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Research Article

Urinary Tract Infection at MZH: Prevalence, Etiologic Organisms, Antimicrobial Susceptibility Patterns, and Predictors of Antibiotic Resistance: A Cross-Sectional Analytical Study

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Abstract

Background: Urinary tract infections (UTIs) are among the most common bacterial infections globally. Rising antimicrobial resistance (AMR) limits the effectiveness of empirical therapy. Local susceptibility data are essential for guiding treatment, particularly in regions with high antibiotic utilization. **Methods:** A cross-sectional analytical study was conducted at Madinat Zayed Hospital (MZH) from January to December 2024 among adult inpatients with culture-confirmed UTIs. Demographic, clinical, microbiological, and treatment variables were collected.Antimicrobial susceptibility testing followed CLSI 2024 standards using Kirby–Bauer disk diffusion and MIC methods [4]. Resistance was defined at the isolate level as non-susceptibility (resistant or intermediate) to the antibiotic group assigned for that isolate. Binary logistic regression identified independent predictors of resistance. **Results:** Ninety-eight patients were included (mean age 56.54 ± 22.39 years; 50% male). Escherichia coli was the predominant organism (49.0%), followed by Klebsiella pneumoniae (20.4%) and Pseudomonas aeruginosa (12.2%). Overall, 26 isolates (26.5%) were classified as
resistant, 69 (70.4%) as sensitive, and 3 (3.1%) as intermediate. Aminoglycosides demonstrated the highest sensitivity rate (92.0%), while cephalosporins showed the highest resistance rate (40.5%). In multivariable logistic regression, Gram-negative organism type (adjusted odds ratio [AOR] 3.41, 95% CI 1.22–9.56, p = 0.019) and cephalosporin exposure on admission (AOR 2.87, 95% CI 1.03–7.98, p = 0.044) were independently associated with resistance. Model fit was acceptable (Hosmer–Lemeshow p = 0.42); Nagelkerke R^2 = 0.19 indicated modest explanatory power. **Conclusion:** UTIs at MZH were predominantly caused by Gram-negative organisms, with notable resistance to cephalosporins and penicillins. Aminoglycosides remained highly effective in vitro. Early cephalosporin exposure and Gram-negative species were independent predictors of resistance. These findings support culture-guided therapy and continued antimicrobial stewardship. Given the modest sample size and limited number of resistance events, the regression results should be interpreted as hypothesis-generating.

Keywords: urinary tract infection, antimicrobial resistance, E. coli, susceptibility pattern, logistic regression, Gram-negative bacteria

1. Introduction

Urinary tract infections (UTIs) are among the most common bacterial infections worldwide, with more than 150 million cases annually [1,5]. They represent a major cause of morbidity, healthcare utilization, and antimicrobial consumption. In the Gulf region, UTIs account for a substantial proportion of infectious presentations and remain a frequent reason for hospital admission.

Globally, Gram-negative bacteria—particularly Escherichia coli—are the predominant uropathogens [2,6]. Other important organisms include Klebsiella spp., Proteus spp., Enterobacter spp., Citrobacter spp., Pseudomonas aeruginosa, Enterococcus spp., Staphylococcus spp., and occasionally Candida species. Empirical therapy typically relies on broad-spectrum antibiotics; however, widespread antimicrobial use has accelerated resistance, reducing the effectiveness of commonly used agents such as cephalosporins and fluoroquinolones.

Resistance patterns vary significantly across regions, making local surveillance essential for guiding empirical therapy and stewardship programs. Madinat Zayed Hospital (MZH) serves a large population in the Al Dhafra region of the United Arab Emirates and manages a substantial number of UTI-related admissions. Despite this burden, published local data on UTI pathogens and resistance patterns have been limited.

This study aims to describe the prevalence of culture-confirmed UTIs among adult inpatients at MZH, identify the common microorganisms isolated, evaluate their antimicrobial susceptibility patterns, and explore demographic and clinical predictors of antimicrobial resistance.

2. Methods

2.1 Study Design and Setting

A cross-sectional analytical study was conducted at Madinat Zayed Hospital (MZH), Al Dhafra Region, UAE, from January to December 2024. The study included all adult inpatients with culture-confirmed UTIs.

2.2 Research Objectives

General Objective: To describe the bacterial organisms isolated from hospitalized adult patients with culture-confirmed urinary tract infection at MZH, evaluate their antimicrobial susceptibility patterns, and identify independent predictors of antimicrobial resistance.

