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"FROM SAMPLE TO SOLUTION: SURVEILLANCE OF UTI BACTERIA AND THEIR ANTIBIOTIC SENSITIVITY IN NORTHWEST INDIA"

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ABSTRACT

Background: Urinary tract infections (UTIs) are among the most common bacterial infections worldwide, with antimicrobial resistance (AMR) posing a growing challenge to effective treatment. This study aimed to assess the culture and antibiotic susceptibility patterns of uropathogens isolated from urine samples in Northwest India, to inform local empirical treatment strategies.

Methods: A total of 298 midstream urine samples from patients with suspected UTIs were analyzed between January and December 2023. Standard microbiological protocols were used for quantitative culture and organism identification. Antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion method, adhering to CLSI guidelines.

Results: Gram-negative organisms accounted for 90.2% of isolates, with *Escherichia coli* being the most prevalent (51%), followed by *Klebsiella* spp. (19%) and *Pseudomonas* spp. (12%). *E. coli* demonstrated high sensitivity to fosfomycin (91%), nitrofurantoin (80%), and imipenem (71%), but high resistance to ampicillin (93%) and ciprofloxacin (88%). *Klebsiella* spp. showed moderate sensitivity to fosfomycin and doxycycline (59% each). Among Gram-positive isolates (9.7%), *Enterococcus* spp. were most susceptible to linezolid (93%) and vancomycin (86%). A concerning degree of resistance was observed across both Gram-negative and Gram-positive organisms.

Conclusion: This study reveals a high prevalence of multidrug-resistant uropathogens in Northwest India, emphasizing the need for regular surveillance and region-specific antibiograms to guide empirical antibiotic therapy. Strengthening antimicrobial stewardship is critical to curb the rise of resistance.

INTRODUCTION

Urinary tract infections (UTIs) are a major global public health concern, representing the most common bacterial infections encountered both in the community and in hospital settings.[1–2] It is estimated that approximately 150 million individuals suffer from UTIs annually worldwide, contributing to a significant economic burden.[3] UTIs are defined as the invasion of the normally sterile urinary tract by pathogenic microorganisms. Both Gram-positive and Gram-negative bacteria can cause UTIs; however, the most frequent pathogen is the Gram-negative facultative anaerobe *Escherichia coli*.[4]

UTIs can involve any part of the urinary tract, with women being particularly susceptible, especially in the form of uncomplicated cystitis.[5] The clinical spectrum includes asymptomatic bacteriuria, uncomplicated UTI, complicated UTI, and recurrent UTI.[6] Gram-negative *Enterobacteriaceae* are commonly implicated in both community-acquired and healthcare-associated UTIs.Antimicrobial resistance (AMR) is defined as the ability of microorganisms to survive exposure to antimicrobials that would normally inhibit or kill them. This results in the persistence and spread of resistant strains.[7–8] Empirical antibiotic therapy, often initiated without microbiological confirmation, has contributed significantly to the emergence of resistant uropathogens. Therefore, targeted therapy, guided by local antimicrobial susceptibility patterns, is essential for effective treatment.[9]

The misuse and overuse of antibiotics have further aggravated resistance among uropathogens.[10] Understanding the antibiotic sensitivity profiles of urinary isolates is crucial for selecting appropriate agents for both treatment and prophylaxis of UTIs. An antibiogramprovides a comprehensive summary of antimicrobial susceptibility patterns for specific organisms and serves as an invaluable tool in antimicrobial stewardship.

Given the paucity of local susceptibility data in this region, the present study aims to isolate and identify uropathogens from patients with symptomatic UTIs and to determine their antibiotic susceptibility profiles. The findings will help inform empirical treatment protocols and support the development of region-specific antimicrobial guidelines.

MATERIALS AND METHODS

Urine samples were collected from patients presenting with signs and symptoms suggestive of urinary tract infection (UTI) and submitted to the central microbiology laboratory of our hospital. Midstream clean-catch urine specimens were collected in sterile containers, following standard collection protocols. Both inpatient and outpatient samples were included in the study, conducted from January to December 2023.

