

Original Research Article

Multidrug-Resistant Bacteria and their Antimicrobial Susceptibility Patterns in Intensive Care Unit at Brazzaville, Republic of Congo: A Retrospective, Observational and Descriptive Study

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Abstract: **Aim:** to describe multidrug-resistant bacteria and their antimicrobial susceptibility patterns in ICU at Brazzaville University Teaching Hospital (CHUB).

Materials and Methods: This was an observational, descriptive, and retrospective study, over 12 months, including all bacteria isolated in infected patients in ICU at CHUB. Epidemiological, clinical and bacteriological parameters were analyzed with Excel 2019. **Results:** 99 Bacteria were identified in 115 samples of 77 patients. Median age of patients was 48 years [32–65 years], 57.1% were females and acute generalized peritonitis represented 26% of diagnoses. Blood cultures (44.4 %), Gram-negative bacilli (77.7 %) were the most represented. *E. coli* (13.1%), *K. pneumoniae* (10.1%), *A. baumannii* (9.1%) and *S. aureus* (8.1%) were most bacteria identified. *E. coli* strains were extended-spectrum beta-lactamase (ESBL)- *E. coli* (82.4%) and carbapenem-resistant *E. coli* (86.4%). *E. coli* was resistant to third-generation cephalosporins (3GC) (86.1%), to fluoroquinolones (81.3%), to aminoglycosides (72.7%). ESBL-producing *K. pneumoniae* represented 76.1% and carbapenem-resistant *K. pneumoniae* represented 23.5% of *K. pneumoniae* strains. *K. pneumoniae* was resistant to piperacillin/tazobactam (83.3%), to aztreonam (71.4%), to quinolones (75.9%) and to aminoglycosides (66.7%). *A. baumannii* strains were resistant to Carbapenem (100%), to 3GC (100%), piperacillin/tazobactam (100%), aminoglycosides (92%), and quinolones (89.2%). *S. aureus* strains were Methicillin-resistant *S. aureus* in 75% and *S. aureus* strains were resistant to piperacillin/tazobactam (90.9%), vancomycin (88.9%), carbapenems (88.2%), 3GC (86%), quinolones (82.6%). **Conclusion:** The Multi-Drug-Resistant bacteria prevalence is very high in ICU at CHUB.

Keywords: Antimicrobial Resistance, Intensive Care Unit, Brazzaville.

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1. INTRODUCTION

Bacterial antimicrobial resistance (AMR) has emerged as one of the leading public health threats of the 21st century [1]. Antibiotic-resistant pathogens are associated with the highest burden and health-care costs and antibiotic-resistant infections caused an estimated 1.27 million deaths globally, disproportionately affecting low-income and middle-income countries [2]. Intensive Care Units (ICUs) present unique conditions (patients are critically ill, immunocompromised, and often subjected to invasive procedures and extended hospital stays) provide an ideal environment for the emergence and spread of resistant pathogens. AMR poses significant challenges for healthcare providers in ICUs, where

timely and effective antibiotic treatment is crucial, directly impacting on clinical outcomes, mortality rates and increased healthcare costs [3].

In response to the AMR threat, World Health Organization (WHO) launched its first Bacterial Priority Pathogens List (BPPL) in 2017, which had the aim of guiding the research and development of new antibacterials and was established based on pathogen resistance profiles, public health impact, and the need for new treatments [2]. Some of bacteria on this list, notably *Escherichia coli* (*E. coli*), *Klebsiella pneumoniae* (*K. pneumoniae*), *Acinetobacter baumannii* (*A. baumannii*), *Pseudomonas aeruginosa* and *Staphylococcus aureus* (*S.*

aureus) have been identified in ICUs in Africa [5-7], and in the Republic of Congo [8, 9]. It's crucial to identify most common bacteria causing infection in ICU patients in order to select an effective probabilistic antibiotic therapy and to implement infection prevention and control measures [10]. However, no data are available on antimicrobial susceptibility patterns of these bacteria in ICUs in the Republic of Congo. This study aims to describe multidrug-resistant bacteria and their antimicrobial susceptibility patterns in ICU at Brazzaville University Teaching Hospital (CHUB), Republic of Congo.

