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Etiological Spectrum and Antimicrobial Resistance Patterns of Uro-pathogens in a Tertiary Care Hospital: A Comprehensive Analysis of Bacterial and Candida Isolates

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ABSTRACT

Background: Urinary tract infections (UTIs) are among the most common bacterial infections encountered in both community and hospital settings, contributing significantly to morbidity and healthcare burden worldwide (1). They affect individuals across all age groups and are a leading cause of antimicrobial prescription.

Materials and Method: The study was carried out at a 1500 bedded tertiary care Centre and teaching hospital located in Central India. The study was conducted over a 12-month period from September 2024 to August 2025. Samples from OPD, IPD, and ICU were processed in the Department of Microbiology.

Results: Among the 40 patients, the largest group (27.50%) consisted of 11 patients in Out of the total urine samples processed in the microbiology laboratory, 505 samples yielded significant microbial growth. The etiological distribution of isolates is presented in Table 1. Among the culture-positive samples, the majority were attributed to Gram-negative bacteria [n = 411 (81.4%)], followed by Gram-positive bacteria [n = 77 (15.3%)] and fungal isolates [n = 17 (3.3%)].

Conclusion: The present study demonstrates that Gram-negative bacteria, particularly Escherichia coli, remain the predominant uropathogens, followed by Gram-positive organisms and Candida species. A high level of antimicrobial resistance was observed among commonly used Access group antibiotics, while relatively better susceptibility was noted with reserve and urinary-specific agents**.**

Keywords*: Urinary tract infections, Uropathogens, Escherichia coli, Antimicrobial resistance, Gram-negative bacteria.*

INTRODUCTION

Urinary tract infections (UTIs) are among the most common bacterial infections encountered in both community and hospital settings, contributing significantly to morbidity and healthcare burden worldwide (1). They affect individuals across all age groups and are a leading cause of antimicrobial prescription.

Gram-negative bacteria, particularly *Escherichia coli*, remain the predominant etiological agents, accounting for the majority of cases. Other commonly implicated organisms include *Klebsiella spp.*, *Pseudomonas spp.*, and Gram-positive bacteria such as *Enterococcus spp.* (2,3).

In recent years, antimicrobial resistance among uropathogens has emerged as a major global health concern. Increasing resistance to commonly used antibiotics such as fluoroquinolones, beta-lactams, and third-generation cephalosporins has been widely reported, limiting therapeutic options (4,5).
Additionally, fungal pathogens, particularly *Candida* species, are increasingly recognized as important causes of urinary tract infections, especially in hospitalized patients, those with indwelling urinary catheters, and individuals receiving prolonged antibiotic therapy (6).

Local surveillance of etiological agents and their antimicrobial susceptibility patterns is essential for guiding empirical therapy and implementing effective antibiotic stewardship strategies. Therefore, the present study was undertaken to analyze the spectrum of uropathogens and their antimicrobial and antifungal susceptibility patterns in urine samples from a tertiary care hospital.

MATERIAL AND METHODS

Study Setting: The study was carried out at a 1500 bedded tertiary care Centre and teaching hospital located in Central India. The study was conducted over a 12-month period from September 2024 to August 2025. Samples from OPD, IPD, and ICU were processed in the Department of Microbiology.

Study design: Cross-sectional study

Sample size: Urinary samples received from OPD/ IPD/ICUs during the specified time period were used for analysis in the study. It also included catheterized urine sample

Inclusion criteria: Only the first isolate recovered during the specified time period per patient with confirmed identification and susceptibility testing results was included for analysis.

Exclusion Criteria: The following were excluded from the study:

- Isolates of screening or surveillance cultures,
- Isolates with ambiguous or intermediate sensitivity results.,
- Duplicate isolate from the same patient.

Sample processing:

Midstream urine (MSU) samples, except in catheterized patients, were collected and processed in accordance with the standard operating procedures of the microbiology laboratory. (7) Culture-positive isolates were further identified and subjected to antimicrobial susceptibility testing (AST) using the VITEK 2 system. Interpretation of AST results was performed in accordance with the Clinical and Laboratory Standards Institute guidelines. (8)

Collection of Urine from Catheterized Patients

Most of the ICU patients in the present study were catheterized, which is a known risk factor for urinary tract infections." In catheterized patients, urine samples were collected aseptically from the sampling port of the indwelling urinary catheter. The catheter tubing was first disinfected using 70% alcohol, and urine was aspirated using a sterile syringe. Samples were transferred to sterile containers and processed promptly.

