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Antibiogram of Bacteria Isolated from Patients with Urological Disorders at Selected Tertiary Health Facilities in Port Harcourt, Nigeria

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ABSTRACT

Antimicrobial resistance among bacterial pathogens associated with urological disorders poses a challenge to effective antimicrobial therapy. Determining local antimicrobial susceptibility patterns and multiple antibiotic resistance (MAR) profiles is important for understanding the resistance burden among bacterial isolates recovered from affected patients. The study determined the antibiogram of bacteria isolated from patients with urological disorders at selected tertiary health facilities in Port Harcourt, Niger. A total of 142 bacterial isolates recovered from 252 patients with urological disorders, were evaluated. The isolates comprised *Klebsiella* spp. (n=73), *Staphylococcus aureus* (n=41), coagulase-negative *Staphylococci* (CoNS) (n=8), *Serratia marcescens* (n=6), *Pseudomonas aeruginosa* (n=6), *Enterobacter* spp. (n=6), and *Escherichia coli* (n=2). Antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar, with results classified as susceptible, intermediate, or resistant. MAR indices were determined for the bacterial isolates. Substantial variation in antimicrobial susceptibility was observed among the bacterial isolates. *S. aureus* demonstrated its highest susceptibility to chloramphenicol (56.1%), followed by vancomycin (51.2%), while resistance was highest to co-trimoxazole (68.3%). *Klebsiella* spp. showed marked resistance to nitrofurantoin (84.9%), meropenem (82.2%), augmentin (82.2%), ceftriaxone (72.6%) and cefepime (68.5%). Both *E. coli* isolates were resistant to meropenem, ceftriaxone, co-trimoxazole, ciprofloxacin and amikacin but were susceptible to nitrofurantoin. *P. aeruginosa* showed complete resistance to gentamicin and cefepime. MAR indices greater than 0.2 occurred in 98.6% of *Klebsiella* spp. and 90.2% of *S. aureus* isolates, with elevated MAR profiles also observed among CoNS, *S. marcescens*, *E. coli* and *P. aeruginosa*. The findings demonstrate a substantial antimicrobial resistance burden among bacterial isolates recovered from patients with urological disorders, characterized by high resistance to several commonly tested antimicrobial agents and elevated MAR indices. Routine antimicrobial susceptibility testing and continued resistance surveillance are therefore important in the management of these infections.

Keywords: Antimicrobial Resistance; Antimicrobial Susceptibility; MAR Index; Urological Disorders; Bacterial Isolates.

Introduction

Urological disorders constitute an important clinical and public health problem and encompass a range of conditions affecting the urinary tract and associated organs. Among these conditions, urinary tract infections (UTIs) are particularly important because they occur frequently in community and healthcare settings and may be associated with recurrent infection, complications and treatment failure. Patients with underlying urological abnormalities, including obstructive conditions, urinary retention and other structural or functional disturbances, may be especially vulnerable to complicated urinary infections and recurrent bacterial colonization (Flores-Mireles et al., 2015; Bonkat et al., 2023).

The bacterial spectrum associated with urinary infections is diverse and includes Gram-negative organisms such as Escherichia coli, *Klebsiella* spp., *Proteus mirabilis, Pseudomonas aeruginosa* and *Enterobacter* spp., as well as Gram-positive organisms including *Staphylococci* (Asadi Karam et al., 2019; Gajdács et al., 2019).

The management of bacterial urinary infections has become increasingly difficult because of the occurrence of antimicrobial resistance (AMR). Resistance among uropathogens can reduce the effectiveness of routinely used antibiotics and complicate empirical treatment (Tandoğdu & Wagenlehner, 2016; Bonkat et al., 2023).

