


Antibiotic Resistance and Resistant Genes among Isolates from Diabetic Patients with Urinary Tract Infections at Benjamin Mkapa Hospital: A Cross-Sectional Study



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Abstract:

Introduction: The emergence of antibiotic-resistant bacteria is a growing public health concern that complicates the prevention, control, and management of bacterial infections and has become a global challenge. Urinary tract infections (UTIs), which are among the most common bacterial infections worldwide, are increasingly associated with antibiotic-resistant pathogens. The present study focused on determining both the phenotypic and genotypic characteristics of antimicrobial-resistant bacteria isolated from diabetic patients with UTIs at Benjamin Mkapa Hospital in the Dodoma region, Tanzania.

Methods: This hospital-based cross-sectional study was conducted at Benjamin Mkapa Hospital (BMH) in Dodoma, Tanzania. Midstream urine samples were collected and inoculated onto blood agar and Cystine-Lactose-Electrolyte-Deficient (CLED) agar. Antibiotic susceptibility testing (AST) was performed using the Kirby-Bauer disc diffusion method, and results were interpreted according to the 2024 Clinical and Laboratory Standards Institute (CLSI) guidelines. Data were expressed as percentages and proportions. Sequencing results were analysed using the BLAST online search tool.

Results: Out of 419 cultured samples, 261 (62.3%) showed significant bacterial growth. The isolates included coagulase-negative staphylococci (CoNS), *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Staphylococcus aureus*. The majority of the isolates were susceptible to amikacin (97%), piperacillin-tazobactam (72%), imipenem (78%), and meropenem (89%). The following genes were detected among the isolates: blaCTX-M-15, blaOXA-1, blaNDM-5, blaTEM-1B, aac(3)-IId, qnrS1, aacA-aphD, blaSHV, and blaTEM.

Discussion: This study investigated antimicrobial resistance patterns and associated resistance genes among uropathogens isolated from diabetic patients with UTIs at Benjamin Mkapa Hospital, Dodoma. Out of 419 samples, 261 (62%) yielded bacterial isolates, with *Escherichia coli* being the most prevalent. All isolates were multidrug-resistant, showing high resistance to commonly used antibiotics such as ceftazidime, amoxicillin/clavulanic acid, ciprofloxacin, and ampicillin, but retained susceptibility to meropenem, amikacin, and imipenem. Molecular analysis revealed the presence of key resistance genes, including blaNDM-5, blaCTX-M-15, and qnrS1. These results indicate a high burden of antimicrobial resistance among diabetic patients with UTIs and emphasize the importance of integrating molecular diagnostics into routine laboratory practice.

Conclusion: Screening for antibiotic resistance genes in parallel with antibiotic susceptibility testing is important for the control and management of resistant isolates.

Keywords: Antibiotic resistance, Diabetes, Urinary tract infection (UTI), Resistance genes, Antibiotics.

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1. INTRODUCTION

Antimicrobial resistance has become a serious public health concern, with the transmission of resistance genes and resistant bacteria being a major focus of global attention [1]. Onanuga *et al.* (2020) reported that multidrug-resistant bacteria pose a significant health threat, complicating the treatment of urinary tract infections due to the limited availability of effective antibiotics. They further noted that urinary tract infections are among the most commonly diagnosed bacterial infections in hospital settings, resulting in substantial antibiotic prescribing following clinical consultations [2].

The widespread use of antibiotics for urinary tract infections (UTIs) has accelerated the emergence of antimicrobial resistance, contributing to increased morbidity, prolonged hospital stays, and higher treatment costs, thereby constituting a major public health concern [1, 2]. UTIs are particularly common among diabetic patients, affecting nearly all age groups and occurring at a much higher rate than among non-diabetic individuals [3].

Many studies have investigated antimicrobial resistance primarily through phenotypic characterisation, often overlooking the contribution of genetic determinants to resistance. Therefore, the present study aimed at determining the phenotypic and genotypic characteristics of antimicrobial-resistant bacteria extracted from diabetic patients with UTIs at Benjamin Mkapa Hospital in the Dodoma region, Tanzania.