Quantitative urine cultures were performed using the calibrated loop technique, which delivers approximately 0.01 mL of the sample onto Blood Agar and MacConkey Agar plates. The inoculated plates were incubated aerobically at 37°C for 24 hours. Bacterial growth was quantified, and colonies yielding $\geq 10^5$ colony-forming units (CFU)/mL were considered indicative of significant bacteriuria. Cultures with no more than two isolates—of which at least one showed $\geq 10^5$ CFU/mL—were deemed positive. Samples yielding three or more different organisms were excluded due to probable contamination.

Isolates were identified by standard microbiological techniques. Antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion method on Mueller-Hinton Agar, following Clinical and Laboratory Standards Institute (CLSI) guidelines. Plates were incubated at 37°C for 24 hours. The antimicrobial agents tested included: cefotaxime, ceftazidime, cefepime, cotrimoxazole, ciprofloxacin, fosfomycin, gentamicin, imipenem, meropenem, nitrofurantoin, doxycycline, amikacin, minocycline, piperacillin-tazobactam, linezolid, vancomycin, and ampicillin. Antibiotics were selected based on the Gram-staining characteristics of the isolates (Gram-positive vs. Gram-negative).

Inclusion criteria:

- All urine culture samples with significant bacteriuria from both male and female patients, irrespective of age.

Exclusion criteria:

- Patients with indwelling urinary catheters
- Immunocompromised individuals
- Patients with anatomical abnormalities like phimosis or paraphimosis
- Patients who had taken antibiotics within the previous 24 hours
- Urine cultures positive for fungal or parasitic organisms

RESULTS

Out of 298 urine samples processed, all showed positive bacterial growth and were analyzed for antibiotic susceptibility patterns. Gram-negative bacteria were the predominant isolates, accounting for 269 out of 298 samples (90.2%), whereas Gram-positive bacteria constituted 29 samples (9.7%). The most frequently isolated organism was Escherichia coli, identified in 153 samples (51%), followed by Klebsiella spp. in 58 samples (19%), and Pseudomonas spp. in 37 samples (12.4%). Enterococcus spp. were the most common Gram-positive isolates, found in 29 samples (9.7%). Acinetobacter spp. accounted for 21 isolates (7%) (Figure 1).

Antibiotic Susceptibility Profiles:

E. coli (Figure 2) showed the highest sensitivity to fosfomycin (91%), followed by nitrofurantoin (80%), imipenem (71%), and gentamicin (65%). It exhibited high resistance to ampicillin (93%), ciprofloxacin (88%), and cefotaxime (87%).

Klebsiella spp. (Figure 3) demonstrated maximum sensitivity to fosfomycin and doxycycline (59% each), followed by imipenem (52%). The lowest sensitivity was observed for ciprofloxacin and cefotaxime (22%).

Pseudomonas spp. (Figure 4) were most sensitive to gentamicin (54%), followed by piperacillin–tazobactam (47%) and amikacin (43%). These isolates showed minimal sensitivity to cefepime (3%) and imipenem (14%).

Enterococcus spp. (Figure 5) exhibited high sensitivity to linezolid (93%) and vancomycin (86%), with moderate sensitivity to nitrofurantoin (64%). Resistance was most pronounced for ciprofloxacin (83%) and tetracycline (76%).

Acinetobacter spp. (Figure 6) were highly sensitive to minocycline (95%) and doxycycline (90%), with poor susceptibility to amikacin, cefepime, and cefotaxime (24% each).

