To determine the bacterial profile and antibiotic susceptibility patterns of pathogens isolated from clinically diagnosed urinary tract infections (UTI) in the north-west indian region.

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Abstract

Background: Urinary tract infections (UTIs) are among the most common bacterial infections worldwide and represent a significant clinical and public health burden, particularly in the context of rising antimicrobial resistance (AMR).

Objectives: The present study aimed to determine the bacterial profile and antibiotic susceptibility patterns of pathogens isolated from clinically diagnosed UTI cases and to identify risk factors contributing to antimicrobial resistance.

Methods: A total of 400 urine samples were cultured aerobically, and bacterial isolates were identified using standard microbiological and biochemical methods. Antibiotic susceptibility testing was performed according to Clinical and Laboratory Standards Institute (CLSI) guidelines using the Kirby-Bauer disc diffusion method. Sociodemographic and clinical characteristics were analysed to assess associations with UTI occurrence and AMR.

Results: Of 400 urine samples, 311 (77.5%) were culture positive, with females contributing a higher proportion of samples (70.58%) compared to males (29.42%). Among culture-positive cases, Gram-negative bacilli (55.1%) predominated, followed by Gram-positive cocci (31.9%), *Candida spp*. (8.1%), and polymicrobial growth (7.9%). *Escherichia coli* was the most frequent isolate (62.2% of GNB), followed by *Klebsiella pneumoniae* (27%) and *Pseudomonas aeruginosa* (11.8%). Among Gram-positive cocci, *Enterococcus* spp. (70%) and *Staphylococcus aureus* (30%) were predominant. Antimicrobial susceptibility testing revealed high resistance rates across major drug classes. In Gram-negative isolates, resistance to gentamicin (71.9–75.7%), ciprofloxacin (42.1–62.1%), and third-generation cephalosporins (up to 74.4%) was common, while carbapenems retained partial efficacy but showed emerging resistance (31–52% resistant). Among Gram-positive bacteria, *S. aureus* demonstrated high resistance to oxacillin (46.7%), erythromycin (51.4%), and ciprofloxacin (78.5%), while glycopeptides and linezolid retained good activity. *Enterococcus faecalis* was largely susceptible to vancomycin and teicoplanin, whereas *E. faecium* exhibited high resistance to multiple drug classes, including fosfomycin (93%) and chloramphenicol (81%).

Conclusion: The study demonstrates a high prevalence of multidrug-resistant (MDR) pathogens in UTI cases, with *E. coli* and *Enterococcus* spp. as the predominant isolates. Resistance to commonly prescribed antibiotics highlights the urgent need for continuous regional surveillance, evidence-based empirical therapy, and strict antimicrobial stewardship programmes to mitigate resistance.

Key words: Urinary tract infections (UTIs), multidrug-resistant (MDR), antimicrobial resistance (AMR), GNB (Gram-negative bacteria), Clinical and Laboratory Standards Institute (CLSI)

1. Introduction

Urinary tract infections (UTIs) are among the most frequent bacterial infections affecting people across all ages, genders, and regions, and they remain a major public health concern due to their contribution to increased morbidity, rising healthcare costs, and significant strain on health systems (Foxman et al., 2014). UTIs occur when pathogenic microorganisms, most often bacteria, colonise and infect any part of the urinary system, including the urethra, bladder, ureters, or kidneys. Although both men and women can be affected, women are disproportionately vulnerable due to anatomical and physiological factors such as a shorter urethra and its proximity to the anal region (Flores-Mireles et al., 2015). Clinically, UTIs can present with a wide spectrum of symptoms, ranging from dysuria, frequency, haematuria, and suprapubic pain to fever, and in severe cases, ascending infections like pyelonephritis can lead to systemic complications, including sepsis, if untreated (Nicolle et al., 2019). These infections are broadly categorised as uncomplicated, often occurring in otherwise healthy individuals, or complicated, which are associated with risk factors such as diabetes, urinary catheterisation, immunosuppression, or anatomical abnormalities (Gupta et al., 2011). *Escherichia coli* is the predominant uropathogen, accounting for most community-acquired and healthcare-associated UTIs, but other species, including *Klebsiella pneumoniae*, *Proteus mirabilis*, *Staphylococcus saprophyticus*, and *Enterococcus spp.,* are also important, particularly in hospital or immunocompromised populations (Flores-Mireles et al., 2015). The bacterial spectrum can vary depending on geography, demographics, hospital environment, and underlying comorbidities, highlighting the importance of local surveillance to guide therapy (Magliano et al., 2012). A critical challenge in UTI management is the rising prevalence of antimicrobial resistance (AMR). Indiscriminate antibiotic use, incomplete courses, self-medication, and poor infection control practices have driven the emergence of multidrug-resistant (MDR) uropathogens, including extended-spectrum beta-lactamase (ESBL)-producing *E. coli* and *Klebsiella pneumoniae*, which significantly limit treatment options (Laupland et al., 2016). Resistance to carbapenems, considered last-resort drugs, further complicates therapy and has been linked to higher mortality, prolonged hospital stays, and increased treatment costs (Logan and Weinstein, 2017). Antibiotic susceptibility testing, particularly using methods such as the Kirby-Bauer disc diffusion technique, plays a key role in guiding effective treatment by providing data on the susceptibility profiles of isolates (CLSI, 2020). Knowledge of local resistance patterns enables clinicians to choose empiric antibiotics more appropriately, reduces treatment failures, and helps prevent the spread of resistance (Hooton et al., 2010). In addition to microbiological testing, understanding the risk factors associated with AMR is essential. Prior antibiotic exposure, recurrent infections, long hospital stays, urinary catheterization, comorbidities such as diabetes, and poor hygiene practices have all been identified as contributing factors (Gajdács et al., 2019). Social and environmental aspects, including limited access to healthcare, inadequate sanitation, and lack of awareness regarding antibiotic misuse, also play significant roles in resistance trends (Prestinaci et al., 2015). Given these challenges, it is necessary to investigate the bacterial profile and susceptibility patterns of UTI pathogens at the local level. Surveillance of AMR trends can inform clinical practice, support antimicrobial stewardship, and guide infection control policies. Furthermore, region-specific data are vital to developing evidence-based treatment protocols that align with the evolving epidemiology of uropathogens (Kumar et al., 2022).