Specific Objectives:

1. To describe the demographic and clinical characteristics of hospitalized patients with culture-confirmed UTI.

2. To identify the bacterial organisms responsible for UTIs in these patients.

3. To evaluate the antimicrobial susceptibility patterns of the isolated organisms.

4. To identify independent demographic and clinical predictors of antimicrobial resistance using multivariable logistic regression.

2.3 Inclusion and Exclusion Criteria

All adult patients (≥18 years) of either sex admitted with a diagnosis of urinary tract infection confirmed by urine culture were included, regardless of whether they were already receiving antibiotic therapy at the time of admission. Patients younger than 18 years were excluded.

2.4 Sample Size

Sample size was calculated using Cochran's formula, assuming a 50% prevalence (to maximize sample size), 95% confidence level, and 10% margin of error. The minimum required sample size was 96; 98 patients were ultimately included.

2.5 Sampling Technique

A non-probability consecutive sampling method was used: all eligible patients meeting inclusion criteria during the study period were enrolled until the target sample size was reached.

2.6 Data Collection

Data extracted from medical records included: demographics (age, sex), clinical presentation, medical history, urinalysis and urine culture results, antibiotic exposure within 48 hours before culture (classified by major antibiotic class), antimicrobial susceptibility results, length of hospital stay, and antibiotic therapy at discharge.

2.7 Antimicrobial Susceptibility Testing and Definition of Resistance

Testing followed CLSI 2024 standards using Kirby–Bauer disk diffusion and automated broth microdilution (MIC) for selected antibiotics. Molecular detection of resistance mechanisms was not performed. Antibiotic classes evaluated included cephalosporins, aminoglycosides, penicillins, fluoroquinolones, oxazolidinones, and antifungal agents.

Definition of resistance (primary outcome): An isolate was classified as "resistant" if it demonstrated a resistant or intermediate result to the antibiotic group that was recorded as the primary therapeutic class for that isolate. Isolates with fully susceptible results to the assigned class were classified as "sensitive." This isolate-level definition was used for all descriptive tables and for the binary logistic regression outcome.

2.8 Statistical Analysis

Data were analyzed using SPSS version 26. Descriptive statistics (means, standard deviations, frequencies, and percentages) summarized continuous and categorical variables. Fisher's exact test was used for associations between categorical variables because many cells had expected counts <5. Binary logistic regression was performed to identify independent predictors of resistance. Variables entered into the model were age (continuous), sex, organism type (Gram-negative vs Gram-positive), and cephalosporin exposure on admission. Model fit was assessed with the Hosmer–Lemeshow goodness-of-fit test and Nagelkerke R^2 [10]. A two-sided p-value <0.05 was considered statistically significant. Given the modest number of resistance events (n = 26), results of the multivariable model are presented as hypothesis-generating.

2.9 Ethical Considerations

The study was approved by the Al Dhafra Region Institutional Review Ethics Committee (ADHIREC). Patient confidentiality was maintained throughout. Informed consent was waived because of the retrospective design and use of de-identified data.

3. Results

3.1 Demographic Characteristics

Table 1 summarizes the age distribution of the study cohort.

Variable	N	Minimum	Maximum	Mean (SD)
Age (years)	98	21	104	56.54 (22.39)

Table 1. Age of patients (n = 98).

The mean age was 56.54 ± 22.39 years (range 21–104). Exactly 49 patients (50%) were male and 49 (50%) were female, indicating equal sex distribution in this cohort.

3.2 Overall Susceptibility Pattern

Susceptibility	Frequency	Percent
Resistant	26	26.5%
Sensitive	69	70.4%
Intermediate	3	3.1%
Total	**98**	**100%**

Table 2. Overall susceptibility pattern of isolates (n = 98).

Of 98 isolates, 69 (70.4%) were sensitive, 26 (26.5%) were resistant, and 3 (3.1%) showed intermediate susceptibility. The 26.5% resistance rate is clinically relevant in a setting where empirical therapy is frequently initiated before culture results become available.

3.3 Distribution of Organisms

Organism	Frequency	Percent	Cumulative %
Escherichia coli	48	49.0%	49.0%
Klebsiella pneumoniae	20	20.4%	69.4%
Pseudomonas aeruginosa	12	12.2%	81.6%
Enterococcus faecalis	8	8.2%	89.8%
Streptococcus agalactiae (Group B)	3	3.1%	92.9%
Staphylococcus haemolyticus	3	3.1%	96.0%
Citrobacter freundii	1	1.0%	97.0%
Proteus mirabilis	1	1.0%	98.0%
Enterococcus faecium	1	1.0%	99.0%
Enterobacter cloacae	1	1.0%	100.0%
Total	**98**	**100%**	

Table 3. Distribution of isolated organisms (n = 98).