2. METHODOLOGY

2.1. Study Design and Setting

This was a hospital-based cross-sectional study conducted from May to December 2024 at Benjamin Mkapa Hospital. Midstream urine samples were collected from diabetic patients with urinary tract infections (UTIs) for culture and sensitivity testing. Laboratory investigations were performed at the University of Dodoma Teaching Laboratory. All isolated bacteria were analyzed for identification and antimicrobial susceptibility.

2.2. Eligibility

2.2.1. Inclusion Criteria

Patients aged 30 years and above with type 1 or type 2 diabetes and diagnosed with urinary tract infections (UTIs) were included in the study.

2.2.2. Exclusion Criteria

Diabetic patients who did not provide consent and those without a diagnosis of urinary tract infection (UTI) were excluded from the study.

2.3. Sample Size and Sampling Techniques

The study involved 399 individuals, as determined by the formula (1) presented below. The sample size was calculated based on the study population, defined as the annual number of patients attending the hospital across all departments (252,000).

$$n = \frac{N}{1 + Ne^2}$$

Where;

N stands for the study population.

e stands for precision level.

95% confidence level of 0.05 was considered.

$$n = \frac{252000}{1 + 252000 \times 0.05^2}$$

$$n = 399.3660856$$

$$n = 399$$

Twenty participants (5%) were non-respondents, resulting in a total sample size of 419. To recruit the estimated sample size, a convenience sampling technique was used.

2.4. Data and Specimen Collection

Demographic details and related factors were collected using a validated and pre-tested questionnaire. All participants were given instructions on how to collect midstream urine (MSU) for culture and susceptibility testing. The collected urine samples were sent to the laboratory for investigation and processed immediately. When immediate processing was not feasible, samples were stored at cold temperatures until culture to minimize overgrowth and preserve organism viability.

2.5. Isolation and Identification of Bacteria

After obtaining written informed consent, socio-demographic characteristics were collected using pre-tested questionnaires. Midstream urine samples were obtained from diabetic patients aged 30 years or older with urinary tract infections (UTIs) for bacterial culture and identification. The urine samples were inoculated onto CLED and blood agar plates and incubated at 37°C for 24 hours [4]. Significant bacteriuria was defined as $\geq 10^5$ CFU/mL of a single bacterial species [4]. Isolated bacteria were identified based on colony morphology, Gram staining, and biochemical tests, including catalase, coagulase, sulfide indole motility (SIM), Kligler iron agar (KIA), citrate, oxidase, and urease tests.

2.5.1. Gram Staining

Gram-positive bacteria appeared purple to bluish, while Gram-negative bacteria appeared reddish to pinkish.

2.5.2. Catalase Test

A drop of hydrogen peroxide was placed on a glass slide, and bacterial colonies were introduced using an applicator stick. A positive reaction was indicated by the appearance of bubbles within 20 seconds; a negative reaction showed no bubbles.

2.5.3. Coagulase Test

Bacterial colonies were mixed with plasma on a glass slide. A positive reaction was indicated by the presence of clots, while a negative reaction was indicated by the absence of clots.

2.5.4. Sulfide Indole Motility (SIM) Test

SIM medium was inoculated by stabbing colonies and incubated at 37°C for 18–24 hours. Hydrogen sulfide production was indicated by the blackening of the media. Indole production was indicated by a red ring on top of the media after the addition of Kovac's reagent. Motility was indicated by diffuse growth away from the stab line; non-motile organisms grew only along the stab line.

2.5.5. Kligler Iron Agar (KIA) Test

KIA was inoculated by stabbing the butt and streaking the slant, then incubated at 37°C for 18–24 hours. Acidic or alkaline reactions were determined by color changes on the slant and butt. Hydrogen sulfide production was indicated by black precipitate formation.

2.5.6. Citrate Test

The medium was inoculated by stabbing the butt and streaking the slant, then incubated at 37°C for 18–24 hours. A positive reaction was indicated by a color change from green to blue, while a negative reaction remained green.

2.5.7. Oxidase Test

A filter paper in a Petri dish was moistened with oxidase reagent, and bacterial colonies were smeared onto the paper using a sterile plastic loop. A positive reaction was indicated by blue coloration within 60 seconds; a negative reaction showed no color change.

