli* Isolated from Diarrhoeic Cattle

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Abstract

Cattle are recognized as important reservoirs of Shiga toxin-producing *Escherichia coli* (STEC), contributing to the transmission of antimicrobial-resistant strains through the food chain and environment. The present study investigated the phenotypic and genotypic antimicrobial resistance profiles of 40 molecularly confirmed STEC isolates recovered from diarrhoeic cattle in Jaipur, Rajasthan. Antimicrobial susceptibility testing was performed against 11 antimicrobial agents using the Kirby-Bauer disc diffusion method. The highest susceptibility was observed against ampicillin/sulbactam, doxycycline, imipenem and chloramphenicol (80% each), whereas the highest resistance was detected against ciprofloxacin (97.5%), nitrofurantoin (95%) and co-trimoxazole (90%). Multidrug resistance was observed in 39 (97.5%) isolates, and resistotyping revealed 24 distinct resistance patterns, with R-1 as the predominant profile (25.0%). Molecular analysis detected *tetA* and *blaTEM* resistance genes in 17.5% and 15.0% of isolates, respectively. The coexistence of virulence-associated STEC with multidrug resistance highlights the potential public health risk posed by cattle as reservoirs of antimicrobial-resistant zoonotic pathogens. These findings emphasize the importance of antimicrobial stewardship, continuous surveillance and One Health approaches to control the emergence and spread of resistant STEC in livestock populations.

Key words: Antimicrobial resistance, Multidrug resistance, Resistotyping, STEC.

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Introduction

Shiga toxin-producing *Escherichia coli* (STEC) is recognized as one of the most significant foodborne zoonotic pathogens affecting both animal and human health worldwide. Cattle serve as the primary reservoir of STEC and shed the organism asymptomatically through faeces, facilitating contamination of food, water, and the environment. Human infection generally occurs through the consumption of contaminated meat, milk, fresh produce, or water, as well as through direct contact with infected animals or their surroundings (Paton and Paton, 1998; Beutin *et al*., 2007; Amézquita-López *et al*., 2014). STEC possesses several important virulence determinants, among which *stx1* and *stx2* are the major pathogenic factors responsible for clinical manifestations ranging from uncomplicated diarrhoea to haemorrhagic colitis and haemolytic uraemic syndrome (HUS), with *Stx2* being more frequently associated with severe disease (Karmali *et al*., 2010; Melton-Celsa, 2014). Additional virulence factors, including *eaeA* encoding intimin and *ehlyA* encoding enterohaemolysin, contribute to bacterial adhesion, colonization, and disease severity. Although serotype O157:H7 remains the most extensively studied, non-O157 STEC serogroups have increasingly been implicated in sporadic infections and foodborne outbreaks across the world (Jajarmi *et al*., 2017; Mughini-Gras *et al*., 2018). Because diarrhoeic cattle can harbour pathogenic STEC strains, continuous surveillance of these organisms is essential to understand their epidemiology and to reduce the risk of zoonotic transmission.

The widespread use of antimicrobial agents in livestock production for disease treatment, prophylaxis, and production enhancement has accelerated the emergence of antimicrobial-resistant *E. coli*, posing a serious challenge to both veterinary and public health. Resistance is primarily mediated through mobile genetic elements such as plasmids, transposons, and integrons carrying transferable resistance genes, facilitating the dissemination of multidrug resistance among bacterial populations (Zhao *et al*.,

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2001; Umpierrez *et al*., 2017). The increasing occurrence of multidrug-resistant STEC is particularly concerning because antimicrobial therapy for STEC infections remains controversial due to the possibility of enhanced Shiga toxin production following exposure to certain antibiotics (Grif *et al.,* 1998). Furthermore, the emergence of resistance to critically important antimicrobials, including carbapenems, highlights the growing public health threat posed by resistant STEC strains (Mir *et al*., 2019). Antimicrobial resistance has been identified by the World Health Organization as one of the leading global health threats, emphasizing the need for integrated surveillance under the One Health framework (WHO, 2024). Despite the importance of dairy farming in Rajasthan, information regarding the phenotypic and genotypic antimicrobial resistance profiles of STEC isolated from diarrhoeic cattle in the Jaipur region remains scarce. Hence, this study was undertaken in Jaipur Region of Rajasthan.