Urine collection from the drainage bag was strictly avoided to prevent contamination. Standard infection control practices were followed during sample collection. This method is in accordance with recommended guidelines for prevention and diagnosis of catheter-associated urinary tract infections (CAUTI) (9,10).

Data Collection and Analysis: As this was a retrospective study, hence the data was retrieved through the Hospital Management information system (HMIS) and analyzed and interpreted using WHO NET 2024 version.

RESULTS

Out of the total urine samples processed in the microbiology laboratory, 505 samples yielded significant microbial growth. The etiological distribution of isolates is presented in Table 1. Among the culture-positive samples, the majority were attributed to Gram-negative bacteria [n = 411 (81.4%)], followed by Gram-positive bacteria [n = 77 (15.3%)] and fungal isolates [n = 17 (3.3%)].

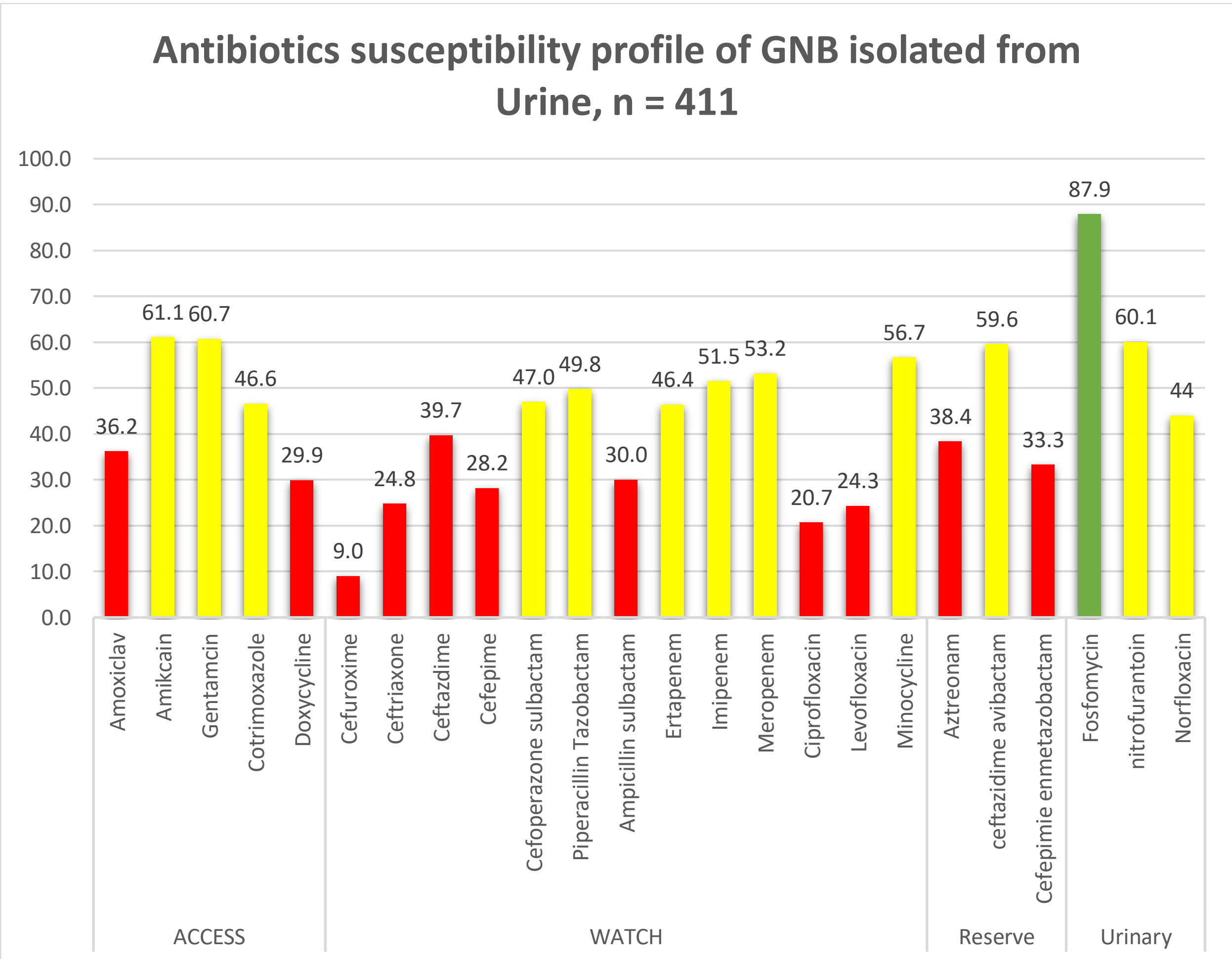
Organism-wise distribution revealed that *Escherichia coli* [n = 236 (46.7%)] was the most frequently isolated pathogen, followed by *Klebsiella pneumoniae* [n = 91 (18.0%)] and *Pseudomonas aeruginosa* [n = 40 (7.9%)] among Gram-negative bacteria. Other Gram-negative bacilli included *Achromobacter spp.*, *Aeromonas spp.*, *Proteus spp.*, *Providencia spp.*, *Morganella spp.*, and *Pseudomonas spp.* other than *P. aeruginosa*.