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The problem is particularly relevant in tertiary healthcare settings, where patients may have recurrent infections, previous antimicrobial exposure, urinary instrumentation and prolonged healthcare contact (Foxman, 2014; Nicolle, 2014). The importance of local surveillance is underscored by the marked variation in antimicrobial resistance patterns among bacterial populations and healthcare settings. The increasing diversity of resistant uropathogens has strengthened the need for reliable antimicrobial susceptibility testing (AST). Phenotypic susceptibility testing provides information on the response of bacterial isolates to individual antimicrobial agents and is an important component of clinical microbiology. Accurate susceptibility information assists antimicrobial selection and provides the basis for local antibiograms (Khan et al., 2019). The European Association of Urology also emphasizes microbiological assessment and antimicrobial stewardship in the management of urological infections (Bonkat et al., 2023). In resource-limited settings, locally generated susceptibility data are particularly valuable because resistance patterns observed elsewhere may not accurately reflect those of patients presenting to individual hospitals.
Evidence from Nigeria indicates that antimicrobial resistance among urinary bacterial isolates is an established concern. Studies from Abakaliki and other Nigerian settings have documented substantial resistance to commonly used antimicrobial agents among urinary isolates (Alo et al., 2015; Onoh et al., 2013). In southern Nigeria, high levels of extended-spectrum β-lactamase production have also been reported among Gram-negative isolates from urine and wound specimens, including *Klebsiella* spp. (Ogefere et al., 2015). These findings indicate the need for contemporary, locally generated susceptibility data to support treatment decisions and antimicrobial stewardship.

Resistance is not restricted to Gram-negative uropathogens. Staphylococcal species may also exhibit resistance to multiple antimicrobial classes, creating therapeutic challenges in urinary and other healthcare-associated infections. The development and persistence of multidrug-resistant *Staphylococcus aureus* have been associated with sustained antimicrobial selection pressure (Chambers & DeLeo, 2009). Coagulase-negative staphylococci are also clinically important because of their capacity to persist in healthcare environments and their association with antimicrobial resistance (Argemi et al., 2019; Becker et al., 2020).

The occurrence of resistant Gram-positive and Gram-negative organisms in the same healthcare environment therefore underscores the need for broad local surveillance.

An additional approach to characterizing antimicrobial resistance is the Multiple Antibiotic Resistance (MAR) index. MAR analysis provides a quantitative description of resistance across multiple antimicrobial agents and can assist in identifying bacterial populations exposed to substantial antimicrobial selection pressure. Krumperman (1983) proposed MAR indexing as an epidemiological approach for identifying populations associated with high-risk antimicrobial exposure. In the present study, MAR values greater than 0.2 were used as the threshold for isolates associated with high-risk antimicrobial exposure, allowing MAR analysis to complement conventional antibiogram data.

The public health relevance of antimicrobial susceptibility surveillance among urological patients is considerable. Inappropriate empirical treatment may expose patients to ineffective antibiotics and contribute to further selection of resistant organisms. Conversely, evidence-based local antibiograms can support more rational antimicrobial selection while informing antimicrobial stewardship, infection prevention and hospital surveillance. The EAU guidelines emphasize antimicrobial stewardship as an important component of the management and prevention of urological infections (Bonkat et al., 2023).

Despite the documented concern about antimicrobial resistance among Nigerian urinary pathogens, contemporary multicentre data among patients with urological disorders in Port Harcourt remain limited. The multicentre nature of the present investigation provides an opportunity to characterize antimicrobial susceptibility patterns among bacterial isolates recovered from patients attending Rivers State University Teaching Hospital (RSUTH), University of Port Harcourt Teaching Hospital (UPTH), and Kelsey-Harrison Hospital (KHH). By combining organism-specific susceptibility profiles with MAR analysis, the study would provide a focused assessment of the phenotypic resistance burden within this patient population.

Accordingly, this study aimed to determine the antibiogram of bacteria isolated from patients with urological disorders attending selected tertiary healthcare facilities in Port Harcourt, Nigeria.

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The findings are intended to provide locally relevant evidence for antimicrobial treatment decisions, resistance surveillance and strengthening of antimicrobial stewardship within tertiary healthcare settings.

Materials and Methods

Study Area and design

The study area was Port Harcourt metropolis River State, Nigeria. The tertiary health facilities within the study area where the work was carried out are University of Port Harcourt Teaching Hospital (UPTH) Rivers State University Teaching Hospital (RSUTH) and Kelsey Harrison Hospital (KHH). The coordinates of the health facilities are 4°53'58''N 6° 55'43'' E, 4°47'03'' N 7° 00'37''E, and 4°47'22'' N 6°59'34'' E respectively.

The study employed a hospital-based, multicentre cross-sectional study design incorporating laboratory procedures to evaluate the antibiogram of bacteria isolated from patients with urological disorders in selected tertiary healthcare facilities in Port Harcourt, Rivers State, Nigeria.