2. MATERIALS AND METHODS

This was a retrospective, observational and descriptive study. We compiled results of bacteriological analyses of all biological samples collected from patients admitted to the General ICU at CHUB in the Republic of Congo. All bacteria isolated from January 1st to December 31st, 2025, were included. We excluded samples from which nonbacterial organisms were isolated. We did not include patients admitted to the ICU with bacteriological test results from samples collected outside the ICU.

The parameters analysed were epidemiological (age and sex of patients), clinical (diagnoses), and bacteriological (type of bacteriological test performed, types of bacteria isolated, names of bacteria identified, and their antimicrobial susceptibility patterns). These parameters were collected using a pre-designed survey form. Statistical analysis of data was performed using Excel 2019 for Windows. Quantitative variables were expressed as mean $\pm$ standard deviation or as median (quartiles), and qualitative variables were expressed as percentages. Patient anonymity and data confidentiality were respected.

CHUB is a Level III healthcare facility of the Republic of Congo with a current capacity of 876 beds distributed across various departments. These include a General ICU, and a Department of Bacteriology and Virology Laboratories.

With 11 beds, the ICU is led by an Anesthesiologist-Intensive Care Physician and has a residency in Anesthesiology and Critical Care. The nurse patient ratio was 1:3 on average a day and night. Medical care was provided by an Anesthesiologist-Intensive Care Physician and three residents during the day, two residents at night.

Bacteriological analysis was performed in the Department of Bacteriology and Virology Laboratories. Microorganisms were identified using Api R strips (Biomérieux): Api 20 E for enterobacteria, Api Staph strips for staphylococci, and Api Strep strips for streptococci. Antibigram testing was performed using agar diffusion methods with antibiotic discs, in accordance with the recommendations of the French Society of Microbiology [11].

3. RESULTS

We recorded 115 bacteriological samples collected from 77 patients, or 1.5 samples per patient. 99 bacteria were identified in 115 samples, representing a positivity rate of 86.1%. Median age of patients was 48 years [32–65 years], with ages ranging from 15 to 89 years. The largest number of patients were under the age of 60 years (63.7%) and 57.1% were females. Acute generalized peritonitis accounted for 26% of the diagnoses (n = 20). Table I presents distribution of patients according to epidemiological and clinical data.

Table I: Distribution of patients according to epidemiological and clinical data

	N=77	Percentage (%)
Age groups in years		
15 - 29	17	22,1
30 - 44	17	22,1
45 - 59	15	19,5
≥ 60	28	36,3
Sexe		
Female	44	57,1
Male	33	42,9
Diagnoses		
Acute generalised peritonitis	20	26,0
Ventilator-associated pneumonia	12	15,6
Severe community-acquired pneumonia	11	14,3
Bacterial encephalitis	10	13,0
Nosocomial urinary tract infection	9	11,8
Bacterial dermatitis and cellulitis	6	7,8
Post-operative peritonitis	5	6,5
Bacteraemia	2	2,6
Perineal gangrene	1	1,3
Gallbladder gangrene	1	1,3

The 115 bacteriological samples consisted 51 blood cultures (44.4 %), 42 urine cultures (36.5 %), 13 tracheal aspirates (15 %), five intraoperative peritoneal samples (4.4 %) and two cyto bacteriological examinations of central line catheter tips (1.7 %).

As regards bacteria identified, these comprised 66 Gram-negative bacilli (GNB) (77.7 %) and 33 Gram-positive cocci (33.3 %). GNB were fermenting in 77.3 % of cases (n=51) and non-fermenting in 22.7 % of cases

(n=15). All 33 Gram-positive cocci (GPC) were fermenting.

Identified GNBs were *E. coli* in 13.1% of cases (n=13), *K. pneumoniae* in 10.1% of cases (n=10), and *A. baumannii* in 9.1% of cases (n=9). The GPC identified were *S. aureus* in 8.1% of cases (n=8), *Staphylococcus non -aureus* in 6.1% of cases (n=6), and *Streptococcus spp.* in 5.1% of cases (n=5). Table II lists all identified bacteria.

