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The prevalence of multidrug-resistant non-lactose bacteria in adult patients with urinary tract infections. A cross-sectional study.

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Abstract

Introduction:

Urinary tract infections (UTIs) are common bacterial infections, and the emergence of multidrug-resistant (MDR) non-lactose fermenting (NLF) bacteria has become a major challenge in their management. This study investigated the prevalence of MDR NLF bacteria and identified the predominant bacterial species isolated from UTI patients at a public hospital in Durban, South Africa.

Aim:

To investigate the prevalence of multidrug-resistant non-lactose fermenting (NLF) bacteria in patients diagnosed with UTIs at the National Health Laboratory Service (NHLS) in Durban, South Africa, and to identify the predominant bacterial species.

Methodology:

This retrospective study utilized laboratory data obtained from the NHLS Academic Affairs and Research Management System (AARMS). Adult patients (≥18 years) diagnosed with UTIs caused by MDR NLF bacteria between January and December 2021 were included. Antimicrobial susceptibility profiles were analysed using Microsoft Excel.

Results:

Of the 345 urine culture records reviewed, 46 isolates were identified as NLF bacteria, representing a prevalence of 13.3%. The *Acinetobacter baumannii* complex was the predominant species (39.1%; 18/46), followed by *Pseudomonas aeruginosa* (21.7%; 10/46) and Proteus mirabilis (17.4%; 8/46). Antimicrobial susceptibility testing revealed extensive resistance, with cefotaxime, ceftriaxone, tigecycline, imipenem, and nitrofurantoin demonstrating 100% resistance.

Conclusion:

MDR NLF bacteria were prevalent among UTI patients, with the Acinetobacter baumannii complex being the most frequently isolated species. High levels of antimicrobial resistance were observed among the isolates.

Recommendation:

Continuous surveillance of antimicrobial resistance patterns and strengthened antimicrobial stewardship programmes are recommended to guide appropriate antibiotic use and improve the management of UTIs caused by MDR NLF bacteria.

Keywords: *Urinary tract infections; multidrug resistance; non-lactose fermenting bacteria; Pseudomonas aeruginosa; Acinetobacter baumannii; antimicrobial resistance; Durban; South Africa.*
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Introduction

Non-fermenting Gram-negative bacilli (NFGNB) are a diverse group of strictly aerobic, non-spore-forming bacteria that do not ferment carbohydrates but instead derive energy through oxidative metabolic pathways (Chiu et al., 2015). Although many of these organisms exist as environmental commensals, they have emerged as important opportunistic pathogens and are increasingly implicated in healthcare-

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associated infections worldwide (Chiu et al., 2015; Tamma et al., 2022). NFGNB account for approximately 15% of all Gram-negative bacilli isolated from clinical specimens (Siou et al., 2009). Studies from Nepal and India have reported prevalence rates ranging from 25.6% to 29.6%, while lower prevalence rates of approximately 15% have been documented in Iran and South Africa (Rahbar et al., 2010; Sharma et al., 2014; Bhagava et al., 2015; Von Knorring et al., 2019). Of particular concern is the growing burden of multidrug resistance (MDR), with studies demonstrating extensive drug resistance in 15% of South African isolates and MDR rates exceeding 35% in India (Von Knorring et al., 2019; Soni et al., 2023).

NFGNB comprises several clinically important bacterial species, including *Pseudomonas* spp., *Acinetobacter* spp., *Stenotrophomonas maltophilia*, *Burkholderia cepacia* complex, and other non-lactose fermenting Gram-negative organisms. Among these, *Pseudomonas aeruginosa* and *Acinetobacter baumannii* are recognized as the predominant opportunistic pathogens in healthcare settings due to their virulence, persistence, and remarkable capacity to develop resistance to multiple antimicrobial agents (Chawla et al., 2013). These organisms are increasingly associated with urinary tract infections (UTIs), particularly among hospitalized and immunocompromised patients, where treatment options are becoming progressively limited.

Urinary tract infections are among the most prevalent infectious diseases globally, affecting approximately 150 million individuals each year and contributing substantially to patient morbidity and healthcare burden (Stamm and Norrby, 2001; McCann et al., 2020). UTIs may involve any part of the urinary tract, including the urethra, bladder, ureters, and kidneys (Foxman et al., 2003). Although they can occur in individuals of any age or sex, women are disproportionately affected, accounting for approximately 75–81% of all reported cases (Salvatore et al., 2011; Kubone et al., 2020). This increased susceptibility is largely attributed to female anatomical and physiological characteristics, including a shorter urethra and its proximity to the anus, which facilitate ascending bacterial colonization (Shimoni et al., 2016; Awkally et al., 2022). Studies conducted in Libya and South Africa have consistently demonstrated a higher prevalence of UTIs among females, with young adults aged 18–28 years showing the highest infection rates, potentially associated with increased sexual activity (Khalifa et al., 2014; Kubone et al., 2020).

