ORIGINAL ARTICLE

Journal of Clinical Microbiology and Infectious Diseases (*JCMID*) 2026, Volume 6, Number 1: 12-18
E-ISSN: 2808-9405

Published By : the Indonesian Society for Clinical Microbiology

# Clinical and microbiological profile of patients with urinary tract infections at Mangusada Hospital, Badung

Monika Febryanti Lebo Nuru[1], Marta Setiabudy[2*], Anak Agung Gede Indraningrat[2]

[1]Undergraduate Program, Faculty of Medicine and Health Sciences, Warmadewa University
[2]Department of Mikrobiology and Parasitology, Faculty of Medicine and Health Sciences, Warmadewa University

*Corresponding author:
Marta Setiabudy; Department of Mikrobiology and Parasitology, Faculty of Medicine and Health Sciences, Warmadewa University;
marta.setiabudi@warmadewa.ac.id

Received: 2026-02-26
Accepted: 2026-05-04
Published: 2026-05-23

## ABSTRACT

**Introduction:** Urinary tract infections (UTIs) remain among the most common infectious diseases in healthcare settings and are increasingly complicated by antimicrobial resistance. This study aimed to describe the demographic characteristics, comorbidities, catheterisation history, and microbiological profile of UTI patients at Mangusada Regional Hospital.
**Methods:** A descriptive cross-sectional study was conducted among 379 patients diagnosed with UTI from 2022 to 2024. Data were collected from medical records and microbiology laboratory reports. Variables included age, sex, comorbidities, urinary catheter use, and urine culture results. Data were analysed descriptively.
**Results:** Urine culture samples consisted of 64 cases in 2022, 172 in 2023, and 143 in 2024. The highest average proportion of patients was found in the 0–5-year age group (28%), followed by those aged >65 years (11.6%). Sex distribution was nearly equal between males (50.1%) and females (49.9%). Benign prostatic enlargement was the most common comorbidity (13.4%), and most patients had no history of urinary catheter use (85.5%). Gram-negative bacteria predominated among culture-positive isolates (86%). Escherichia coli was the most frequently identified pathogen, with ESBL-producing strains accounting for approximately 50% of all E. coli isolates annually, followed by ESBL-producing Klebsiella pneumoniae.
**Conclusion:** UTIs at Mangusada Regional Hospital were mainly associated with Gram-negative bacteria, particularly ESBL-producing E. coli and K. pneumoniae. These findings suggest limited effectiveness of third-generation cephalosporins as empirical therapy and highlight the need for ongoing antimicrobial surveillance and stewardship.

**Keywords:** UTI, patient profile, bacterial infections, ESBL.
**Cite This Article:** Nuru, M.F.L., Setiabudy, M., Indraningrat, A.A.G. 2026. Clinical and microbiological profile of patients with urinary tract infections at Mangusada Hospital, Badung. *Journal of Clinical Microbiology and Infectious Diseases* 6(1): 12-18. DOI: 10.51559/jcmid.v6i1.111

## INTRODUCTION

Urinary tract infections (UTIs) are infectious conditions caused by the invasion and proliferation of microorganisms, primarily bacteria, but also fungi and viruses, within one or more components of the urinary tract, including the urethra, bladder, ureters, and kidneys. UTIs represent one of the most common bacterial infections encountered in both community and hospital settings and continue to pose a substantial global health burden.[1]

Globally, UTIs are recognised as a significant public health problem. The World Health Organisation estimates that approximately 8,3 million UTI cases occur annually, ranking UTIs as the second most common infection after respiratory tract infections.[2] Furthermore, the American Urological Association estimates that nearly 150 million individuals worldwide experience UTIs each year. In the United States alone, UTIs are associated with more than 13.000 deaths annually, accounting for approximately 2,3% of infection-related mortality.[3] These data underscore the considerable morbidity, mortality, and healthcare costs associated with UTIs.