Table II: identified bacteria

	N=99	Percentage (%)
Gram-negative fermenting bacilli (n=51)		
<i>Escherichia coli</i>	13	13,1
<i>Klebsiella pneumoniae</i>	10	10,1
<i>Enterobacter cloacae</i>	5	5,1
<i>Proteus mirabilis</i>	3	3,1
<i>Citrobacter koseri</i>	3	3,1
<i>Klebsiella oxytoca</i>	3	3,1
<i>Morganella morganii</i>	2	2,1
<i>Klebsiella terrigena</i>	2	2,1
<i>Enterobacter aerogenes</i>	2	2,1
<i>Pantoea spp</i>	2	2,1
<i>Raoultella ornithinolytica</i>	2	2,1
<i>Enterobacter hafnia</i>	1	1,1
<i>Enterobacter spp</i>	1	1,1
<i>Serratia spp</i>	1	1,1
<i>Burkholderia cepacea</i>	1	1,1
Gram-negative non-fermenting bacilli (n=15)		
<i>Acinetobacter baumannii</i>	9	9,1
<i>Morganella morganii</i>	2	2,1
<i>Burkholderia cepacea</i>	1	1,1
<i>Stenotrophomonas maltophilia</i>	1	1,1
<i>Pseudomonas luteola</i>	1	1,1
<i>Pseudomonas spp</i>	1	1,1
Gram-positive cocci (n=33)		
<i>Staphylococcus aureus</i>	8	8,1
<i>Staphylococcus non aureus</i>	6	6,1
<i>Streptococcus spp</i>	5	5,1
<i>Enterococcus faecium</i>	3	3,1
<i>Enterococcus spp</i>	3	3,1
<i>Staphylococcus epidermidis</i>	3	3,1
<i>Staphylococcus spp</i>	2	2,1
<i>Staphylococcus haemolyticus</i>	1	1,1
<i>Streptococcus agalactiae</i>	1	1,1
<i>Streptococcus pneumoniae</i>	1	1,1

E. coli strains were extended-spectrum beta-lactamase (ESBL)-producing in 82.4% of cases, with resistance to amoxicillin-clavulanic acid (91.7%), third-generation cephalosporins (3GC) (86.1%), to fluoroquinolones (81.3%), and to piperacillin/

tazobactam (66.7%). Carbapenemases were produced by 86.4% of *E. coli* strains. Acquired resistance to aminoglycosides was also identified in 72.7% of *E. coli* strains. The antimicrobial susceptibility pattern of *E. coli* is shown in figure 1.