DISCUSSION

This study generated a comprehensive urine culture-based antibiogram from samples collected at SMS Medical College and Hospital, Jaipur, offering insights into the local prevalence and antimicrobial susceptibility patterns of uropathogens. The most frequently isolated organism was *Escherichia coli*, consistent with findings from numerous regional and international studies.[11–13]

Historically, multidrug-resistant (MDR) organisms were largely confined to nosocomial or healthcare-associated infections. However, a disturbing trend has emerged in recent years, with MDR organisms increasingly being reported from community-acquired infections as well. Fluoroquinolones were once the mainstay of empirical treatment for UTIs due to their broad spectrum and initial low resistance rates. However, resistance to this class has escalated significantly over the past decade.[14] The World Health Organization (WHO) has identified *E. coli* as one of the high-priority antibiotic-resistant pathogens based on surveillance data from 17 countries, with ciprofloxacin resistance in uropathogenic*E. coli* (UPEC) ranging from 8% to 65%. In response, the WHO launched the Global Antimicrobial Resistance Surveillance System (GLASS) in 2015 to strengthen international AMR monitoring.[15]

In our study, Gram-positive bacteria exhibited high sensitivity to linezolid (93%) and vancomycin (86%), while showing considerable resistance to ciprofloxacin (83%), tetracycline (74%), and ampicillin (52%). Among Gram-negative isolates, *E. coli* was highly sensitive to fosfomycin (91%) and nitrofurantoin (80%), followed by imipenem (71%) and gentamicin (65%). However, resistance was alarmingly high to ampicillin (93%), ciprofloxacin (88%), cefotaxime (87%), and ceftazidime (82%) (Table 2). *Klebsiella* spp. showed maximum sensitivity to fosfomycin and doxycycline

(59%), and moderate sensitivity to imipenem (52%), but high resistance to ciprofloxacin (78%), cefotaxime (78%), cefepime (77%), and ceftazidime (76%) (Table 3). *Pseudomonas* spp. were only moderately sensitive to gentamicin (54%) and piperacillin–tazobactam (47%), while exhibiting extensive resistance to cefepime (97%), ciprofloxacin (86%), imipenem (84%), and ceftazidime (76%) (Table 4). *Acinetobacter* spp. showed high sensitivity to minocycline (95%) and doxycycline (90%) but were largely resistant to cefotaxime, cefepime, and amikacin (76%) (Table 6).

Findings from international literature echo similar concerns. A 2012 study from Sudan by Ibrahim et al. reported 92.7% MDR *E. coli*, with 32.7% extended-spectrum beta-lactamase (ESBL) positivity, and high resistance to cotrimoxazole (88.3%), ciprofloxacin (58.4%), and cefotaxime (92.5%).[16] In Nigeria, Olorunmola et al. (2013) observed *E. coli* resistance to fluoroquinolones ranging from 65.7% to 86.9%, while nitrofurantoin showed the lowest resistance (7.3%).[17] Similarly, Alizadeh et al. (2018) reported wide-ranging fluoroquinolone resistance (5–64.7%), cotrimoxazole resistance (4.2–88.2%), and third-generation cephalosporin resistance (15–87%) across different Iranian regions.[18] Woldaii et al. (2016) observed *E. coli* resistance of 30% to ciprofloxacin and only 7% to ceftriaxone in a community antibiogram study in Texas, USA.[19]

There is a well-established association between antibiotic resistance and the level of exposure to specific antibiotics. High local prescription rates of fluoroquinolones and cotrimoxazole have been directly linked to elevated resistance.[20–21] Conversely, reduced or discontinued use of certain antimicrobials over time may contribute to improved susceptibility. These findings reinforce the urgent need for judicious antimicrobial use, effective stewardship programs, and adherence to global strategic frameworks, such as the one proposed by WHO, which advocates awareness campaigns, surveillance, infection prevention, and rational antibiotic use.

A key limitation of our study was the inability to differentiate between inpatient and outpatient samples, which could have provided further insights into the resistance dynamics between community-acquired and hospital-acquired infections.

CONCLUSION

The present study demonstrates a high level of antibiotic resistance among both Gram-positive and Gram-negative uropathogens. This highlights the growing challenge posed by antimicrobial resistance (AMR), which remains a critical public health concern. Given the regional variability in resistance patterns, institution-specific antibiograms are essential to guide effective empirical therapy. Continuous surveillance, judicious antibiotic use, and robust antimicrobial stewardship programs are imperative to combat the evolving threat of AMR.

