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ESBL (Extended–Spectrum Beta–Lactamase) – Producing Enterobacteriaceae in Hospitalized UTI – Prevalence and Molecular Characterization.

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ABSTRACT

Background: UTIs are among the most prevalent hospital-acquired infections (HAIs) and are frequently brought on by members of the Enterobacteriaceae family. The appearance of Extended - Spectrum Beta - Lactamase (ESBL) – producing strains is a grave danger to antimicrobial therapy and has led to restricted antimicrobial options and to high morbidity. **Aim:** The purpose of this study was to determine the frequency and pattern of ESBL-producing Enterobacteriaceae that were isolated from hospitalized patients' urine samples, as well as to evaluate their pattern of antibiotic susceptibility.

Methods: The isolates came from 899 samples of urine collected at SGT Hospital, Gurugram, during a six-month period and yielded 109 non- duplicate Enterobacteriaceae “isolates. Identification was performed using standard biochemical assays of the isolates. In accordance with the standards established by the Clinical and Laboratory Standards Institute (CLSI), the Kirby-Bauer disk diffusion method (mKB) has been utilised to conduct the test for antimicrobial susceptibility. blaSHV, blaCTX-M, and blaTEM were discovered by multiplex PCR in twenty randomly selected ESBL-positive isolates. The Double Disk Synergy Test (DDST) was utilised in order to screen and validate the production” of ESBL.

Results: Of the 899 urine samples, 12.1% (109/899) were significantly positive for the presence of enterobacteriaceae. “*Escherichia coli* (83.4%) and *Klebsiella pneumoniae* (6.4%) were the predominant isolates” found. It was determined that 51 isolates (46.8%) produced ESBL by phenotypic screening, of which E.coli accounted for 88.2% of ESBL producers. A high level of resistance was noted for Amoxicillin (76.1%), ampicillin (69.7%), and cefepime (68.8%), while fosfomycin (89.0% sensitive) and aztreonam (87% sensitive) were highly effective. The blaSHV gene was found in 95% of the 20 isolates, blaCTX -M in 40%, and blaTEM was not found, based on PCR analysis.

Conclusion: According to the study, blaSHV-carrying *E. coli* is primarily responsible for the high incidence of ESBL-producing Enterobacteriaceae (46.8%) in UTI isolates from hospitalized patients. Controlling the spread of these multidrug-resistant bacteria requires constant antimicrobial surveillance, appropriate antimicrobial use, and the application of infection control strategies.

Keywords: ESBL, Enterobacteriaceae, blaSHV, antimicrobial resistance, blaCTX-M, hospitalized patients, urinary tract infection, β - lactamase.

1. INTRODUCTION

UTIs are a major health care burden, estimated to be 1-4% of all healthcare-associated infections (HAIs) worldwide [1]. UTIs can occur in any age group, and they are among the most crucial sources of morbidity and increasing health care costs [2]. While various microorganisms can infect the urinary tract, members of the Enterobacteriaceae family, specifically *Klebsiella pneumoniae* and *E. coli*, are the predominant etiological agents in both community-acquired and hospital-acquired UTIs [3-5].

Increasingly, antimicrobial resistance has worsened the worldwide spread of UTIs and their “clinical management [9]. The production of Extended-Spectrum β -lactamase (ESBLs) is one of the key resistance mechanisms of Gram-negative bacteria [6]. While susceptible to β -Lactamase inhibitors (e.g., clavulanic acid) [6], Carbapenems do not work on ESBLs. ESBL-producing strains of *K. pneumoniae* and *E. coli* frequently exhibit co-resistance to other antibiotic classes, such as aminoglycosides and fluoroquinolones, thus reducing” the choice of empiric therapy and the risk of clinical complications like sepsis and long hospital stays [7, 12].

The genetic determinants of ESBLs are typically plasmid-mediated and lead to the rapid spread of the gene(s) between different bacterial species [11]. The most clinically relevant ESBL families are TEM, SHV, and CTX-M [8]. The TEM and SHV family of derivatives were once common, but CTX-M has rapidly spread globally making it a major contributor to cephalosporin resistance in UTI pathogens [5,12].