UTIs are broadly classified as uncomplicated or complicated infections. Uncomplicated UTIs typically occur in healthy, non-pregnant individuals with normal urinary tract anatomy and function, whereas complicated UTIs are associated with structural or functional abnormalities, indwelling catheters, immunosuppression, or other underlying medical conditions that predispose individuals to persistent or recurrent infections (Flores-Mireles et al., 2015; Lichtenberger and Hooton, 2016). Recurrent and complex UTIs are associated with substantial morbidity and may progress to serious complications, including pyelonephritis and bacteraemia (Jarvis, 1996). Clinically, UTIs commonly present with urinary urgency, increased frequency, dysuria, suprapubic pain, haematuria, and, in some cases, cloudy or foul-smelling urine associated with pyuria, leukocyturia, and bacteriuria (Mandokhail et al., 2015; Kaur and Kaur, 2021). Upper UTIs affecting the kidneys may additionally present with fever, chills, nausea, vomiting, and flank pain (Hooton, 2012). However, these symptoms alone are insufficient for definitive diagnosis, emphasizing the importance of microbiological identification of the causative pathogen through urine culture and antimicrobial susceptibility testing (Schmiemann et al., 2010).

The pathogenesis of UTIs begins when uropathogens adhere to the urethral epithelium and ascend into the bladder using specialized adhesins. If immune clearance is unsuccessful, bacterial proliferation and toxin production may facilitate further tissue invasion and inflammation (Mancuso et al., 2023). In complicated UTIs, pathogens frequently form biofilms on indwelling urinary catheters, enhancing bacterial persistence and significantly increasing resistance to antimicrobial therapy. Opportunistic Gram-negative bacteria such as *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, *Proteus mirabilis*, and *Morganella morganii* are particularly important causative agents in these settings (Niall et al., 2011).

Pseudomonas aeruginosa is one of the most frequently isolated Gram-negative pathogens implicated in healthcare-associated infections, causing pneumonia, bloodstream infections, wound infections, and UTIs, particularly in immunocompromised individuals (Stover et al., 2000; Ito et al., 2021). Its pathogenicity is attributed to a combination of host susceptibility and bacterial virulence factors, including fimbriae, flagella, and invasive enzymes that facilitate colonization, tissue penetration, and immune evasion (Sadikot et al., 2005; Driscoll et al., 2007). Of increasing concern is the emergence of carbapenem-resistant *P. aeruginosa*, with resistance mechanisms including porin downregulation, efflux pump overexpression, antibiotic modification, and target site alterations (Livermore, 2002).

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Global surveillance studies indicate significant regional MDR prevalence, particularly in Latin America, Europe, and Africa, highlighting the urgent need for enhanced antimicrobial stewardship and diagnostic surveillance (Lee et al., 2022).

Similarly, *Acinetobacter baumannii* has emerged as one of the most clinically significant multidrug-resistant pathogens worldwide. This non-motile, non-fermentative Gram-negative coccobacillus is associated with pneumonia, meningitis, bacteremia, wound infections, and UTIs, particularly among critically ill patients in intensive care units (Peleg et al., 2008; Rosenthal et al., 2021). Its ability to survive desiccation and persist in hospital environments contributes to its transmission and clinical importance. The *Acinetobacter calcoaceticus-baumannii* complex, which includes *A. baumannii*, accounts for approximately 80% of reported *Acinetobacter* infections and is associated with significant morbidity and mortality (El-Badawy et al., 2021). Although carbapenems and colistin have historically been used as last-resort therapeutic options, increasing resistance to both agents threatens treatment efficacy (Lee et al., 2017).

Proteus mirabilis is another important opportunistic pathogen and a common cause of complicated UTIs, particularly among patients with urinary tract abnormalities or long-term indwelling catheters (Sabbuba et al., 2003). Its clinical manifestations include cystitis, pyelonephritis, prostatitis, and catheter-associated UTIs, with women aged 20–50 years most frequently affected (Nakamura et al., 2019). *Morganella morganii*, although less prevalent, has emerged as a notable opportunistic pathogen with inherent resistance to several β-lactam antibiotics due to the presence of inducible AmpC β-lactamase genes, further complicating treatment (Kohlmann et al., 2018).

