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ORIGINAL RESEARCH

Bacteriological Profile and Antibiotic Resistance Patterns of Uropathogenic Bacteria at HPGRB

Bashizi Cito[1,2,*], Kabagale Ansima Corneille[1,*], Iragi Mulume Gates[1], Kashindi Kikombe Bruno[1], Kandi Charles Ruhimbasa[1], Muhindo Hamuli Gloire[1], Jonathan Bahaya[1], Zigashane Lameck Kawala[3], Olivier Mushagalusa Makeshe[3,4], David Lupande Mwenebitu[1,3,5,6]

[1]Faculty of Medicine, Catholic University of Bukavu, Bukavu, Democratic Republic of Congo; [2]Clinical Research Department, Center for Tropical Diseases and Global Health, Bukavu, Democratic Republic of Congo; [3]Laboratory Department, Center for Tropical Diseases and Global Health, Bukavu, Democratic Republic of Congo; [4]Laboratory Section, Higher Institute of Medical Techniques of Bukavu, Bukavu, Democratic Republic of Congo; [5]Microbiology Unit, Provincial General Reference Hospital of Bukavu, Bukavu, Democratic Republic of Congo; [6]Global Health and Infectious Diseases Research Center (GHIDRC) Higher Institute of Medical Techniques of Bukavu, Bukavu, Democratic Republic of Congo

*These authors contributed equally to this work

Correspondence: Bashizi Cito; Kabagale Ansima Corneille, Email bashizicito@gmail.com; kabagale.ansima@ucbukavu.ac.cd

Background: Urinary tract infections (UTIs) represent a major public health concern, particularly in low- and middle-income countries, where they are highly prevalent and increasingly associated with antimicrobial resistance. In the Democratic Republic of Congo (DRC), data on the bacteriological profile and antibiotic susceptibility patterns of uropathogens remain scarce. This study aimed to describe the bacteriological profile, antibiotic resistance patterns, and factors associated with multidrug resistance (MDR) among uropathogens at the Hôpital Provincial Général de Référence de Bukavu (HPGRB).

Methods: A retrospective descriptive and analytical study was conducted from July 1 to December 31, 2024, in the Microbiology Department of HPGRB. Urine cultures and Kirby–Bauer antibiograms (EUCAST and CLSI 2024 guidelines) from 380 positive samples were analyzed. Bivariate (χ^2/Fisher) and multivariate logistic regression were used to identify factors associated with MDR. The production of extended-spectrum β-lactamases (ESBL) was detected and selected by the search for the champagne cork between clavulanic acid and ceftazidime alone or simply resistance to ceftazidime in the absence of the champagne cork.

Results: Among 380 patients with positive urine cultures (55% female), children (40.4%) and elderly patients (41.6%) were the most affected. *Escherichia coli* (62%) and *Klebsiella pneumoniae* (21%) predominated, showing high resistance to third-generation cephalosporins and quinolones. Presumed ESBL phenotypes were observed in 76.2% of *E. coli* and 83.3% of *K. pneumoniae*, with MDR rates of 70% and 82%, respectively. Surgery department admission was the only independent predictor of MDR (adjusted OR 5.43; 95% CI 1.63–18.09; p = 0.006).

Conclusion: UTIs at HPGRB are dominated by *Enterobacterales* with high MDR and presumed ESBL rates, though last-line antibiotics remain effective. Continuous surveillance, confirmatory ESBL testing, and targeted antibiotic stewardship are urgently needed to preserve therapeutic options.

Keywords: urinary tract infection, antibiotic resistance, MDR, ESBL, *E. coli*, *K. pneumoniae*, DR Congo

Introduction

The urinary tract represents the second most common site of community-acquired bacterial infection after the respiratory system and is the leading cause of reported nosocomial infections.[1] Globally, approximately 150–250 million people experience a urinary tract infection (UTI) each year.[2] UTIs affect both women and men, although their prevalence is considerably higher in women, mainly due to anatomical and physiological factors. The prevalence also varies according to age, sex, and race.[1,2]

In Africa, the prevalence of UTIs varies widely between regions. A systematic review published in 2022 estimated the overall prevalence in sub-Saharan Africa at 32.12%.[3] In the Democratic Republic of Congo (DRC), available data remain

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scarce, although UTIs continue to pose a major public health challenge. A study conducted at the University Clinics of Lubumbashi reported a frequency of 30.21%, with a predominance among women (72.68%) and *Escherichia coli* identified as the most frequently isolated pathogen.[4]

In the South Kivu region, studies on antibiotic resistance exist, but few are specifically devoted to urinary tract infections. Nevertheless, according to available data, a study conducted in Bukavu revealed a predominance of *E. coli* and *K. pneumoniae*, with a high level of resistance ranging from 84.3% to 100% to amoxicillin, ampicillin, amoxicillin-clavulanic acid, ceftazidime, ceftriaxone, and cefuroxime.[5]

A significant gap remains with regard to urinary tract infections among the country's pediatric population. Pediatric population is particularly vulnerable due to inadequate hygiene practices.[6] From a bacteriological standpoint, these infections are mainly caused by bacteria from the digestive flora.[2,7] A study conducted in 2019 in a neighboring province, North Kivu, among children also confirmed a female predominance (61.8%) and highlighted strong resistance to common antibiotics, particularly ampicillin, amoxicillin, and gentamicin.[7]

Enterobacterales particularly *E. coli* and *Klebsiella pneumoniae* are the main pathogens implicated in UTIs, as shown by several studies conducted in DRC,[4,6] including in the city of Bukavu.[5] Although these species are consistently predominant, their antibiotic resistance profiles are dynamic, evolving over time under the influence of multiple factors.[8] This variability has serious consequences, creating a vicious cycle that exacerbates antimicrobial resistance.[9]

This cycle is further aggravated by the structural weaknesses of the Congolese health system. On one hand, the high prevalence of infectious diseases is favored by low socioeconomic conditions and poor sanitation, factors that encourage the excessive use of antibiotics.[10] On the other hand, the lack of up-to-date local studies to guide empirical antibiotic therapy limits clinicians' ability to choose effective treatments.[6,10] Consequently, this situation compromises therapeutic management and contributes to the spread of multidrug-resistant bacteria, perpetuating the resistance cycle.[11]

The treatment of urinary tract infections is based on antibiotic therapy adapted to the patient's age, clinical severity and antibiogram results.[12] In current practice, probabilistic treatment is often introduced before the bacteriological results are obtained, especially in febrile children. First-line antibiotics for treating urinary tract infections in DRC and the region for both adults and children include ampicillin, amoxicillin, amoxicillin-clavulanic acid, and certain Third-generation cephalosporins.[5,6] Currently, Quinolones and Aminoglycosides are more commonly used for empirical treatment. However, prescribing remains dependent on the clinician's assessment and the patient's condition.[7]

This study was conducted at the Hôpital Provincial Général de Référence de Bukavu (HPGRB) to determine recent trends in the susceptibility and resistance patterns of bacterial isolates to commonly used antibiotics in urinary tract infections. The findings are expected to contribute to optimizing patient management and promoting the rational use of antibiotics.