India is geographically and culturally diverse, and regional variations influence disease patterns, antibiotic use, and healthcare access. Punjab, located in the northwest part of the country, is known for intensive agriculture, a strong private healthcare sector, and widespread antibiotic availability without prescription (Yadav & Pandey, 2023). This easy accessibility contributes to frequent self-medication and irrational antibiotic use, which accelerates antimicrobial resistance, especially in urinary pathogens (Bhargava et al., 2022). In contrast, the Northeastern region of India—which includes states such as Assam, Meghalaya, Manipur, Nagaland, Mizoram, Tripura, Arunachal Pradesh, and Sikkim—is geographically isolated and has a different healthcare delivery structure. Although healthcare facilities are improving, several northeastern states still face gaps in diagnostic infrastructure, especially microbiology laboratories capable of culture and sensitivity testing (Deka et al., 2021). Limited surveillance and overuse of empirical therapy contribute to antimicrobial resistance trends similar to those seen in Punjab, but with less documentation (Borah et al., 2022). The current study seeks to address these gaps by identifying the bacterial pathogens responsible for UTIs, assessing their antibiotic resistance profiles, and examining factors contributing to AMR in the northwest indian region. Findings from this study will provide valuable insights into local epidemiology, improve targeted antibiotic use, and contribute to strategies aimed at reducing the global burden of antimicrobial resistance in UTIs in this region of India.

2. Materials and Methods

2.1 Study Design and Setting

A diagnostic lab-based cross-sectional study was conducted at Lovely Diagnostic Centre, Ferozepur, Punjab, India. Microbiological analyses, including bacterial isolation, identification, and antimicrobial susceptibility testing.

2.2 Study Population

The study population comprised clinically diagnosed patients with urinary tract infections (UTIs) presenting with symptoms such as dysuria, frequent urination, hematuria, fever, and lower abdominal pain. Both male and female patients of all age groups were included.

Sample Size

A total of 400 urine samples were collected from clinically diagnosed UTI patients.

2.3 Inclusion Criteria

- Patients clinically diagnosed with UTIs.
- Patients of all age groups and genders.
- Patients providing informed consent.\

2.4 Exclusion Criteria

- Patients who had received antibiotics within 48 hours prior to sample collection.
- Patients with incomplete medical records.
- Samples showing visible contamination or improper collection.

2.5 Sample Collection

Midstream clean-catch urine samples (20–30 mL) were collected in sterile containers using aseptic techniques. All samples were transported to the microbiology laboratory within 2 hours of collection under cold storage conditions.

2.6 Microbiological Analysis

2.6.1 Bacterial Isolation and Identification

Urine samples were inoculated onto Cysteine Lactose Electrolyte Deficient (CLED) agar, MacConkey agar, and Blood agar using the semi-quantitative streak plate method. The plates were incubated aerobically at 37°C for 24–48 hours. Significant bacteriuria was defined as a colony count of $\geq 10^5$ CFU/mL. Isolates were identified on the basis of colony morphology, Gram staining, and standard biochemical tests, including catalase, oxidase, indole, citrate utilisation, and urease tests.

2.6.2 Antibiotic Susceptibility Testing

Antibiotic susceptibility testing was performed by the Kirby–Bauer disc diffusion method on Mueller–Hinton agar following Clinical and Laboratory Standards Institute (CLSI) guidelines (CLSI, 2023). The antibiotic panel included Erythromycin (15 µg), Clindamycin (2 µg), Gentamicin (10 µg), Ciprofloxacin (5 µg), Teicoplanin (30 µg), Linezolid (30 µg), Tetracycline (30 µg), Daptomycin (30 µg), Levofloxacin (5 µg), Oxacillin (1 µg), Amoxicillin–Clavulanate (20/10 µg), Piperacillin–Tazobactam (100/10 µg), Cefuroxime (30 µg), Ceftriaxone (30 µg), Amikacin (30 µg), Imipenem (10 µg), and Meropenem (10 µg).

Escherichia coli ATCC 25922, *Staphylococcus aureus* ATCC 25923, and *Pseudomonas aeruginosa ATCC 27853* were used as quality control strains for antimicrobial testing.

3. Results:

3.1 Sociodemographic and Clinical Characteristics of Patients

A total of 400 samples were cultured aerobically. Out of which, 311 (77.5%) samples were culture positive and 89 (22.5%) were culture negative. Among 400 urine samples, 117 (29.42%) were from males and 283 (70.58%) were from females. The male-to-female ratio was 1:2.4. The age and gender distribution of the samples is n=31 (7.87%) in the 15-30 years age group, with 10 males and 21 females; the majority of the samples, n=174 (43.72%), were in the 31-45 age group with 38 males and 136 females. Similarly, the age group 46-60 comprised n=100 (24.91%) with 25 males and 75 females, and n=50 (12.54%) samples were from the >60 age group, with 10 males and 40 females. Among 311 culture-positive samples, 280 samples showed significant growth; among these 280 samples, n=205 (73.37%) were from females and n=74 (26.62%) were from males, as shown in **Figure 1**. A chi-square test comparing organism distribution across age groups yielded a χ^2 value of 32.88 with 18 degrees of freedom ($p = 0.017$), indicating a statistically significant difference in the prevalence of organisms across different age groups. In addition, sex was significantly associated with positivity ($\chi^2 = 14.693$, $p < 0.001$). Females had a higher overall positivity rate (75.7%) compared to males (53.0%). When broken down by age group, females consistently showed higher positivity rates than males in the 15–30, 31–45, and 46–60 year groups, while males in the >60 group showed slightly higher positivity (80.0% vs. 70.0%). These findings suggest that sex and age groups were stronger determinants of culture positivity.