The rapid emergence of multidrug resistance among these organisms has become a major global health concern. Excessive and inappropriate use of broad-spectrum antimicrobials, inaccurate diagnosis, and misuse of prescribed antibiotics have accelerated the development of resistance (John and McGowan, 2006). Resistance mechanisms include enzymatic degradation of antibiotics, target site modification, loss of outer membrane porins, and activation of efflux pumps, all of which severely limit available therapeutic options (Fluit et al., 2022). Recent studies have demonstrated alarming resistance rates, with *P. aeruginosa* and *A. baumannii* showing complete resistance to multiple first-line agents, including ampicillin, piperacillin, cefotaxime, and ceftriaxone, while *Proteus mirabilis* and *Morganella morganii* have exhibited substantial resistance to cephalosporins, nitrofurantoin, and β-lactam combinations (Motbainor et al., 2020; Shaaban et al., 2022; Hrbacek et al., 2020).

Given the increasing prevalence of multidrug-resistant NFGNB in UTIs, continuous epidemiological surveillance and antimicrobial susceptibility testing are essential for guiding appropriate empirical therapy and improving patient outcomes. Narrow-spectrum antimicrobial agents, when appropriate, may help reduce selective pressure and slow resistance development. Furthermore, infection prevention measures, antimicrobial stewardship programs, and ongoing resistance monitoring remain critical strategies for controlling the spread of MDR pathogens. Therefore, this study aims to investigate the prevalence and antimicrobial resistance patterns of multidrug-resistant non-lactose fermenting Gram-negative bacteria isolated from UTI patients in Durban, South Africa, thereby contributing to the growing body of evidence needed to inform targeted treatment strategies and strengthen infection control practices.

Research Methodology

Study design

This study employed a cross-sectional retrospective design aimed at investigating urinary tract infections (UTIs) caused by multidrug-resistant non-lactose fermenting bacteria. A quantitative approach was utilized, and retrospective laboratory data were assessed.

Study setting and population.

This retrospective study was conducted using data obtained from a public hospital in Durban, KwaZulu-Natal, South Africa. Laboratory results were retrieved from the National Health Laboratory Service (NHLS) database within the Microbiology Department. The study population comprised adult patients diagnosed with UTIs caused by multidrug-resistant non-lactose fermenting bacteria, based on urine specimens tested between January 2021 and December 2021.

Sampling and sample size

Data sampling was conducted by retrieving laboratory results from the NHLS Academic Affairs and Research Management System (AARMS) for patients of both genders (male and female) diagnosed with UTIs caused by multidrug-resistant non-lactose fermenting bacteria. These

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patients had undergone microscopy, culture, and sensitivity (MCS) testing between January 2021 and December 2021. A total of 345 patient records were included in the study, all from individuals aged 18 years and above.

Eligibility criteria

Inclusion criteria

This study included adult patients (18 years and older), both male and female, who were either inpatients or presented with symptoms of UTI and were diagnosed with multidrug-resistant non-lactose fermenting bacteria, based on NHLS laboratory data.

Exclusion criteria

The study excluded data from paediatric patients diagnosed with UTIs. Duplicate and triplicate laboratory results were also excluded from the analysis.

Efforts to address potential sources of bias: Exclusion criteria.

All eligible laboratory records meeting the inclusion criteria during the study period were included to reduce selection bias.

Duplicate and triplicate records were excluded to prevent overrepresentation of individual cases.

Standardised NHLS laboratory procedures were used for bacterial identification and antimicrobial susceptibility testing to minimise information bias.

Quality control measures routinely implemented by the NHLS laboratory were followed to ensure the reliability of laboratory results.

Patient identifiers were removed to maintain confidentiality and reduce the risk of data handling errors.

Data collection and sample analysis

Study data were obtained from the NHLS AARMS database for the period between January 2021 and December 2021. The results were derived from urine specimens, including midstream urine (MSU) and catheter specimen urine (CSU).

Standard operating procedure for urine culture

Urine culture and antimicrobial susceptibility testing were performed routinely by NHLS laboratories according to standard operating procedures.

1. The first voided urine sample of the morning was preferred for urinalysis, as it is typically more concentrated and preserves formed elements better, reducing the risk of lysis or distortion.
2. A minimum specimen volume of **0.5 mL** was required for testing.
3. Specimens were analysed within **2 hours** of collection.