Materials and Methods

Study Design and Setting

This was a retrospective, descriptive and analytical study conducted in the Microbiology Department of the Hôpital Provincial Général de Référence de Bukavu (HPGRB), located in Bukavu, South Kivu Province, Democratic Republic of Congo. The study was based on the review of clinical and microbiological data obtained from patients' medical records and laboratory registers at HPGRB. It covered a six-month period, from July 1 to December 31, 2024.

Study Population and Sampling

The study population included all hospitalized and outpatient individuals who underwent urine culture testing during the study period. Patients of all ages and both sexes were eligible for inclusion if they had a positive urine culture result with a complete antibiotic susceptibility test (antibiogram). Exclusion criteria comprised negative or contaminated urine cultures, incomplete laboratory results, or inconclusive bacterial identification. A consecutive exhaustive inclusion of all patients meeting the eligibility criteria during the study was performed (convenience exhaustive sampling).

Patient and Isolate Selection Criteria

To avoid-overrepresentation of patients with recurrent or multiple episodes and comply with international recommendations for antimicrobial resistance surveillance, only the first positive urine culture per patient during the study period (1 July 2024–31 December 2024) was included. Subsequent isolates from the same patient within the same period were considered duplicates and excluded, regardless of species or resistance profile. Patient identification was based on the unique hospital registration number recorded in the Open-Clinic software and cross-checked with laboratory registers.

Sample Collection and Microbiological Analysis

Urine samples were transported to the laboratory within a maximum of two hours after collection. Each sample was inoculated on CLED and MacConkey agar plates and incubated at 37°C for 24 hours. Bacterial identification was performed based on morphological, biochemical, and enzymatic characteristics using standard microbiological methods.

Significant bacteriuria was defined as $\geq 10^5$ CFU/mL for clean-catch mid-stream urine specimens and $\geq 10^3$ CFU/mL for catheterized specimens, in the presence of a single predominant microorganism. Although many international guidelines (EAU, IDSA, CLSI) accept 10^3 CFU/mL in symptomatic non-pregnant women with pyuria, we deliberately retained the more conservative threshold of 10^5 CFU/mL for mid-stream specimens in order to increase specificity in our context of high contamination rates and limited systematic urinalysis with microscopy. This conservative approach is also used by several reference surveillance laboratories in low- and middle-income countries for the same reasons.[13,14]

Culture showing growth of three or more different bacterial morphotypes, or growth of usual skin/contaminant flora at any colony count in the absence of a clearly predominant pathogen, or with >10 squamous epithelial cells per low-power field on direct examination were considered contaminated and excluded.

Antimicrobial Susceptibility Testing

Antibiotic susceptibility testing was performed using the Kirby–Bauer disk diffusion method. Antimicrobial susceptibility testing was first interpreted using the 2024 guidelines of the European Committee on Antimicrobial Susceptibility Testing. When it was not possible to interpret the results, especially for species, antibiotic combinations not covered by EUCAST, breakpoints from the Clinical and Laboratory Standards Institute (M100-S34, 2024) were used as a complement. Bacterial isolates were categorized as Susceptible (S), Susceptible, Intermediate resistant (I), or Resistant (R) based on their inhibition response at standard antibiotic concentrations.

Multidrug-resistant (MDR) bacteria were defined according to the joint criteria of the European Centre for Disease Prevention and Control (ECDC) and the U.S. Centers for Disease Control and Prevention (CDC) ie., non-susceptibility to at least one agent in three or more antimicrobial categories commonly used for treatment.[15] Extensively drug-resistance (XDR) bacteria were defined as non-susceptible to at least one agent in all but two or fewer antimicrobial categories (ie., bacterial isolates remain susceptible to agents in only one or two categories). Pan-drug Resistant (PDR) bacteria were defined as non-susceptible to all agents in all antimicrobial categories.

In this study, the production by *Enterobacterales* of extended-spectrum β-lactamases (ESBL) was determined using the double-disc synergy (DDS) test and / or the resistance to third-generation cephalosporins (C3G) (ceftazidime being the C3G that was tested on many isolates).[16]

Age Group Classification

For analytical purposes, patients were categorized into six age groups:

- Infant: <1 year
- Child: 1–12 years
- Adolescent: 12–18 years
- Adult: 18–40 years
- Senior: 40–60 years
- Very old: >60 years

Data Collection and Statistical Analysis

Data were extracted from the patient's records and corresponding laboratory registers, then encoded and cleaned in Microsoft Excel 2021. The final dataset was analyzed using RStudio version 2024.12.1 + 563. Descriptive statistics were expressed as frequencies and percentages for categorical variables, and medians for continuous variables (eg., age).

Bivariate associations between MDR status (or specific antibiotic resistance, eg., ceftazidime) and patient characteristics (gender, age group, department) were assessed using χ^2 tests or Fisher's exact tests when appropriate (expected cell counts <5). Factors associated with MDR in bivariate analysis ($p < 0.10$) or deemed clinically relevant (eg., gender, age group, department) were included in a multivariate logistic regression model to identify independent predictors. Adjusted OR with 95% CI were reported. Model fit was evaluated using pseudo-R^2 and likelihood ratio tests; instability due to small subgroups (quasi-complete separation) was noted where applicable. XDR and PDR were estimated based on non-susceptibility to agents in all but ≤2 categories (XDR) or all categories (PDR), following Magiorakos et al,[15] with isolates having <5 tested categories excluded. Bivariate associations between BLSE status and patient characteristics (gender, age group, department) were assessed using χ^2 tests or Fisher's exact tests when appropriate (expected cell counts <5). A p-value < 0.05 was considered statistically significant. Results were presented using tables and figures for clarity.