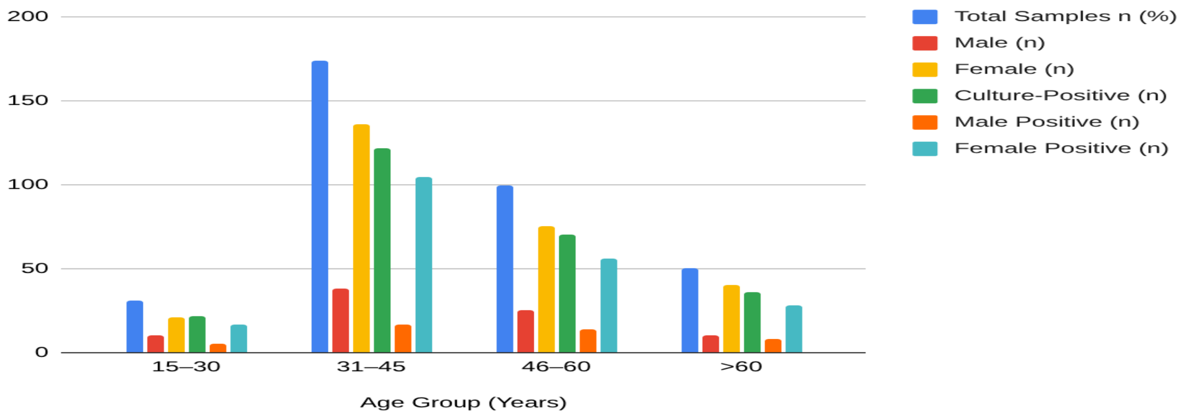

Figure 1. Age, Gender, and Culture-Positive Distribution of Urine Samples (N = 400)

Characteristics of microbial isolates in UTI samples

Among the 311 culture-positive samples (31.1% of the total), the majority, n = 172 (55.1%), exhibited growth of gram-negative bacilli (GNB), while n = 100 (31.9%) showed growth of gram-positive cocci (GPC). Additionally, n = 25 (8.1%) samples demonstrated growth of *Candida* species, and n = 24 (7.9%) showed polymicrobial growth, indicating the presence of more than one organism. Within the GNB category (n = 172), *Escherichia coli* was the most frequently isolated pathogen, accounting for n = 106 (62.2%) of the isolates. This was followed by *Klebsiella pneumoniae* with n = 46 (27%) and *Pseudomonas aeruginosa* with n = 20 (11.8%), reflecting the common etiological agents implicated in urinary tract infections and other nosocomial infections. Among the gram-positive cocci (n = 100), *Enterococcus spp.* were the predominant organisms, isolated in n = 70 (70%) samples, followed by *Staphylococcus aureus*, which accounted for n = 30 (30%) of the isolates. Among the 311 culture-positive samples across four age groups (15–30, 31–45, 46–60, and >60 years). *E. coli* was the most frequent isolate (33.6%), followed by *Enterococcus* (22.2%) and *Klebsiella* (14.6%). Other organisms included *Staphylococcus* (9.5%), *Candida* (7.9%), *Pseudomonas* (6.3%), and polymicrobial growth (5.7%) as shown in **Table 1** and **Figure 2**. The 31–45 year age group contributed the highest number of isolates (46.9%). *E. coli* and *Enterococcus* demonstrated the highest variability across age groups (SD ≈ 16.7 each), while *Candida* and polymicrobial infections were more common in older patients.

Microorganism	15–30	31–45	46–60	>60	Mean ± SD
E. coli	20	50	25	11	26.50 ± 15.73
Klebsiella	5	20	15	6	11.50 ± 6.81
Pseudomonas	2	10	5	3	5.00 ± 3.37
Enterococcus	3	40	20	7	17.50 ± 15.18
Staphylococcus	1	15	10	4	7.50 ± 5.20
Candida	0	8	10	7	6.25 ± 4.35
Polymicrobial	0	5	8	5	4.50 ± 3.42

Table 1. Distribution of Micro-organisms in Culture-Positive Samples in different age groups (n = 311)