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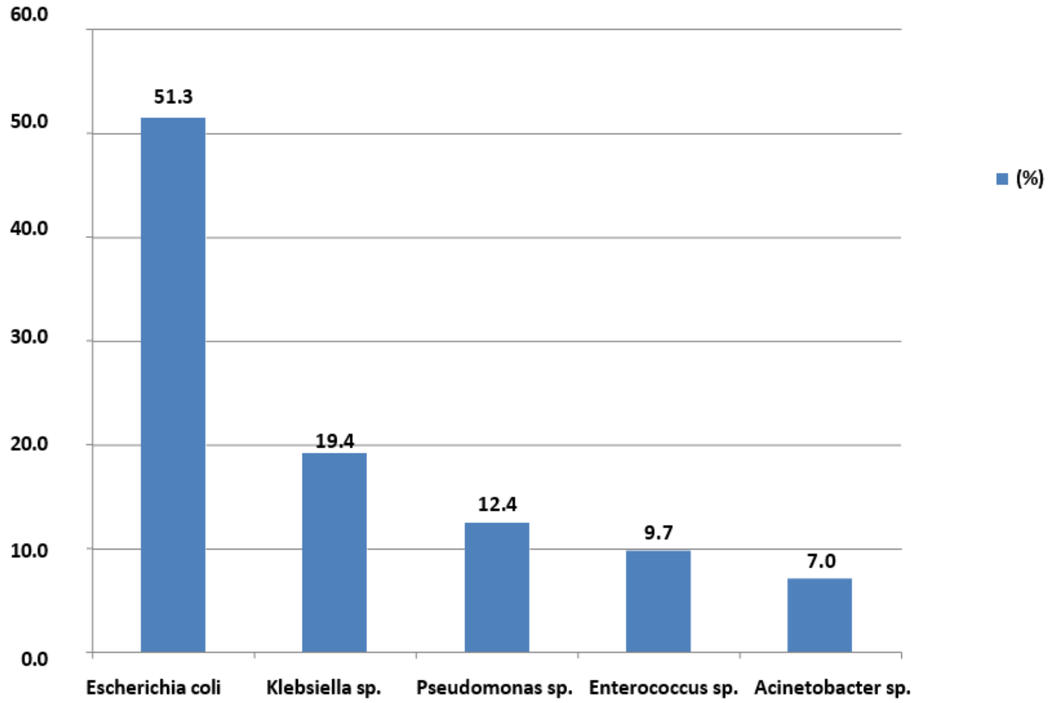
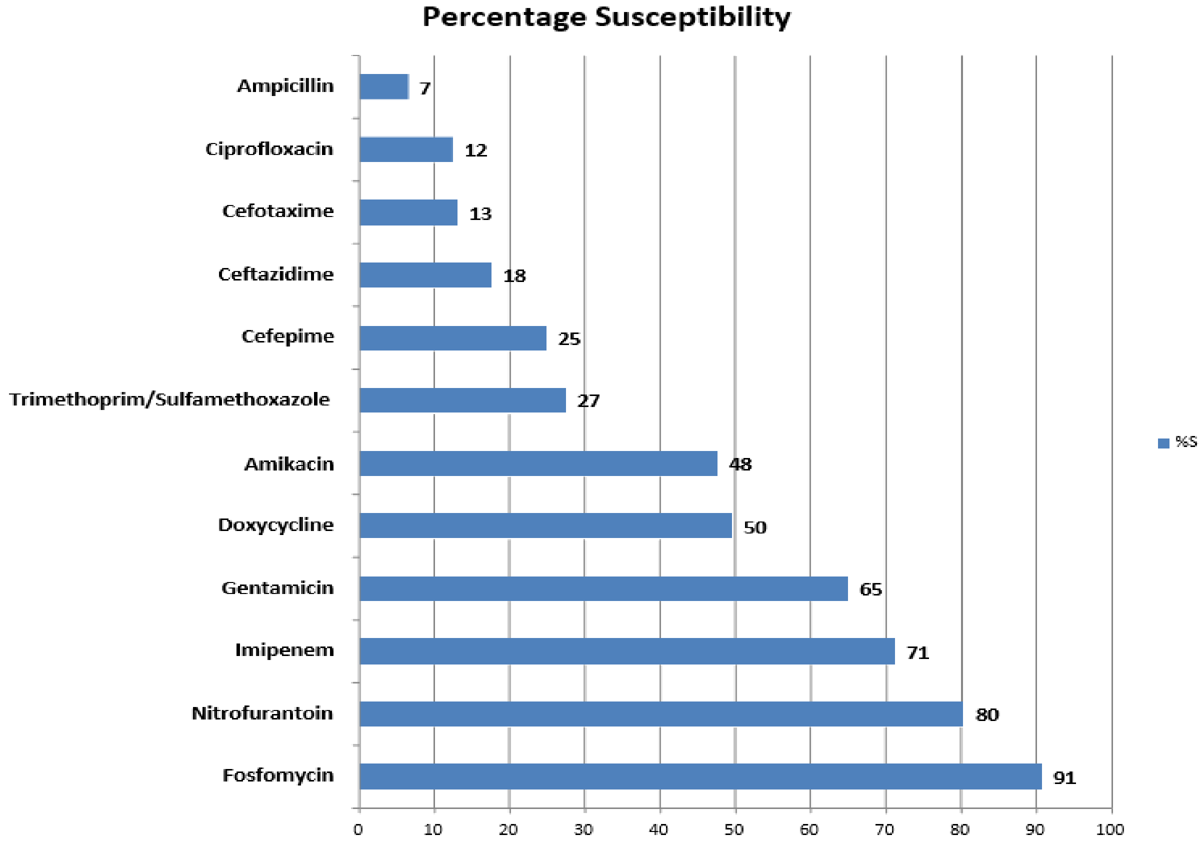
Figure 1. Distribution of uropathogens in urine cultures (N = 298)