Among Gram-positive organisms, *Enterococcus spp.* [n = 66 (13.0%)] were the predominant isolates. Fungal isolates comprised various *Candida* species, predominantly *Candida albicans*, followed by *Candida tropicalis* and *Candida parapsilosis.*

Table 1: Etiological distribution of Urinary isolates

SN	Gram Negative Organisms	Number (%)
1	Acinetobacter baumannii	6 (1.2)
2	Citrobacter sp.	7 (1.3)
3	Enterobacter cloacae complex	5 (0.9)
4	Escherichia coli	236 (46.7)
5	Klebsiella pneumoniae	91 (18.0)
6	pseudomonas aeruginosa	40 (7.9)
7	Serratia marcescens	9 (1.8)
8	Miscellaneous GNB	17 (3.3)
9	Enterococcus Spp.	66 (13.0)
10	Staphylococcus aureus	1 (0.1)
11	CONS	10 (1.9)
12	Candida albicans	3 (0.5)
13	Candia nonalbicans	14 (2.7)
	Total	**505**

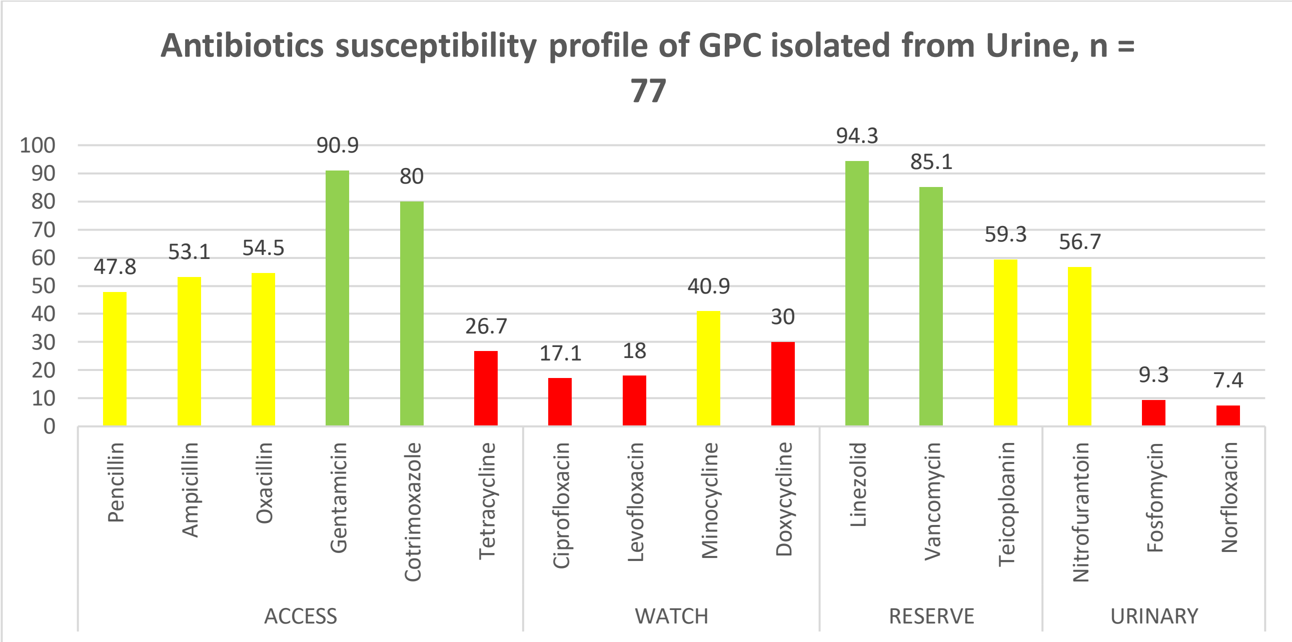
Antibiotics were categorized into Access, Watch, and Reserve (AWaRe) groups in accordance with the World Health Organization AWaRe classification, which is designed to promote optimal antibiotic selection and antimicrobial stewardship. (11) The Access group includes first- and second-line agents with lower resistance potential, the Watch group comprises broader-spectrum antibiotics with a higher risk of resistance development, and the Reserve group consists of last-resort agents reserved for the treatment of multidrug-resistant infections. Antibiotics with known intrinsic resistance for specific organisms were identified and excluded from susceptibility interpretation.