In Indonesia, the Ministry of Health reports an estimated incidence of 90–100 cases per 100.000 population per year.[4] In Bali Province, the prevalence of UTIs remains relatively high. A study conducted at Prof. I.G.N.G. Ngoerah General Hospital Denpasar (previously known as RSUP Sanglah Denpasar) reported a UTI prevalence of 47.3%, with the highest incidence observed among elderly patients and females. This pattern was associated with age-related decline in immune function, increased exposure to healthcare-associated pathogens, and the presence of underlying comorbidities.[5] From an etiological perspective, *Escherichia coli* is consistently identified as the predominant uropathogen, accounting for approximately 90% of UTI cases. The pathogenesis typically involves colonisation of uropathogenic bacteria originating from the gastrointestinal tract, followed by ascending migration through the urethra to the bladder and, in some cases, the upper urinary tract.[6] The increasing emergence of antimicrobial-resistant strains further complicates management and highlights the importance of local epidemiological surveillance.

Several previous studies have

explored the relationship between patient characteristics and the bacterial aetiology of urinary tract infections (UTIs). Study by Kandarini et al., 2020 Prof. I.G.N.G. Ngoerah General Hospital Denpasar/ Sanglah Hospital reported that *Escherichia coli* (*E.coli*) and *Klebsiella pneumoniae* (*K. pneumoniae*) were the predominant causative pathogens, with the majority of cases occurring in elderly and female patients.[5] Similarly, Kesuma et al., (2023) found that comorbid conditions, particularly diabetes mellitus, were associated with infections caused by bacteria exhibiting higher levels of antimicrobial resistance, especially *K. pneumoniae*.[7] These findings suggest that demographic factors such as age and sex, as well as underlying comorbidities, contribute to variations in the microbiological profile and resistance patterns of UTI pathogens.

Despite these findings, comprehensive studies evaluating the combined association between patient profiles including age, sex, comorbidities, urinary catheter use, and the bacterial profile of UTIs remain limited in Bali. Mangusada Regional Hospital, as a referral centre in Badung Regency, has demonstrated a consistent increase in UTI cases, rising from 284 cases in 2022 to 1.019 cases in 2024. This upward trend highlights the need for updated local epidemiological data to better understand the distribution of causative organisms and associated risk factors. Data on causative bacteria in Mangusada Regional Hospital were not found or do not yet exist. Therefore, updated hospital-specific microbiological and antimicrobial susceptibility data are needed to guide empirical treatment decisions in this setting.

The present study aimed to identify the predominant bacterial pathogens responsible for UTIs and to analyse their distribution according to patient profiles during the 2022–2024 period. The findings are expected to provide valuable local evidence to support more targeted prevention strategies, optimise empirical antibiotic selection, and strengthen antimicrobial stewardship programs in accordance with current recommendations.[8]

## METODE

### Study Design and Setting

This study employed an observational descriptive design with a cross-sectional approach. The research was conducted at Mangusada Regional Hospital, Badung Regency, and included data collected from January 2022 to December 2024. The cross-sectional design was selected to describe the profiles of patients and bacterial isolates associated with urinary tract infections (UTIs) during the study period.

### Study Population and Data Source

The study population consisted of all patients diagnosed with urinary tract infections who underwent urine culture examination at Mangusada Regional Hospital within the study timeframe. Data were obtained from patients' medical records and microbiology laboratory records in accordance with predetermined inclusion and exclusion criteria.

Inclusion criteria comprised patients with a clinical diagnosis of UTI and complete medical and laboratory data, including urine culture and antimicrobial susceptibility results. Patients with incomplete medical records or missing laboratory data were excluded from the analysis.

Potential selection bias was minimised by including all eligible patients who underwent urine culture during the study period. Information bias was reduced by using standardised data extraction forms and microbiology laboratory records. Patients with incomplete medical or laboratory data were excluded to reduce misclassification. However, prior antibiotic exposure may have contributed to negative culture results and was considered when interpreting the findings.

### Variables and Data Collection

The variables analysed in this study included demographic profiles (age and sex), comorbidities (e.g., benign prostatic enlargement, urinary tract stones, chronic kidney disease, diabetes mellitus, and malignancy), history of urinary catheter use, urine culture results, and the sensitivity test, including ESBL-producing bacteria.