Study Population and Ethical Consideration

The study population comprised patients with urological disorders attending the selected tertiary health facilities in Port Harcourt, Rivers State, namely Rivers State University Teaching Hospital (RSUTH), University of Port Harcourt Teaching Hospital (UPTH), and Kelsey-Harrison Hospital (KHH), during the study period. Eligible participants who met the inclusion criteria were recruited for the study, and urine specimens were collected for microbiological and antimicrobial susceptibility investigations.

Ethical approval was obtained from the appropriate institutional research ethics committees of the participating health facilities before commencement of the study. Written informed consent was obtained from each participant after the purpose and procedures of the study had been explained.

Participation was voluntary, and participants were informed of their right to withdraw at any time without consequences. Confidentiality and anonymity of participants' information were maintained, and all data were used strictly for research purposes.

Determination of Sample Size

The sample size for the study was calculated using Cochran formula (Eqn. 1) based on the requirement for prevalence value by the formula, a prevalence value of 60% (0.6) was obtained from a previous study (Kolawole *et al*., 2009). Insertion of this value into equation 1 yielded a sample size of 368.

$$n = \frac{Z^2 P (1-P)}{d^2} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots \quad \text{(Eqn. 1)}$$

Where;
n = sample size
z = statistic for level of confidence (1.96)
p = Expected prevalence or proportion (18%)
d = precision (0.05)

$$\frac{(1.96)^2 x 0.6\ (1-0.6)}{(0.05)^2}$$

$$\frac{3.8416\ x\ 0.6\ (0.4)}{0.0025}$$

$$\frac{3.8416\ x\ 0.24}{0.0025}$$

$$\frac{0.92184}{0.0025} = 368$$

The calculated minimum sample size was 368, but only 252 eligible participants/samples were available during the study period. Hence, the final sample size of 252.

Sample Collection and Identification of Isolates

Midstream urine specimens were collected aseptically from eligible participants into sterile, appropriately labelled universal containers and transported promptly to the microbiology laboratory for processing. Samples were cultured on appropriate selective and differential media and incubated under standard conditions. Suspected bacterial isolates were identified based on colony morphology, Gram staining, and standard biochemical tests, and the identity of each isolate was confirmed by cross-checking the results against the identification schemes in the laboratory manual of Cheesbrough (2006).

Antibiotic Susceptibility Testing

Antibiotic susceptibility testing was performed using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar. Bacterial suspensions equivalent to a 0.5 McFarland standard were prepared.

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Results were interpreted as Susceptible (S), Intermediate (I), or Resistant (R) according to Clinical and Laboratory Standards Institute criteria (CLSI, 2026) [quality control reference strains used are; *Escherichia coli* ATCC 25922, *Staphylococcus aureus* ATCC 25923, *Pseudomonas aeruginosa* ATCC 27853, and *E. coli* ATCC 35218. The antimicrobial agents tested varied according to the bacterial group and included agents such as: nitrofurantoin (30µg), ceftriaxone (30µg), meropenem (10µg), co-trimoxazole (25µg), levofloxacin (5µg), gentamicin (10µg), ciprofloxacin (5µg), augmentin (30µg), cefepime (30µg), amikacin (30µg), ceftazidime (30µg), aztreonam (30µg), ceftazidime (30µg), chloramphenicol (30µg), cephapirin (30µg), erythromycin (15µg), and azithromycin (15µg).

Multiple Antibiotic Resistance Index

The MAR index of the bacterial isolates was determined and presented according to bacterial species. The isolates with MAR indices greater than 0.2 were classified as originating predominantly from high-risk environments associated with frequent antibiotic exposure (Krumperman, 1983).

Statistical analysis

Data derived were analyzed using Statistical Package for Social Sciences (SPSS) version 20.0. Results were presented as frequencies and percentages for susceptible, intermediate and resistant isolates.

Results

Results of the frequency and distribution of the 142 bacterial isolates recovered from patients with urological disorders across the three hospitals are presented in Figure 1. *Klebsiella* spp. constituted the largest group with 73 isolates, followed by *S. aureus* with 41. Coagulase-negative *Staphylococci* (CoNS) accounted for 8 isolates, while *S. marcescens*, *E. coli*, *P. aeruginosa* and *Enterobacter* spp. accounted for 6, 2, 6 and 6 isolates, respectively.