2.5.8. Urease Test

The medium was inoculated by stabbing the butt and streaking the slant, then incubated at 37°C for 18–24 hours. A positive reaction was indicated by a color change from yellow to pink, while a negative reaction remained yellow.

2.6. Susceptibility Testing of Antimicrobials

A suspension of isolated microorganisms was prepared, and turbidity was adjusted to match a 0.5 McFarland turbidity standard. Antimicrobial susceptibility testing (AST) was performed using the Kirby-Bauer disk diffusion method. The inoculated Mueller-Hinton agar (MHA) plates were incubated at 37°C for 16–18 hours. The following antimicrobial agents were tested based on local treatment guidelines: amoxicillin/clavulanic acid (20/10 µg), ampicillin (10 µg), gentamicin (10 µg), ceftazidime (30 µg), piperacillin/tazobactam (100/10 µg), ceftriaxone (30 µg), ciprofloxacin (5 µg), nitrofurantoin (100 µg), cefoxitin (30 µg), amikacin (30 µg), meropenem (10 µg), and imipenem (10 µg). All antibiotic disks were obtained from Oxoid UK Ltd. Reference strains of *Staphylococcus aureus* (ATCC 25923), *Escherichia coli* (ATCC 25922), *Klebsiella pneumoniae* (ATCC 700603), and *Pseudomonas aeruginosa* (ATCC 27853) were used to validate antimicrobial susceptibility testing. Zones of inhibition were measured and reported in millimeters (mm) according to the 2024 CLSI guidelines.

2.7. DNA Extraction for Molecular Techniques

DNA extraction for molecular analysis was performed according to the protocol described by Dashti *et al.* (2009) using the Genra Puregene DNA Isolation Kit. Five microliters (5 µL) of extracted DNA was mixed with 45 µL of pre-aliquoted Reddy-Load PCR Mix, containing 1.25 units of Taq DNA polymerase, 75 mM Tris-HCl (pH 8.8), 20 mM (NH₄)₂SO₄, 1.5 mM MgCl₂, 0.01% (v/v) Tween 20, 0.2 mM of each deoxynucleotide triphosphate (dATP, dCTP, dGTP, and dTTP), and picomoles of each primer. Primers for detection of antimicrobial resistance genes - version 06.11.2018 were used (**Appendix 1**). PCR amplification was performed in a programmable thermal cycler [5]. The reaction included an initial denaturation at 95°C for 5 minutes, followed by 32 cycles of denaturation at 94°C for 1 minute, annealing at 57°C for 1 minute, and extension at 70°C for 1 minute, with a final extension at 72°C for 10 minutes.

PCR products were purified by ethanol precipitation. Twenty-five microliters (25 µL) of template suppression reagent (TSR) was added to the pellet, mixed, and heated at 95°C for two minutes. For sequencing PCR, 1 µL of each PCR product was mixed with 3.2 picomoles of either the forward or reverse primer and 8 µL of dye-terminator-ready reaction mix. Sequencing PCR was performed in a thermal cycler programmed for 30 cycles of 96°C for 20 seconds, 50°C for 20 seconds, and 60°C for four minutes. The PCR products were purified again and stored on ice until sequencing using an automated DNA sequencer [5]. Representative agarose gel electrophoresis of PCR products from *E. coli* isolates carrying the various tested resistant genes is shown in **Appendix 2**.

2.8. Data Analysis

Data analysis was performed using the Statistical Package for the Social Sciences (SPSS), version 20. Descriptive data were presented as proportions and percentages, while continuous data were summarized using the median and interquartile range (IQR). Sequencing results were analyzed using BLAST, an online sequence alignment tool.

2.9. Ethical Considerations

Ethical approval for the study (Ref. No. OUT/PG202000391) was granted by the Open University of Tanzania, and a certificate of ethical clearance (Ref. No. NIMR/HQ/R.8a/Vol.IX/4640) was obtained from the National Institute for Medical Research (NIMR), Tanzania. Participation in this study was entirely voluntary, and written informed consent was obtained from all participants before enrollment.