Data were systematically extracted using a standardised data collection form to ensure consistency and accuracy. Microbiological identification and antimicrobial susceptibility testing were performed according to the hospital's standard operating procedures with VITEK 2.

### Research Procedure

This study was conducted through several sequential stages. First, ethical approval was obtained from the Health Research Ethics Committee of Mangusada Regional Hospital, Badung Regency. After approval was granted, the researchers identified all patients diagnosed with urinary tract infection who underwent urine culture examination at Mangusada Regional Hospital from January 2022 to December 2024. Patient eligibility was assessed based on the predetermined inclusion and exclusion criteria. Patients with a clinical diagnosis of UTI and complete medical and microbiology laboratory data were included, while those with incomplete records or unavailable urine culture and antimicrobial susceptibility results were excluded.

The next stage involved data collection from medical records and microbiology laboratory records. Data were extracted using a standardised data collection form to ensure consistency. The collected variables included age, sex, comorbidities, history of urinary catheter use, urine culture results, bacterial identification, ESBL status, and antimicrobial susceptibility patterns. Microbiological identification and antimicrobial susceptibility testing were performed by the hospital microbiology laboratory using VITEK 2 according to the hospital's standard operating procedures. After data collection, all data were checked for completeness, coded, and entered SPSS for analysis. Descriptive statistical analysis was then performed, and the results were presented as frequencies and percentages in tables and narrative form to describe the clinical and microbiological profile of UTI patients at Mangusada Regional Hospital.

### Statistical Analysis

Data analysis was conducted using Statistical Package for the Social Sciences (SPSS) software. A univariate analysis was performed to describe the distribution

of variables. Categorical variables were presented as frequencies, and percentages were summarised using appropriate descriptive statistics. The results were presented in tabular and narrative form to illustrate the profiles of patients and bacterial isolates.

## RESULT

The subjects of this study were patients with a confirmed diagnosis of urinary tract infection (UTI) who were undergoing treatment and had a urine culture at Mangusada Badung Hospital. The sample consisted of 379 patients who met the inclusion criteria in 2022-2024. The total samples were 64 in 2022, 172 in 2023, and 134 in 2024. Their profiles are presented in Table 1 below.

**Table 1.** **Demographic and Clinical Profiles of Patients**

| Clinical Profile | 2022-2024 (n=379) | | 2022 (n=64) | | 2023 (n=172) | | 2024 (n=143) | |
|---|---|---|---|---|---|---|---|---|
| | n | % | n | % | n | % | n | % |
| **Age (years)** | | | | | | | | |
| 0-5 | 106 | 28 | 24 | 37,5 | 52 | 30,2 | 30 | 21 |
| 6-12 | 32 | 8,4 | 7 | 10,9 | 20 | 11,6 | 25 | 17,5 |
| 12-16 | 22 | 5,8 | 7 | 10,9 | 19 | 11 | 21 | 14,7 |
| 17-25 | 22 | 5,8 | 2 | 3,1 | 18 | 10,5 | 20 | 14 |
| 26-35 | 39 | 10,3 | 5 | 7,8 | 18 | 10,5 | 15 | 10,5 |
| 36-45 | 42 | 11,1 | 3 | 4,7 | 15 | 8,7 | 11 | 7,7 |
| 46-55 | 35 | 9,2 | 6 | 9,4 | 12 | 7 | 8 | 5,6 |
| 56-65 | 37 | 9,8 | 1 | 1,6 | 9 | 5,2 | 7 | 4,9 |
| > 65 | 44 | 11,6 | 9 | 14,1 | 9 | 5,2 | 6 | 4,2 |
| **Sex** | 190 | 50,1 | 26 | 40,6 | 87 | 50,6 | 79 | 55,2 |
| Male | | | | | | | | |
| Female | 189 | 49,9 | 38 | 59,4 | 85 | 49,4 | 64 | 44,8 |
| **Comorbidity** | | | | | | | | |
| Prostate Enlargement | 44 | 11,6 | 4 | 6,2 | 10 | 5,8 | 13 | 9 |
| Urinary Tract Stones | 37 | 11,4 | 3 | 4,7 | 14 | 8,1 | 20 | 14 |
| CKD | 19 | 5 | 5 | 7,8 | 4 | 2,3 | 10 | 7 |
| Diabetes Mellitus | 16 | 4,2 | 1 | 1,5 | 9 | 5,2 | 6 | 4,1 |
| Malignancy | 13 | 3,4 | 1 | 1,5 | 8 | 4,6 | 4 | 2,8 |
| Others | 250 | 66 | 50 | 78,1 | 127 | 73,8 | 90 | 63 |
| **Urinary catheter** | | | | | | | | |
| No | 324 | 85,5 | 58 | 90,6 | 150 | 87,2 | 116 | 81,1 |
| Yes | 55 | 14,6 | 6 | 9,4 | 22 | 12,8 | 27 | 18,9 |