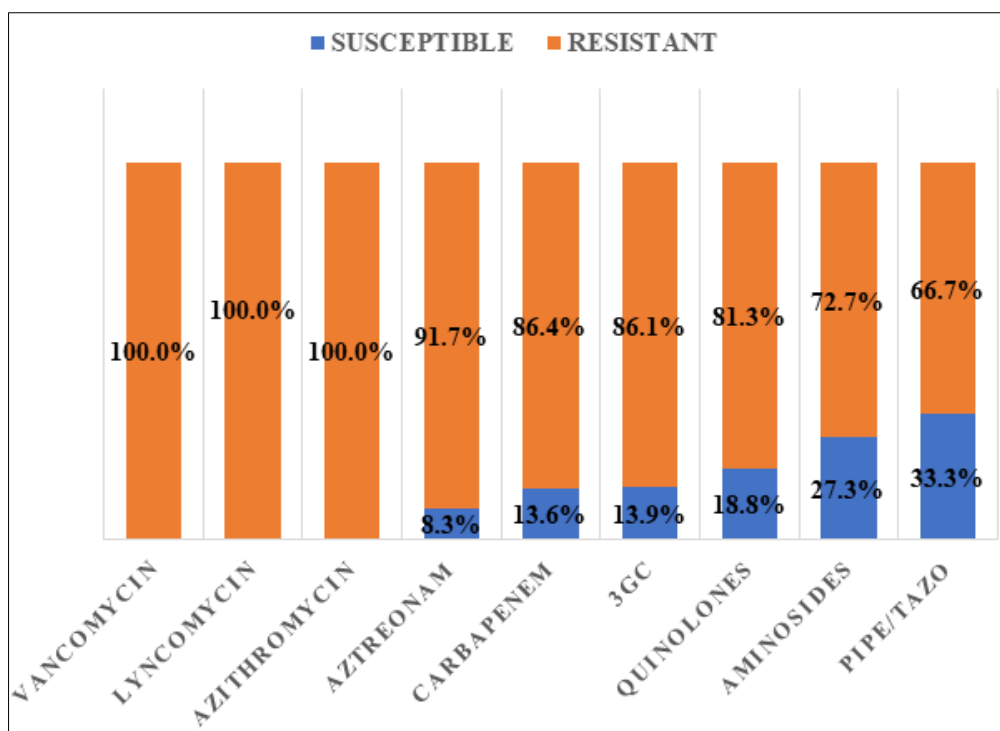


Figure 1: *E. coli* antimicrobial susceptibility patterns
3GC: third-generation cephalosporins; **Pipe/Tazo:** piperacillin + tazobactam

ESBL-producing *K. pneumoniae* strains represented 76.1% of *K. pneumoniae* strains identified as resistant to penicillins (100%), piperacillin/tazobactam (83.3%), aztreonam (71.4%), and 3GC antibiotics (49.6%). Susceptibility to carbapenems was preserved in 76.5% of *K. pneumoniae* strains, with carbapenemase

production observed in 23.5% of *K. pneumoniae* strains. Acquired resistance to quinolones (75.9%) and aminoglycosides (66.7%) was observed. The antimicrobial susceptibility pattern of *K. pneumoniae* is shown in figure 2.

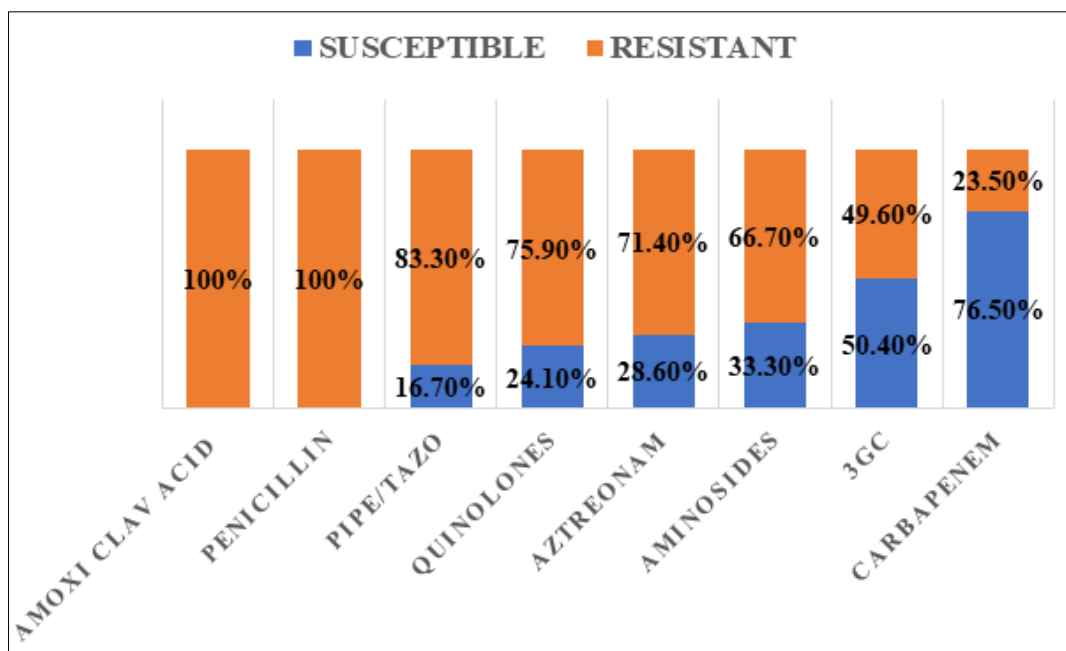


Figure 2: *Klebsiella pneumoniae* antimicrobial susceptibility patterns
Amoxi Clav Acid: Amoxicillin + clavulanic acid; **3GC:** third-generation cephalosporins; **Pipe/Tazo:** piperacillin + tazobactam