Quality control

Quality control measures included the following:

- All culture media were inspected for contamination before use.
- Inoculating loops were examined to ensure they were properly shaped (round) and free from dents, bends, corrosion, or residual incinerated material.

Inoculation of culture media for urine specimens

A flamed and cooled 1/1000 mL wire loop (for MSU) and 1/100 mL wire loop (for CSU) were immersed just below the surface of a well-mixed, uncentrifuged urine specimen. A loopful of the specimen was then transferred onto a labelled Cysteine Lactose Electrolyte Deficient (CLED) agar plate as the initial inoculum. The specimen was streaked across the entire plate to isolate single colonies without re-flaming the loop. Subsequently, a loopful of urine was transferred onto the paper disc located on a labelled segment of the AMS agar plate. Both the CLED and AMS agar plates were incubated at 37°C for 24 hours.

Interpretation of colony count

Colony counts were interpreted as follows:

- **$<10^4$ CFU/mL** (equivalent to 1–9 colonies): *Not significant growth*
- **10^4–10^5 CFU/mL** (equivalent to 10–100 colonies): *Doubtful significant growth*
- **$>10^5$ CFU/mL** (equivalent to >100 colonies): *Significant growth*

Statistical analysis

Data were analysed using Microsoft Excel version XX. Descriptive statistics, including frequencies, percentages, tables, and graphs, were used to summarise bacterial species distribution and antimicrobial resistance patterns.

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Ethical considerations

Ethical approval for this study was obtained on 20 January 2025 from the Research Ethics Committee of Mangosuthu University of Technology. Approval was also granted by the National Health Laboratory Service (NHLS) Academic Affairs and Research Management System (AARMS) to access and utilise patient laboratory results. The ethical clearance number is: RD5/15/2025

Informed consent was not required, as the study involved the analysis of retrospective laboratory data. Patient confidentiality was strictly maintained throughout the study. No patient names or identifying information were used, and access to the data was limited to the researcher and the supervisor.

Research Results/ findings

A total of 399 patients' data results were received from NHLS AARMS from January 2021 to December 2021. After applying the filtration criteria, the dataset was refined to 345 patient records. Of these, only 46 met the eligibility requirements and were included in the final analysis. The study population comprised both males and females, with 11 (23.9%) males and 35 (76.1%) females.

Table 1. Statistical data of the gender demographic

Gender	Males	Females
Total number	11 (23.9%)	35 (76.1%)

Table 1: Descriptive summary table

Bacterial species	Number of Isolates	Prevalence (%)
1. Acinetobacter baumannii complex	18	39.1
2.Pseudomonas aeruginosa	10	21.7
3. Proteus mirabilis	8	17.4
4.Providencia rettgeri	3	6.5
5. Acinetobacter baumannii	2	4.3
6. Morganella morganii	1	2.2
7. Pseudomonas luteola	1	2.2
8.Pseudomonas putida	1	2.2
9. Stenotrophomonas maltophilia	1	2.2
10. Acinetobacter haemolyticus	1	2.2
Total number of Isolated NLFs	46	

This table summarises the prevalence of multidrug non-lactose fermenting organisms and the number of isolated bacterial species that were obtained from patients with UTIs in Durban, KwaZulu-Natal, South Africa. A total of 46 isolates of NLFs were retained, out of 345 data results retrieved from NHLS AARMS. The prevalence of NLF was 13.3%.

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Figure 1: Distribution of non-lactose fermenting bacteria in patients with UTI.