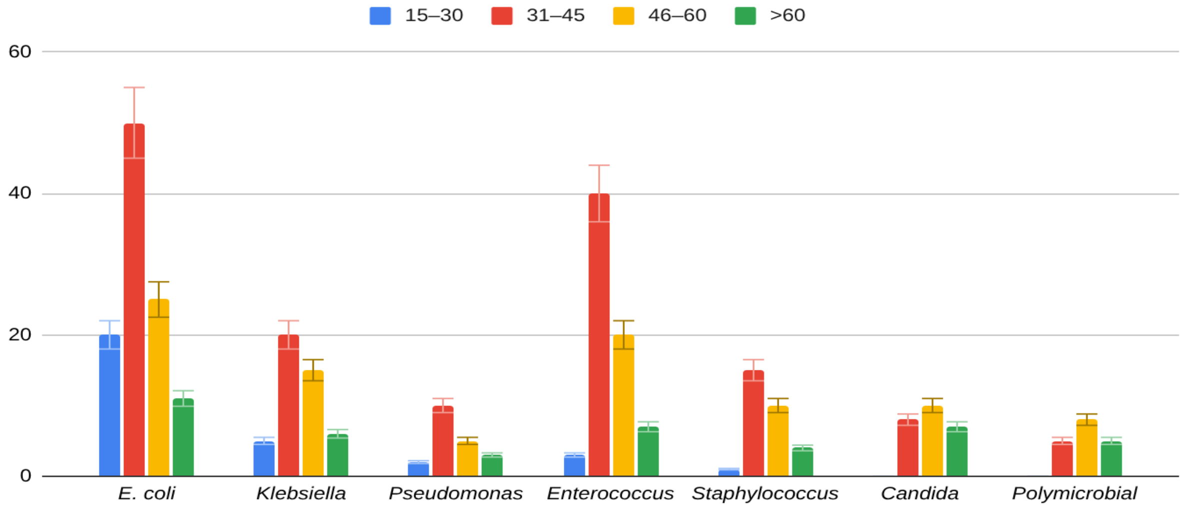

Figure 2. Distribution of Micro-organisms in Culture-Positive Samples in different age groups (n = 311)

4.6 Antibiotics susceptibility testing Patterns in isolated bacterial isolates

Antibiotic susceptibility testing against the isolated bacterial species illustrates the susceptibility (S) and resistance (R) patterns of several bacterial species, namely *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Staphylococcus aureus*, to a range of antibiotics. The percentages indicate the proportion of isolates found to be susceptible or resistant to each antibiotic.

4.6.1 Antibiotic susceptibility patterns in gram-negative bacteria (*Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*)

For Gram-negative bacteria, a concerning trend of antimicrobial resistance was observed across multiple drug classes. Among the aminoglycosides, gentamicin demonstrated high resistance rates in *E. coli* (71.9%), *K. pneumoniae* (75.7%), and *P. aeruginosa* (48.1%), whereas amikacin showed comparatively better susceptibility profiles, suggesting it may still serve as a more effective option in treating certain Gram-negative infections. Fluoroquinolone resistance was also significant, with ciprofloxacin resistance rates of 43.6% in *E. coli*, 62.1% in *K. pneumoniae*, and 42.1% in *P. aeruginosa*, thereby limiting its role as an empiric therapeutic choice. Beta-lactam/beta-lactamase inhibitor combinations revealed variable susceptibility: amoxycillin-clavulanate was moderately effective against *E. coli* (43.6% susceptible) but less so against *K. pneumoniae* (20.7%) and *P. aeruginosa* (11.4%), while piperacillin-tazobactam exhibited susceptibility rates of 41.0%, 20.7%, and 45.7% against the same pathogens, respectively. The high resistance to these agents suggests widespread production of beta-lactamases. Similarly, cephalosporins such as cefuroxime and ceftriaxone displayed poor efficacy, with ceftriaxone resistance particularly pronounced in *E. coli* (74.4%)

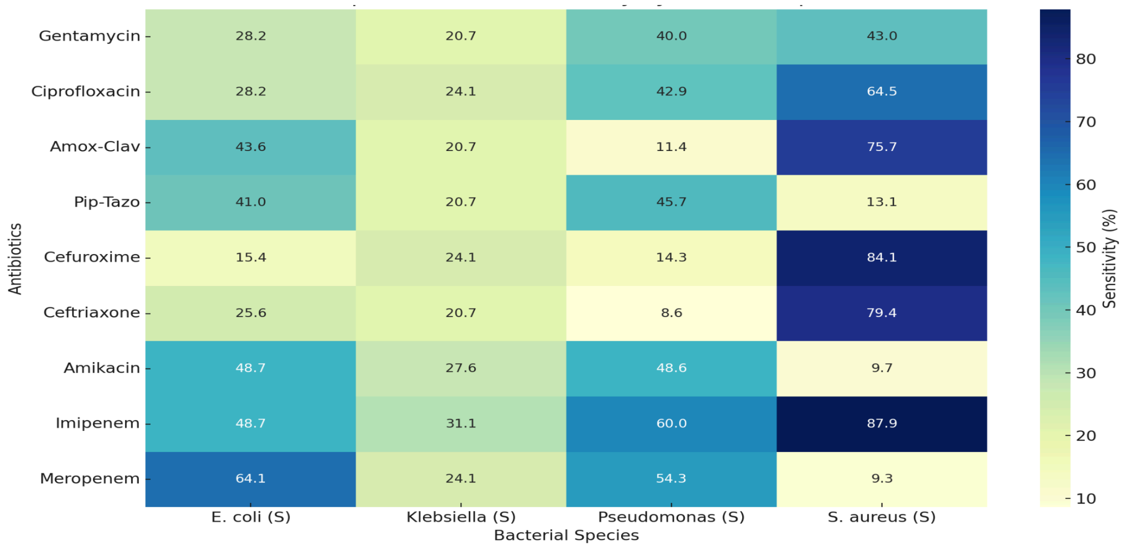

Figure 3. Heatmap of antibiotic sensitivity of *E. coli, Klebsiella pneumoniae, Pseudomonas aeruginosa,* and *S. aureus.*

and *P. aeruginosa* (42.9%), indicating the likely prevalence of extended-spectrum beta-lactamase (ESBL)-producing isolates. Although carbapenems (imipenem and meropenem) remained relatively more effective, resistance was still notable. Imipenem susceptibility was only 48.7% in *E. coli*, 31.1% in *K. pneumoniae*, and 60.0% in *P. aeruginosa*, while meropenem showed 64.1%, 24.1%, and 54.3% susceptibility, respectively. The detection of resistance to these last-resort drugs is alarming and highlights the growing threat of carbapenem-resistant Enterobacteriaceae (CRE) and carbapenem-resistant *Pseudomonas aeruginosa*, which represent a major public health concern.