All *A. baumannii* strains were resistant to carbapenems (100%). These carbapenem-resistant *Acinetobacter baumannii* (CRAB) strains were also resistant to 3GC (100%), piperacillin/tazobactam (100%), aminoglycosides (92%), and quinolones (89.2%), typical characteristics of highly resistant CRAB

strains (XDR: Extensively Drug-Resistant). Susceptibility to colistin was not tested. Five XDR-CRAB strains were also resistant to tigecycline, a characteristic of pan-resistant CRAB strains (PDR: Pandrug-Resistant). The antimicrobial susceptibility pattern of *A. baumannii* is shown in figure 3.

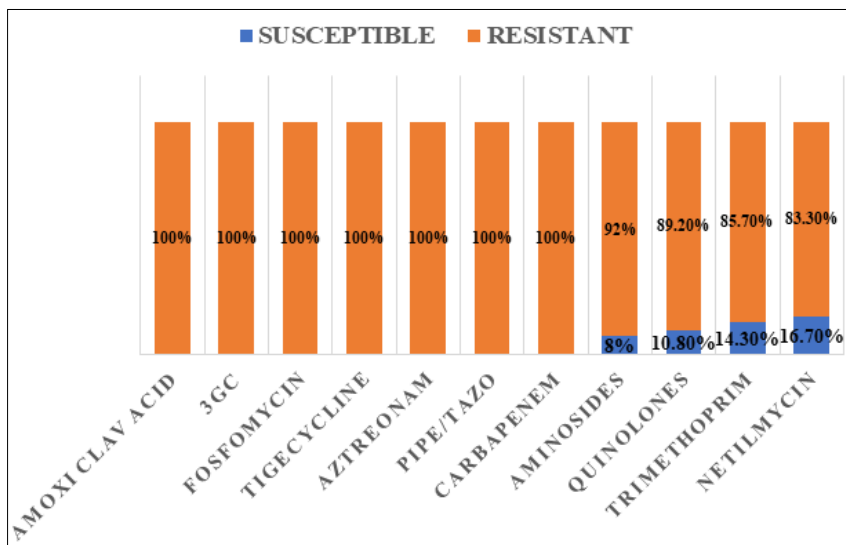


Figure 3: *Acinetobacter baumannii* antimicrobial susceptibility patterns

Amoxi Clav Acid: Amoxicillin + clavulanic acid; *3GC*: third-generation cephalosporins; *Pipe/Tazo*: piperacillin + tazobactam

Methicillin-susceptible *S. aureus* (MSSA) accounted for 25% of *S. aureus* strains and 75% were Methicillin-resistant *S. aureus* (MRSA). *S. aureus* strains were resistant to piperacillin/tazobactam (90.9%), vancomycin (88.9%), carbapenems (88.2%), 3GC

(86%), quinolones (82.6%), amoxicillin-clavulanic acid (81.8%), aminoglycosides (80%), and fosfomycin (60%). The antimicrobial susceptibility pattern of *S. aureus* is shown in figure 4.