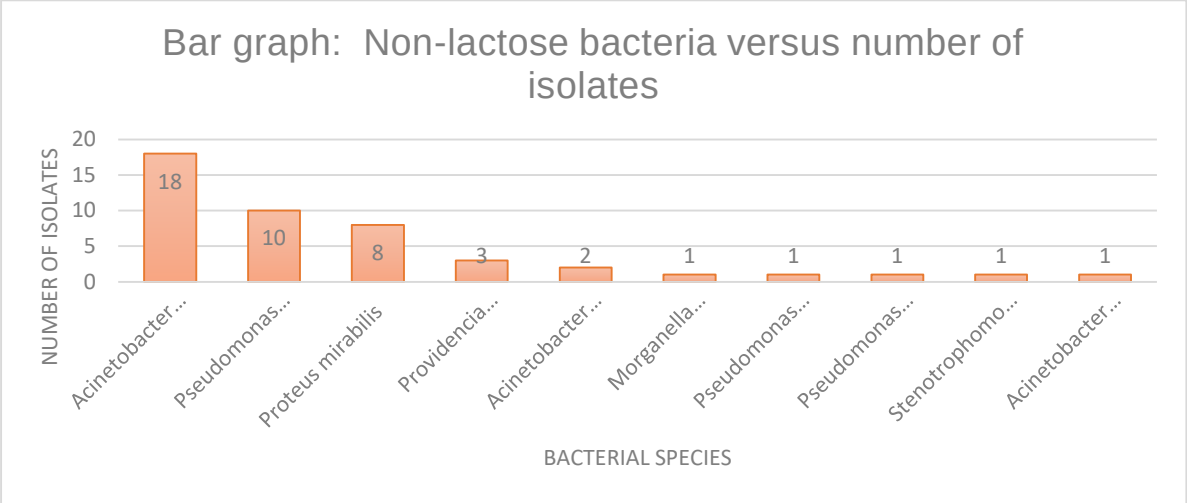

Figure 1 shows the distribution of non-lactose fermenting bacteria identified in patients with UTI based in Durban, KwaZulu-Natal, South Africa, between January 2021 and December 2021. NLF microorganisms are represented according to the number of isolates.

Figure 2: Prevalence of non-lactose fermenting bacteria in patients with UTI.

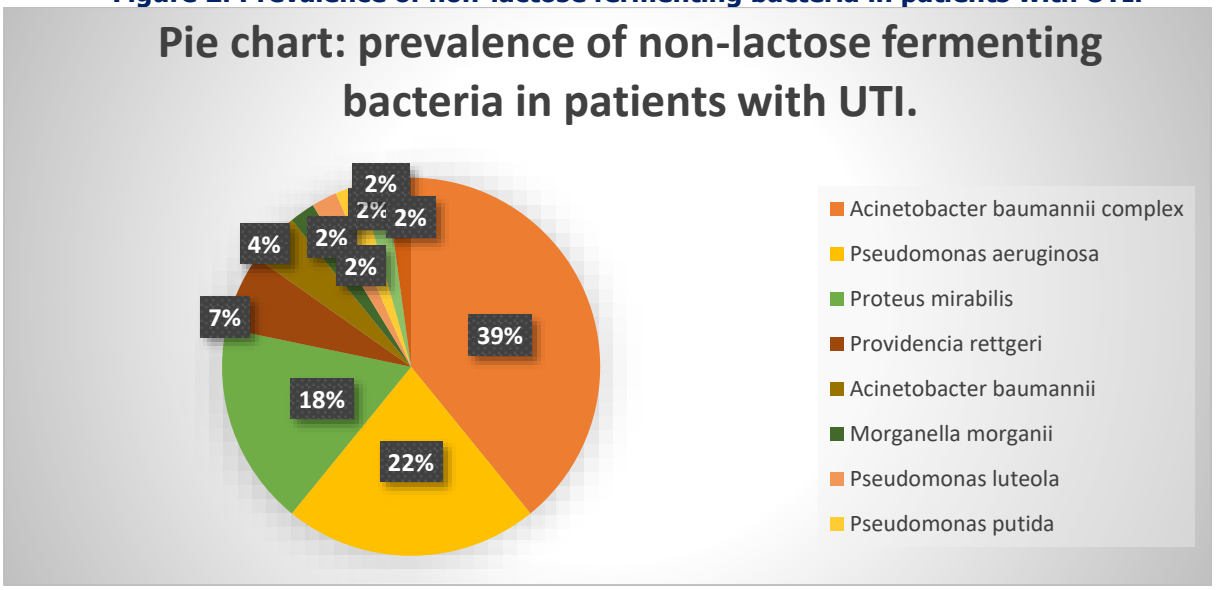

Figure 2 depicts the prevalence in percentages of NLF pathogens in patients with UTI, based in Durban, KwaZulu-Natal, South Africa, from January 2021 to December 2021.