Result of the antibiotic susceptibility as presented in Table 1 revealed that, among the 41 *S. aureus* isolates, the highest susceptibility was recorded for chloramphenicol (56.1%), followed by vancomycin (51.2%) and ceftriaxone (39.0%). Resistance was highest to co-trimoxazole (68.3%), followed by augmentin (65.9%), azithromycin (63.4%), ciprofloxacin (61.0%) and cephapirin (61.0%).

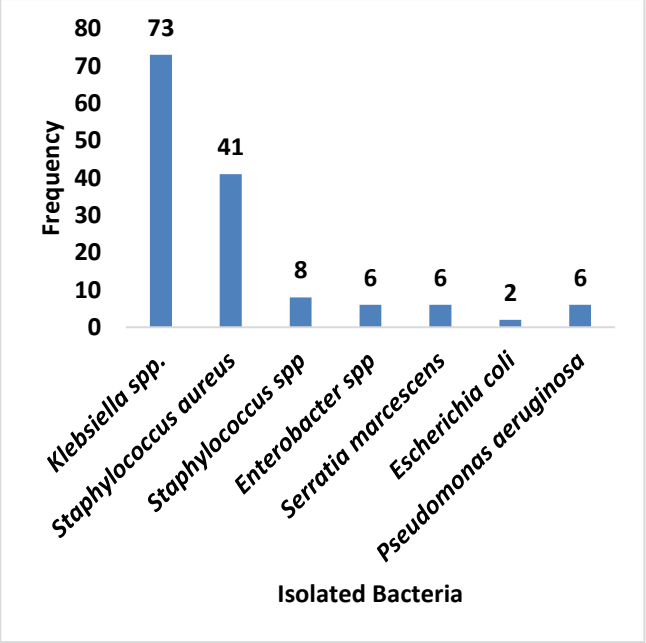

Figure 1: Distribution of bacteria isolated from patients with urological disorders across three Hospitals

While meropenem and erythromycin each recorded 58.5% resistance

Among the eight coagulase-negative *Staphylococci* (CoNS) isolates, susceptibility was highest to cephapirin (62.5%), followed by ceftriaxone (50.0%). Meropenem, erythromycin and gentamicin each showed 37.5% susceptibility. Resistance was highest to co-trimoxazole and chloramphenicol (75.0% each), followed by levofloxacin, augmentin and vancomycin (62.5% each) (Table 1).

Antibiotic susceptibility pattern of the other bacteria isolated from patients with urological disorders are as presented in Table 2.

Among the 73 *Klebsiella* spp. isolates, susceptibility was highest to ciprofloxacin (43.8%), followed by aztreonam (27.4%), levofloxacin (21.9%), and cefepime and ceftazidime (20.6% each). Resistance was particularly high to nitrofurantoin (84.9%), augmentin (82.2%), ceftriaxone (72.6%), meropenem (68.5%), cefepime (68.5%), co-trimoxazole (67.1%) and gentamicin (65.8%).

All six *S. marcescens* isolates were susceptible to ceftazidime.

Susceptibility was also high to augmentin (83.3%) and co-trimoxazole (66.7%). Complete resistance (100%) was recorded against meropenem, ceftriaxone, gentamicin, cefepime and amikacin.

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Table 1: Antibiotic susceptibility pattern of *Staphylococcus aureus* and coagulase-negative *Staphylococci* (CoNS) isolated from patients with urological disorders

Antibiotic (Concentration)	*Staphylococcus aureus* n=41 n (%)			Coagulase-negative *Staphylococci* (CoNS) n=8 n (%)		
	S	I	R	S	I	R
Azithromycin (10µg)	8(19.5)	7(17.1)	26(63.4)	2(25)	2(25)	4(50)
Meropenem (10µg)	9(22)	8(19.5)	24(58.5)	3(37.5)	1(12.5)	4(50)
Erythromycin (30µg)	12(29.3)	5(12.2)	24(58.5)	3(37.5)	2(25)	3(37.5)
Ceftriaxone (10µg)	16(39)	9(22)	16(39)	4(50)	1(12.5)	3(37.5)
Co-trimoxazole (10µg)	6(14.6)	7(17.1)	28(68.3)	1(12.5)	1(12.5)	6(75)
Levofloxacin (30µg)	10(24.4)	11(26.8)	20(48.8)	1(12.5)	2(25)	5(62.5)
Gentamycin (10µg)	12(29.3)	10(24.4)	19(46.3)	3(37.5)	1(12.5)	4(50)
Ciprofloxacin (30µg)	11(26.8)	5(12.2)	25(61)	2(25)	2(25)	4(50)
Augmentin (30µg)	9(22)	5(12.2)	27(65.9)	2(25)	1(12.5)	5(62.5)
Vancomycin (30µg)	21(51.2)	10(24.4)	10(24.4)	1(12.5)	2(25)	5(62.5)
Chloramphenicol (30µg)	23(56.1)	9(22)	9(22)	1(12.5)	1(12.5)	6(75)
Cephapirin (30µg)	10(24.4)	6(14.6)	25(61)	5(62.5)	1(12.5)	2(25)