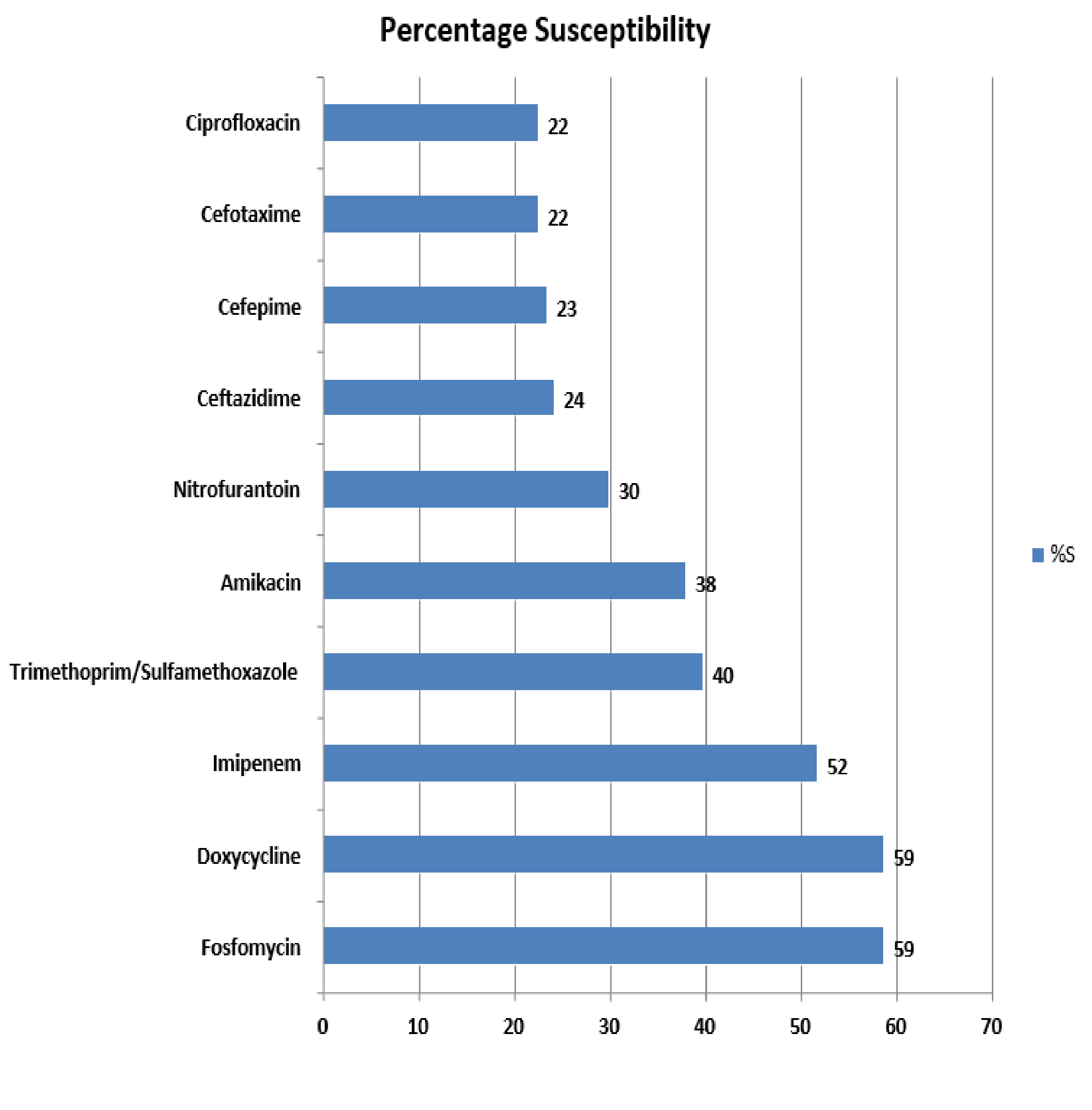
Legend:
Percentage of bacterial isolates from urine samples (Jan–Dec 2023), Department of Nephrology, SMS Medical College, Jaipur. E. coli was the most common (51.3%), followed by Klebsiella, Pseudomonas, Enterococcus, and Acinetobacter spp.