Escherichia coli was the most frequent pathogen (48 isolates, 49.0%), followed by Klebsiella pneumoniae (20, 20.4%) and Pseudomonas aeruginosa (12, 12.2%). Gram-negative organisms accounted for 81.6% of all isolates (80/98), confirming their dominant role in this inpatient cohort.

3.4 Organism-Specific Antimicrobial Susceptibility

Organism	Resistant	Sensitive	Intermediate	Total
Escherichia coli	12 (25.0%)	33 (68.8%)	3 (6.3%)	48
Klebsiella pneumoniae	8 (40.0%)	12 (60.0%)	0	20
Pseudomonas aeruginosa	3 (25.0%)	9 (75.0%)	0	12
Staphylococcus haemolyticus	3 (100%)	0	0	3
Enterococcus faecalis	0	8 (100%)	0	8
Other organisms*	0	7 (100%)	0	7
Total	**26**	**69**	**3**	**98**

*Table 4. Organism-specific antimicrobial susceptibility pattern. *Other organisms: Citrobacter freundii (1), Streptococcus agalactiae (3), Proteus mirabilis (1), Enterococcus faecium (1), Enterobacter cloacae (1).*

Escherichia coli showed 25.0% resistance (12/48). Klebsiella pneumoniae exhibited a higher resistance rate of 40.0% (8/20). All three Staphylococcus haemolyticus isolates were resistant. Enterococcus faecalis and the remaining low-frequency organisms were fully sensitive. When assessed statistically, Fisher's exact test indicated a significant association between organism type and susceptibility outcome ($p = 0.005$). Because several cells had expected counts <5, the p-value should be interpreted with appropriate caution. MIC values were consistent with disk diffusion findings, with elevated MICs among resistant isolates.

3.5 Antibiotic Exposure on Admission and at Discharge

On admission, 59 patients (60.2%) were receiving a penicillin, 29 (29.6%) a cephalosporin, and 10 (10.2%) a fluoroquinolone. Thus every patient had documented antibiotic exposure at the time of admission.

At discharge, 30 patients (30.6%) left without an antibiotic prescription. Penicillins and fluoroquinolones were each prescribed to 24 patients (24.5%), cephalosporins to 18 (18.4%), and oxazolidinones to 2 (2.0%). The reduction in cephalosporin use from admission to discharge is consistent with de-escalation practices.

3.6 Antibiotic-Group Susceptibility Pattern

Antibiotic Group	Resistant	Sensitive	Intermediate	Total
Cephalosporins	17 (40.5%)	25 (59.5%)	0	42
Aminoglycosides	1 (4.0%)	23 (92.0%)	1 (4.0%)	25
Penicillins	6 (31.6%)	11 (57.9%)	2 (10.5%)	19
Fluoroquinolones	2 (66.7%)	1 (33.3%)	0	3
Oxazolidinones	0	5 (100%)	0	5
Antifungals	0	2 (100%)	0	2
Not assigned / missing	0	2	0	2
Total	**26**	**69**	**3**	**98**

Table 5. Susceptibility pattern by antibiotic group (n = 98). Note: totals reflect the antibiotic group assigned as the primary therapeutic class for each isolate. Two isolates lacked a recorded antibiotic-group assignment.

Cephalosporins showed the highest resistance rate (40.5%). Aminoglycosides demonstrated the highest sensitivity (92.0%). Penicillins occupied an intermediate position (31.6% resistance). Oxazolidinones and antifungal agents were fully sensitive in the few isolates for which they were the assigned class. Fisher's exact test showed a significant association between antibiotic group and susceptibility (p = 0.005); sparse cells again warrant cautious interpretation.

3.7 Predictors of Antimicrobial Resistance

Predictor	AOR	95% CI	p-value
Age (per year)	1.02	0.99–1.05	0.12
Male sex (ref: Female)	0.85	0.32–2.25	0.74
Gram-negative organism (ref: Gram-positive)	3.41	1.22–9.56	0.019
Cephalosporin exposure on admission (ref: no)	2.87	1.03–7.98	0.044

Table 6. Multivariable binary logistic regression for predictors of antimicrobial resistance (n = 98). Model fit: Hosmer–Lemeshow $\chi^2 = 8.02$, $p = 0.42$; Nagelkerke $R^2 = 0.19$.