Key: S = Susceptible; I = Intermediate; R = Resistant.

Both *E. coli* isolates were susceptible to nitrofurantoin (100%). One isolate (50.0%) was susceptible to levofloxacin. Complete resistance (100%) was recorded against meropenem, ceftriaxone, co-trimoxazole, ciprofloxacin and amikacin.

Among the six *P. aeruginosa* isolates, the highest susceptibility was observed for nitrofurantoin (83.3%), followed by co-trimoxazole, levofloxacin, augmentin and ceftazidime (66.7% each). Complete resistance was recorded against gentamicin and cefepime (100% each), while aztreonam showed 83.3% resistance. Meropenem, ceftriaxone and amikacin each showed 66.7% resistance.

Enterobacter spp. showed the most favourable susceptibility profile among the Gram-negative groups described in this study. Complete susceptibility (100%) was recorded for cefepime. Ceftriaxone, co-trimoxazole, nitrofurantoin and aztreonam each showed 83.3% susceptibility.

Multiple Antibiotic Resistance Index

The MAR index distribution demonstrated substantial resistance across several bacterial groups. Among the 41 *S. aureus* isolates, MAR values ranged from 0.1 to 0.8. The largest proportion had a MAR index of 0.7 (24.4%), followed by 0.8 (21.9%). Among the eight CoNS isolates, four (50.0%) had a MAR index of 0.8, while 87.5% had MAR values above 0.2. For *Klebsiella* spp., 28 (38.4%) had a MAR index of 0.8 and 19 (26.0%) had a MAR index of 0.7. All six *S. marcescens* isolates had MAR indices ≥0.3. Both *E. coli* isolates had MAR indices of 0.7 and 0.8. All six *P. aeruginosa* isolates had MAR indices above 0.2. In contrast, all of the *Enterobacter* spp. isolates had MAR indices greater than or equal to 0.1 (Table 3).

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Table 2: Antibiotic susceptibility pattern of other bacteria isolated from patients with urological disorders

Antibiotic (Concentration)	*Klebsiella* spp. n=73 n (%)			*S. marcescens* n=6 n (%)			*E. coli* n=2 n (%)			*P. aeruginosa* n=6 n (%)			*Enterobacter* spp. n=6 n (%)		
	S	I	R	S	I	R	S	I	R	S	I	R	S	I	R
Meropenem (10µg)	12(16.4)	11(15.1)	50(68.5)	0(0)	0(0)	6(100)	0(0)	0(0)	2(100)	0(0)	2(33.3)	4(66.7)	4(66.7)	2(33.3)	0(0)
Ceftriaxone (10µg)	9(12.3)	11(15.1)	53(72.6)	0(0)	0(0)	6(100)	0(0)	0(0)	2(100)	0(0)	2(33.3)	4(66.7)	5(83.3)	1(16.7)	0(0)
Co-trimoxazole (10µg)	10(13.7)	14(19.2)	49(67.1)	4(66.7)	2(33.3)	0(0)	0(0)	0(0)	2(100)	4(66.7)	2(33.3)	0(0)	5(83.3)	1(16.7)	0(0)
Levofloxacin (30µg)	16(21.9)	16(21.9)	41(56.2)	1(16.7)	4(66.7)	1(16.7)	1(50)	1(50)	0(0)	4(66.7)	2(33.3)	0(0)	4(66.7)	2(33.3)	0(0)
Gentamicin (10µg)	10(13.7)	15(20.5)	48(65.8)	0(0)	0(0)	6(100)	0(0)	1(50)	1(50)	0(0)	0(0)	6(100)	0(0)	6(100)	0(0)
Ciprofloxacin (30µg)	32(43.8)	6(8.2)	35(47.9)	0(0)	4(66.7)	2(33.3)	0(0)	0(0)	2(100)	0(0)	5(83.3)	1(16.7)	0(0)	5(83.3)	1(16.7)
Augmentin (30µg)	5(6.9)	8(10.9)	60(82.2)	5(83.3)	1(16.7)	0(0)	0(0)	1(50)	1(50)	4(66.7)	2(33.3)	0(0)	4(66.7)	2(33.3)	0(0)
Nitrofurantoin (30µg)	5(6.9)	6(8.2)	62(84.9)	0(0)	2(33.3)	4(66.7)	2(100)	0(0)	0(0)	5(83.3)	1(16.7)	0(0)	5(83.3)	1(16.7)	0(0)
Cefepime (30µg)	15(20.6)	8(10.9)	50(68.5)	0(0)	0(0)	6(100)	0(0)	1(50)	1(50)	0(0)	0(0)	6(100)	6(100)	0(0)	0(0)
Amikacin (30µg)	14(19.2)	15(20.6)	44(60.3)	0(0)	0(0)	6(100)	0(0)	0(0)	2(100)	0(0)	2(33.3)	4(66.7)	0(0)	5(83.3)	1(16.7)
Ceftazidime (30µg)	15(20.6)	15(20.6)	43(58.9)	6(100)	0(0)	0(0)	0(0)	2(100)	0(0)	4(66.7)	1(16.7)	1(16.7)	2(33.3)	4(66.7)	0(0)
Aztreonam (30µg)	20(27.4)	33(45.2)	20(27.4)	0(0)	1(16.7)	5(83.3)	0(0)	1(50)	1(50)	0(0)	1(16.7)	5(83.3)	5(83.3)	1(16.7)	0(0)