Figure 2. Antibiotic susceptibility pattern of *Escherichia coli* (N = 153)



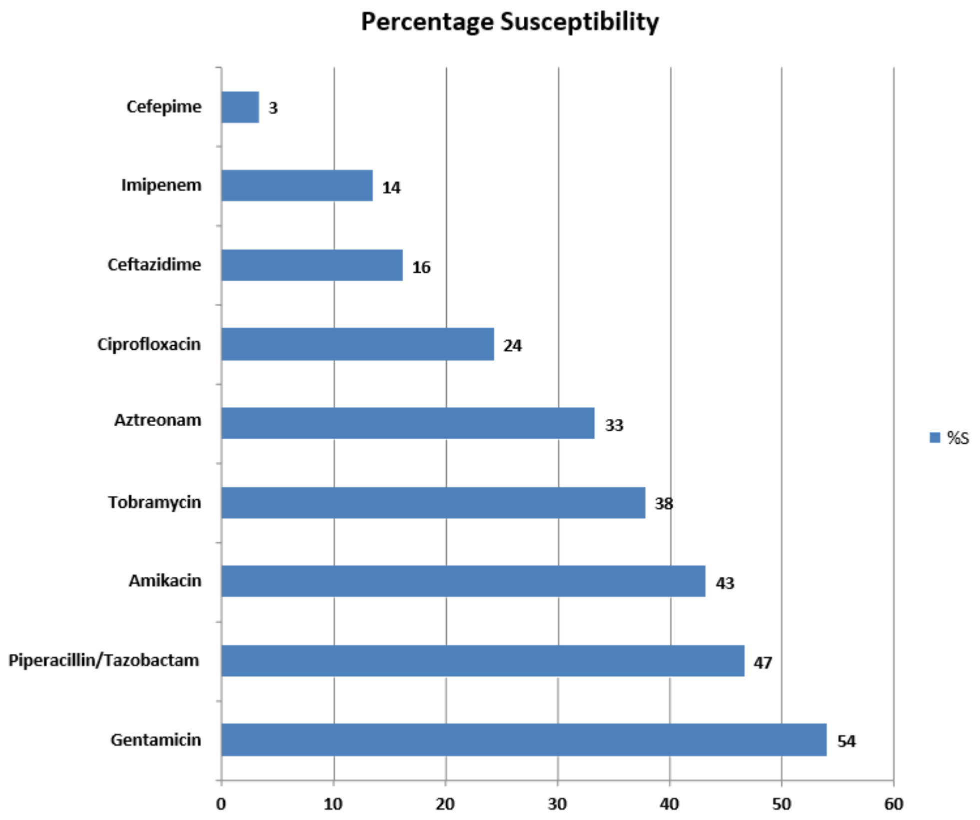
Legend:
Percentage susceptibility of *E. coli* isolates from urine samples (Jan–Dec 2023), Nephrology Department, SMS Medical College, Jaipur. Highest sensitivity was observed to fosfomycin (91%), nitrofurantoin (80%), and imipenem (71%).

