


Antimicrobial susceptibility testing data analysis over 3 years at the Yaoundé General Hospital, Cameroon

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Background: Antimicrobial resistance (AMR) is a major health concern with high rates in low-income countries. Bacteriology laboratories sustain the fight against AMR by providing antibiotic susceptibility testing (AST) results to ensure appropriate therapies. These laboratories generate a lot of data, which are usually used for prospective interventions. Our study conducted in a lower-middle-income hospital setting aimed to describe the profile of bacteria isolated from the specimens received over 3 years, assess their susceptibility profile and identify potential gaps or area of improvement from the analysis of our data.

Methods: Monthly data were retrieved from registers for all specimens received between January 2020 until December 2022. Data were compiled and analysed using the R and WHONET software.

Results: Out of 3582 specimens received, 797 were culture positive (22.3%). *Escherichia coli* and *Klebsiella pneumoniae* were frequently isolated (30.5% and 24.2%, respectively). AST results analysis showed high resistance of Gram-negative bacteria to penams and cepheems, whereas low resistance was observed to carbapenems. Susceptibility to antibiotics based on the AWaRe antibiotic classification was variable. The bacteriological profile in the various types of specimen was established and rational information to design a therapeutic protocol adapted to our hospital setting was obtained.

Conclusions: AST results may not only be used for prospective guidance for treatment, but rather cumulative data analysis can contribute to design effective antibiotic prescriptions and improve general practices at the laboratory. This is, however, dependent on a good record-keeping, standardization of practices and collaboration between clinicians and laboratory scientists.

Introduction

Antimicrobial resistance (AMR) is a global health concern considered as the next pandemic and threat worldwide.¹ It is estimated that by 2050 up to 10 million deaths could occur annually due to AMR.² Although the development of antibiotic resistance (ABR) can arise from pathogens' natural defence mechanisms, it is enhanced by inappropriate behaviours, overuse or misuse of antibiotics in humans, animals and the environment.^{3,4,5} In parallel, there has not been much discovery of new antibiotics over the past two decades. Even if intensive research is ongoing, leading to promising future discovery,⁶ it is urgent to target other effective areas of interventions, which could quickly help in the control of ABR. Such areas

of interventions include antimicrobial stewardship. Antimicrobial stewardship is an integrated and multidisciplinary approach to select appropriate drugs for appropriate patients for a proper duration to minimize the risk of developing AMR. This approach also promotes implementation of guidelines, and continuous medical education.⁷ The impact of antimicrobial stewardship in reducing AMR was clearly demonstrated by several studies;^{8,9} however, it is also advisable that such interventions should be designed and implemented based on available resources and expertise.¹⁰ The selection of the appropriate drug for the appropriate patient mainly relies on the use of the antibiotic susceptibility testing (AST) results, which definitely provide the insight of which antibiotic to use based on the pathogen isolated. Bacteriology laboratories

performing AST may therefore generate a lot of data, which are frequently used for prospective interventions, either readjustment of a patient's treatment or surveillance. This paper describes how the analysis of retrospective data generated from AST could be used as part of the antibiotic stewardship process at the level of the health facility. Specifically, the study aimed to describe the profile of bacteria isolated from the specimens received over 3 years, assess their antibiotic susceptibility profile and identify potential gaps or areas of improvement from the analysis of our data.

Methods

Setting

The study was conducted at the bacteriology laboratory of the Yaoundé General Hospital. This is a first-category health facility in Yaoundé, the capital city of Cameroon, with a general capacity of 200 beds and up to 21 medical and subsurgical specialties. The health facility has many reference pools such as the oncology management centre. The bacteriology unit receives specimen from inpatients and outpatients.

Data entry system

Data retrieved from the registers were entered into the WHONET[®] software. This is a free desktop Windows application for the management and analysis of microbiology laboratory data with a particular focus on AMR surveillance. It has been developed and supported by the WHO Collaborating Centre for Surveillance of Antimicrobial Resistance at the Brigham and Women's Hospital in Boston, MA, USA. WHONET supports local, national, regional and global surveillance efforts in over 2300 hospitals, public health, animal health and food laboratories in over 130 countries worldwide.¹¹ Aerobic bacteria isolated from specimens received from January 2020 until December 2022 were recorded and their susceptibility profiles were analysed. The specimens considered were urine, stool, blood, catheters, body fluids and pus (from wounds, swabs or surgery). Genital samples were not included. Anaerobic bacteria were not included in the study.

Laboratory methods

Culture and identification methods

The general culturing method was an incubation at 36°C ± 5°C in aerobic conditions or in a 5% CO₂-enriched atmosphere in a jar, for blood-enriched culture media.

Urine samples were plated on cystine lactose electrolyte-deficient (CLED) agar. Stool samples were both simultaneously plated on Hektoen and Salmonella Shigella agar, whereas another part was enriched in Muller-Kauffmann or selenite-F broth before plating on to agar after 24 h incubation. Blood samples were collected on diphasic culture bottles, which were incubated at aerobic conditions for at least seven days, and cross-checked every 48 h. Pus specimens were directly plated on blood-enriched based media and incubated in a jar under a 5% CO₂-enriched environment.

Identification was performed using Gram staining, and biochemical orientation tests such as catalase and oxidase. API 20E[®] mini galleries were used for identification of Enterobacteriaceae isolates. For *Staphylococcus* species, identification was confirmed after coagulase and DNase tests, whereas for *Streptococcus* species, blood agar haemolytic patterns, Gram staining and Streptokit[®] were used for general group identification.