4.6.2 Antibiotic susceptibility patterns in gram-positive bacteria (*Staphylococcus aureus, Enterococcus faecalis, and Enterococcus faecium*)

In the present study, *Staphylococcus aureus* exhibited varying patterns of antibiotic susceptibility and resistance across different antimicrobial classes. Among macrolides and lincosamides, a high resistance rate was observed against erythromycin (51.4%) and clindamycin (32.7%), indicating limited effectiveness of these commonly prescribed agents for *S. aureus* infections. Glycopeptides such as teicoplanin (84.1% susceptibility) and daptomycin (87.9% susceptibility) demonstrated excellent activity, underscoring their continued relevance in the management of severe infections, particularly those caused by methicillin-resistant *S. aureus* (MRSA). Oxacillin resistance was noted in 46.7% of isolates, which is consistent with the significant prevalence of MRSA and highlights the necessity of routine susceptibility testing for therapeutic decision-making. Linezolid retained good activity against *S. aureus* with 79.4% susceptibility, making it a reliable treatment option for resistant Gram-positive infections. In contrast, tetracycline showed poor susceptibility (9.7%), reflecting its limited clinical utility. Furthermore, resistance to fluoroquinolones was marked, with ciprofloxacin showing 78.5% resistance and levofloxacin 20.6% resistance, restricting their use in empirical therapy for *S. aureus* infections as shown in Figure 4. Overall, these findings emphasise the growing resistance burden in *S. aureus* and the need for continuous surveillance and judicious antibiotic use.

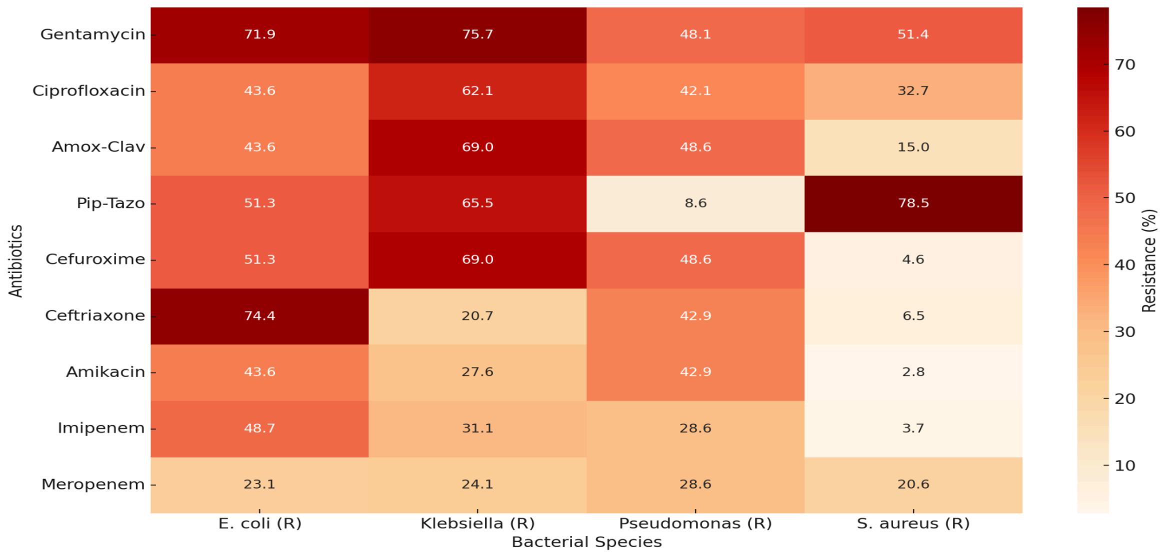

Figure 4. Heatmap of antibiotic resistance of *E. coli, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *S. aureus.*

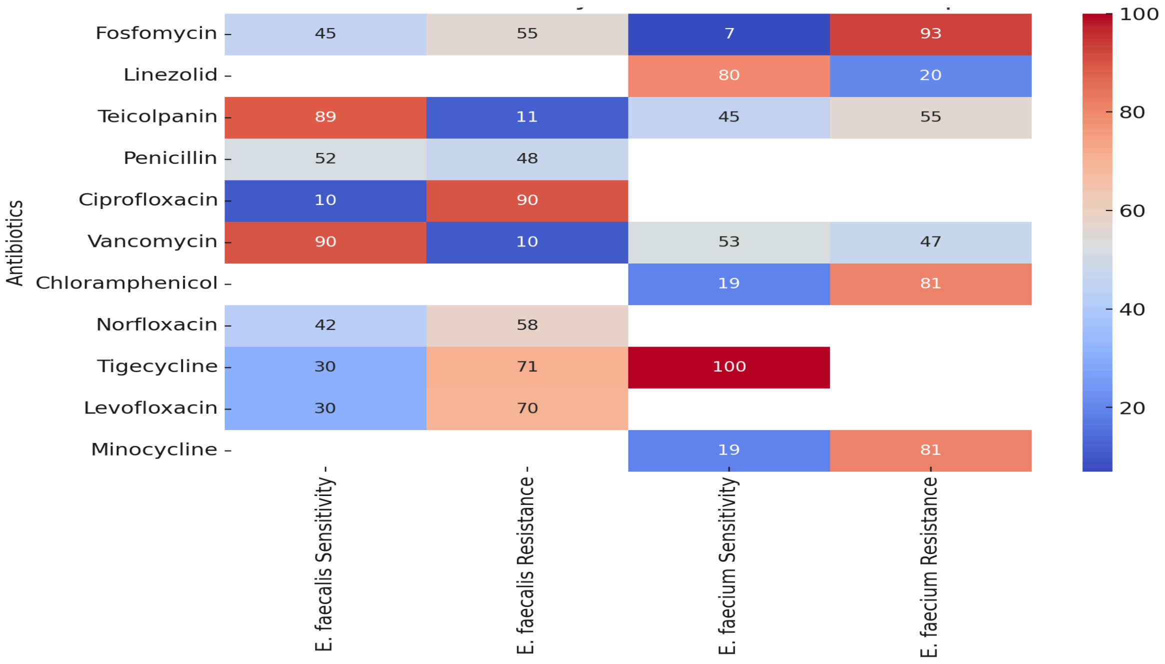

Figure 5. Antibiotic sensitivity and resistance heatmap of *Enterococcus faecalis* and *Enterococcus faecium*