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Antibiotic susceptibility test

AK: Amikacin
AMC: Amoxicillin clavulanic acid
AMP_AML: Ampicillin amoxicillin
FEP: Cefepime
CTX: Cefotaxime
FOX: Cefoxitin
CXM: Cefuroxime
CAZ: Ceftazidime
CRO: Ceftriaxone
Cephalexin
CIP: Ciprofloxacin
COL: Colistin
ETP: Ertapenem
GEN: Gentamicin
IMI: Imipenem
MEM: Meropenem
NIT: Nitrofurantoin
TZP: Piperacillin tazobactam
TGC: Tigecycline
TMS: Trimethoprim sulfamethoxazole

Organism Identification

Acinetobacter baumannii complex isolated from patient A1-A18 = 18 patients
Pseudomonas aeruginosa isolated from patient B1-B10 = 10 patients
Proteus mirabilis isolated from patient C1-C8 = 8 patients
Providencia rettgeri isolated from patient D1-D3 = 3 patients
Acinetobacter baumannii isolated from patient E1-E2= 2 patients
Morganella morganii isolated from patient F1 = 1 patient
Pseudomonas luteola isolated from patient G1 = 1patient
Pseudomonas putida isolated from patient H1 = 1patient
Stenotrophomonas maltophilia isolated from patient I1 = 1 patient
Acinetobacter haemolyticus isolated from patient J1 = 1 patient

Table 2Antimicrobial susceptibility patterns of individual isolates and antimicrobial agents used.

Name of the organisms	Group ID	NIT	TGC	CRO	FOX	CXM	ETP	AK	COL	Cephalexin
Acinetobacter baumannii complex	A1	-	S	R	-	-	-	S	S	-
	A2	-	S	R	-	-	-	-	S	-
	A3	-	S	R	-	-	-	-	S	-
	A4	-	S	R	-	-	-	S	S	-
	A5		S	R	-	-	-	-	S	-
	A6	-	S	R	-	-	-	-	S	-
	A7	-	S	R	-	-	-	-	S	-
	A8	-	S	R	-	-	-	-	S	-
	A9	-	I	R	-	-	-	-	S	-
	A10	-	S	R	-	-	-	-	S	-
	A11	-	S	R	-	-	-	-	S	-
	A12	-	S	R	-	-	-	-	S	-
	A13	-	S	R	-	-	-	-	S	-
	A14	-	S	R	-	-	-	-	S	-
	A15	-	S	R	-	-	-	-	S	-
	A16	-	S	R	-	-	-	-	S	-
	A17	-	S	R	-	-	-	-	S	-
	A18	-	S	R	-	-	-	-	S	-

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Name of the organisms	Patient ID	NIT	TGC	CRO	FOX	CXM	ETP	AK	COL	Cephalexin
Proteus mirabilis	C1	R	R	S	S	S	S	S	-	S
	C2	R	I	S	S	S	S	S	-	S
	C3	R	I	S	S	S	S	S	-	S
	C4	R	R	S	S	S	S	S	-	S
	C5	R	R	S	S	S	S	I	-	S
	C6	R	R	S	S	S	S	S	-	S
	C7	R	R	S	S	S	S	S	-	S
	C8	R	S	S	R	S	S	S	-	S

Name of the organisms	Patient ID	NIT	TGC	CRO	FOX	CXM	ETP	AK	COL	Cephalexin
Pseudomonas aeruginosa	B1	-	R	R	-	-	-	S	S	-
	B2	-	R	R	-	-	-	S	S	-
	B3	-	R	R	-	-	-	S	S	-
	B4	-	R	R	-	-	-	S	S	-
	B5	-	R	R	-	-	-	S	S	-
	B6	-	R	R	-	-	-	S	S	-
	B7	-	R	R	-	-	-	S	S	-
	B8	-	R	R	-	-	-	S	R	-
	B9	-	R	R	-	-	-	S	S	-
	B10	-	R	R	-	-	-	S	S	-

Name of the organisms	Patient ID	NIT	TGC	CRO	FOX	CXM	ETP	AK	COL	Cephalexin
Acinetobacter baumannii	E1	-	S	R	-	-	-	-	S	-
	E2	-	S	R	-	-	-	R	S	-

Name of the organisms	Patient ID	NIT	TGC	CRO	FOX	CXM	ETP	AK	COL	Cephalexin
Providencia rettgeri	D1	R	R	R	R	R	R	S	-	R
	D2	R	R	R	R	R	R	I	-	-
	D3	S	S	S	S	S	S	S	-	R

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Name of the organism	Patient ID	NIT	TGC	CRO	FOX	CXM	ETP	AK	COL	Cephalexin
Morganella morganii	F1	R	R	R	I	R	S	S	-	R

Name of the organism	Patient ID	NIT	TGC	CRO	FOX	CXM	ETP	AK	COL	Cephalexin
Pseudomonas luteola	G1	-	S	S	-	-	-	S	-	-