ESBL-producing Enterobacteriaceae are a recognized threat to global health, and there is an urgent need for ongoing, local epidemiological surveillance. Local patterns of antibiotic use and patient population characteristics have a significant influence on local resistance patterns [10]. Determining the incidence “of ESBL-producing Enterobacteriaceae in hospitalized UTI patients, together with their antibiotic resistance pattern and the molecular distribution of, blaSHV, blaCTX-M, and blaTEM resistance genes.

MATERIALS AND METHODS

1.1 Study Setting and Period

This was a prospective and observational study carried out in the Department of Microbiology at SGT Hospital (SGTH), Budhera, Gurugram, Haryana. The study was carried out between May 2023 and October 2023 for a total of six” months.

2.2 Study Population and Sample Collection

The “population under study consisted of 200 individuals.

Patients hospitalized in the inpatient department had their midstream urine samples taken consecutively with a clinical suspicion of UTI during the study period.

2.3 Inclusion and Exclusion Criteria

Avoiding the inclusion of items in a study that” would bias the results. Exclusion and inclusion criteria.

Enterobacteriaceae were only included when recovered from significant amounts in the urine of hospitalised patients. Isolates that were Gram – positive, non-Enterobacteriaceae Gram-negative isolates, and clinically insignificant colony counts were excluded from the study.

2.4 Urine Culture and Bacterial Isolation

The urine samples were processed using semi-quantitative culturing methods. Samples were “streaked on Cystine Lactose Electrolyte-Deficient (CLED) agar using a sterile nichrome wire loop, and they were then incubated for 18 to 24 hours at 37°C. Per Kass criterion, a colony count of $\geq 10^5$ Colony Forming Units (CFUs)/mL is deemed” significant.

2.5 Identification of Enterobacteriaceae

Conventional microbiological techniques were employed to ascertain the bacterial species. These included Gram staining, motility testing using the hanging drop technique, as well as a wide range of “biochemical assessments: Catalase, Oxidase, Triple Sugar Iron (TSI) agar, Indole production, Citrate utilization, Nitrate Reduction, and Urease Tests” [13].

2.6 Antimicrobial Susceptibility Testing (AST)

Mueller-Hinton agar (MHA) “was tested for antimicrobial susceptibility using the Modified Kirby-Bauer disk diffusion method. Bacterial suspension concentrations were adjusted to a 0.5 McFarland standard. Aztreonam (30 µg), Nitrofurantoin (300 µg), Ceftriaxone (30 µg), Amikacin (30 µg), Ampicillin (10 µg), Ciprofloxacin (5 µg), Piperacillin-tazobactam (100/10 µg), Ceftazidime (30 µg), Fosfomycin (200 µg), Cotrimoxazole (25 µg), Amoxicillin-clavulanic acid (20 µg), Levofloxacin (30 µg), and Gentamicin (10 µg) are the antibiotics” that are including in it. The zone diameter (Sensitive, Intermediate, or Resistant) “was measured and interpreted using the Clinical and Laboratory Standards Institute (CLSI) 2022 standards [12]. The quality control strain used was *E. coli* ATCC 25922.

2.7 Phenotypic Detection of ESBL Production

Isolates resistant to or less susceptible to third-generation cephalosporins (cefotaxime, ceftazidime, and ceftriaxone) were found to be potential ESBL producers. The phenotype was confirmed using the DDST in accordance” with CLSI recommendations [15]. The “antibiotic disks that were tested were Cefotaxime/clavulanic acid (30µg/10µg), Ceftazidime (30µg), Cefotaxime (30µg), and Ceftazidime/clavulanic acid (30µg/10µg). The zone diameter of the clavulanate-combined disk grew by at least 5 mm in comparison to the regular disk, indicating” the synthesis of ESBL.