S = Susceptible; I = Intermediate; R = Resistant.

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Table 3: Multiple Antibiotic Resistance Index Distribution among Bacterial Isolates

MAR Index	*S. aureus* n=41 n (%)	CoNS n=8 n (%)	*Klebsiella* spp. n=73 n (%)	*S. marcescens* n=6 n (%)	*E. coli* n=2 n (%)	*P. aeruginosa* n=6 n (%)	*Enterobacter* spp. n=6 n (%)
0.1	1(2.4)	1(12.5)	0(0)	0(0)	0(0)	0(0)	6(100)
0.2	3(7.3)	0(0)	1(1.4)	0(0)	0(0)	0(0)	0(0)
0.3	3(7.3)	1(12.5)	2(2.7)	2(33.3)	0(0)	1(16.7)	0(0)
0.4	3(7.3)	0(0)	9(12.3)	0(0)	0(0)	2(33.3)	0(0)
0.5	6(14.6)	1(12.5)	5(6.8)	0(0)	0(0)	3(50)	0(0)
0.6	6(14.6)	0(0)	9(12.3)	3(50)	0(0)	0(0)	0(0)
0.7	10(24.4)	1(12.5)	19(26)	1(16.7)	1(50)	0(0)	0(0)
0.8	9(21.9)	4(50)	28(38.4)	0(0)	1(50)	0(0)	0(0)
Total	**41(100)**	**8(100)**	**73(100)**	**6(100)**	**2(100)**	**6(100)**	**6(100)**

Key: MAR index <0.2 = low-risk source; MAR index >0.2 = high-risk source; MAR index >0.4 = high-risk contamination; CoNS = Coagulase-negative *Staphylococci*.

Discussion

The study demonstrated a substantial antimicrobial resistance burden among bacterial isolates recovered from patients with urological disorders. The overall antibiogram revealed widespread resistance to commonly tested antimicrobial agents, including co-trimoxazole, augmentin, ceftriaxone, ciprofloxacin, gentamicin and meropenem, although susceptibility varied considerably among bacterial species. This pattern indicates a substantial burden of multidrug-resistant uropathogens and may complicate empirical treatment in tertiary healthcare settings. Comparable resistance patterns have been documented among urinary isolates in Nigeria. Alo et al. (2015) reported substantial resistance among urinary pathogens in Abakaliki, while Onoh et al. (2013) documented considerable resistance to commonly used agents among uropathogens in Abakaliki. A South-South Nigerian tertiary-hospital study likewise reported a high level of resistance to commonly prescribed antibiotics and emphasized the need for antimicrobial stewardship (Onukak et al., 2021).