Name of the organism	Patient ID	NIT	TGC	CRO	FOX	CXM	ETP	AK	COL	Cephalexin
Stenotrophomonas maltophillia	I1	-	-	-	-	-	-	-	-	-

Name of the organism	Patient ID	NIT	TGC	CRO	FOX	CXM	ETP	AK	COL	Cephalexin
Pseudomonas putida	H1	-	I	I	-	-	-	S	-	-

Name of the organism	Patient ID	NIT	TGC	CRO	FOX	CXM	ETP	AK	COL	Cephalexin
Acinetobacter haemolyticus	J1	-	S	S	-	-	-	S	S	-

Discussion

This study aimed to determine the prevalence of multidrug-resistant non-lactose fermenting bacteria among patients with urinary tract infections (UTIs) and to assess their antimicrobial resistance patterns using retrospective laboratory data. The findings contribute to the existing body of knowledge regarding antimicrobial resistance patterns observed among UTI patients in South Africa and highlight the growing clinical importance of multidrug-resistant non-lactose fermenting pathogens.

Prevalence of UTIs according to gender

In the present study, the results revealed that 76.1% of patients diagnosed with UTIs were female, while 23.9% were male. Therefore, females were the population most affected by UTIs compared to males. These findings are consistent with previous studies conducted by Khalifa et al. (2014), where a higher prevalence of UTIs was also observed among females. In their study involving 582 patients enrolled at Sobrata Hospital, 51.72% were female, and 11.34% were male. Furthermore, in the same study, 926 patients were enrolled from a clinic in Algmel City, where 38.2% were female and 18.5% were male (Khalifa et al., 2014). Similarly, Al-Awkally et al. (2022) reported comparable findings, indicating that UTIs were more prevalent among females than males. This increased susceptibility may be attributed to anatomical and physiological factors, including the shorter female urethra and its closer proximity to the anus, which facilitate bacterial entry into the urinary tract.

4.3 Prevalence and antimicrobial susceptibility patterns of predominant non-lactose fermenting uropathogens.

The present study revealed that non-lactose fermenting organisms constituted 13.3% of all UTI isolates, with the *Acinetobacter baumannii* complex identified as the predominant pathogen (39.1%). These findings indicate that multidrug-resistant non-lactose fermenting organisms continue to act as opportunistic pathogens that often go undetected yet contribute substantially to the increasing burden of nosocomial infections, particularly among patients with UTIs.

The *Acinetobacter baumannii* complex exhibited a high level of multidrug resistance, showing complete resistance

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to cefotaxime/ceftriaxone (100%) and marked resistance to cefepime (88.9%), ceftazidime (88.9%), ciprofloxacin (88.9%), piperacillin-tazobactam (88.9%), and trimethoprim-sulfamethoxazole (88.9%). However, all isolates remained susceptible to colistin (100%). These findings highlight the concerning emergence of multidrug-resistant *A. baumannii* as an important urinary pathogen, limiting the effectiveness of commonly used empirical antimicrobial agents in UTI management. The observed susceptibility to colistin suggests that it remains a valuable last-line treatment option.

The second most prevalent non-lactose fermenting pathogen identified was *Pseudomonas aeruginosa*, accounting for 21.7% of isolates. The *P. aeruginosa* isolates exhibited complete resistance to cefotaxime/ceftriaxone (100%) and tigecycline (100%), indicating limited efficacy of these antimicrobial agents. Conversely, the isolates demonstrated complete sensitivity to amikacin (100%) and gentamicin (100%), suggesting that aminoglycosides remain effective therapeutic options for UTIs caused by *P. aeruginosa* in hospital settings.

Lastly, *Proteus mirabilis* had a prevalence of 17.4%. The isolates demonstrated complete resistance to imipenem (100%) and nitrofurantoin (100%), suggesting limited therapeutic value of these agents. In contrast, complete sensitivity was observed to cefepime (100%), cefotaxime/ceftriaxone (100%), ceftazidime (100%), ciprofloxacin (100%), cefuroxime (100%), piperacillin-tazobactam (100%), ertapenem (100%), and cephalexin (100%). These findings suggest that a broad range of β-lactam and fluoroquinolone antimicrobial agents remain highly effective against *P. mirabilis*, providing several options for both empirical and targeted treatment. However, the resistance observed to imipenem and nitrofurantoin highlights the need for continuous local antimicrobial surveillance.