2.8 DNA Extraction and PCR Detection of blaSHV, blaCTX-M, and blaTEM

Twenty randomly chosen, phenotypically confirmed ESBL-producing isolates underwent molecular phenotyping. As directed by the manufacturer, “genomic DNA was extracted from overnight cultures using the HiPurA Bacterial Genomic DNA Purification Kit (HiMedia Laboratories, Mumbai, India) [16]. The blaSHV, blaCTX-M, and blaTEM genes were identified using the multiplex Real-Time PCR” method based on the HI-PCR. HiMedia Laboratories' Gene

Quantification Probe PCR Kit [1436] was used to measure extended beta-lactamases, or ESBLs. The 25µl reaction mixtures were subjected to “thermal cycling (TC-4000, Bangalore Genei, India) with denaturation at 95°C for 10 minutes and 40 cycles of denaturation at 95°C for 15 seconds, followed by annealing/extension at 60°C for” 30 seconds.

2.9 Ethical Approval

The “study protocol was reviewed and approved by the Institutional Ethics Committee, Faculty of Medicine and Health Sciences (FMHS), SGT University, Haryana (Approval No”: SEC/FMHS/M.SC/29/04/23-03).

3 RESULTS

3.3 Sample Processing and Demographics

Hospitalized individuals provided 899 urine samples over the course of the six-month trial period. Significant bacterial growth corresponding to the Enterobacteriaceae family was observed in 109 samples (12.1%), while 790 samples (87.8%) exhibited no Significant growth.

Among the 109 culture-positive cases, females were notably more affected, accounting for 79 cases (72.5%), compared to 30 cases (27.5%) in males. The age group of 19 to 45 years had the highest infection incidence, representing 56.8% (n=62) of the positive cultures, followed by patients aged 46-60 years (17.4%, n=19).

Table 1. Age and Gender Distribution of Culture–Positive Patients (n=109)

Age Group (Years)	Male (%)	Female (%)	Total (%)
0-18	2 (18.1%)	9 (81.8%)	11 (10.0%)
19-45	12 (19.3%)	50 (80.6%)	62 (56.8%)
46-60	9 (47.3%)	10 (52.6%)	19 (17.4%)
Above 60	7 (41.1%)	10 (58.8%)	17 (15.5%)
Total	30 (27.5%)	79 (72.5%)	109 (100%)

3.4 Distribution of Bacterial Isolates

Following this were *Citrobacter freundii* (2.7%, n=3), *Proteus mirabilis* (4.5%, n=5), *Klebsiella pneumoniae* (6.4%, n=7), and *Klebsiella oxytoca* (2.7%, n=3).

3.5 Overall Antimicrobial Resistance Pattern

The isolates displayed high levels of resistance to standard empirical therapies. Amoxicillin resistance was found to be the highest (76.1%), followed by ampicillin (69.7%), cefepime (68.8%), ceftriaxone (66.9%), and ciprofloxacin (56.8%). Conversely, the isolates retained higher susceptibility to fosfomycin (11.0% resistant), aztreonam (22.0% resistant), piperacillin – tazobactam (23.8% resistant), and gentamicin (26.6% resistant).

Table 2. Antimicrobial Resistance Profile of major Enterobacteriaceae Isolates

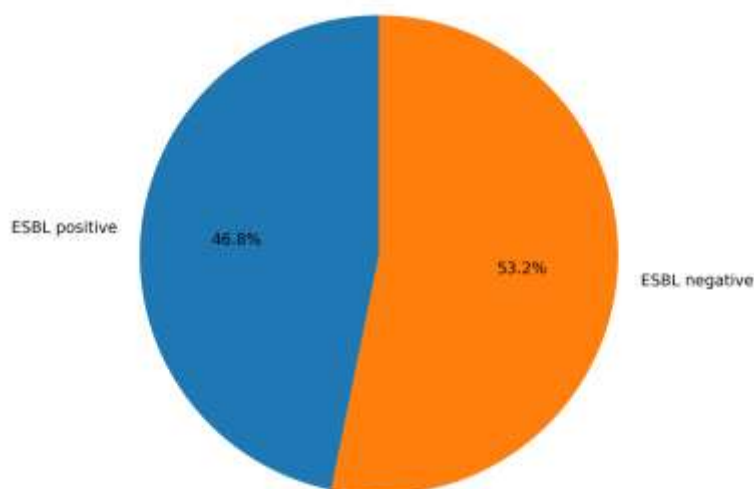
Antibiotic	<i>E.coli</i> (n=91) Resistance %	<i>P. mirabilis</i> (n=5) Resistance %	<i>K. oxytoca</i> (n=3) Resistance %	<i>C. freundii</i> (n=3) Resistance %	<i>K. pneumoniae</i> (n=7) Resistance %
Ampicillin	72.55	80.0%	66.6%	66.6%	57.1%
Amoxicillin	75.8%	100%	-	66.6%	57.1%
Ceftriaxone	69.2%	60.0%	66.6%	66.6%	57.1%
Cefotaxime	50.5%	80.0%	66.6%	66.6%	28.5%
Cefepime	70.3%	60.0%	33.3%	0.0%	42.8%
Ceftazidime	35.1%	20.0%	66.6%	0.0%	28.5%
Ciprofloxacin	58.2%	80.0%	33.3%	33.3%	42.8%
Levofloxacin	49.4%	80.0%	66.6%	66.6%	42.8%
Amikacin	47.2%	20.0%	66.6%	33.3%	28.5%
Gentamicin	27.4%	20.0%	33.3%	0.0%	14.2%
Nitrofurantoin	37.3%	40.0%	33.3%	0.0%	42.8%
Cotrimoxazole	42.8%	40.0%	33.3%	33.3%	14.2%
Pip-Tazobactam	23.0%	20.0%	33.3%	0.0%	42.8%
Aztreonam	23.0%	20.0%	0.0%	-	14.2%
Fosfomycin	-	-	0.0%	0.0%	28.5%