Graph 1. AST profile of Gram-negative uropathogens by AWaRe classification (n = 411)

The antimicrobial susceptibility profile of Gram-negative bacilli isolated from urine samples is depicted in Graph 1. Antibiotics were categorized according to the WHO AWaRe classification into Access, Watch, Reserve, and urinary-specific agents.

Among the Access group antibiotics, moderate susceptibility was observed for amikacin (61.1%) and gentamicin (60.7%), whereas lower susceptibility was noted for ampicillin (36.2%). In the Watch group, higher susceptibility was observed with piperacillin-tazobactam (49.8%) and meropenem (53.2%), Imipnem (51.5%) while cefepime (28.2%) and ceftazidime (39.7%) demonstrated comparatively lower effectiveness. Ampicillin-sulbactam showed moderate activity (30.0%). Among Urinary group antibiotics, fosfomycin exhibited the highest susceptibility (87.9%), followed by nitrofurantoin (60.1%). Among the reserved group, moderate susceptibility was seen with cefepime-enmetazobactam (33.3%) and aztreonam (38.4%), while ceftazidime-avibactam showed relatively higher activity (59.6%). Overall, higher susceptibility was observed with urinary-specific agents compared to commonly used first-line antibiotics.



Graph 2. AST profile of Gram Positive uropathogens by AWaRe classification (n = 411)

The antimicrobial susceptibility profile of Gram-positive cocci isolated from urine samples is depicted in Graph 2. Among the Access group antibiotics, higher susceptibility was observed for gentamicin (90.9%) and cotrimoxazole (80%), while moderate susceptibility was noted for ampicillin (53.1%) and oxacillin (54.5%). Penicillin showed relatively lower susceptibility (47.8%). In the Watch group, overall lower susceptibility was observed, with tetracycline (26.7%), ciprofloxacin (17.1%), and levofloxacin (18%) showing reduced effectiveness. Minocycline demonstrated moderate susceptibility (40.9%). Among the Reserve group antibiotics, linezolid exhibited the highest susceptibility (94.3%), followed by vancomycin (85.1%) and teicoplanin (59.3%). Among urinary-specific agents, nitrofurantoin demonstrated moderate susceptibility (56.7%), whereas fosfomycin (9.3%) and norfloxacin (7.4%) showed low susceptibility. Overall, higher susceptibility was observed with reserve antibiotics compared to Access and Watch group agents.

Table 2. Antifungal susceptibility testing of fungal isolates

Total no. of fungal isolates	**Amphotericin B**	**Micafungin**	**Caspofungin**	**Fluconazole**	**Voriconazole**
17	17 (100)	17 (100)	17 (100)	14 (85.7)	17

Antifungal susceptibility testing of fungal isolates is summarized in Table 2. A total of 17 Candida isolates were recovered from urine samples. All isolates (100%) were found to be susceptible to amphotericin B, micafungin, and caspofungin. High susceptibility was also observed for voriconazole (100%), while slightly lower susceptibility was noted for fluconazole (85.7%).