Results

In our study of 380 patients with positive urine cultures, women accounted for 55% of the group, while men comprised 45% (Figure 1).

As can be seen in Figure 2, young adults account for about 41.6% of cases, the pediatric population 40.3% and 18.2% of cases concern very elderly patients. The most represented age group was between 18 and 65 years old. The median age of our population was 28 years. Among the pediatric population, the 2–4-year age group was the most represented. A male predominance was observed among infants under 1 year of age (35.7%; n = 25). Conversely, beyond one year of age, a female predominance was noted (Table 1).

As can be seen in Figure 3, the breakdown by hospital department indicates that pediatrics and internal medicine are the most represented with 39.5% and 26.1%, respectively.

The monthly distribution of cases does not suggest a marked seasonality as can be seen in Figure 4, but variations may be linked to patient flows.

Table 2 shows that *E. coli* (53.9%, 205/380) is by far the most isolated germ in all age groups, followed by *K. pneumoniae* (18.6%, 71/380).

The analysis by hospital department confirms a high prevalence of *Enterobacterales* in all departments, with a predominance in pediatrics 39.6% (132/333) followed by Internal Medicine 25.8% (86/333). Non-fermenting Gram-negative bacilli (*Pseudomonas spp., Acinetobacter sp., S. maltophilia*) were also observed in Internal Medicine and

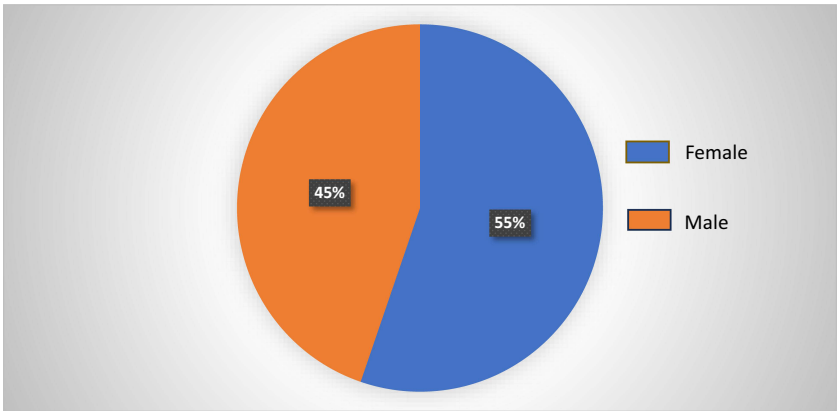

Figure 1 Distribution of patients by sex.

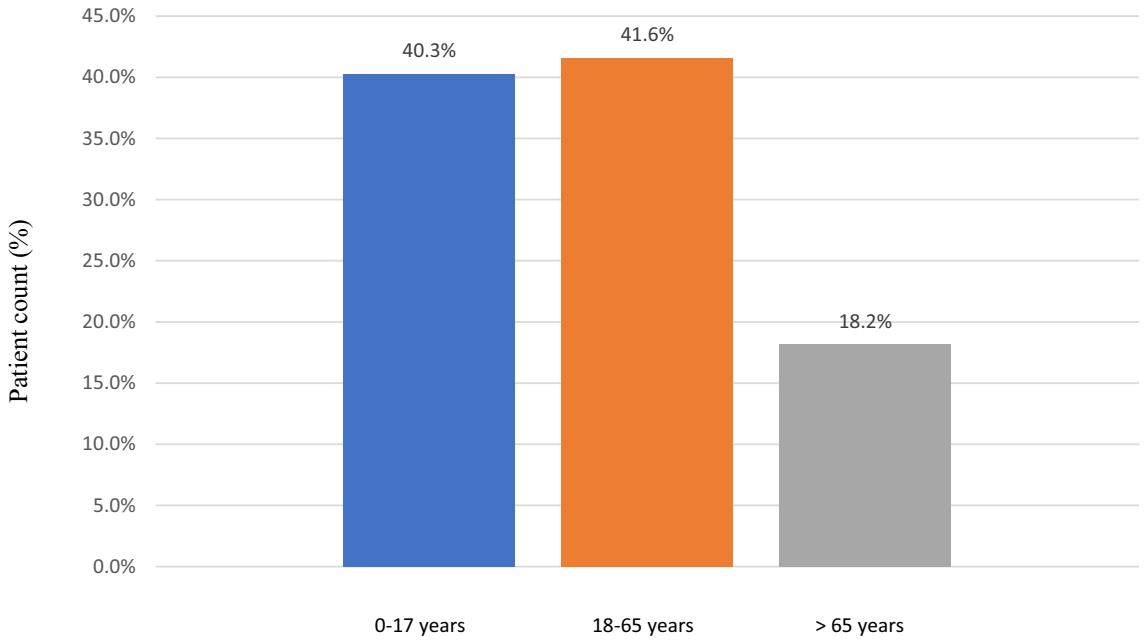

Figure 2 Age distribution of patients.

Pediatrics; 29.6% (8 / 27) for each departments. Gram-positive (*E. faecalis, Streptococcus sp. and S. aureus*) have been observed mainly in pediatrics 45% (9/20) and internal medicine 30% (6/20) (Table 3).

As we can see in Table 4, our study showed a high resistance of *E. coli* to Amoxicillin-clavulanic acid 98.4% (179/182), 3rd generation cephalosporins: ceftazidime 76.5% (144/188), ceftriaxone 63.9% (103/161) and to a lesser extent, to fluoroquinolones: norfloxacin and ciprofloxacin, respectively 65.8% (52/79) and 63.6% (110/173). We note in the same table that *K. pneumoniae* also showed strong resistance to Amoxicillin-clavulanic acid 96.7% (59/61), 3rd generation Cephalosporins: Ceftazidime 83.3% (55/66), Ceftriaxone 77.8% (42/54) and to a lesser extent, fluoroquinolones: ciprofloxacin 67.3% (37/55), norfloxacin 62.5% (15/24). Both *E. coli* and *K. pneumoniae* showed similar resistance trends ($p > 0.05$) to most antibiotics tested, except for Piperacillin-tazobactam, Amikacin, nitrofurantoin, meropenem and gentamycin ($p < 0.05$). By bivariate analysis, however, the resistance rates of *E. coli* compared to *K. pneumoniae* were significantly higher to imipenem (OR = 5.33, p = 0.031), piperacillin-tazobactam (OR = 2.45, p = 0.009), amikacin (OR = 3.05, p = 0.001), nitrofurantoin (OR = 3.90, p = <0.01), meropenem (OR = 4.62, p = 0.003) and gentamicin (OR = 2.04, p = 0.027).