3.6 Phenotypic Detection of ESBL Producers

Based on the “DDST, 51 (46.8%) of the 109 clinical isolates were found to produce ESBL. ESBL generation was more common in female patients (72.5% of all ESBL instances, n = 37) than in male patients (27.04%, n = 14) (p = 0.094). The age group of 20 to 40 years old had the highest frequency of ESBL isolates (33.3%, n=17).

Among the ESBL- producing strains, *E. coli* was the dominant species, comprising” 88.2% (n=45) of all ESBL isolates. *Citrobacter freundii* and *Proteus mirabilis* accounted for 3.9% (n=2) each, while *K. oxytoca* and *K. pneumoniae* each accounted for 1.9% (n=1).

Figure 1. Phenotypic ESBL detection by DDST among culture-positive Enterobacteriaceae isolates (n=109).

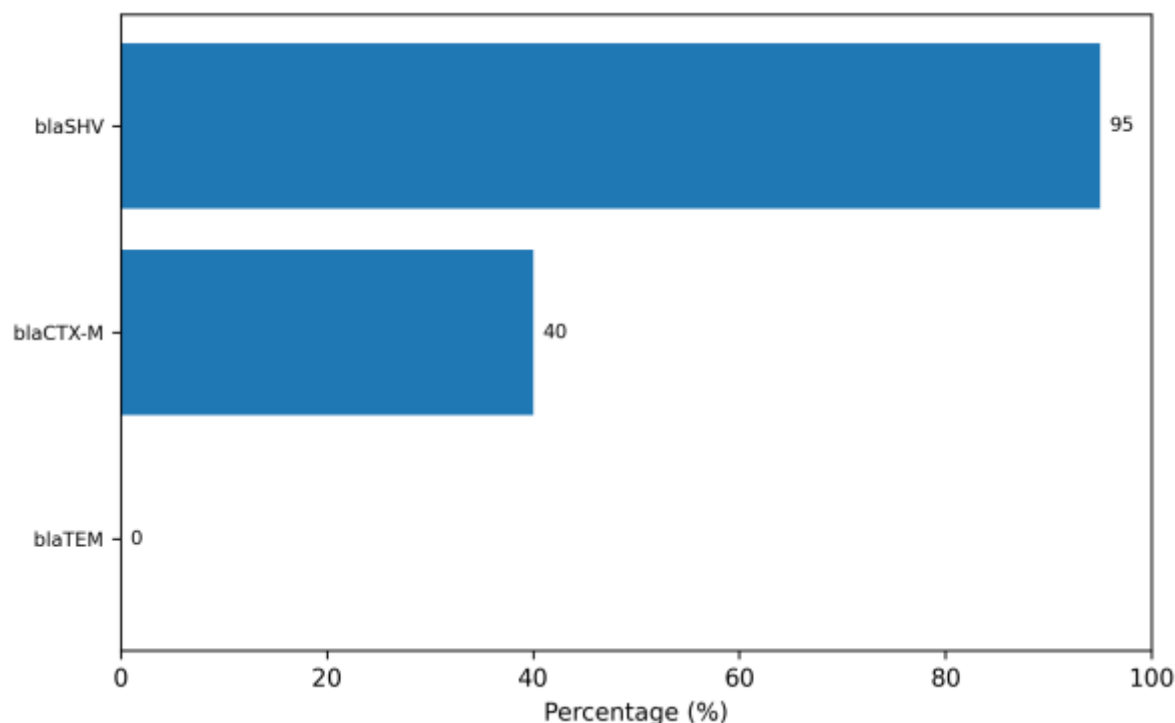


3.7 Molecular Characterization of ESBL Genes

Multiplex PCR was successfully performed on 20 randomly selected DDST-positive ESBL isolates. Molecular screening revealed an overwhelming predominance of the blaSHV gene, which was found in 95.0% (19/20) of the isolates. The blaCTX-M gene was co- found in 40.0% (8/20) of the isolates. Notably, the blaTEM gene was absent (0%) in all tested samples.

E.coli represented the primary reservoir for these genes, accounting for 85% (17/20) of the PCR - confirmed isolates.

Figure 2. Using multiplex real-time PCR, ESBL-associated genes were found in 20 randomly chosen phenotypically confirmed ESBL isolates.



4. DISCUSSION

This study shows that ESBL-producing Enterobacteriaceae are highly prevalent in the hospital setting (46.8%) and indicates a significant and increasing problem for empirical antimicrobial therapy of UTIs. A total of 12.1% (3/25) significant bacteriuria were isolated in our patient group and compared well with other previous institutional studies from the Indian subcontinent, such as Behera et al. (12.6% significant growth) and Shrestha et al. (9% growth) [17, 18].