Materials and Methods

A total of 40 Shiga toxin-producing *Escherichia coli* (STEC) isolates recovered from faecal samples of diarrhoeic cattle and previously identified by cultural, biochemical, and molecular methods in our earlier investigation (Chaudhary *et al*., 2026) were included in the present study. These confirmed non-O157 STEC isolates were used to determine their phenotypic antimicrobial susceptibility and genotypic antimicrobial resistance profiles

Antimicrobial Susceptibility Testing

The antimicrobial susceptibility of the 40 STEC isolates was evaluated using the Kirby–Bauer disc diffusion method on Mueller-Hinton agar. Briefly, each isolate was subcultured in 5 mL of Luria-Bertani (LB) broth and incubated at 37°C for 6-8 h under shaking conditions to obtain actively growing cultures. The bacterial suspension was uniformly inoculated onto Mueller-Hinton agar plates using a sterile cotton swab. Commercial antibiotic discs representing 11 commonly used antimicrobial agents were aseptically placed on the agar surface at an appropriate distance to prevent overlapping inhibition zones. The inoculated plates were incubated aerobically at 37°C for 18-24 h, after which the diameters of the inhibition zones were measured in millimetres. Based on the CLSI (2020) interpretative criteria, isolates were classified as susceptible (S), intermediate (I), or resistant (R) to each antimicrobial agent.

Molecular Detection of Antibiotic-Resistant Genes in *E. coli*

To detect antibiotic-resistant genes in the STEC isolates (n=40), simplex PCR assays were conducted for beta-lactamase genes (e.g., *blaTEM*) and tetracycline resistance genes (e.g., *tetA*)) using specific primers and amplification conditions (Table 1). The PCR reaction mixture (10 µL total volume) comprised 1.0 µL of 10× PCR buffer, 1.0 µL of dNTP mix, 1.0 µL of each primer, 2.0 µL of genomic DNA template, 0.4 µL of Taq DNA polymerase, and 4.6 µL of nuclease-free water. PCR amplification conditions for both β-lactamase (TEM) *blaTEM* gene and Tetracycline resistance *tetA gene* included initial denaturation at 94°C/5 min, followed by 35 cycles each of denaturation at 94°C/1 min, annealing at 51°C/1 min *blaTEM* gene (56°C/1 min for *tetA gene*), and elongation at 72°C/1 min, and final extension at 72°C/5 min (Maynard *et al.*, 2003; Randall *et al*., 2011). PCR amplification products were analyzed by electrophoresis on a 1.5% agarose gel in 1× TAE buffer at 100 V for 1 h. The gel was stained with an appropriate DNA-binding dye and visualized under UV illumination using the Fusion Solo S gel documentation system (Vilber, France). The presence of distinct DNA bands corresponding to the expected amplicon sizes was considered indicative of successful amplification.

Results and Discussion

A total of 40 STEC isolates recovered from diarrhoeic cattle were evaluated for antimicrobial susceptibility against 11 antimicrobial agents. The antibiogram revealed an alarmingly high prevalence of multidrug resistance (MDR), with 39 (97.5%) isolates exhibiting resistance to three or more antimicrobial classes, indicating extensive antimicrobial selection pressure within cattle production systems. Similar high frequencies of MDR among bovine STEC have been reported globally and are considered a major concern because cattle serve as the principal reservoir of zoonotic STEC capable of transmitting resistant bacteria to humans through contaminated food, water and the environment (Mukherjee *et al*., 2021; Schierack *et al*., 2023; Chaudhary *et al*., 2026).