Bivariate analysis revealed a statistically significant association between sex and multidrug resistance (p = 0.04). Furthermore, a significant difference was also observed between hospital departments and multidrug resistance ($p < 0.01$), with the highest prevalence noted in Pediatrics (38.3%, n = 106) and Internal medicine (27.8%, n = 77). However, adjusted

Table 1 Distribution of the Pediatric Population

Parameters	Male N = 70 (%)	Female N = 82 (%)	P value
Age			
0–1	25 (35.7)	19 (23.1)	0.1211
2–4	25 (35.7)	30 (36.5)	
5–9	9 (12.8)	22 (26.8)	
10–17	11 (15.7)	11 (13.4)	
Department			
Pediatrics	68 (97.1)	80 (97.5)	0.7825
Intensive care	1 (1.4)	2 (2.4)	
Surgery	1 (1.4)	0 (0)	

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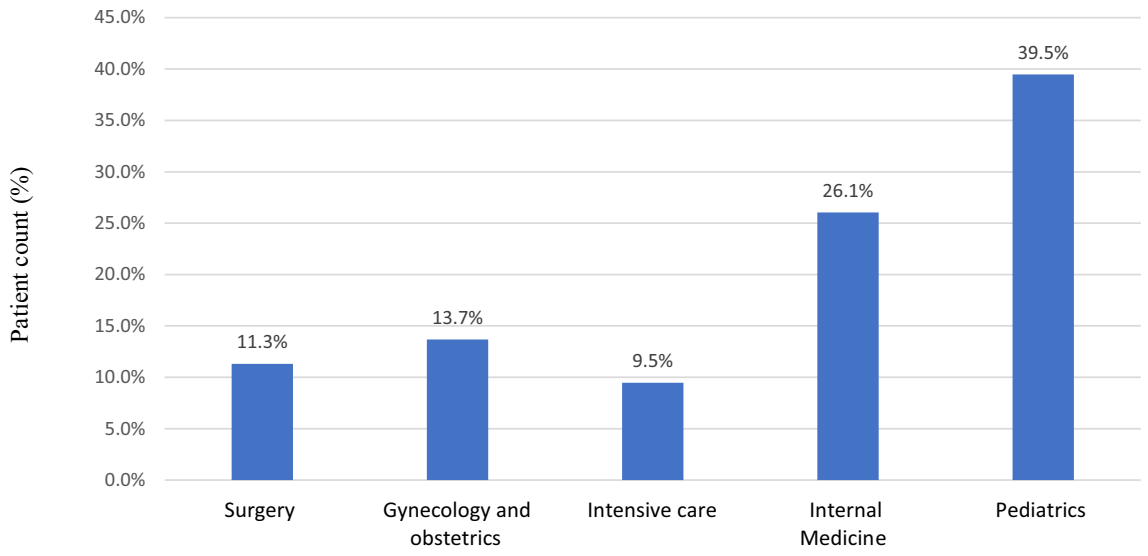

Figure 3 Distribution of patients by department.

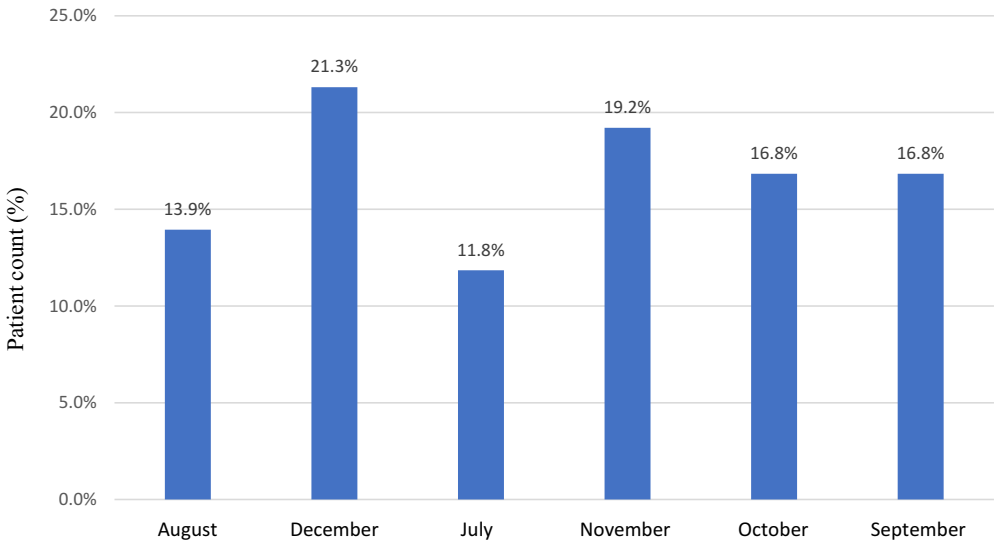

Figure 4 Distribution of patients by period of diagnosis.

multivariate analysis indicated that patients hospitalized in surgery had a higher risk of multidrug resistance compared to patients in Gynecology obstetrics department (OR = 5.43; 95% CI: 1.63–18.09; p = 0.006). Estimates for some age groups were unstable due to small cell counts. No PDR isolates were identified in this study (Table 5).

Figure 5 shows a predominance of *E. coli* (69.6% MDR) and *K. pneumoniae* (83.1% MDR), the main Enterobacterales involved in MDR infections. Other genera such as *Enterobacter spp., Citrobacter freundii* and *Enterococcus spp*. also have high rates of resistance, while non-fermenting bacilli, including *Pseudomonas spp*. and *Acinetobacter spp*., have more variable levels.

Using our screening method for beta-lactamase detection in Enterobacterales, we observed the following epidemiological patterns: The highest prevalence was reported in the Internal Medicine department, followed by Pediatrics. Female patients were predominant, and the most represented age group was 18–65 years. A statistically significant difference was observed when comparing departments with ESBL production (Table 6).