UTIs were the most prevalent, occurring in 73% of the patients, as is usual in every country in the world. This was likely caused by a number of anatomical predispositions, such as a “shorter urethra and the proximity to the perianal region. Young-to-middle-aged adults (19–45 years old) in the current study had the highest infection burden, as reported by Yadav et al. in the 20–40 age range” (46.03%) [20].

With 83.4% of all Enterobacteriaceae infections, *E. coli* was the most significant uropathogen; *K. pneumoniae* came in second with 6.4%. The conclusion that *E. coli* is the primary target of antibiotic stewardship for UTIs is supported by the overwhelming dominance of *E. coli* in both Mohamed and Parajuli trials (68.9% and 68.4%, respectively) [19, 21].

The overall antimicrobial susceptibility profile was alarming, as resistance was present for most of the basic beta-lactam antibiotics, with resistance to amoxicillin, ampicillin, ceftriaxone, and cefepime at near or above 70%, respectively. The fluoroquinolone resistance rate was also high, with 56.8% showing resistance to ciprofloxacin. These patterns resemble those that Teklu et al.

reported in Ethiopia, for amoxicillin-clavulanic acid (71.6%) and cefepime (60.3%) [22]. Fortunately, the effectiveness of piperacillin-tazobactam and aztreonam (both >75% sensitive) and fosfomycin (72.9% sensitive) as carbapenem-sparing drugs remains high, and they continue to be useful in severe or complicated cases in our setting.

The frequency of ESBL producers in the hospital was 46.8%, which is similar to other parts of the region, like 48.2% reported by Shaikh et al., North India [23] and 40.8% reported by Sharif et al., Iran [24]. The genotypic distribution of these ESBLs, however, had unique local characteristics. Multiplex PCR revealed that blaSHV was the most prevalent genetic determinant associated with ESBL production in our patients (95.0%), followed by blaCTX-M (40.0%), and blaTEM was not detected. This is different from the outcome of Sahoo et al., who reported the highest frequency of blaTEM (76.25%) and blaCTX-M (71.87%) [25]. The presence of the blaSHV genes in a high proportion of isolates – mainly *E. coli* isolates - may be due to particular regional plasmid transmission patterns and regional antimicrobial prescribing practices.