Figure 3. Antibiotic susceptibility pattern of Klebsiella spp. (N = 58)



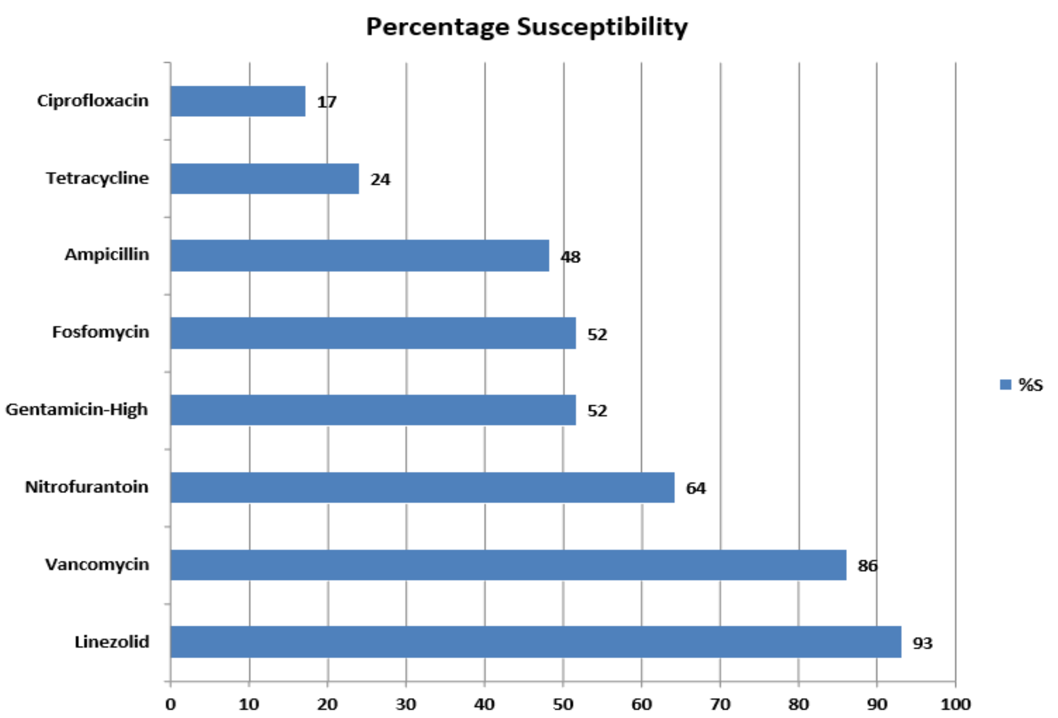
Legend:
Percentage susceptibility of Klebsiella spp. isolates from urine cultures (Jan–Dec 2023), Nephrology Department, SMS Medical College, Jaipur. Highest sensitivity was observed to fosfomycin and doxycycline (59%), followed by imipenem (52%).