Table 2 Age Distribution of Crops

Germs	0–17 Years Old		18–65 Years Old		>65 Years Old		Total	
	N	%	N	%	N	%	N	%
Fermenting Gram-negative bacilli								
Enterobacterales								
E. coli	79	38.5	83	40.4	43	20.9	205	53.9
K. pneumoniae	41	57.7	23	32.3	7	9.8	71	18.6
Enterobacter spp.	4	22.2	11	61.1	3	16.6	18	4.7
E. aerogenes	2	18.1	9	81.8	0	0	11	2.8
Citrobacter spp.	2	20	5	50	3	30	10	2.6
Klebsiella spp.	4	57.1	2	28.5	1	14.2	7	1.8
Proteus spp.	1	14.2	6	85.7	0	0	7	1.8
Other (Salmonella sp., M. morganii)	3	75	1	25	0	0	4	1
Total	**136**	**40.8**	**140**	**42**	**57**	**17.1**	**333**	**87.6**
Non-fermenting Gram-negative bacilli								
Pseudomonas spp.	5	26.3	6	31.5	8	42.1	19	5
Acinetobacter sp	3	50	2	33.3	1	16.6	6	1.5
S. maltophilia	0	0	2	100	0	0	2	0.5
Total	**8**	**29.6**	**10**	**37**	**9**	**33.3**	**27**	**7.1**
Gram-positive cases								
E. faecalis	5	38.4	5	38.4	3	23	13	3.4
Streptococcus sp	1	25	3	75	0	0	4	1.05
S. aureus	3	100	0	0	0	0	3	0.7
Total	**9**	**45**	**8**	**40**	**3**	**15**	**20**	**5.2**
Total Gen	**153**	**40.2**	**158**	**41.5**	**69**	**18.1**	**380**	**100**

Table 3 Bacteriological Profile of Germs by Department

Culture	Department										Total	
	Surgery		Gynecology-Obstetrics		Intensive Care		Internal Medicine		Paediatrics			
	N	%	N	%	N	%	N	%	N	%	N	%
Fermenting Gram-negative bacilli												
Enterobacterales												
E. coli	18	8.7	39	19	22	10.7	49	23.9	77	37.5	205	53.9
K. pneumoniae	6	8.4	7	9.8	3	4.2	15	21.1	40	56.3	71	18.6
Enterobacter spp.	4	22.2	1	5.5	3	16.6	5	27.7	5	27.7	18	4.7
E. aerogenes	4	36.3	0	0	2	18.1	4	36.3	1	9	11	2.8
Citrobacter spp.	3	30	0	0	0	0	5	50	2	20	10	2.6
Klebsiella spp.	0	0	0	0	0	0	3	42.8	4	57.1	7	1.8
Proteus spp.	1	14.2	1	14.2	0	0	4	57.1	1	14.2	7	1.8
Other *(Salmonella sp, M. morganii)*	1	25	0	0	0	0	1	25	2	50	4	1
Total	**37**	**11.1**	**48**	**14.4**	**30**	**9**	**86**	**25.8**	**132**	**39.6**	**333**	**87.6**

(*Continued*)

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Table 3 (Continued).

Culture	Department										Total	
	Surgery		Gynecology-Obstetrics		Intensive Care		Internal Medicine		Paediatrics			
	N	%	N	%	N	%	N	%	N	%	N	%
Non-fermenting Gram-negative bacilli												
Pseudomonas spp.	3	15.7	1	5.2	4	21	6	31.5	5	26.3	19	5
Acinetobacter sp	2	33.3	0	0	1	16.6	0	0	3	50	6	1.5
S. maltophilia	0	0	0	0	0	0	2	100	0	0	2	0.5
Total	**5**	**18.5**	**1**	**3.7**	**5**	**18.5**	**8**	**29.6**	**8**	**29.6**	**27**	**7.1**
Gram-positive cases												
E. faecalis.	1	7.6	1	7.6	1	7.6	5	38.4	5	38.4	13	3.4
Streptococcus sp	0	0	2	50	0	0	1	25	1	25	4	1.05
S. aureus	0	0	0	0	0	0	0	0	3	100	3	0.7
Total	**1**	**5**	**3**	**15**	**1**	**5**	**6**	**30**	**9**	**45**	**20**	**5.2**
Total	**43**	**11.3**	**52**	**13.6**	**36**	**9.4**	**100**	**26.3**	**149**	**39.2**	**380**	**100**

Table 4 Prevalence and Comparative Resistance Profiles of *E. coli* and *K. pneumoniae*

Antibiotic	*E. coli* %R (n/N)	*K. pneumoniae* %R (n/N)	χ^2	p-value (χ^2)	Odds Ratio (95% CI)	p-value (OR)
Imipenem	4.5 (3/67)	20.0 (5/25)	3.74	0.053	5.33 (1.17–24.31)	0.031*
Piperacillin-Tazobactam	25.6 (40/156)	45.8 (22/48)	6.15	0.013*	2.45 (1.25–4.80)	0.009*
Amikacin	16.0 (26/163)	36.7 (22/60)	9.95	0.002*	3.05 (1.56–5.97)	0.001*
Nitrofurantoin	25.7 (46/179)	57.4 (31/54)	17.45	<0.001*	3.90 (2.06–7.35)	<0.001*
Levofloxacin	58.3 (109/187)	57.8 (37/64)	0.00	1.000	0.98 (0.55–1.74)	0.947
Amoxicillin-Clavulanic acid	98.4 (179/182)	96.7 (59/61)	0.07	0.799	0.49 (0.08–3.03)	0.446
Ciprofloxacin	63.6 (110/173)	67.3 (37/55)	0.11	0.737	1.18 (0.62–2.24)	0.619
Cefotaxime	33.3 (1/3)	50.0 (1/2)	0.00	1.000	2.00 (0.05–78.25)	0.711
Norfloxacin	65.8 (52/79)	62.5 (15/24)	0.00	0.956	0.87 (0.34–2.23)	0.765
Cotrimoxazole	0 (0/0)	0.0 (0/1)	-	-	-	-
Cefuroxime	33.3 (1/3)	100.0 (1/1)	0.00	1.000	-	-
Cephalexin	75.0 (3/4)	50.0 (1/2)	0.00	1.000	0.33 (0.01–11.94)	0.547
Ceftriaxone	63.9 (103/161)	77.8 (42/54)	2.91	0.088	1.97 (0.96–4.04)	0.064
Ceftazidime	76.5 (144/188)	83.3 (55/66)	1.07	0.301	1.56 (0.75–3.24)	0.230
Meropenem	5.7 (8/141)	21.7 (10/46)	8.53	0.003*	4.62 (1.70–12.55)	0.003*
Gentamicin	52.7 (88/167)	69.5 (41/59)	4.36	0.037*	2.04 (1.09–3.85)	0.027*

Note: P-value less than 0.05*.