5. STRENGTHS AND LIMITATIONS

Strengths: This study is successful in the use of both phenotypic (DDST) and advanced genotypic (Multiplex Real-Time PCR) methods for mapping the spread of ESBL, with a more robust pathogen characterization of ESBL resistance mechanisms than phenotypic screening alone. **Limits:** This study may not accurately represent the prevalence of UTIs in the area or community because it was conducted at a single tertiary care facility. Furthermore, the molecular detection of the genes discovered was limited to a random subsample of 20 ESBL-positive isolates using PCR.

6. CONCLUSION

The burden of ESBL-producing Enterobacteriaceae among hospitalized UTI patients is alarmingly high (46.8%), significantly compromising the efficacy of conventional β -lactam and cephalosporin therapies. *E. coli* remains the preeminent uropathogen, and the robust presence of the blaSHV gene points to established local plasmid reservoirs. With nearly three-quarters of isolates demonstrating multi-drug resistance characteristics, reliance on empirical prescribing without culture confirmation risks therapeutic failure.

7. CLINICAL IMPLICATIONS / RECOMMENDATIONS

To mitigate the rapid escalation of ESBL-driven resistance, hospitals must prioritize routine phenotypic and genotypic surveillance integrated with rigorous antimicrobial stewardship. Empirical antibiotic guidelines for hospitalized UTIs should be continuously updated against local antibiograms; based on current data, agents like fosfomycin and piperacillin-tazobactam should be prioritized over highly compromised third-generation cephalosporins. Strict adherence to catheter care protocols and infection prevention measures is vital to disrupt the nosocomial transmission of these resistant blaSHV and blaCTX-M strains.

8. REFERENCES

1. Yang X, Chen H, Zheng Y, Qu S, Wang H, Yi F. Disease burden and long-term trends of urinary tract infections. *Front Public Health*. 2022;27:10-88.
2. Flores-Mireles AL, Walker JN, Caparon M, Hultgren SJ. Urinary tract infections: epidemiology, mechanisms of infection and treatment options. *Nature Reviews Microbiology*. 2015 May;13(5):269-84.
3. Korkmazer R, Kayaaslan B, Kaya-Kalem A, Oktay Z, Eser F, Hasanoğlu İ, Güner R. Causative Microorganisms in Community-Acquired Urinary Tract Infections and Risk Factors for the Development of Infection with Extended-Spectrum β -Lactamase-Producing Species. *Infectious Diseases & Clinical Microbiology*. 2024 Jun 28;6(2):112.
4. Bayaba S, Founou RC, Tchouangueu FT, Dimani BD, Mafo LD, Nkengkana OA, Founou LL, Noubom M. High prevalence of multidrug resistant and extended-spectrum β -lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* isolated from urinary tract infections in the West region, Cameroon. *BMC infectious diseases*. 2025 Jan 24;25(1):115.
5. Zhou Y, Zhou Z, Zheng L, Gong Z, Li Y, Jin Y, Huang Y, Chi M. Urinary tract infections caused by uropathogenic *Escherichia coli*: mechanisms of infection and treatment options. *International journal of molecular sciences*. 2023 Jun 23;24(13):10537.
6. Rawat D, Nair D. Extended-spectrum β -lactamases in Gram Negative Bacteria. *Journal of global infectious diseases*. 2010 Sep;2(3):263.
7. Jo SB, Ahn ST, Joo HJ, Kim JW, Oh MM. Carbapenem resistance and ESBL-producing Enterobacteriaceae in patients with urological Infections from 2012 to 2021 in three Korean hospitals. *Diagnostics*. 2025 Aug 11;15(16):2004.
8. Castanheira M, Simner PJ, Bradford PA. Extended-spectrum β -lactamases: an update on their characteristics, epidemiology and detection. *JAC-antimicrobial resistance*. 2021 Sep 1;3(3):dlab092.
9. Sampathkumar R, Saranya R, Gnanasekaran D, Thakran V, Aslam H, Pascal S. Antibiotic resistance in urinary tract infections: A study on trends and contributing factors in outpatient care among Indian patients. *Bioinformation*. 2024 Dec 31;20(12):1908.
10. Azzam A, Khaled H, Samer D, Nageeb WM. Prevalence and molecular characterization of ESBL-producing Enterobacteriaceae in Egypt: a systematic review and meta-analysis of hospital and community-acquired infections. *Antimicrobial Resistance & Infection Control*. 2024 Dec 5;13(1):145.
11. Stadler T, Meinel D, Aguilar-Bultet L, Huisman JS, Schindler R, Egli A, Seth-Smith HM, Eichenberger L, Brodmann P, Hübner P, Bagutti C. Transmission of ESBL-producing Enterobacteriaceae and their mobile genetic elements—identification of sources by whole genome sequencing: study protocol for an observational study in Switzerland. *BMJ open*. 2018 Feb;8(2):e021823..
12. Clinical Laboratory Standard Institute. Performance Standard for Antimicrobial Susceptibility Testing; Thirty-Two Information Supplement. M100-S32. Wayne, Pennsylvania, USA: Clinical Laboratory Institute; 2022
13. Franco-Duarte R, Černáková L, Kadam S, S. Kaushik K, Salehi B, Bevilacqua A, Corbo MR, Antolak H, Dybka-Święć K, Leszczewicz M, Relison Tintino S. Advances in chemical and biological methods to identify microorganisms—from past to present. *Microorganisms*. 2019 May 13;7(5):130.
14. Hi-PCR Extended-spectrum beta-lactamase (ESBLs) Gene Quantification Probe PCR Kit