Clinical and diagnostic implications

To mitigate the potential complications associated with UTIs and prevent the misclassification of infections as multidrug-resistant, early urine testing is recommended for patients presenting with clinical symptoms of UTI. Prompt diagnosis facilitates the identification of the causative pathogen and enables the administration of targeted and appropriate antimicrobial therapy. Therefore, routine microscopic examination, culture, and antimicrobial susceptibility testing should be incorporated into standard diagnostic practice.

This study successfully determined the antimicrobial susceptibility profiles of non-lactose fermenting pathogens causing UTIs and identified the *Acinetobacter baumannii* complex as the predominant species. These findings underscore the importance of early detection, accurate microbial identification, and evidence-based antimicrobial use in improving patient outcomes and controlling the spread of hospital-acquired infections.

Generalisability of the study

Although this study was conducted at a single public hospital in Durban, KwaZulu-Natal, the findings may apply to similar public healthcare settings managing urinary tract infections caused by multidrug-resistant non-lactose fermenting organisms, particularly within South Africa and other resource-limited settings. The antimicrobial resistance patterns identified in this study provide valuable local epidemiological data that may assist clinicians and microbiology laboratories in guiding empirical treatment decisions and strengthening antimicrobial stewardship interventions. However, caution should be exercised when generalising the findings to broader populations, as resistance patterns may vary across different hospitals, provinces, and patient populations due to differences in healthcare practices, antimicrobial prescribing behaviours, and infection prevention measures. Further multicentre studies involving larger and more diverse populations are recommended to improve the external validity and broader applicability of these findings.

Conclusion

This study has demonstrated that effective collaboration among scientists, healthcare professionals, and academic researchers is essential to address the evolving patterns of antimicrobial resistance. The observed resistance profiles of common pathogenic organisms such as *Acinetobacter baumannii* and *Pseudomonas aeruginosa* highlight the need for ongoing surveillance and integrated, coordinated strategies to mitigate this growing public health threat.

Limitations

This study faced several limitations that should be acknowledged.

Firstly, the sample size was relatively small due to the occurrence of duplicate and triplicate isolates, which reduced the number of unique samples available for analysis.

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Secondly, the study was conducted over 12 months at a single hospital in Durban, which limits the generalisability of the findings to a broader population, as participants were drawn from a limited geographic area.

Additionally, the retrospective design of the study constrained access to demographic data. Variables such as race and age were inconsistently recorded, and in some cases, the accuracy of the age data was questionable.

Recommendations

It is recommended that stricter antimicrobial stewardship programmes be implemented to minimise the unnecessary use of broad-spectrum antibiotics through the regular updating of antibiotic guidelines based on local resistance patterns. Routine antimicrobial susceptibility testing should be encouraged before prescribing antimicrobial agents for UTIs.

In addition, stricter adherence to infection prevention and control practices, including proper hand hygiene, sterilisation protocols, and appropriate disposal of healthcare waste, is essential to prevent the environmental spread of resistant bacteria.

Health education programmes should also be implemented to inform patients about the importance of completing prescribed antibiotic courses and avoiding self-medication, thereby reducing the risk of developing and transmitting multidrug-resistant infections.

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Acronyms and abbreviations

NFGNB – Non-Fermenting Gram-Negative Bacilli
UTI – Urinary tract infections
MDR – Multi-Drug Resistance
AST – Antimicrobial susceptibility tests
KZN – KwaZulu-Natal
NHLS – National Health Laboratory Service
AARMS – Academic Affairs Research Management System
SOP – Standard Operating Procedure
P. aeruginosa – *Pseudomonas aeruginosa*
A. baumannii – *Acinetobacter baumannii*
P. mirabilis – *Proteus mirabilis*
M. morganii – *Morganella morganii*
ABC – *Acinetobacter baumannii* complex

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Conflict of Interest

The authors declare that there are no conflicts of interest regarding the publication of this study. This study was conducted as part of a student research project undertaken in fulfilment of university training requirements and under a Memorandum of Understanding (MoU) between the university and the industry partner. No external funding was received.

Author contributions

The student researcher conceptualised the study, conducted the literature review, collected and analysed the data, interpreted the findings, and drafted the manuscript. The supervisor provided guidance on the study design, methodology, data interpretation, manuscript review, and overall supervision of the research project. All authors reviewed and approved the final manuscript.

Data availability

The data supporting the findings of this study are contained within this manuscript. The underlying NHLS dataset is not publicly available due to confidentiality requirements and the terms of the Memorandum of Understanding (MoU).

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