3. RESULTS

Midstream urine samples were collected from 419 diabetic patients diagnosed with urinary tract infections. Of these, 261 (62.3%) showed significant bacterial growth, whereas 158 (37.7%) showed non-significant growth. The majority of participants were female (219, 52%). Most participants were aged 50–59 years (160, 38%), with a

median age of 58 years (IQR: 52-65). Primary school education was the most common level of education (167, 40%), and most participants were self-employed (178, 43%). Nearly half of the participants belonged to the lower-income category (207, 49%).

The bacterial isolates included *Escherichia coli*, coagulase-negative staphylococci (CoNS), *Staphylococcus aureus*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa*. Susceptibility to amikacin, meropenem, piperacillin-tazobactam, and imipenem was 97%, 89%, 72%, and 78%, respectively. Varying degrees of resistance were observed for ampicillin (61%), ceftriaxone (39%), ceftazidime (92%), cefoxitin (41%), ciprofloxacin (64%), amoxicillin/clavulanic acid (65%), gentamicin (47%), and nitrofurantoin (64%) (Table 1).

Out of 261 cultured samples with significant growth, *Escherichia coli* (109, 41.8%) was the most prevalent bacterial isolate, followed by *Staphylococcus aureus* (79, 30.3%), coagulase-negative staphylococci (CoNS) (36, 13.8%), *Pseudomonas aeruginosa* (22, 8.4%), and *Klebsiella pneumoniae* (15, 5.7%). Varying resistance patterns were observed among the isolates to the tested

antibiotics. *E. coli* showed high resistance to ceftazidime (88%), amoxicillin/clavulanic acid (73%), ciprofloxacin (60%), and ampicillin (59%). CoNS exhibited 100% resistance to ampicillin, cefoxitin, amikacin, amoxicillin/clavulanic acid, and ceftazidime. *S. aureus* showed high resistance to ceftazidime (100%), ampicillin (91%), ciprofloxacin (82%), and nitrofurantoin (82%). *K. pneumoniae* was highly resistant to nitrofurantoin and gentamicin (both 100%) and ciprofloxacin (53%). *P. aeruginosa* exhibited high resistance to ampicillin, nitrofurantoin, and ceftazidime (all 100%), as well as ciprofloxacin (68%) (Table 2).

The isolates exhibited multidrug resistance to the tested antibiotics, which was defined as resistance to two or more antibiotics. Among the 109 *E. coli* isolates, 25 (23%) were resistant to six of the tested antibiotics. Of the 79 *S. aureus* isolates, 28 (35%) were resistant to more than six antibiotics. Among 36 coagulase-negative staphylococci (CoNS) isolates, 21 (58%) were resistant to five antibiotics. Of the 15 *K. pneumoniae* isolates, 9 (60%) were resistant to three antibiotics, and among 22 *P. aeruginosa* isolates, 11 (50%) were resistant to three antibiotics (Table 3).

Table 1. Overall susceptibility patterns of isolates from diabetic patients who were diagnosed with UTI (N=261).

Antibiotics	Sensitive n (%)	Intermediate n (%)	Resistant n (%)
AM(10 µg)	80(31)	0(0)	159(61)
FOX (30µg)	131(50)	0(0)	108(41)
AK(30µg)	254(97)	0(0)	7(3)
CIP(5 µg)	87(33)	7(3)	167(64)
NIT (100 µg)	65(25)	28(11)	168(64)
CN(10 µg)	109(42)	29(11)	123(47)
PIT(100/10µg)	189(72)	29(11)	43(17)
AMC (20/10µg)	92(35)	0(0)	169(65)
CAZ(30 µg)	7(2)	15(6)	239(92)
CRO(30 µg)	110(42)	50(19)	101(39)
MRP(10µg)	232(89)	7(3)	22(8)
IPM (10 µg)	203(78)	29(11)	29(11)

Abbreviations: AM, Ampicillin; FOX, Cefoxitin; CN, Gentamycin; AK, Amikacin; CIP, Ciprofloxacin; PIT, Piperacillin-Tazobactam; MRP, Meropenem; AMC, Amoxicillin/Clavulanic; CAZ, Ceftazidime; CRO, Ceftriaxone; NIT, Nitrofurantoin; IPM, Imipenem; µg, Microgram.

Table 2. Overall proportion of isolates resistant to tested antibiotics.