DISCUSSION

In the present study, Gram-negative bacteria were the predominant uropathogens, accounting for 81.4% of isolates, followed by Gram-positive bacteria (15.3%) and fungal isolates (3.3%). This finding is consistent with recent studies, which report

Gram-negative organisms as the major contributors to urinary tract infections, often comprising around 80–90% of isolates. (12) The predominance of Gram-negative bacilli is attributed to their virulence factors, including adhesins, biofilm formation, and ability to colonize the uroepithelium.Among the isolates, *Escherichia coli* (46.7%) was the most common pathogen, followed by *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*. Similar distributions have been consistently reported in recent literature, where *E. coli* remains the leading uropathogen, followed by *Klebsiella spp.* and other non-fermenters. (13) The persistence of *E. coli* as the dominant organism highlights its strong adaptability and pathogenic potential in both community and hospital settings.

The antimicrobial susceptibility profile of Gram-negative isolates in the present study revealed reduced susceptibility to commonly used Access group antibiotics such as ampicillin, ceftriaxone, and fluoroquinolones. Comparable findings have been reported in recent studies demonstrating high resistance rates to ampicillin, trimethoprim-sulfamethoxazole, and fluoroquinolones, thereby limiting their role in empirical therapy. (14) This trend reflects the widespread and often inappropriate use of these antibiotics, leading to increased selective pressure and emergence of resistant strains. In contrast, relatively higher susceptibility was observed with aminoglycosides and beta-lactam/beta-lactamase inhibitor combinations, while carbapenems and fosfomycin demonstrated better activity. Similar observations have been reported in recent studies, where carbapenems, aminoglycosides, and fosfomycin retain good efficacy against resistant uropathogens.(13) However, the increasing reliance on these higher-end antibiotics is concerning, as it may contribute to the emergence of multidrug-resistant and carbapenem-resistant organisms.

The application of the WHO AWaRe classification in the present study provides an important perspective on antibiotic utilization. A higher resistance was observed among Access group antibiotics, while better susceptibility was noted among Reserve group drugs. This pattern aligns with global observations, where increased resistance to commonly used first-line agents necessitates the use of broader-spectrum or reserve antibiotics. Such findings underscore the urgent need for antimicrobial stewardship programs to preserve the efficacy of existing antibiotics.

Among Gram-positive isolates, *Enterococcus spp.* was the predominant organism. The susceptibility pattern demonstrated preserved activity of linezolid and vancomycin, which is consistent with recent reports indicating retained effectiveness of these agents against Gram-positive uropathogens. (15) However, reduced susceptibility to fluoroquinolones and other commonly used antibiotics highlights the emerging resistance trends in Gram-positive organisms as well.

An important aspect of this study was the identification of fungal isolates, primarily *Candida* species, accounting for 3.3% of cases. Candiduria is increasingly being reported, particularly in hospitalized and catheterized patients, and is associated with risk factors such as prolonged antibiotic use and invasive devices. The antifungal susceptibility pattern in the present study showed excellent activity of amphotericin B and echinocandins, with high susceptibility to azoles. These findings are comparable to recent studies reporting good susceptibility of Candida isolates to these antifungal agents.

Overall, the present study highlights the evolving antimicrobial resistance patterns among uropathogens. The high prevalence of resistance to commonly used antibiotics, coupled with increasing dependence on reserve drugs, emphasizes the need for continuous surveillance, rational antibiotic prescribing, and strict infection control practices. The integration of AWaRe classification further strengthens the clinical relevance of the findings and supports its role in guiding antimicrobial stewardship strategies.

CONCLUSION

The present study demonstrates that Gram-negative bacteria, particularly *Escherichia coli*, remain the predominant uropathogens, followed by Gram-positive organisms and *Candida* species. A high level of antimicrobial resistance was observed among commonly used Access group antibiotics, while relatively better susceptibility was noted with reserve and urinary-specific agents.

The findings highlight the growing challenge of antimicrobial resistance in urinary isolates, necessitating regular surveillance of local antibiograms. The inclusion of the WHO AWaRe classification provides valuable insight into antibiotic usage patterns and supports its role in guiding rational antimicrobial therapy. Overall, the study underscores the importance of antimicrobial stewardship, judicious antibiotic use, and adherence to infection control practices to curb the emergence and spread of resistant uropathogens.

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