15. Paterson DL, Bonomo RA. Extended-spectrum β -lactamases: a clinical update. Clinical microbiology reviews. 2005 Oct;18(4):657-86.
16. HiPurA Bacterial Genomic DNA Purification Kit (Cat No. MB505,Himedia Laboratories, Mumbai, India
17. Behera B, Debbarma M, Rout B, Baral P, Das S, Jena L, Panigrahy R. Prevalence of ESBL Producing Bacteria in Community-Acquired UTI from Eastern Part of India. J Pure Appl Microbiol. 2022; 16:1682-8.
18. Shakya P, Shrestha D, Maharjan E, Sharma VK, Paudyal R. ESBL production among *E. coli* and *Klebsiella spp.* causing urinary tract infection: a hospital based study. Open Microbiol. J. 2017; 11:23.
19. Mohamed ES, Khairy RM, Abdelrahim SS. Prevalence and molecular characteristics of ESBL and AmpC β -lactamase producing Enterobacteriaceae strains isolated from UTIs in Egypt. Antimicrob. Resist. Infect. Control. 2020; 9:1-9.
20. Yadav K, Prakash S. Screening of ESBL producing multidrug resistant *E. coli* from urinary tract infection suspected cases in Southern Terai of Nepal. J Infect Dis Diagn. 2017; 2:116.
21. Parajuli NP, Maharjan P, Parajuli H, Joshi G, Paudel D, Sayami S, et al. High rates of multidrug resistance among uropathogenic *Escherichia coli* in children and analyses of ESBL producers from Nepal. Antimicrob. Resist. Infect. Control. 2017; 6:1-7.
22. Teklu DS, Negeri AA, Legese MH, Bedada TL, Woldemariam HK, Tullu KD. Extended-spectrum beta-lactamase production and multi-drug resistance among Enterobacteriaceae isolated in Addis Ababa, Ethiopia. Antimicrob. Resist. Infect. Control. 2019; 8:1-2.
23. Shaikh S, Fatima J, Shakil S, Rizvi SM, Kamal MA. Risk factors for acquisition of extended spectrum beta lactamase producing *Escherichia coli* and *Klebsiella pneumoniae* in North-Indian hospitals. Saudi J. Biol.Scie. 2015; 22:37-41.
24. Sharif MR, Soltani B, Moravveji A, Erami M, Soltani N. Prevalence and risk factors associated with extended spectrum beta lactamase producing *Escherichia coli* and *Klebsiella pneumoniae* isolates in hospitalized patients in Kashan (Iran). Electron. physician. 2016; 8:2081.
25. Sahoo S, Otta S, Swain B, Kar SK. Detection and genetic characterization of extended-spectrum beta-lactamases producers in a tertiary care hospital. J. Lab. Physicians. 2019; 11:253-8.