Isolates	AM n(%)	FOX n(%)	AK n(%)	CIP n(%)	NIT n(%)	CN n(%)	PIT n(%)	AMC n(%)	CAZ n(%)	CRO n(%)	MRP n(%)	IPM n(%)
<i>E.coli</i> (N=109)	65(59)	36(33)	0(0)	65(60)	44(41)	51(47)	36(33)	80(73)	95(88)	51(47)	15(14)	22(20)
CoNS (N=36)	36(100)	36(100)	36(100)	14(39)	22(62)	14(39)	0(0)	36(100)	36(100)	14(39)	0(0)	0(0)
<i>S.aureus</i> (N=79)	72(91)	36(46)	7(9)	65(82)	65(82)	36(46)	7(9)	36(46)	79(100)	29(37)	7(9)	7(9)
<i>K.pneumoniae</i> (N=15)	7(47)	0(0)	0(0)	8(53)	15(100)	15(100)	0(0)	7(47)	7(47)	0(0)	0(0)	0(0)
<i>P.aeruginosa</i> (N=22)	22(100)	NA	0(0)	15(68)	22(100)	7(32)	0(0)	NA	22(100)	7(32)	0(0)	0(0)

Abbreviations: AM, Ampicillin; FOX, Cefoxitin; AK, Amikacin; CIP, Ciprofloxacin; CN, Gentamycin; PIT, Piperacillin-Tazobactam; AMC, Amoxicillin/Clavulanic; CAZ, Ceftazidime; MRP, Meropenem; CRO, Ceftriaxone; NIT, Nitrofurantoin, IPM, Imipenem; µg, Microgram.

Table 3. Multi-drug resistant pattern of isolates from diabetes patients diagnosed with UTI.

Isolate	Resistance n (%)							
	R0	R1	R2	R3	R4	R5	R6	^R6
<i>E.coli</i> (N=109)	0(0)	0(0)	17(16)	0(0)	20(18)	24(22)	25(23)	23(21)
<i>S.aureus</i> (N=79)	0(0)	0(0)	0(0)	12(15)	24(30)	15(19)	0(0)	28(35)
CoNS (N=36)	0(0)	0(0)	0(0)	0(0)	0(0)	21(58)	9(25)	6(17)
<i>K.pneumoniae</i> (N=15)	0(0)	0(0)	0(0)	9(60)	6(40)	0(0)	0(0)	0(0)
<i>P.aeruginosa</i> (N=22)	0(0)	0(0)	0(0)	11(50)	0(0)	6(27)	5(23)	0(0)

Note: R0, Sensitive to all tested antibiotics; R1, R2, R3, R4, R5, R6, ^R6, Resistant to one, two, three, four, five, six, and more than six of the tested antibiotics.

Table 4. Antimicrobial resistance gene and associated antibiotic resistant pattern.

Isolates	Antibiotic Class	**AMR Gene	Antibiotics	Resistant Isolates n(%)
<i>E.coli</i> (N=109)	Aminoglycoside	<i>aac(3)-IId</i>	Gentamicin	51(47)
	Beta -Lactam	<i>blaCTX-M-15</i> <i>blaNDM-5,blaOXA-1</i> , and <i>blaTEM-1B</i>	Ceftazidime	95(88)
			Ceftriaxone	51(47)
			Cefoxitin	36(33)
			Meropenem	15(14)
			Imipenem	22(20)
			Amoxicillin/clavulanic acid	80(73)
			Ampicillin	65(59)
	Quinolone	<i>qnrS1</i>	Ciprofloxacin	65(60)
<i>S.aureus</i> (N=79)	Aminoglycoside	<i>aacA-aphD</i>	Gentamicin	36(46)
<i>K. pneumoniae</i> (N=15)	Cephalosporins, Penicillin	<i>blaSHV</i> , <i>blaTEM</i>	Ceftazidime	7(47)
			Ampicillin	7(47)