Figure 4. Antibiotic susceptibility pattern of Pseudomonas spp. (N = 37)



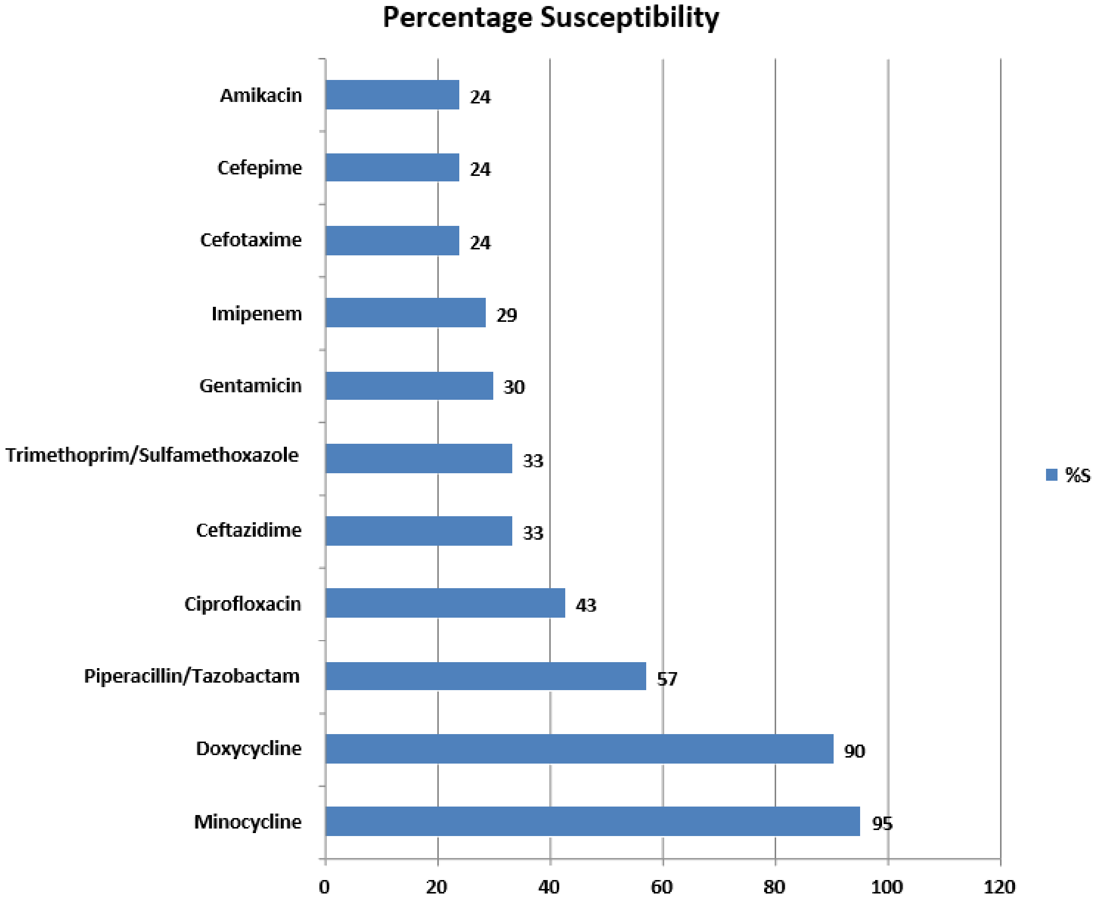
Legend:
Percentage susceptibility of Pseudomonas spp. isolates from urine cultures (Jan–Dec 2023), Nephrology Department, SMS Medical College, Jaipur. Highest sensitivity was observed to gentamicin (54%), followed by piperacillin–tazobactam (47%) and amikacin (43%).

Figure 5. Antibiotic susceptibility pattern of Enterococcus spp. (N = 29)



Legend:
Susceptibility profile of Enterococcus spp. from urine samples (Jan–Dec 2023), Nephrology Department, SMS Medical College, Jaipur. Highest sensitivity was observed to linezolid (93%) and vancomycin (86%), followed by nitrofurantoin (64%).

Figure 6. Antibiotic susceptibility pattern of Acinetobacter spp. (N = 21)



Legend:
Susceptibility profile of Acinetobacter spp. from urine samples (Jan–Dec 2023), Nephrology Department, SMS Medical College, Jaipur. The highest sensitivity was noted for minocycline (95%) and doxycycline (90%), with poor response to cefotaxime, cefepime, and amikacin (24% each)