Table 5 Factors Associated with MDR: Univariate and Multivariate Analyses

Characteristic	MDR N = 277 (%)	Non-MDR N = 101 (%)	p-value (Bivariate)	Adjusted OR (95% CI)	p-value (Multivariate)
Gender					
Female (ref)	141 (50.9)	68 (67.3)	0.004*	1.00	
Male	136 (49.1)	33 (32.7)		1.09 (0.66–1.78)	0.740

(*Continued*)

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Table 5 (Continued).

Characteristic	MDR N = 277 (%)	Non-MDR N = 101 (%)	p-value (Bivariate)	Adjusted OR (95% CI)	p-value (Multivariate)
Department					
Gynaecology & Obstetrics (ref)	26 (9.4)	26 (25.7)	<0.001*	1.00	
Intensive care	27 (9.7)	9 (8.9)		1.69 (0.62–4.63)	0.307
Internal Medicine	77 (27.8)	22 (21.8)		1.27 (0.51–3.16)	0.610
Paediatrics	106 (38.3)	42 (41.6)		Unstable	–
Surgery	41 (14.8)	2 (2.0)		5.43 (1.63–18.09)	0.006*
Age group					
Infant (<1 year) (ref)	33 (11.9)	10 (9.9)	0.058	1.00	
Child (1–12 years)	68 (24.5)	30 (29.7)		0.66 (0.13–3.37)	0.612
Adolescent (12–18 years)	11 (4.0)	1 (1.0)		Unstable	–
Adult (18–40 years)	55 (19.9)	29 (28.7)		Unstable	–
Senior (40–60 years)	39 (14.1)	17 (16.8)		Unstable	–
Very old (>60 years)	71 (25.6)	14 (13.9)		Unstable	–

Note: P-value less than 0.05*.

Discussion

Prevalence and Demographic Distribution

The main objective of this study was to determine the sensitivity and resistance profiles of bacterial isolates to antibiotics commonly used in urinary tract infections (UTIs) at HPGRB.

Our findings revealed a high prevalence of UTIs, with a predominance among women (55%) and a significant proportion of infections in children (40.3%) and young adults (41.6%). This sex distribution aligns with regional data, such as the study by Mbuya et al in Lubumbashi, where 72.6% of 216 confirmed UTI cases occurred in females.[4] Similarly, Odongo et al in Uganda,

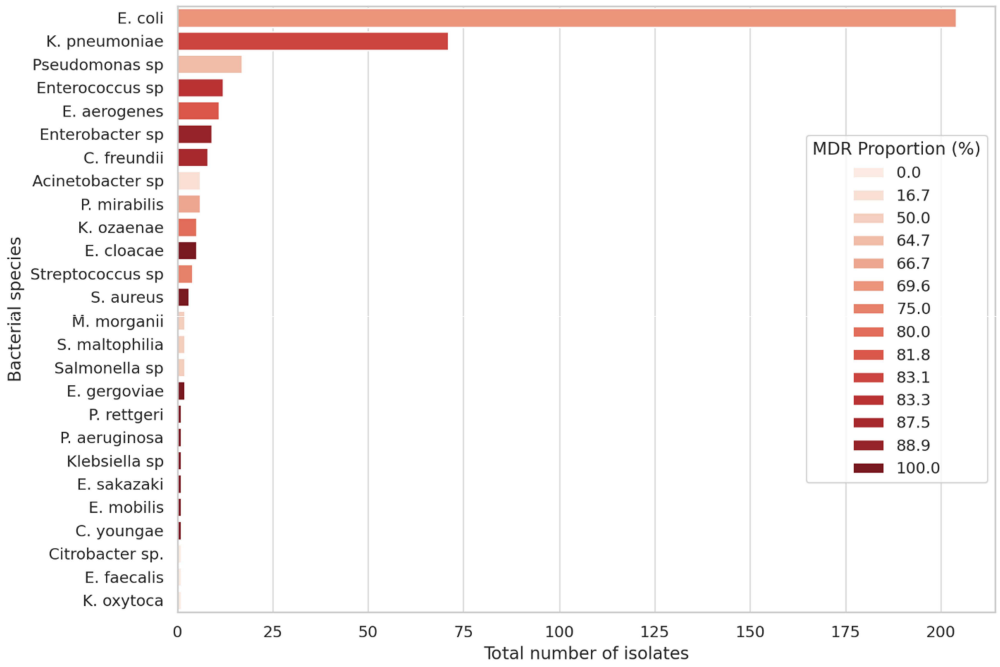

Figure 5 Prevalence of multidrug-resistant germs.

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Table 6 Prevalence of Extended-Spectrum Beta-Lactamase (ESBL)-Producing *Enterobacterales*

Characteristic	ESBL-Positive N = 239 (%)	ESBL-Negative N = 69 (%)	χ^2	p-value
Department				
Surgery	35 (14.6%)	0 (0.0%)	18.834	0.0008*
Gynaecology-Obstetrics	44 (18.4%)	15 (21.7%)		
Acute Medicine	28 (11.7%)	22 (31.9%)		
Internal Medicine	81 (33.9%)	22 (31.9%)		
Paediatrics	51 (21.3%)	10 (14.5%)		
Sex				
Female	130 (54.4%)	43 (62.3%)	1.063	0.303
Male	109 (45.6%)	26 (37.7%)		
Age group				
0–17 years	94 (39.3%)	29 (42.0%)	2.195	0.334
18–65 years	99 (41.4%)	32 (46.4%)		
>65 years	46 (19.2%)	8 (11.6%)		

Note: P-value less than 0.05*.