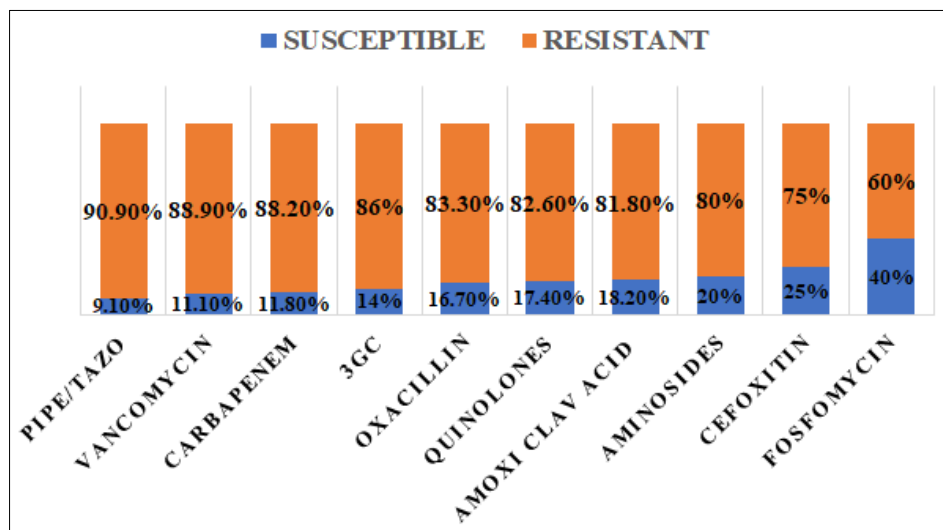


Figure 4 : *Staphylococcus aureus* antimicrobial susceptibility patterns.

Amoxi Clav Acid: Amoxicillin + clavulanic acid; *3GC*: third-generation cephalosporins; *Pipe/Tazo*: piperacillin + tazobactam

4. DISCUSSION

Our study presents first findings on bacterial AMR in ICU in the Republic of Congo. We conducted an observational, descriptive study consisting of a

retrospective analysis of the results of all bacterial culture samples collected over a 12-month period in the ICU at CHUB. Because of the retrospective data collection, we have no information regarding sampling

protocols for biological fluids analyzed. The observational and descriptive approach does not allow us to study the associated factors and prognostic factors of bacterial AMR in our ICU. However, our results highlight certain findings that warrant further discussion.

We report a very high positivity rate (86.1%) for bacteriological tests carried out. Essola *et al.*, reported a 15.3% positivity rate for bacteriological tests in nosocomial infections in ICU in Libreville [12]. Guibla *et al.* reported a 64.6% positivity rate for blood cultures and a 31.4% positivity rate for urine cultures in community-acquired and nosocomial sepsis in ICU in Bobo-Dioulasso [13]. Our data are similar to those of Guibla *et al.*, probably because both studies concerned community-acquired and nosocomial infections, unlike the study by Essola *et al.*, in Libreville [12].

Multidrug-resistant Gram-negative bacterial (MDR-GNB) represent the main challenge in terms of infections in ICUs worldwide [14]. The “critical group” on WHO BPPL for 2024 consists exclusively of MDR-GNBs [2]. We report a prevalence of 77 % of GNB, which is comparable to the findings of Leye *et al* (92.7 %) in Dakar [7], and Essola *et al* (65%) in Libreville [12], both of whom studied nosocomial infections in an ICU. Comparable data have been reported from several ICUs around the world. MDR-GNB infections represent a major public health challenge, due to increasing antibiotic resistance, a reduction in treatment options and their association with increased morbidity and mortality [15].

In our series, *E. coli* was the most common pathogen (13.1%), with 82.4% of strains secreting ESBL and 86.4% of strains resistant to carbapenems. A commensal bacterium, *E. coli* is a rod-shaped bacterium belonging to the Gram-negative group and the Enterobacteriaceae family. *E. coli* strains become pathogenic in the presence of certain “virulence factors,” notably host-related factors and genes transmitted via plasmids, transposons, or bacteriophages [16]. In Gabon, *E. coli* and *A. baumannii* rank first among pathogens isolated in cases of bacteremia in ICU at Libreville, and 60% of *E. coli* strains are resistant to carbapenems [5]. In Dakar, *E. coli* ranks second (21.3%) among nosocomial infections in ICUs, and its antimicrobial susceptibility pattern reveals resistance rates of 81% to ciprofloxacin, 54% to ceftriaxone, 48% to gentamicin, and only 2% to imipenem [7]. The predominance of *E. coli* in our series could be explained, in part, by the frequency of intra-abdominal infections (particularly peritoneal infections) among causes of sepsis in ICU at Brazzaville [8]. Furthermore, in general population, *E. coli* (15.68%) is one of the three most commonly found GNB in domestic wastewater in Brazzaville [17] and he was identified in 20% of bacterial strains isolated in artisanal fish dishes sold by street vendors in Brazzaville [18]. The 86.4% resistance to carbapenems is the result of resistance acquired in a hospital because, in Brazzaville, *E. coli*

strains have low resistance to carbapenems, ranging from 0 to 12.5% in general population [17, 18]. *ESBL-producing E. coli* strains were identified in 43.3% of cases in general population and in hospitals, including ICUs [19].