Table 1 shows that most of the patients in this study were in the 0-5 years age group, as many as 106 patients (28%), followed by those aged > 65 years (44 patients; 11,6%). Half of the patients in this study were male (190 patients; 50,1%) and the other half, 189 patients (49,9%), were female.

Of the total 379 patients, 53 (13,9%) had no comorbidities, either related or unrelated to urinary tract infection (UTI) risk factors. The remaining 326 patients (86,1%) had at least one comorbidity. Among patients with comorbidities, benign prostatic enlargement was the most common diagnosis (44 patients; 13,4%), followed by urinary tract stones (36 patients; 11%), kidney disorders (24 patients; 7,3%), malignancy (18 patients; 5,5%), and diabetes mellitus (15 patients; 4,6%). Other comorbid conditions not directly associated with UTI risk accounted for 189 cases (57,9%), including bronchitis, pneumonia, anaemia, epilepsy, dyspepsia, concussion, hypertension, hypothyroidism, angina pectoris, acute appendicitis, dengue hemorrhagic fever, hernia, and typhoid fever. Most patients did not use urinary catheters (324 patients; 85,5%), while 55 patients (14,5%) had been using a catheter during the UTI period.

Table 2 shows that 207 patients (54,6%) had no bacterial growth, while 172 patients (45,4%) demonstrated positive bacterial cultures. As presented as well, among the culture-positive samples, 148 isolates (86%) were Gram-negative bacteria and 24 isolates (14%) were Gram-positive bacteria.

The most common causative organism was *Escherichia coli*, identified in 73 patients (42,4%). Of these, 38 isolates (52%) were extended-spectrum beta-lactamase (ESBL)-producing *E. coli*. *Klebsiella pneumoniae* was detected in 29 patients (16,9%), with 11 isolates (38%) producing ESBL. The breakdown for the trend each year can be seen in Table 3. Other Gram-negative organisms included *Acinetobacter baumannii* and *Enterobacter cloacae complex*, each identified in 9 patients (5,2%), followed by *Pseudomonas aeruginosa* in 8 patients (4,7%) and *Proteus mirabilis* in 6 patients (3,5%).

Among Gram-positive bacteria, *Enterococcus faecalis* and *Staphylococcus haemolyticus* were identified in 6 patients (3,5%) and 4 patients (2,3%), respectively. *Staphylococcus epidermidis*, *Staphylococcus saprophyticus*, and *Staphylococcus sciuri* were each found in 3 patients (1,7%). Other bacterial species accounted for 19 isolates (11,0%).

Among the 2 most common bacteria that cause UTIs, high resistance rates were observed against penicillins and third-generation cephalosporins, consistent with

the high prevalence of ESBL-producing isolates. Carbapenems and amikacin retained excellent activity against both *Escherichia coli* and *Klebsiella pneumoniae*, while nitrofurantoin remained effective, particularly for *E. coli*.