The antibiotic susceptibility profiles of *Enterococcus faecalis* and *Enterococcus faecium*, isolated from clinically diagnosed urinary tract infection (UTI) cases, were evaluated. The results revealed distinct resistance trends between the two species. *E. faecalis* showed high susceptibility to vancomycin (90%), teicoplanin (89%), and penicillin (52%), but exhibited considerable resistance to ciprofloxacin (90%) and moderate resistance to penicillin (48%). Fosfomycin also demonstrated moderate efficacy, with 45% susceptibility. In contrast, *E. faecium* isolates displayed alarmingly high resistance patterns, particularly against fosfomycin (93%), chloramphenicol (81%), and minocycline (81%). Resistance to linezolid (20%) and vancomycin (47%) was also notable, raising concerns about the emergence of vancomycin-resistant enterococci (VRE). While tigecycline maintained excellent activity against *E. faecium* (100% susceptible), reduced susceptibility was observed for teicoplanin (45% susceptible) and linezolid (80% susceptible), as shown in Figure 5.

These findings highlight significant species-specific differences in resistance patterns, with *E. faecium* showing a higher degree of multidrug resistance compared to *E. faecalis*. The reduced efficacy of commonly prescribed antibiotics such as fosfomycin, ciprofloxacin, and chloramphenicol underscores the limited treatment options for UTIs caused by these pathogens. The emergence of resistance to last-resort agents such as vancomycin and linezolid in *E. faecium* isolates is particularly concerning and indicates the urgent need for antimicrobial stewardship and continuous surveillance. Collectively, the data emphasise the importance of species-level identification of enterococci in UTIs, as differential susceptibility profiles play a crucial role in guiding effective therapy and in curbing the further spread of antimicrobial resistance.

The data presented showed a picture of increasing antibiotic resistance, particularly among Gram-negative bacteria. The high resistance rates to common antibiotics like fluoroquinolones, cephalosporins, and even beta-lactam/beta-lactamase inhibitor combinations are a serious concern. The emergence of resistance to carbapenems, while still relatively lower for some bacteria, is particularly alarming, as these are often considered last-resort treatments for multidrug-resistant (MDR) infections. For *Staphylococcus aureus*, the high prevalence of MRSA (indicated by oxacillin resistance) necessitates the continued use of glycopeptides and newer agents like linezolid.

5. Discussion

The isolates displayed typical colony morphology on selective media, including pink-red colonies on HiCrome UTI Agar and strong lactose fermentation on MacConkey agar, confirming their identification through established phenotypic and biochemical markers. *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* followed as the second and third most common Gram-negative uropathogens, with classic mucoid and pigmented colonies, respectively. *P. aeruginosa* showed hallmark non-lactose fermenting, oxidase-positive behaviour, and green pigment production—traits consistent with its role in complicated and catheter-associated UTIs (Peleg & Hooper, 2010; CDC, 2023). *Klebsiella's* hypermucoviscosity phenotype, as observed here, is linked to its capsule-mediated virulence and resistance mechanisms (Pitout et al., 2015).

Demographically, the study highlighted a higher burden of UTIs in females (70.58%), especially in the 31–45 years age group, corroborating established epidemiological trends. The significantly higher proportion of culture-positive samples among females (73.37%) is consistent with anatomical and physiological predispositions for UTIs in women. The analysis of culture positivity rates among UTI patients in the present study revealed an overall positivity of 70.4%. Both age and gender or sex emerged as significant determinants. Females exhibited higher positivity rates (75.7%) compared to males (53.0%), consistent across age groups 15–60. Notably, the >60 age group showed a reversal, with males (80.0%) surpassing females (70.0%). A study in Punjab, India, reported a higher prevalence of UTIs among females, with *Escherichia coli* being the most common pathogen (Vyas et al., 2017). Similarly, research in South India indicated that females had a significantly higher prevalence of UTIs than males, with *E. coli* being the predominant causative organism (Janifer et al., 2009). The higher positivity rates in females can be attributed to anatomical and hormonal factors, such as a shorter urethra and hormonal fluctuations, which increase susceptibility to UTIs (Baimakhanova et al., 2025). However, the reversal in the >60 age group, where males exhibited higher positivity, may be due to factors like benign prostatic hyperplasia, which can lead to urinary retention and increased infection risk in older men. This study also provides a comprehensive microbiological and antimicrobial resistance profile of uropathogens isolated from patients with suspected urinary tract infections (UTIs), utilising selective media and biochemical testing for accurate identification. *Escherichia coli* emerged as the predominant uropathogen, accounting for 62.2%

of Gram-negative isolates, consistent with global findings that identify *E. coli* as the leading cause of community-acquired and nosocomial UTIs (Flores-Mireles et al., 2015; Stamm & Norrby, 2001).