The observed resistance to multiple antimicrobial classes is consistent with the long-recognized ability of *S. aureus* to develop and maintain resistance under antimicrobial selection pressure (Chambers & DeLeo, 2009). Nigerian studies have also documented substantial antimicrobial resistance among clinical *S. aureus* isolates. Nwankwo & Nasiru (2011) reported variable but substantial resistance among clinical *S. aureus* isolates in a tertiary institution in Kano, while Onanuga & Temedie (2011) reported multidrug-resistant *S. aureus* among self-medicated healthy adults in the Niger Delta. The relatively preserved activity of vancomycin observed in the present study is noteworthy, although continued surveillance remains necessary.

Coagulase-negative *Staphylococci* demonstrated substantial resistance to several tested antimicrobial agents. Resistance was particularly high to co-trimoxazole and chloramphenicol, followed by levofloxacin, augmentin and vancomycin, whereas cephapirin demonstrated the highest susceptibility. The finding is consistent with the broader concern surrounding antimicrobial resistance among CoNS. Becker et al. (2020) describe CoNS as important healthcare-associated organisms with substantial resistance potential, while Argemi et al. (2019) highlighted their pathogenicity and genomic capacity to harbour clinically relevant resistance determinants. These characteristics make the resistance observed among the CoNS isolates in the present study clinically important.

The predominance of resistance among *Klebsiella* spp. is consistent with evidence of increasing resistance among *Klebsiella* and other Gram-negative urinary pathogens.

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Ogefere et al. (2015) documented extended-spectrum β-lactamase-producing Gram-negative isolates from urine and wound specimens in southern Nigeria and reported reduced susceptibility to several commonly used agents. Gajdács et al. (2019) also demonstrated substantial resistance trends among common urinary pathogens in a tertiary-care setting. The very high resistance to meropenem observed in the present study is particularly concerning because carbapenems are important agents for serious infections caused by resistant Gram-negative bacteria. However, the present phenotypic data do not by themselves establish ESBL or carbapenemase production. Such mechanisms would require dedicated phenotypic or molecular confirmation. The observed pattern nevertheless warrants close surveillance given the documented emergence of carbapenem-resistant Enterobacterales in Nigerian hospitals (Olalekan et al., 2020).

The six *Serratia marcescens* isolates demonstrated complete resistance to meropenem, ceftriaxone, gentamicin, cefepime and amikacin, while all isolates were susceptible to ceftazidime. High resistance was also recorded against aztreonam and nitrofurantoin. The extensive resistance profile is compatible with the recognized capacity of *Serratia* species to express multiple intrinsic and acquired resistance mechanisms. Mahlen (2011) reviewed the clinical significance and antimicrobial resistance of *Serratia*, including resistance associated with chromosomal AmpC β-lactamases, reduced permeability and efflux mechanisms. Given the small number of *S. marcescens* isolates in the present study, the findings should be interpreted cautiously but still warrant attention within hospital antimicrobial-surveillance programmes.

Although only two *Escherichia coli* isolates were recovered, both demonstrated marked resistance, including complete resistance to meropenem, ceftriaxone, co-trimoxazole, ciprofloxacin and amikacin. In contrast, both isolates were susceptible to nitrofurantoin. The small number of *E. coli* isolates limits generalization of this finding; nevertheless, the observed resistance to fluoroquinolones and cephalosporins is consistent with resistance patterns reported among Nigerian urinary isolates (Iregbu & Nwajiobi-Princewill, 2013; Onoh et al., 2013).

The preserved activity of nitrofurantoin is also of clinical interest because it remained active against these isolates in the present study.

Pseudomonas aeruginosa demonstrated complete resistance to gentamicin and cefepime, with additional high resistance to aztreonam, meropenem, ceftriaxone and amikacin. However, comparatively higher susceptibility was observed to nitrofurantoin, co-trimoxazole, levofloxacin, augmentin and ceftazidime. The resistance pattern is clinically important because *P. aeruginosa* urinary tract infections occur particularly in hospitalized patients and may be associated with poor outcomes when definitive antimicrobial therapy is not appropriate (Lamas Ferreiro et al., 2017). The findings therefore reinforce the importance of organism-specific susceptibility results for guiding treatment.