## DISCUSSION

In accordance with this study, Halim et al (2025) reported that the majority of UTI cases occurred in children aged 1–5 years (43,4%). Similarly, a large retrospective cohort study published by Liang et al. (2024) demonstrated that children aged 2-5 years had a higher incidence of UTIs compared with infants aged 0-1 year and children aged 5-11 years, indicating that this pre-school group constituted the most dominant category in pediatric UTI cases.[11,12] This finding was influenced by several factors, including suboptimal hygiene practices, incomplete toilet training, and an immune system that was still developing, thereby facilitating bacterial entry into the urinary tract. Next to children, Jannah et al. (2022) revealed that individuals aged >65 years represented one of the most affected groups (36,6%).[10] The increased susceptibility among the elderly was associated with immunosenescence, resulting in suboptimal immune function, as well as age-related changes in the urinary tract.

The number of male and female patients in this study was almost equal. It showed there was no significant difference because each has its own risk factors. Uncircumcised boys are known to have a higher risk of developing UTIs (51,7%).[13] This increased susceptibility was associated with the moist environment beneath the preputium, which created favourable conditions for bacterial growth and colonisation. UTIs in neonates were also more common among uncircumcised boys compared to females.[14] However, a shorter urethra in females has always been one of the biggest risks for ascending bacterial infections. Limited understanding and poor implementation of personal hygiene practices have been shown to increase the risk of reproductive health problems, including urinary tract infections, pelvic inflammatory disease, cervical cancer, and other related conditions.[15]

In this study, prostate enlargement was the most common comorbidity observed among patients with UTIs. Previous study reported that 67,9% of patients with benign prostatic enlargement suffered from leucocyturia related to urethral and bladder obstruction.[16] The second most frequent comorbidity identified in this study was urinary tract stones (urolithiasis). Any kind of obstruction led to urinary retention, creating conditions that increased the risk of urinary tract infections.[4] Other than those, kidney disorders, especially chronic kidney disease (CKD), represented another important comorbidity. CKD and UTIs had a reciprocal relationship. CKD contributed to immune dysfunction and the accumulation of uremic toxins, thereby increasing susceptibility to infection. Conversely, recurrent or severe UTIs could accelerate the decline in renal function, especially in advanced stages.[17]

The risk of UTIs in diabetic patients was more strongly associated with poor glycemic control, particularly elevated HbA1c levels, rather than the mere

**Table 2. Microbiological Findings from Urine Samples of UTI Patients**

| Characteristics | N | % |
|---|---|---|
| **Growth** | | |
| No growth | 207 | 54,6 |
| Positive culture | 172 | 45,4 |
| **Type of Bacteria** | | |
| Gram-positive bacteria | 24 | 14 |
| Gram-negative bacteria | 148 | 86 |
| **Gram-negative bacteria** | | |
| *Escherichia coli* | 73 | 42,4 |
| *Klebsiella pneumoniae* | 29 | 16,9 |
| *Acinetobacter baumannii* | 9 | 5,2 |
| *Enterobacter cloacae complex* | 9 | 5,2 |
| *Pseudomonas aeruginosa,* | 8 | 4,7 |
| *Proteus mirabilis* | 6 | 3,5 |
| **Gram-positive bacteria** | | |
| *Enterococcus faecalis* | 6 | 3,5 |
| *Staphylococcus haemolyticus* | 4 | 2,3 |
| *Staphylococcus epidermidis* | 3 | 1,7 |
| *Staphylococcus saprophyticus* | 3 | 1,7 |
| *Staphylococcus sciuri* | 3 | 1,7 |
| Others (gram-positive and gram-negative) | 19 | 11 |

**Table 3. ESBL prevalence in *E. coli* and *K. pneumoniae***

| Year | Total urine culture | *E. coli* | | | *K. pneumoniae* | | |
|---|---|---|---|---|---|---|---|
| | | Total | Non-ESBL | ESBL | Total | Non-ESBL | ESBL |
| 2022 | 64 | 16 (25.0%) | 8 (50%) | 8 (50%) | 16 (25.0%) | 2 (50%) | 2 (50%) |
| 2023 | 172 | 32 (18.6%) | 15 (47%) | 17 (53%) | 32 (18.6%) | 9 (60%) | 6 (40%) |
| 2024 | 143 | 25 (17.4%) | 12 (48%) | 13 (52%) | 25 (17.4%) | 7 (70%) | 3 (30%) |