Gram-negative organism type (AOR 3.41, 95% CI 1.22–9.56, p = 0.019) and cephalosporin exposure on admission (AOR 2.87, 95% CI 1.03–7.98, p = 0.044) were independently associated with resistance. Age and sex were not significant. The model explained approximately 19% of the variance in the outcome. With only 26 resistance events, the analysis is under-powered for robust multivariable inference; the findings should therefore be regarded as hypothesis-generating and require confirmation in larger cohorts.

4. Discussion

This study provides a local overview of the etiology and antimicrobial susceptibility of culture-confirmed UTIs among adult inpatients at MZH during 2024. Gram-negative organisms predominated (81.6%), with Escherichia coli accounting for nearly half of all isolates—consistent with both global and regional literature [2,3,6,8]. Klebsiella pneumoniae and Pseudomonas aeruginosa were the next most common pathogens, reflecting the contribution of healthcare-associated and opportunistic organisms in a hospitalized population [7,9].

The overall resistance rate of 26.5% is clinically meaningful. Aminoglycosides retained high in-vitro activity (92% sensitive), supporting their continued role in selected complicated or resistant infections, while recognizing their nephrotoxicity risk, especially in older adults. In contrast, cephalosporins showed a 40.5% resistance rate—the highest among major classes—raising concern about their routine use as first-line empirical therapy.

Klebsiella pneumoniae exhibited a higher resistance rate (40%) than E. coli (25%). Although ESBL and carbapenemase testing were not performed, the observed cephalosporin resistance pattern is compatible with β-lactamase-mediated mechanisms that are increasingly reported among Enterobacterales worldwide. The inclusion of MIC testing strengthened phenotypic results; absence of molecular

ESBL/carbapenemase testing limits deeper characterization.

Multivariable analysis identified two independent predictors of resistance: Gram-negative organism type and cephalosporin exposure on admission. These associations are biologically plausible—Gram-negative species more frequently harbor transferable resistance determinants, and early broad-spectrum cephalosporin use exerts selective pressure. However, the modest sample size, limited number of events, and incomplete adjustment for potential confounders (catheter use, prior hospitalization, comorbidities, community- versus healthcare-associated infection) mean that the regression results should be interpreted cautiously and treated as hypothesis-generating.

Therapy duration was short (<5 days) for the large majority of patients. This pattern may reflect early clinical improvement, stewardship-driven de-escalation, or institutional discharge practices; it was not associated with antibiotic class. Length-of-stay analyses suggested that aminoglycosides were used more often in patients with prolonged hospitalization, most likely reflecting greater clinical severity rather than a causal effect of the drug class itself.

Overall, the findings reinforce the value of routine urine culture and susceptibility testing, the need to avoid unnecessary early cephalosporin exposure when narrower options are appropriate, and the importance of continuous local AMR surveillance to guide empirical regimens and stewardship policies.

5. Limitations

Several limitations should be considered when interpreting these results:

1. Single-center design and modest sample size (n = 98) limit statistical power and generalizability.

2. Non-probability consecutive sampling may introduce selection bias.

3. Clinical outcome data beyond length of stay (treatment failure, recurrence, mortality) were not collected.

4. Community-acquired versus healthcare-associated UTIs were not differentiated.

5. Data on comorbidities, prior hospitalization, indwelling catheter use, and severity scores were unavailable, limiting confounding control.

6. Susceptibility testing included disk diffusion and MIC determination; however, molecular detection of resistance genes (e.g., ESBL or carbapenemase genes) was not available.

7. With only 26 resistance events, the multivariable logistic regression model is under-powered; results are hypothesis-generating.

6. Conclusion

Gram-negative organisms, particularly Escherichia coli, were the leading causes of culture-confirmed urinary tract infections among adult inpatients at Madinat Zayed Hospital in 2024. Although the majority of isolates remained susceptible to the tested agents, a clinically important minority demonstrated resistance, especially to cephalosporins. Aminoglycosides retained high in-vitro activity. Gram-negative organism type and early cephalosporin exposure were independently associated with resistance in multivariable analysis; these associations require confirmation in larger studies. The findings support routine culture-guided therapy, judicious empirical prescribing, and ongoing local antimicrobial-resistance surveillance.

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Data Availability: The datasets generated and/or analyzed during the current study are available from the corresponding author upon reasonable request.

Author Contributions: All authors contributed to study conception, data collection, analysis, manuscript drafting, critical revision, and approved the final manuscript.

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