Among the antimicrobials tested, the highest susceptibility was observed against ampicillin/sulbactam, doxycycline, imipenem and chloramphenicol (80% each), suggesting that these agents still retain comparatively good activity against most STEC isolates. In contrast, susceptibility to amikacin (12.5%), cefotaxime (27.5%), tetracycline (20%), gentamicin (10%), ciprofloxacin (2.5%), co-trimoxazole (2.5%) and nitrofurantoin (2.5%) was markedly reduced (Table 2). The extremely high resistance observed against ciprofloxacin (97.5%), nitrofurantoin (95%), co-trimoxazole (90%), amikacin (80%), tetracycline (77.5%), gentamicin (77.5%) and cefotaxime (70%) reflects the increasing antimicrobial selection pressure in food animals. Similar resistance profiles have been reported in bovine STEC isolates from India and other countries, where extensive use of fluoroquinolones, tetracyclines and β-lactams has

Table 1: Primers used for detection of *blaTEM* and *tetA* genes in STEC isolates

Gene	Target gene	Primer sequence (5´-3´)	Amplicon size (bp)	References
β-lactamase (TEM)	*blaTEM*	F-5´GAGTATTCAACATTTTCGT3´ R-5´ACCAATGCTTAATCAGTGA3´	857	Maynard *et al.*, 2003
Tetracycline resistance	*tetA*	F-5´GGTTCACTCGAACGACGTCA3´ R- 5´CTGTCCGACAAGTTGCATGA3´	577	Randall *et al.*, 2011

Table 2: Antibiotic sensitivity pattern of STEC Isolates

Name of antibiotics	Symbol	Concen-tration	Antibiotic Sensitivity Pattern		
			Sensitive	Intermediate	Resistant
Amikacin	AK	30 µg	5 (12.5%)	3 (7.5%)	32 (80.0%)
Ampicillin/Sulbactum	A/S	10/10 µg	32 (80.0%)	1 (2.5%)	7 (17.5%)
Cefotaxime	CTX	5 µg	11 (27.5%)	1 (2.5%)	28 (70.0%)
Doxycycline	DO	30 µg	32 (80.0%)	2 (5.0%)	6 (15.0%)
Imipenem	IPM	10 µg	32 (80.0%)	0	8 (20.0%)
Tetracycline	TE	30 µg	8 (20.0%)	1 (2.5%)	31 (77.5%)
Chloramphenicol	C	30 µg	32 (80.0%)	5 (12.5%)	3 (7.5%)
Ciprofloxacin	CIP	5 µg	1 (2.5%)	0 (0%)	39 (97.5%)
Co-Trimoxazole (Trimethoprim/ Sulfamethoxazole)	COT	25 µg	1 (2.5%)	3 (7.5%)	36 (90.0%)
Gentamicin	GEN	10 µg	4 (10.0%)	5 (12.5%)	31 (77.5%)
Nitrofurantoin	NIT	300 µg	1 (2.5%)	1 (2.5%)	38 (95.0%)

contributed to the emergence and persistence of resistant clones (Gyles, 2007; Mukherjee *et al*., 2021).

Although antimicrobial therapy is generally not recommended in human STEC infections because antibiotic exposure may induce bacteriophage-mediated Shiga toxin release and increase the risk of haemolytic uraemic syndrome (HUS), monitoring antimicrobial resistance in livestock isolates remains epidemiologically important. Resistant STEC circulating in cattle may serve as reservoirs of transferable resistance determinants that can disseminate to other enteric bacteria through horizontal gene transfer, thereby contributing to the growing burden of antimicrobial resistance within the One Health framework (Pacheco and Sperandio, 2012; Schierack *et al*., 2023).

Resistotyping further demonstrated substantial phenotypic diversity among the isolates. A total of 24 distinct resistotypes were identified, indicating continuous diversification of resistance patterns under antimicrobial pressure. The distribution of different resistance profiles among STEC isolates is summarized in Table 3. Resistotype R-1 was the predominant pattern, accounting for 25% of all resistotypes, and was characterized by simultaneous resistance to amikacin, cefotaxime, tetracycline, ciprofloxacin, co-trimoxazole, gentamicin and nitrofurantoin. The predominance of a single MDR resistotype suggests the circulation of a successful resistant clone or the widespread dissemination of common mobile resistance determinants among bovine STEC populations. Conversely, Resistotype R-3 exhibited the broadest resistance spectrum, including resistance to nine antimicrobial agents, highlighting the emergence of highly resistant isolates capable of surviving exposure to multiple therapeutic options. The occurrence of numerous unique resistotypes indicates ongoing acquisition and rearrangement of resistance genes through plasmids, transposons and integrons, which facilitate adaptation under farm-level antimicrobial selection pressure (Schierack *et al*., 2023; Valat *et al*., 2024).