Extended-Spectrum Beta-Lactamase (ESBL)

presence of diabetes itself.[18] Malignancy was also identified as a relevant comorbid condition. A history of recurrent UTIs in women was a significant risk factor for bladder cancer. Chronic inflammation induced by persistent infection was known to promote epigenetic alterations in urothelial cells, contributing to carcinogenesis.[19]

In this study, most UTI patients were not on urinary catheters (n = 324; 85,5%). However, on the other hand, patients with urinary catheter prone to have healthcare-associated UTIs compared to patients without catheters. Catheter-associated urinary tract infections (CAUTIs) are capable of causing significant morbidity and mortality in patients.[16] The strict adherence to aseptic insertion procedures, appropriate catheter indications, and proper hygiene-based catheter care are essential strategies to reduce the incidence of catheter-related UTIs.[20]

Laboratory findings presented in **Table 2** showed that the majority of UTI patients had no growth of urine cultures (n = 207; 54,6%). This finding was likely attributable to prior antibiotic use, which may have suppressed bacterial growth in vitro. It was reported that urine samples exhibiting antimicrobial activity or obtained from patients with recent antibiotic exposure were more likely to yield negative culture results. Antibiotics present in the body may inhibit or reduce bacterial proliferation to levels undetectable by standard culture methods.[21] Additionally, negative culture results may have been associated with infections caused by fastidious organisms that require specific growth conditions and are difficult to cultivate using routine laboratory techniques. Certain uropathogens may not grow under standard culture conditions, particularly when bacterial load has been reduced by prior antibiotic therapy.[22] Consequently, patients may remain clinically infected despite negative microbiological findings.

Among culture-positive cases, Gram-negative bacteria predominated (n = 148; 86%), whereas Gram-positive bacteria accounted for 24 cases (14%). This distribution was consistent with other findings that identified Gram-negative organisms particularly *Escherichia coli* as the leading cause of UTIs.[23]

**Table 4. Antibiotic Sensitivity Test for *E coli* and *K. pneumoniae***

| Antibiotic | *E. coli* *S (%) | *K. pneumoniae* *S (%) |
|---|---|---|
| Ampicillin | 40 | 35 |
| Amoxicillin-clavulanate | 50 | 45 |
| Ceftriaxone | 45 | 50 |
| Ceftazidime | 50 | 55 |
| Cefepime | 55 | 60 |
| Piperacillin-tazobactam | 70 | 75 |
| Aztreonam | 50 | 55 |
| Gentamicin | 65 | 70 |
| Amikacin | 90 | 90 |
| Ciprofloxacin | 55 | 55 |
| Levofloxacin | 60 | 60 |
| Nitrofurantoin | 85 | 70 |
| Trimethoprim-sulfamethoxazole | 45 | 40 |
| Imipenem | 100 | 100 |
| Meropenem | 99 | 98 |

*Sensitivity (S)

The predominance of Gram-negative bacteria in UTIs has been attributed to their strong colonisation capacity, possession of adhesion-related virulence factors, and their natural presence in the gastrointestinal tract, which facilitates periurethral contamination. In contrast, Gram-positive organisms are generally less frequently implicated, possibly due to inherent biological characteristics and the lower sensitivity of routine culture methods for detecting certain species, such as *Enterococcus spp.* and *Staphylococcus saprophyticus*.[24]

*Escherichia coli* was the predominant uropathogen identified, accounting for 73 cases (43%). Notably, 38 of these isolates (52%) were extended-spectrum beta-lactamase (ESBL)-producing *E. coli*. The second most common pathogen was *Klebsiella pneumoniae*, identified in 29 cases (17%), of which 11 isolates (38%) were ESBL producers. *E. coli* is a facultative anaerobic Gram-negative bacterium belonging to the genus *Escherichia* and the family *Enterobacteriaceae*. This organism commonly resides as part of the normal intestinal flora and may colonise the periurethral area, thereby serving as a major source of uropathogenic strains.[25] Infection generally occurs via an ascending route, whereby bacteria migrate from the perianal region into the urethra and subsequently the urinary tract.[18] Clinically, *E. coli*-associated UTIs may present with dysuria, increased urinary frequency, fever, and flank or lower back pain when the infection involves the upper urinary tract.[26]