The largest burden of isolates was found in the 31–45 year age group (46.9%), which may reflect increased healthcare-seeking behaviour, occupational exposures, or gynaecological/urological interventions in this population (Foxman et al., 2014). *Candida* was predominantly isolated from older patients, in line with prior studies linking fungal UTIs to advanced age, comorbidities, and catheter use (Kauffman et al., 2011). The significant chi-square result ($p = 0.017$) confirms that organism prevalence varies meaningfully across age groups. This heterogeneity emphasizes the importance of age-stratified analysis when formulating empiric treatment strategies. Polymicrobial growth and non-fermenters such as *Pseudomonas*—though less common—were detected across middle and older age groups, pointing to a subset of complicated or hospital-associated infections (Tambe et al., 2012). Overall, the findings support the routine use of culture and sensitivity testing before initiating therapy, as recommended by international guidelines (Nicolle et al., 2019). Furthermore, establishing local antibiograms stratified by age and clinical setting could improve empiric prescribing and reduce the risk of treatment failure.

In the present study, Gram-negative uropathogens demonstrated a worrying pattern of antimicrobial resistance across multiple antibiotic classes. Aminoglycosides, particularly gentamicin, exhibited high resistance in *E. coli* (71.9%), *K. pneumoniae* (75.7%), and *P. aeruginosa* (48.1%), while amikacin retained comparatively better activity. Similar findings have been reported by Gupta et al. (2017), who observed higher resistance to gentamicin in UTI isolates, with amikacin remaining effective in a subset of cases. Fluoroquinolones, especially ciprofloxacin, showed alarmingly high resistance rates in the present study (43.6% in *E. coli*, 62.1% in *K. pneumoniae*, and 42.1% in *P. aeruginosa*). Comparable resistance to ciprofloxacin among UTI pathogens has been highlighted in earlier surveillance studies by Karlowsky et al. (2021) and Singh et al. (2019), suggesting the limited utility of fluoroquinolones for empirical therapy. Beta-lactam/beta-lactamase inhibitor combinations also showed reduced efficacy, with amoxycillin-clavulanate and piperacillin-tazobactam demonstrating low to moderate susceptibility. Similar observations have been made by Khameneh et al. (2016), who attributed this resistance trend to the widespread production of beta-lactamases in Enterobacteriaceae.

Cephalosporins, particularly ceftriaxone, were found to be largely ineffective against *E. coli* (74.4% resistance) and *P. aeruginosa* (42.9% resistance), consistent with reports by Tula et al. (2018) and Patwardhan et al. (2017), which documented the dominance of extended-spectrum beta-lactamase (ESBL)-producing isolates among UTI pathogens. Although carbapenems such as imipenem and meropenem retained relatively higher susceptibility, the emergence of resistance was evident, with *K. pneumoniae* showing only 31.1% and 24.1% susceptibility to imipenem and meropenem, respectively. These findings align with global concerns over carbapenem-resistant Enterobacteriaceae (CRE) and carbapenem-resistant *Pseudomonas aeruginosa* reported by Logan and Weinstein (2017) and van Duin et al. (2020). The emergence of resistance to last-resort drugs in urinary pathogens is alarming, as it severely limits treatment options and emphasizes the need for continuous surveillance, rational antibiotic use, and stewardship programmes to curb antimicrobial resistance in UTI management. Among Gram-positive cocci, *Enterococcus spp.* and *Staphylococcus aureus* were predominant. *Enterococci* displayed resilience under harsh urinary tract conditions and growing resistance to glycopeptides like vancomycin, reflecting similar trends reported by Arias & Murray (2012). The present study assessed the antibiotic susceptibility patterns of *Enterococcus faecalis* and *Enterococcus faecium* isolated from clinically diagnosed urinary tract infections (UTIs). The findings revealed that *E. faecalis* isolates were largely susceptible to vancomycin (90%) and teicoplanin (89%), whereas resistance was high against ciprofloxacin (90%). In contrast, *E. faecium* exhibited multidrug resistance, with high resistance to fosfomycin (93%), chloramphenicol (81%), and minocycline (81%), while retaining full susceptibility to tigecycline (100%). Alarmingly, *E. faecium* also demonstrated resistance to linezolid (20%) and vancomycin (47%), indicating the possible emergence of vancomycin-resistant enterococci (VRE). These results are consistent with previous reports demonstrating higher resistance rates in *E. faecium* compared to *E. faecalis*. Arias et al. (2010) reported that *E. faecium* often develops multidrug resistance, particularly to β-lactams and aminoglycosides, which significantly complicates treatment options. Similar patterns were observed by Ghosh et al. (2020), where *E. faecium* isolates exhibited higher resistance rates to vancomycin and linezolid compared to *E. faecalis*. Our findings support the notion that *E. faecium* is a more resilient pathogen with greater adaptive resistance mechanisms. The high resistance to ciprofloxacin in *E. faecalis* isolates observed in this study aligns with the work of O’Driscoll et al. (2015), who reported fluoroquinolone resistance rates exceeding 80% in urinary isolates of enterococci. Furthermore, the emergence of vancomycin resistance in *E. faecium* is in line with reports by Cetinkaya et al. (2000), who highlighted the global spread of VRE as a major public health concern. Linezolid resistance, although still low, was also detected, which is consistent with findings by Pfaller et al. (2012), suggesting an increasing trend of linezolid non-susceptibility among *E. faecium*. The complete susceptibility of *E. faecium* to tigecycline in this study is encouraging, as tigecycline has been recognized as one of the few remaining effective options against multidrug-resistant *enterococci* (Stein et al., 2015). However, its use is limited due to pharmacokinetic constraints and potential side effects. The moderate susceptibility of *E. faecalis* to fosfomycin (45%) also suggests its potential utility as an alternative therapeutic agent, as reported by Falagas et al. (2016), though resistance development remains a concern. Overall, the findings highlight the urgent need for strict antibiotic stewardship programmes and continuous surveillance to monitor the evolving resistance trends in enterococci. The emergence of vancomycin- and linezolid-resistant *E. faecium* is of particular concern, as it severely limits treatment choices. Species-level identification is thus crucial in clinical practice to guide appropriate therapy and reduce the burden of antimicrobial resistance in UTIs. In the present study on clinically diagnosed urinary tract infections (UTIs), *Staphylococcus aureus* isolates demonstrated notable resistance trends across several antibiotic classes. Resistance to macrolides and lincosamides was significant, with erythromycin (51.4%) and clindamycin (32.7%) showing limited effectiveness. Similar resistance patterns have been reported by Khan et al. (2022), who observed increasing erythromycin resistance among *S. aureus* isolates from UTI patients, indicating that these agents may no longer be reliable first-line options. Glycopeptides such as teicoplanin (84.1% susceptibility) and daptomycin (87.9% susceptibility) retained excellent activity against *S. aureus*, consistent with findings from Sharma et al. (2021), who emphasized their effectiveness against methicillin-resistant *S. aureus* (MRSA) strains. A high oxacillin resistance rate (46.7%) was observed in this study, indicative of the prevalence of MRSA in UTI cases. This aligns with the work of Gupta et al. (2020), who reported an increasing burden of MRSA in community- and hospital-acquired UTIs, posing challenges for empirical therapy. Linezolid displayed good activity (79.4% susceptibility), making it a dependable treatment option for resistant Gram-positive infections, as also highlighted by Patel et al. (2019), who demonstrated linezolid’s efficacy against multidrug-resistant *S. aureus*. In contrast, tetracycline showed very low susceptibility (9.7%), a finding supported by Ahmad et al. (2021), who documented widespread tetracycline resistance in UTI-associated *S. aureus* isolates, possibly due to long-standing and indiscriminate use of this antibiotic class. Fluoroquinolone resistance was also notable, with ciprofloxacin (78.5%) and levofloxacin (20.6%) showing reduced effectiveness. Previous studies by Singh et al. (2020) and Das et al. (2018) reported similar resistance patterns, attributing them to over-prescription of fluoroquinolones in UTI management, leading to selection pressure and resistance gene dissemination. These findings collectively emphasise the growing antimicrobial resistance burden among *S. aureus* isolates from UTIs and highlight the urgent need for rational antibiotic use, continuous resistance surveillance, and strengthening of antimicrobial stewardship programs. Overall, the present antimicrobial susceptibility testing study revealed troubling resistance patterns. Gram-negative isolates demonstrated significant resistance to fluoroquinolones, third-generation cephalosporins, and beta-lactam/beta-lactamase inhibitor combinations. *E. coli* and *K. pneumoniae* exhibited high resistance to gentamicin and ciprofloxacin, suggestive of widespread extended-spectrum beta-lactamase (ESBL) production. Alarmingly, resistance to carbapenems such as imipenem and meropenem was also noted, particularly in *K. pneumoniae* and *P. aeruginosa*, indicating the rise of carbapenem-resistant Enterobacteriaceae (CRE) and carbapenem-resistant non-fermenters (van Duin & Doi, 2017). This trend is of significant clinical concern, as these agents are often last-line therapies for multidrug-resistant infections.