analyzing 82 community-acquired isolates, also reported a strong female predominance (96.3%), which they attributed to anatomical and hormonal factors.[17] Regarding pediatric population, female sex was predominant (82/152, 53.9%). Our finding is consistent with the study by *Mashako* et al[7] in North Kivu, which also reported a significant female predominance (61.8%, 21/39; $p < 0.05$). Another study conducted in Kimpese, Kongo Central, by *Mafuta* et al[12] found that female children had a significantly higher risk of developing a urinary tract infection compared to male children (OR = 2.79; 95% CI: 1.67–4.65). In contrast, our study found no statistically significant difference between sexes ($p = 0.1211$). These findings suggest that, despite the observed female predominance in our study, urinary tract infections also affect male children considerably in Bukavu. Our study shows a male predominance in the 0–1 year age group (n = 25, 35.7%). Beyond one year of age, however, females become more prevalent. This finding is consistent with the results of *Maria* et al ($p < 0.0001$)[18] and aligns with other studies that also reported a slight improvement.[2,19]

Bacteriological Profile

Gram-negative bacilli were clearly predominant, with *E. coli* (53.9%) and *K. pneumoniae* (18.7%) as the leading etiological agents in adults and children. These results are consistent with those of *Kabego* et al, who, a decade earlier in the same institution, reported *E. coli* (58.5%) and *Klebsiella spp*. (21.9%) as the most frequent isolates among 643 positive urine cultures.[5] Comparable findings were also observed in Lubumbashi, where *E. coli* accounted for 40.2% and *K. pneumoniae* for 24.07% of 216 positive urine cultures.[4] The predominance of *E. coli* in adults and children as the main uropathogenic is further supported by several national and international reviews.[3,17,18,20,21]

Antibiotic Resistance Trends

Our study showed a high resistance of *E. coli* and *K. pneumoniae* to the same antibiotics: Amoxicillin-clavulanic acid (98.4% and 96.7% respectively), 3rd generation Cephalosporins: Ceftazidime (76.5% and 83.3% respectively), Ceftriaxone (63.9% and 77.8% respectively) and to a lesser extent, to Fluoroquinolones: norfloxacin (65.8% and 62.5% respectively) and ciprofloxacin (63.6% and 67.3% respectively). These rates are considerably higher than those reported by *Kabego* et al[5] ten years earlier at the same hospital, where resistance to amoxicillin–clavulanic acid, ceftazidime, and ciprofloxacin in *E. coli* and *Klebsiella* spp. ranged between 11% and 16%. By contrast, *Irenge* et al[11] in 2023 found that 75% of *E. coli* and 87.2% of *K. pneumoniae* isolates from Bukavu were resistant to ciprofloxacin, confirming the sharp rise in resistance over the past decade. The growing resistance to Fluoroquinolones and Third-generation cephalosporins among Enterobacterales in Bukavu has been repeatedly documented. This resistance profile

forces a shift toward antibiotic combinations or alternative classes, including aminoglycosides. While carbapenems remain highly effective, stewardship guidelines limit their routine use in UTIs to prevent further selection pressure. In the long term, this dynamic risks exacerbating the global burden of antimicrobial resistance, driven by the rapid spread of resistance determinants beyond the urinary tract.[5,11,22]

Both *E. coli* and *K. pneumoniae* showed similar resistance trends ($p > 0.05$) to most antibiotics tested. Bivariate analysis revealed that infection with *Klebsiella* was associated with significantly higher odds of resistance to several antibiotics: imipenem (OR = 5.33, $p = 0.031$), meropenem (OR = 4.62, $p = 0.003$), nitrofurantoin (OR = 3.90, $p < 0.01$), amikacin (OR = 3.05, $p = 0.001$), piperacillin-tazobactam (OR = 2.45, $p = 0.009$), and gentamicin (OR = 2.04, $p = 0.027$). This situation is particularly alarming, as these antibiotics serve as second-line or last-resort treatments for many serious infections.[6,10] Our findings underscore the need for molecular studies to elucidate the underlying resistance mechanisms in *K. pneumoniae* and *E. coli*. In the DRC, antibiotic use has become uncontrolled, with self-medication being prevalent. Consequently, establishing stringent control over both the prescription and consumption of these critical drugs is imperative.

On a positive note, carbapenems (imipenem and meropenem) and amikacin retained good in vitro activity and remain viable therapeutic alternatives. Similar trends have been observed in African and international studies, although the increasing reliance on carbapenems raises concern for the potential emergence of carbapenemase-producing strains.[4,8,10]

Multidrug Resistance (MDR) and Contributing Factors

The proportion of MDR strains observed approximately 70% for *E. coli* and 82% for *K. pneumoniae* is high compared to other African studies, yet consistent with regional findings. Irenge et al[8] analyzed 449 clinical isolates from South Kivu and sequenced 37 MDR *K. pneumoniae* ESBL-producing strains, confirming the circulation of conjugative plasmids encoding resistance genes. *Kadima* et al,[22] in a retrospective study of 712 isolates, reported 29.4% MDR bacteria, while Bikioli-Bolombo et al[11] found 31.4% MDR/XDR isolates both demonstrating the persistence of resistant pathogens in Bukavu's hospitals.

A significant association was observed between hospital departments and the prevalence of MDR ($p < 0.01$). The highest rates were found in Pediatrics (38.3%, n = 106) and Internal Medicine (27.8%, n = 77). This pattern may be explained by several factors. Patients in these departments often resort to self-medication with antibiotics or traditional remedies prior to seeking formal care. Upon presentation, they frequently enter healthcare facilities that are under-resourced, lacking both the diagnostic equipment and specialized personnel required for guiding appropriate antibiotic therapy. This cycle of empirical treatment and inadequate stewardship likely contributes to the selection and spread of MDR strains.[9]

There are insufficient studies on the molecular biology of multi-resistance in certain germs; however, *Irenge* et al[8] conducted SNP-based phylogenetic analysis of MDR ESBL-producing *K. pneumoniae* strains from Bukavu (DRC), revealing high genetic diversity: 37 isolates distributed across 16 distinct clusters, each with a unique MLST profile. The most frequent STs were ST607 and ST48 (n = 6 each), ST340 (n = 5), and ST39 (n = 4); ST15, ST874, ST1777, and ST37 (n = 2 each); others (ST14, ST16, ST502, ST337, ST967, ST11, ST309, ST2094) as single isolates. These Congolese lineages share STs with other sub-Saharan and global strains (64.9%; eg., ST14, ST15, ST39, ST48, ST340, ST607), but differ in phylogeny, virulence gene content, and carbapenem susceptibility (unlike international clones).