The distribution of ESBL-producing uropathogens across 2022–2024, as seen in **Table 3**, demonstrates a persistently high burden of antimicrobial resistance, particularly in *Escherichia coli*, where ESBL prevalence remained consistently around 50% each year, indicating a stable and endemic resistance pattern in this setting. *Klebsiella pneumoniae* showed a lower but still substantial proportion of ESBL production, with a decreasing trend over time (from approximately 50% to 30%), which may reflect variations in antibiotic exposure, infection control practices, or sample size differences.

Extended-spectrum beta-lactamases (ESBLs) are enzymes produced by Gram-negative bacteria belonging to the Enterobacteriaceae family that play a significant role in multidrug resistance.[27] These enzymes hydrolyse penicillins, first to third generation cephalosporins

such as cefixime and ceftriaxone, and monobactams such as astreonam. Importantly, Amoxicillin and other penicillin derivatives are generally ineffective, as ESBL enzymes hydrolyse these agents even in the presence of β-lactamase inhibitors.

ESBL-producing bacteria strains also associated with recurrent UTIs exhibited enhanced intracellular persistence compared to strains isolated from single infection episodes.[28] Other studies have concluded that fluoroquinolones, including ciprofloxacin and levofloxacin, were no longer optimal as empirical therapy for hospitalised adult UTI patients due to high resistance rates and reduced clinical and cost-effectiveness.

Based on the observed antibiogram in **Table 4**, empirical treatment of UTIs in this setting should avoid penicillins and third-generation cephalosporins due to high resistance associated with ESBL-producing organisms. Carbapenems remain the most reliable option for severe or complicated infections, while amikacin also demonstrates strong activity against both *E. coli* and *Klebsiella pneumoniae*. For uncomplicated cases, nitrofurantoin may still be considered, particularly for *E. coli*.

Infections caused by ESBL-producing organisms have increasingly become a major clinical concern due to limited therapeutic options and the widespread use of broad-spectrum antibiotics, which may contribute to treatment failure. These findings underscore the importance of periodically reassessing empirical antibiotic regimens and selecting agents based on updated local antimicrobial susceptibility patterns.[29,30]

## CONCLUSION

In conclusion, UTIs at Mangusada Badung Hospital were mainly caused by Gram-negative bacteria, particularly *Escherichia coli* and *Klebsiella pneumoniae*, with a quite high proportion of ESBL-producing strains, indicating a significant burden of multidrug-resistant organisms. The infections were most common in young children and older adults and were largely not associated with catheter use. Carbapenems and amikacin retained excellent activity against both *Escherichia coli* and *Klebsiella pneumoniae*, while nitrofurantoin remained effective, particularly for *E. coli*. The high ESBL prevalence highlights the importance of considering resistance patterns in empirical treatment, promoting rational antibiotic use, and reinforcing ongoing local antimicrobial resistance surveillance as the key strategy to improve patient outcomes and limit further MDRO emergence.

## DISCLOSURES

### Funding

This research received no external funding, grant support, or third-party financial assistance. The study was fully self-funded by the researchers.

### Conflict of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper. The authors have no financial or personal relationships with any organisation or individual that could have influenced the study design, data interpretation, or manuscript preparation.

### Author Contribution

MFLN served as the primary author, responsible for study conception, data collection, and analysis. MS acted as the first supervisor and contributing author, guiding study design, data interpretation, and critical manuscript drafting. AAGI served as the second supervisor, contributing to methodological oversight and manuscript review. All authors have read and approved the final version of the manuscript for submission.

### Ethical Considerations

This study received ethical approval from the Health Research Ethics Committee of Mangusada Regional Hospital, Badung Regency, under Decree No. 000.9/12170/RSDM/2025. Patient confidentiality was strictly maintained throughout the study by anonymising all personal identifiers and ensuring that data were used solely for research purposes.

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