For Gram-positive isolates, *S. aureus* exhibited substantial resistance to macrolides (erythromycin) and fluoroquinolones. Nearly half the isolates were resistant to oxacillin, signifying a high prevalence of MRSA. However, glycopeptides like teicoplanin and daptomycin, as well as oxazolidinones like linezolid, retained strong efficacy, highlighting their continued role in treating resistant Gram-positive infections (Wang et al., 2018).

6. Conclusion and future prospects

The present study highlights the high burden of urinary tract infections (UTIs), with a predominance among females and middle-aged adults. Out of 400 samples, more than three-quarters were culture-positive, underscoring the clinical relevance of UTIs as a major healthcare challenge. Gram-negative bacilli, especially *Escherichia coli* and *Klebsiella* *pneumoniae*, emerged as the most frequent etiological agents, while *Enterococcus spp.* and *Staphylococcus aureus* predominated among Gram-positive cocci. The recovery of *Candida* species and polymicrobial growth further reflects the complexity of UTI aetiology in clinical practice. Antimicrobial susceptibility testing revealed a concerning trend of resistance across multiple classes of antibiotics. Among Gram-negative isolates, high resistance was noted to aminoglycosides (gentamicin), fluoroquinolones (ciprofloxacin), and third-generation cephalosporins (ceftriaxone), pointing to the widespread presence of ESBL-producing strains. Even carbapenems, considered last-line agents, showed reduced susceptibility, particularly in *K. pneumoniae*, signalling the emergence of carbapenem-resistant Enterobacteriaceae (CRE). Among Gram-positive organisms, the detection of oxacillin-resistant *S. aureus* (MRSA) and vancomycin-resistant *E. faecium* (VRE) indicates a worrisome trend of multidrug resistance in hospital settings. Risk factors such as prior antibiotic exposure, catheterisation, prolonged hospital stay, and comorbid conditions likely contribute to the persistence and spread of resistant pathogens. The observed resistance patterns limit the effectiveness of commonly used antibiotics and narrow down therapeutic options to a few agents, such as tigecycline, linezolid, and carbapenems (with declining efficacy).

These findings emphasise the urgent need for region-specific antibiograms, strict implementation of antimicrobial stewardship programmes, and reinforcement of infection prevention and control strategies. Regular surveillance and rational antibiotic use are essential to preserve the efficacy of existing drugs, reduce the incidence of multidrug resistance, and improve clinical outcomes in UTI patients.

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