In our study, *K. pneumoniae* ranked second (10.1%) among pathogens isolated in ICU, with 76.1% of strains secreting ESBL and 23.5% secreting carbapenemases. *K. pneumoniae* is also one of the three most commonly found GNB in domestic wastewater in Brazzaville [17]. *K. pneumoniae* alone accounts for 20% of deaths related to AMR worldwide, making this bacterium an “absolute priority” pathogen [20]. In ICU at Libreville [5], *K. pneumoniae* ranks second among nosocomial infections, with 20% of strains producing carbapenemases, 90% resistant to ceftriaxone, and 80% resistant to ciprofloxacin. *K. pneumoniae* is the most commonly isolated pathogen (32.03%) in nosocomial infections in ICU at Dakar, with 81% resistance to ciprofloxacin, 90% to ceftriaxone, 82% to gentamicin, and 11% to imipenem. In a Mexican study on “critically prioritized” GNBs in neonatal, pediatric, and adult ICUs, *K. pneumoniae* was the most commonly isolated pathogen (27.02%), with 83.76% of strains producing ESBL between 2019 and 2021 in Yucatán [10]. In ICU at CHUB, peritonitis is the leading cause of sepsis [8], which may explain why *K. pneumoniae* ranked second in our series, behind *E. coli*. Indeed, among MDR-GNBs, *E. coli* is most commonly responsible for severe abdominal sepsis [21].

Third most common pathogen (9.1%), *A. baumannii* has the highest level of bacterial AMR in our series, with 100% resistance to carbapenems — a characteristic of *Carbapenem-Resistant Acinetobacter baumannii* (CRAB) — and 89.2% of CRAB isolates were highly resistant, meeting the criteria for the *XDR-CRAB* profile (*Extensively Drug-Resistant*). Furthermore, some *XDR- CRAB* strains tested positive for resistance to tigecycline, a characteristic of *PDR- CRAB* strains (*Pandrug-Resistant*). In ICU at Dakar, the most resistant pathogen was also *Acinetobacter spp.*, with 38% resistance to imipenem [8], even though this GNB ranked only third among the most common pathogens in nosocomial infections. In Yucatán, Mexico, *A. baumannii* was the most represented GNB in adult ICUs only and the most resistant MDR-GNB in all of them, neonatal, adult, and obstetric ICUs between 2019 and 2021, with more than 80.3% of CRAB strains and 47.54% of XDR-CRAB strains [10]. In Khartoum, out of 100 clinical isolates from ICUs, 38.0% were confirmed as *A. baumannii* strains with 100% resistance to carbapenems (CRAB), only 39.5% sensitivity to colistin, and 60.5% of the isolated *A. baumannii* strains were classified as *XDR-CRAB* strains [22]. In Sub-Saharan Africa, the overall prevalence of CRAB was estimated at 20% in a 2020 meta-analysis [23]. Classified as a “critical” priority bacterium on WHO BPPL, *A. baumannii* is an urgent public health problem [2]. First