A particularly noteworthy observation was the detection of 20% phenotypic resistance to imipenem, a carbapenem considered a last-resort antimicrobial for severe multidrug-resistant Gram-negative infections in human medicine. Because carbapenems are not routinely used in livestock production, the presence of imipenem-resistant STEC isolates may reflect environmental dissemination of carbapenem-resistant Enterobacteriaceae or acquisition of mobile resistance determinants from human or environmental sources. Similar findings have recently been highlighted as an emerging public health concern due to the increasing movement of carbapenem resistance genes across animal, environmental and human interfaces (Hussain *et al*., 2019; Valat *et al*., 2024).

Molecular characterization of the STEC isolates further supported the phenotypic findings. Among the 40 isolates, the *tetA gene* was detected in 17.5% (7/40**)**, whereas the *blaTEM* gene was detected in 15.0% (6/40) of the isolates (Fig. 1, 2). The *tetA* gene encodes an energy-dependent efflux pump that actively exports tetracycline from the bacterial

Table 3: Resistotyping of STEC isolates from diarrheic cattle

Resistotype	Resistotype Pattern	No. of isolates	%
R-1	AK, CTX, TE, CIP, COT, GEN, NIT	10	25%
R-2	AK, TE, CIP, COT, GEN, NIT	2	5%
R-3	AK, CTX, IPM, TE, C, CIP, COT, GEN, NIT	1	2.5%
R-4	AK, A/S, CTX, TE, CIP, COT, GEN, NIT	2	5%
R-5	IPM, CIP, COT, GEN, NIT	1	2.5%
R-6	CTX, CIP, GEN, NIT	2	5%
R-7	AK, CTX, TE, COT, GEN, NIT	1	2.5%
R-8	AK, A/S, DO, TE, C, CIP, COT, GEN, NIT	1	2.5%
R-9	AK, CTX, CIP, COT	1	2.5%
R-10	CTX, DO, TE, CIP, COT, NIT	1	2.5%
R-11	TE, CIP, COT, GEN, NIT	2	5%
R-12	AK, CTX, IPM, TE, CIP, COT, GEN, NIT	3	7.5%
R-13	AK, CTX, DO, IPM, TE, CIP, COT, GEN, NIT	1	2.5%
R-14	CIP, COT, NIT	1	2.5%
R-15	AK, TE, CIP, COT, NIT	1	2.5%
R-16	AK, IPM, TE, C, CIP, GEN, NIT	1	2.5%
R-17	AK, A/S, CTX, TE, CIP, COT, NIT	1	2.5%
R-18	AK, A/S, CTX, DO, TE, CIP, COT, GEN, NIT	2	5%
R-19	AK, CTX, IPM, TE, CIP, COT, NIT	1	2.5%
R-20	AK, CIP, COT, NIT	1	2.5%
R-21	AK, CTX, CIP, COT, GEN, NIT	1	2.5%
R-22	AK, CTX, TE, CIP, COT, NIT	1	2.5%
R-23	AK, CIP, COT, GEN, NIT	1	2.5%
R-24	CTX, CIP	1	2.5%

cell, thereby reducing intracellular drug concentrations, while *blaTEM* encodes a β-lactamase enzyme capable of hydrolysing β-lactam antibiotics and conferring resistance to penicillins and related compounds. Detection of these genes confirms the circulation of plasmid-mediated resistance mechanisms within bovine STEC populations and supports their role as reservoirs of transferable antimicrobial resistance genes (Gyles, 2007; Valat *et al*., 2024).