Note: **AMR gene, Antimicrobial resistance gene

Among the 261 sequenced isolates, *Escherichia coli* (109, 41.8%) was the most prevalent, followed by *Staphylococcus aureus* (79, 30.3%), coagulase-negative staphylococci (CoNS) (36, 13.8%), *Klebsiella pneumoniae* (15, 5.7%), and *Pseudomonas aeruginosa* (22, 8.4%). Of the 109 sequenced *E. coli* isolates, 58 (53.2%) carried at least one resistance gene, including *blaOXA-1*, *blaNDM-5*, *blaTEM-1B*, and *blaCTX-M-15*, which are associated with resistance to carbapenems, cephalosporins, and penicillins. Additionally, 30 (27.5%) *E. coli* isolates harbored the *aac(3)-IId* gene, conferring resistance to aminoglycosides, while 15 (13.8%) carried the *qnrS1* gene, associated with resistance to quinolones. Six (5.5%) *E. coli* isolates did not carry any resistance genes.

Among the 79 *S. aureus* isolates, 12 (15.2%) harbored the *aacA-aphD* gene, conferring resistance to aminoglycosides, whereas the remaining 67 (84.8%) isolates carried no resistance genes. Of the 15 sequenced *K. pneumoniae* isolates, 8 (53.3%) carried the *blaSHV* and *blaTEM* genes, which confer resistance to cephalosporins and penicillins, while the remaining 7 (46.7%) isolates had no resistance genes. No resistance genes were detected in the sequenced CoNS or *P. aeruginosa* isolates (Table 4).

4. DISCUSSION

This study aimed to determine antimicrobial resistance patterns and associated resistance genes among isolates from patients with diabetes mellitus (DM) suffering from urinary tract infections (UTIs). A total of 261 (62%) isolates from 419 cultured samples were analyzed.

The bacterial isolates included *E. coli* (109, 26%), *S. aureus* (79, 19%), coagulase-negative staphylococci (CoNS) (36, 9%), *K. pneumoniae* (15, 4%), and *P. aeruginosa* (22, 5%). *E. coli* was the most frequently isolated organism, consistent with previous studies from Eastern India, Dhaka, Bangladesh, Dilla University, Ethiopia, and Ghana [3, 6–9]. The high prevalence of *E. coli* may be attributed to its commensal presence in the bowel, fecal contamination, and strong adhesion to epithelial cells in diabetic individuals [6, 8].

All 261 isolates (100%) exhibited multidrug resistance (MDR), defined as resistance to two or more antibiotics. This rate was higher than reported in studies from India and Ethiopia [6, 8], and may reflect poor adherence to antibiotic regimens, misuse of antibiotics, and over-the-counter availability. High resistance rates were observed for ceftazidime (92%), amoxicillin/clavulanic acid (65%), nitrofurantoin (64%), ciprofloxacin (64%), and ampicillin (61%). Conversely, isolates were highly susceptible to meropenem (89%), amikacin (97%), imipenem (78%), and piperacillin–tazobactam (72%) [10, 11]. Differences in resistance across studies may be influenced by geographic location, antibiotic availability, and prescribing practices.

E. coli isolates demonstrated high resistance to ceftazidime (88%), amoxicillin/clavulanic acid (73%), ciprofloxacin (60%), and ampicillin (59%), slightly higher than reports from Dhaka, Surabaya, Indonesia, and Saudi Arabia [7, 12, 13], but lower than Addis Ababa, Ethiopia [14]. CoNS exhibited 100% resistance to ampicillin,

cefoxitin, amikacin, amoxicillin/clavulanic acid, and ceftazidime, consistent with findings from Ethiopia [8]. *S. aureus* isolates were 91% resistant to ampicillin, 82% resistant to ciprofloxacin and nitrofurantoin, and 100% resistant to ceftazidime, exceeding resistance rates reported in Surabaya, Indonesia [12]. *K. pneumoniae* isolates were 100% resistant to nitrofurantoin and gentamicin, and 53% resistant to ciprofloxacin, showing higher or comparable resistance to studies in India and Indonesia [6, 12, 15]. *P. aeruginosa* isolates were 100% resistant to ampicillin and ceftazidime and 68% resistant to ciprofloxacin, higher than previous reports from India and Indonesia [6, 12, 16]. Variations may be explained by differences in geography, lifestyle, and health education, as well as by study period and sample size.