pathogen in nosocomial infections, *A. baumannii* frequently infects critically ill patients in ICUs and accounts for approximately 20% of infections in ICUs through the world. Its antimicrobial resistance and environmental resilience are main factors contributing to the widespread and pervasive spread of *A. baumannii* in hospitals [24]. The presence of *CRAB* (100%), *XDR-CRAB* (89.2%), and *PDR-CARB* in our ICU is a warning. This could be due to inappropriate antibiotic use, as reported by Elombila *et al.*, [9]. In ICU at CHUB, 62.5% of patients receive antibiotics — in combination in 92.5% of cases — with only 16.5% compliance in antibiotic selection. Furthermore, *A. baumannii*'s ability to form a biofilm facilitates its adhesion to abiotic and biotic surfaces, such as medical devices surfaces, host and healthcare personnel tissues [24]. Therefore, inappropriate antibiotic prescriptions practices only cannot explain the exceptionally high resistance of *A. baumannii* strains in our ICU. Microbiological analysis of surfaces, invasive and non-invasive medical devices, and healthcare workers hands in our ICU could be the first step toward identifying potential sources of contamination and strengthening infection prevention and control measures in our ICU. In Mali, bacteria of *Acinetobacter* genus were second most bacteria commonly found on surfaces and medical devices in ICU, after *Staphylococcus* genus [25]. In Uganda, *A. baumannii* was the most frequently MDR-GNB isolated on healthcare workers hands in two ICU in Kampala, between 2016 and 2018 [26]. With our descriptive study, we cannot analyze the link between this high-level AMR of *A. baumannii* and sepsis mortality in our ICU. Further studies are needed to analyze this link.

S. aureus was the fourth most common bacterium (8.1%) in our series, with 75% of *MRSA*, 82.6% resistant to quinolones, 90.9% resistant to piperacillin/tazobactam, 88.9% resistant to vancomycin, 88.2% resistant to carbapenems, 86% resistance to 3GC, 81.8% resistance to amoxicillin-clavulanic acid, 80% resistance to aminoglycosides, and 60% resistance to fosfomycin. In Dakar, Leye *et al.* found a 5% prevalence of *MRSA* with 100% resistance to ciprofloxacin, 70% to gentamicin, and 16% to chloramphenicol in nosocomial infections in ICU [7]. In Uganda, *S. aureus* (14%) was the third most commonly isolated pathogen in nosocomial infections in ICU, with 1.9% of *MRSA* [27]. In Libreville, 12 *S. aureus* isolates were identified among 43 positive isolates from nosocomial infections in ICU, but susceptibility to cefoxitin was not studied [11]. In a recent meta-analysis, the prevalence of *MRSA* in Africa was estimated to 42.2%, but the large majority of studies did not involve ICUs [28]. In Brazzaville, *S. aureus* was isolated from smoked fish meals in 5 out of 25 isolates, and 3 strains were *MRSA*, in general population [18]. In hospitals (excluding ICUs), the antimicrobial susceptibility pattern of community-acquired *S. aureus* strains showed 100% resistance to nalidixic acid, 69.2% resistance to ciprofloxacin, and 61.5% resistance to levofloxacin, norfloxacin, and ofloxacin, and

nosocomial strains exhibited 96.2% resistance to nalidixic acid, 77.8% resistance to ofloxacin, 70.4% to norfloxacin and ciprofloxacin, and 59.6% to levofloxacin [29]. Susceptibility to cefoxitin was not tested. This high prevalence of *MRSA* in our series is a cause for concern and highlights the need to assess and strengthen hygiene and infection control measures in our ICU. The major components of preventing and controlling *MRSA* include hand and environmental hygiene (as part of standard precautions), patient isolation, and patient/staff decolonization. Improving hand hygiene practice is especially important where the risk of infection is highest, e.g. in intensive care [30].

5. CONCLUSION

The 'critical' priority BGNs on WHO BPPL play a central role in bacterial AMR in ICU at CHUB. Most common bacteria were: *E. coli*, *K. pneumoniae*, *A. baumannii* and *S. aureus*. All *A. baumannii* strains were *CRAB*. *MRSA* strains predominated over *S. aureus* strains. *ESBL-producing E. coli* and *carbapenem-resistant E. coli* were predominant. *K. pneumoniae* strains were *ESBL-producing* in majority, but susceptible to carbapenems. MDR-bacteria prevalence is very high in ICU at CHUB. Further studies are needed to identify associated factors and to investigate prognostic factors for MDR-bacteria infected patients in our ICU.

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