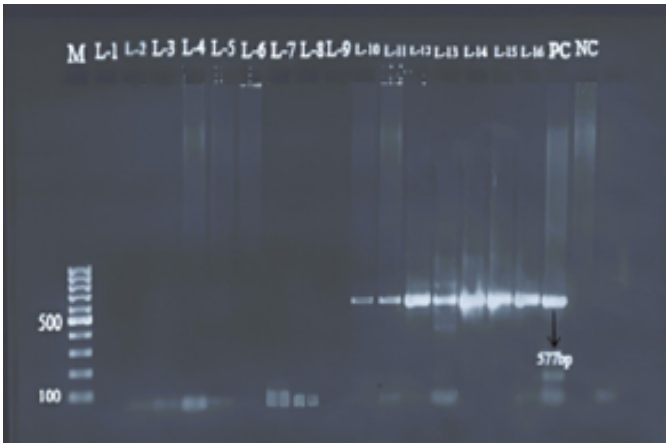


Fig. 1: PCR amplification product of tetracycline resistance (*tetA*) gene (577 bp) in STEC isolates

The molecular findings showed a general agreement with the phenotypic resistance profile. The widespread tetracycline resistance observed phenotypically is consistent

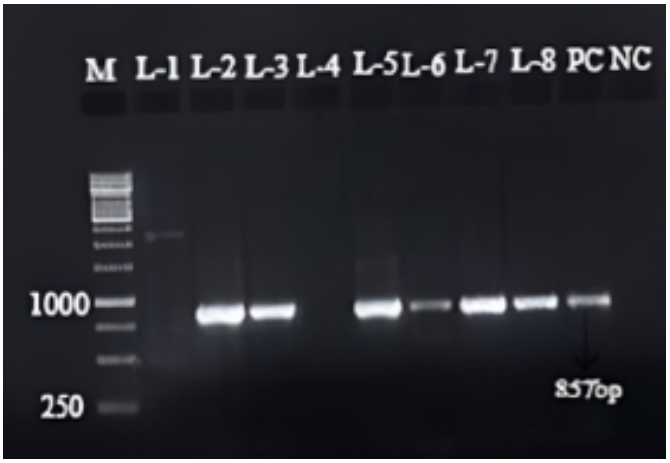


Fig. 2: PCR amplification product of β-lactamase (*blaTEM*) gene (857 bp) in STEC isolates

with the detection of *tetA*, whereas the presence of *blaTEM* supports the occurrence of β-lactam resistance among STEC isolates. However, the proportion of phenotypically resistant isolates exceeded the number carrying these two genes, suggesting that additional resistance determinants such as *tetB, tetM, blaCTX-M, blaSHV*, *AmpC* β-lactamases or multidrug efflux systems may also contribute to the observed resistance phenotype. Similar genotype–phenotype discrepancies have been reported previously, highlighting the complexity of antimicrobial resistance mechanisms in livestock-associated *E. coli* (Tello *et al.*, 2020;

Messele *et al.*, 2022).

When interpreted together with the virulence profiling conducted in the present investigation, the antimicrobial resistance findings become more significant. The predominance of *stx2*-positive isolates, together with the detection of *eaeA* and *ehlyA* in the same bovine VTEC isolates reported in our previous study (Chaudhary *et al*., 2026), suggests the coexistence of virulence and multidrug resistance within bovine STEC populations. Such strains possess enhanced pathogenic potential while simultaneously carrying resistance determinants that facilitate persistence under antimicrobial pressure. Mobile genetic elements carrying resistance genes may coexist with virulence-associated genes, thereby promoting the emergence and dissemination of highly adapted zoonotic clones. Similar convergence of antimicrobial resistance and virulence has been reported in diarrhoeic cattle and is increasingly recognized as a major challenge for both veterinary medicine and public health (Schierack *et al*., 2023).

Conclusion

The present study revealed a very high prevalence of multidrug resistance among STEC isolates recovered from diarrhoeic cattle in the Jaipur region of Rajasthan. The coexistence of extensive phenotypic resistance, diverse resistotypes and transferable resistance genes *(tetA* and *blaTEM*) indicates the potential role of cattle as reservoirs for antimicrobial-resistant zoonotic pathogens. The detection of resistant STEC strains carrying virulence-associated characteristics highlights a significant public health concern under the One Health framework. Continuous antimicrobial surveillance, judicious antibiotic usage and implementation of effective farm-level antimicrobial stewardship practices are essential to control the emergence and dissemination of resistant STEC in livestock populations.

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