Resistance genes were detected among the isolates. Most *E. coli* isolates harbored blaNDM-5, blaOXA-1, blaTEM-1B, and blaCTX-M-15, conferring resistance to carbapenems, ampicillin, amoxicillin/clavulanic acid, and cephalosporins, consistent with studies from referral hospitals in Tanzania and government clinics in Karakudi [17, 18]. Additionally, qnrS1 genes, conferring quinolone resistance, and aac(3)-IIId, conferring aminoglycoside resistance, were identified, aligning with previous reports [17-19]. Among *K. pneumoniae*, blaSHV and blaTEM were detected [20-22]. *S. aureus* isolates harbored the aacA-aphD gene, similar to observations from Pakistan [23]. These resistance genes likely contributed to the observed antimicrobial resistance patterns.

Antimicrobial resistance is particularly concerning in patients with diabetes mellitus due to immune compromise, poor glycemic control, bladder dysfunction, and vascular complications [16, 24]. The aminoglycoside resistance observed in this study may be attributed to the detected resistance gene, highlighting the need for routine molecular diagnostics in hospital laboratories to complement phenotypic testing and guide precision antibiotic therapy.

This study has limitations. Convenience sampling may not fully represent diabetic patients in other regions of Tanzania, as the findings reflect the characteristics of patients seeking care at Benjamin Mkapa Hospital. Future studies should include multiple hospitals in Dodoma to provide a more comprehensive understanding of antimicrobial-resistant pathogens in diabetic patients with UTIs.

CONCLUSION

This study demonstrates a high burden of multidrug-resistant (MDR) uropathogens among diabetic patients with urinary tract infections at Benjamin Mkapa Hospital, Tanzania. *Escherichia coli*, *Staphylococcus aureus*, coagulase-negative staphylococci, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* were the predominant isolates, with *E. coli* being the most frequent. All isolates exhibited resistance to two or more antibiotics, with particularly high resistance to ceftazidime, amoxicillin/clavulanic acid, ciprofloxacin, and ampicillin. At the same time, susceptibility remained higher for meropenem, amikacin, imipenem, and piperacillin-tazobactam.

Genotypic analysis identified clinically important resistance genes, including blaNDM-5, blaOXA-1, blaTEM-1B, blaCTX-M-15, qnrS1, aac(3)-IIId, blaSHV, and aacA-aphD, which likely contribute to the observed resistance patterns. These findings highlight the urgent need for routine culture and susceptibility testing, integrated molecular diagnostics, and targeted antibiotic stewardship programs to guide effective therapy and limit the spread of resistant pathogens in this high-risk population.

Despite the study's limitations due to convenience sampling, the results emphasize the need to expand surveillance across multiple hospitals in Dodoma to achieve a more comprehensive understanding of antimicrobial resistance among diabetic patients with UTIs.

AUTHORS' CONTRIBUTIONS

It is hereby acknowledged that all authors have accepted responsibility for the manuscript's content and consented to its submission. They have meticulously reviewed all results and unanimously approved the final version of the manuscript.

LIST OF ABBREVIATIONS

DM	=	Diabetes Mellitus
KIA	=	Kligler Iron Agar
MHA	=	Mueller-Hinton Agar
TSR	=	Template Suppression Reagent

ETHICS APPROVAL AND CONSENT TO PARTICIPATE

Ethical approval for the study (Ref. No. OUT/PG202000391) was granted by the Open University of Tanzania, and a certificate of ethical clearance (Ref. No. NIMR/HQ/R.8a/Vol.IX/4640) was obtained from the National Institute for Medical Research (NIMR), Tanzania.

HUMAN AND ANIMAL RIGHTS

All procedures performed in studies involving human participants were in accordance with the ethical standards of institutional and/or research committees and with the 1975 Declaration of Helsinki, as revised in 2013.

CONSENT FOR PUBLICATION

Participation in this study was entirely voluntary, and written informed consent was obtained from all participants before enrollment.

STANDARDS OF REPORTING

STROBE guidelines were followed.

AVAILABILITY OF DATA AND MATERIALS

The data and supporting information are available in the article.