In contrast to the other Gram-negative isolates, *Enterobacter* spp. demonstrated a comparatively favourable susceptibility profile. Complete susceptibility was observed to cefepime, while high susceptibility was recorded for ceftriaxone, co-trimoxazole, nitrofurantoin and aztreonam. Comparable susceptibility variation among *Enterobacter* populations has been described in the literature, while Davin-Regli et al. (2019) emphasize that *Enterobacter* species possess multiple mechanisms through which antimicrobial resistance can emerge. Continued surveillance is therefore appropriate despite the comparatively favourable profile observed in the present isolates.

The MAR findings provide an additional measure of the multiple-antibiotic resistance burden among the bacterial isolates. Krumperman (1983) established MAR indexing as an epidemiological approach for distinguishing bacterial populations associated with different levels of antimicrobial exposure. In the present study, the majority of bacterial isolates exhibited MAR indices above 0.2. The highest proportion was recorded among *Klebsiella* spp. (98.6%), followed by *S. aureus* (90.2%), while CoNS, *S. marcescens*, *E. coli* and *P. aeruginosa* also demonstrated predominantly elevated MAR values. In contrast, *Enterobacter* spp. showed comparatively lower MAR indices. Similar high MAR levels have been reported among urinary isolates in South-South Nigeria (Onukak et al., 2021).

The high MAR profile observed among *S. aureus* is noteworthy, as most isolates were distributed within the higher MAR categories, particularly between 0.5 and 0.8.

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Comparable multidrug-resistance among clinical *Staphylococcus aureus* isolates has been documented in Nigeria (Nwankwo & Nasiru, 2011; Onanuga & Temedie, 2011). CoNS also demonstrated considerable MAR values, with half of the isolates recording a MAR index of 0.8. The finding is consistent with the recognized ability of CoNS to persist in healthcare environments and harbour resistance determinants (Becker et al., 2020).

Klebsiella spp. exhibited the greatest MAR burden, with 98.6% of isolates having MAR values greater than 0.2 and the largest proportion concentrated at a MAR index of 0.8. High resistance burdens among *Klebsiella* spp. and other Gram-negative urinary pathogens have been reported in Nigeria (Ogefere et al., 2015), while Navon-Venezia et al. (2017) described *Klebsiella pneumoniae* as an important global vehicle and reservoir for antimicrobial resistance. The high MAR profile observed here therefore warrants continued surveillance and stewardship measures.

The MAR profile of *S. marcescens* was similarly elevated, with all isolates having MAR values of at least 0.3. The small number of isolates limits broad inference, but the finding is consistent with the recognized multidrug-resistance potential of *Serratia* species described by Mahlen (2011). Both *E. coli* isolates also demonstrated high MAR values; however, interpretation should remain cautious because of the very small sample size. Comparable multiple-antibiotic resistance among urinary *E. coli* has been documented in Nigerian studies (Iregbu & Nwajiobi-Princewill, 2013; Onoh et al., 2013).

P. aeruginosa showed uniformly elevated MAR profiles, with all isolates exceeding the 0.2 threshold and half recording a MAR index of 0.5. The high MAR profile is consistent with the importance of antimicrobial stewardship in managing hospital-associated *P. aeruginosa* infections. Lamas Ferreiro et al. (2017) demonstrated the clinical importance of appropriate definitive antimicrobial treatment in hospitalized patients with *P. aeruginosa* urinary tract infection. The present findings therefore support continued susceptibility surveillance for this organism.

In contrast, *Enterobacter* spp. demonstrated lower MAR indices. The comparatively lower resistance burden should nevertheless be interpreted cautiously because the number of isolates was small.

Davin-Regli et al. (2019) describe the capacity of *Enterobacter* species to acquire and express multiple resistance mechanisms, reinforcing the need for continued surveillance.

Conclusion

The study demonstrated substantial antimicrobial resistance among bacterial isolates recovered from patients with urological disorders attending the three tertiary health facilities in Port Harcourt. Resistance was particularly pronounced among *Klebsiella* spp., *S. aureus*, CoNS, *S. marcescens*, *E. coli* and *P. aeruginosa*, while *Enterobacter* spp. demonstrated comparatively favourable susceptibility to several tested antimicrobial agents. The high proportion of isolates with MAR indices above 0.2 further demonstrated a considerable multiple-antibiotic resistance burden among the bacterial isolates evaluated.

The findings support the need for routine urine culture and antimicrobial susceptibility testing before antibiotic prescription, particularly given the high resistance observed among several bacterial groups. The study also emphasizes antimicrobial stewardship and continued surveillance of resistant bacteria isolates.

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