Prevalence of Extended-Spectrum Beta-Lactamase (ESBL)-Producing Enterobacterales

In our study, we identified 239 ESBL-producing strains among 333 isolated *Enterobacterales*, representing a prevalence of 71.7%. It is among the highest prevalences in the world.[23] This rate is substantially higher than that reported in Kinshasa (17.8%, 92/516),[24] a difference attributable to the identification methods employed. In Kinshasa, BLSE was detected using a synergy test combining clavulanic acid with cefotaxime, ceftazidime, and cefepime discs, while our study relied on the search for the champagne cork between clavulanic acid and ceftazidime alone or simply resistance to ceftazidime in the absence of the champagne cork. A statistically significant difference was observed between hospital departments and ESBL production ($p = 0.0008$). The highest prevalence was recorded in internal medicine (33.9%, n = 81), followed by pediatrics (21.3%, n = 51), likely due to increased antibiotic use in these departments.

According to *Irenge* et al,[8] *Enterobacterales* producing ESBL in the DRC mainly carry the genes $bla_{\text{CTX-M-15}}$ (prevalent in 33/37 MDR *K. pneumoniae* isolates), $bla_{\text{TEM-1}}$ (31/37 isolates), and various bla_{SHV} variants (SHV-1, −28, −62, −110, −121). These genes are often redundant, conferring an ESBL phenotype in 100% of MDR isolates. However, in Kinshasa, a study revealed *bla*CTX-M-15 as the dominant ESBL (30.4% [n = 31]), followed by $bla_{\text{CTX-M-28}}$ (20.6% [n = 21]), $bla_{\text{TEM-68}}$ (17.6% [n = 18]), $bla_{\text{CTX-M-3}}$ and $bla_{\text{TEM-104}}$ (9.8% each [n = 10]), $bla_{\text{SHV-12}}$ and $bla_{\text{CTX-M-22}}$ (4.9% each [n = 5]), and others in low proportions ($bla_{\text{TEM-168}}$: 1.96% [n = 2]; $bla_{\text{CTX-M-34}}$, $bla_{\text{CTX-M-62}}$, $bla_{\text{SHV-2}}$, $bla_{\text{SHV-5}}$: 0.98% each [n = 1]).[24] Given the high proportion of ESBL-producing strains in our study, more molecular studies are urgently needed to effectively combat antibiotic resistance in our setting.

Public Health Implications and Recommendations

These findings underscore the urgent need for context-adapted interventions. Priority actions include:

1. Implementation of antibiotic stewardship programs to rationalize prescriptions and preserve the efficacy of last-line antimicrobials;
2. Strengthening diagnostic capacity, including broader access to culture and sensitivity testing as well as molecular assays; and
3. Education and awareness campaigns for both healthcare workers and the general population to promote prudent antibiotic use and infection prevention practices.

Study Limitations

This study has certain limitations. It was monocentric, based on samples from a single hospital in Bukavu, which may restrict the generalizability of the results to the entire province. Consequently, our analysis was necessarily limited to a screening approach based on the presence of champagne cork and/or resistance to C3G (ceftazidime) as an indicator of the presumed presence of ESBL-producing *Enterobacterales*. We were unable to confirm the presence of ESBL genes using molecular approaches. The small subgroups in the multivariate models caused instability, warranting larger-scale studies. Finally, the 6-month period may not reflect seasonal variations.

Conclusion

This study highlights the predominance of *E. coli* and *K. pneumoniae* as the main uropathogens responsible for urinary tract infections at HPGRB. The high prevalence of MDR strains, particularly against Third-generation cephalosporins and Fluoroquinolones, reflects a worrying trend consistent with regional and continental data.

Carbapenems and amikacin remain largely effective. However, their increasing use risks driving the emergence of resistant strains. This would undermine this advantage. This situation calls for urgent action, including the establishment of a structured regional antibiotic surveillance system alongside strong antimicrobial stewardship programs. In the absence of coordinated surveillance, educational initiatives for healthcare providers, and locally tailored, evidence-based protocols, these advanced treatment options may become obsolete. Priority should therefore be given to developing sustainable stewardship frameworks that reflect regional capacity and resistance patterns. Moreover, improving diagnostic capacities, ensuring adherence to infection prevention and control measures, and raising awareness among healthcare workers and the general population are critical steps to curb the spread of resistant pathogens. Continued research, including molecular investigations, will be essential to better characterize resistance mechanisms and support evidence-based therapeutic strategies in the region.

Abbreviations

DRC, Democratic Republic of Congo; UTIs, Urinary tract infections; HPGRB, Hôpital Provincial Général de Référence de Bukavu; CLED, Cysteine Lactose Electrolyte Deficient; CLSI, Clinical and Laboratory Standards Institute; EUCAST, European Committee on Antimicrobial Susceptibility Testing; MDR, Multidrug-resistant; CFU, Colony Forming Unit; ECDC, European Centre for Disease Prevention and Control; CDC, Centers for Disease Control and Prevention; MDR, Multidrug-resistant; ESBL, Extended-spectrum β-lactamase.

Data Sharing Statement

The finding of this study is generated from the data collected and analyzed based on the stated methods and materials. All generated data are included in the manuscript. The original dataset supporting this finding is available upon request from the corresponding author (Bashizi Cito).

Ethics Approval

This work is part of an ongoing research study on antibacterial resistance in hospital settings in Bukavu. The study received approval from the Ethics Committee of the Université Catholique de Bukavu (P.O. Box 285, Bukavu, Democratic Republic of the Congo), under reference number n°UCB/CIE/NC/014/2016. The principles of confidentiality and discretion were scrupulously observed, and all data were analysed in strict accordance with the anonymity of the participants. Our research was not a clinical trial; however, it was conducted in accordance with the principles of the Declaration of Helsinki. This compliance is demonstrated by the fact that the study protocol received formal approval from the ethics committee of Université Catholique de Bukavu. This ensured that the research met rigorous ethical standards concerning participant welfare and data integrity.

Consent to Participate

The data for this retrospective study were sourced from hospital patient records and laboratory registries. The analysis was conducted with a strict guarantee of anonymity, and the results were used exclusively for scientific and care improvement purposes. Due to the retrospective nature of the study, informed consent was waived by the ethics committee.

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Author Contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis, and interpretation, or all these areas; took part in drafting, revising, or critically reviewing the article; gave final approval of the version to be published; agreed on the journal to which the article has been submitted; and agreed to be accountable for all aspects of the work.

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Disclosure

The authors declare that they have no competing interests in this work.

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