FUNDING

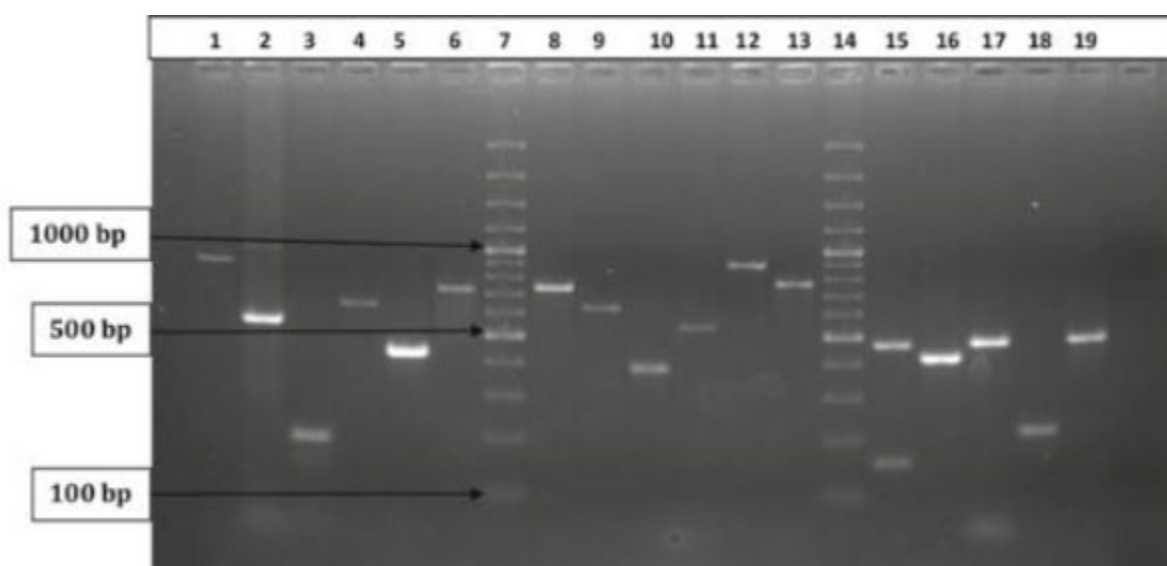
None.

CONFLICT OF INTEREST

The authors declare no conflict of interest, financial or otherwise.

APPENDIX**Appendix 1. Primers used for screening resistant genes.**

Target Gene	Primer Name	5'-3' Sequence	Source
<i>aac(3)-IId</i>	aac(3)-IIdF	TGA AAC GCT GAC GGA GCC TC	List of primers for detection of antimicrobial resistance genes - version 06.11.2018
	aac(3)-IIdR	GTC GAA CAG GTA GCA CTG AG	
<i>blaCTX-M</i>	CTXM1-F3	GAC GAT GTC ACT GGC TGA GC	
	CTXM1-R2	AGC CG C CGA CGC TAA TAC A	
<i>blaNDM-5</i>	NDM-5-F	GCTCTAGAATGGCTCCAGATGACAAACA T	
	NDM-5-R	GCTCTAGATGGGTTCGAGGTCAGGATAG G	
<i>blaOXA-1</i>	OXA-1 F	ATGAAAAACACAATACATATCAACTTCG C	
	OXA-1R	GTGTGTTTAGAATGGTGATCGCATT	
<i>blaTEM</i>	TEM-F	ATGAGTATTCAACAT TTC CG	
	TEM-R	CCAATGCTTAATCAG TGA GG	
<i>qnrS1</i>	QnrS1-F	ATTATTTGTTACAGACCCGG	
	QnrS1-F	GCTAACTTTGCAACAGTGCC	
<i>aacA-aphD</i>	aacA-aphD F	TAA TCC AAG AGC AAT AAG GGC	
	aacA-aphDR	GCC ACA CTA TCA TAA CCA CTA	
<i>blaSHV</i>	SHV-F	TTCGCCTGTGTATTATCTCCCTG	
	SHV-R	TTAGCGTTGCCAGTGYTCG	

Appendix 2. The representative gel picture (PCR products).

Agarose gel electrophoresis of PCR products with representative *E. coli* isolates carrying the various tested resistant genes. Lane 1: blaTEM (867 bp), lane 2: blaCTXM (540 bp), lane 3: blaOXA-1 (198 bp), lane 7, 14: 100 bp plus ladder, lane 8: aac(3)-IId (740 bp).

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