AST

The Kirby-Bauer disc diffusion method was the antibiotic susceptibility technique performed at the laboratory over the 3 years surveyed. The

main brands supplied were Oxoid[®] and Bio-Analyse[®]. The disc concentrations were those recommended by the EUCAST guidelines of the corresponding year. Discs of antibiotics were placed on the top of Mueller-Hinton agar, inoculated with a 0.5 McFarland suspension of the isolate. After a minimum of 16 h incubation, diameters of the inhibitory zones were measured manually using an electronic sliding caliper. Susceptibility results were interpreted based on the EUCAST guidelines.

Ethics

We received administrative authorization to perform data analysis. Ethical clearance was delivered by the Institutional Research Ethics Committee, with the reference number 121/UY1/FMSB/VDRC/DAASR/CSO.

Results

Statistics of samples received from 2020 to 2022

In total, 3582 samples were received for culture between 2020 and 2022. The most frequent samples were urine, followed by blood and stool samples. The number of samples increased over the years for urine, blood, stool, pus and body fluids. The proportions of positive samples per type of specimen in 2020 and 2022 are presented in Table 1. The overall percentage positivity of specimens cultured decreased between 2020 and 2022. The proportion of positive urine samples also considerably reduced, from 33.7% to 11.4%. The highest positivity rates were observed for catheters and suppurated specimens.

Age group and sex distribution of patients with positive cultured samples

The age group and sex demographics of patients with positive cultures are presented in Table 2. The mean age of patients with positive culture samples was 45 years. We observed a slight male predominance in 2021 and 2022.

Pathogens isolated from specimens

The most frequent bacteria isolated from the various types of specimen are presented in Table 3.

Over the 3 years' time frame, *Escherichia coli*, *Klebsiella pneumoniae* and *Staphylococcus aureus* remained the most frequent bacteria isolated in urine. Other bacteria such as *Citrobacter*, *Enterobacter* and *Proteus mirabilis* were isolated with variable frequency over the years. *Staphylococcus saprophyticus*, considered for urine samples, was isolated only in the year 2022.

Staphylococcus aureus was the most prevalent bacterium isolated from blood cultures, followed by *K. pneumoniae*. CoNS species were also isolated with decreasing occurrence from 11.8% in 2020 to 5% in 2022.

Apart from a high prevalence of *Pseudomonas aeruginosa* observed in suppurated specimens collected in 2020, the main bacterium isolated in these specimens was *K. pneumoniae* followed by *S. aureus*. *Streptococcus* species were isolated only in 2020.

S. aureus was the most prevalent bacterium isolated from catheters in 2020 then the prevalence decreased by 10%–15% in 2021 and 2022. Globally, *E. coli* and *K. pneumoniae* tend to be the most frequent bacteria isolated from catheters. The frequency of bacteria isolated from body fluids over the years was variable.

Table 1. Proportion of positive samples per type of specimen

Type of samples		Samples received/positive (+) samples	2020	2021	2022
Samples from sterile sites	Blood	Samples received, <i>n</i>	265	297	244
		+ samples, <i>n</i> (%)	68 (25.7)	60 (20.2)	78 (32)
	Body fluid	Samples received, <i>n</i>	34	56	122
		+ abdominal fluid, <i>n</i> (%)	5 (14.7)	2 (3.6)	0
		+ CSF, <i>n</i> (%)	1 (3)	2 (3.6)	3
		+ knee fluid, <i>n</i> (%)	1 (3)	0	0
		+ others: biopsy, cyst, pleural, <i>n</i> (%)	2 (6)	2 (3.6)	2
	Catheters	Samples received, <i>n</i>	22	14	62
		+ urine catheters, <i>n</i> (%)	8 (36)	8 (57)	39 (63)
		+ venous catheters, <i>n</i> (%)	6 (27)	3 (21.4)	5 (8)
Urine	Samples received, <i>n</i>	347	587	709	
	+ samples, <i>n</i> (%)	117 (33.7)	160 (27.3)	81 (11.4)	
Total	Samples received, <i>n</i>	668	954	1137	
	+ samples, <i>n</i> (%)	208 (31.1)	237 (24.8)	208 (18.3)	
Samples from non- sterile sites	Pus	Samples received, <i>n</i>	53	106	118
		+ samples, <i>n</i> (%)	24 (45.3)	59 (55.7)	56 (47.5)
	Stool	Samples received, <i>n</i>	147	289	100
+ samples, <i>n</i> (%)		3 (2)	1 (0.3)	1 (1)	
Total	Samples received, <i>n</i>	200	395	218	
	+ samples, <i>n</i> (%)	27 (13.5)	60 (15.2)	57 (26.1)	
Total samples from sterile and non- sterile sites	Samples received, <i>n</i>	868	1349	1355	
	+ samples, <i>n</i> (%)	235 (27)	297 (22)	265 (19.6)	

Table 2. Sex and age group distribution of patients with positive samples

		2020	2021	2022
Sex, <i>n</i> (%)	Female	127 (54)	141 (47.6)	122 (46.2)
	Male	108 (46)	156 (52.4)	143 (53.8)
Age (years)	Mean	45	46	46
	Min	0	1	1
	Max	91	98	93
Age group (years), <i>n</i> (%)	0–4	16 (6.8)	18 (6)	24 (9)
	5–14	9 (3.7)	15(5)	7 (3)
	15–24	29 (12.3)	25 (8.4)	12 (5)
	25–34	33 (14.1)	57 (19.1)	13 (5)
	35–44	22 (9.2)	31 (10.4)	55 (21)
	45–54	25 (10.4)	21 (7)	65 (24)
	55–64	49 (20.9)	47 (16)	42 (16)
	65–74	32 (13.5)	47 (16)	30 (11)
	75–84	14 (6.1)	25 (8.4)	14(5)
	>85	6 (3)	11 (3.7)	3 (1)
Total	235	297	265	

For stool culture, *Salmonella typhi* was the main bacterium isolated in 2020 (2%) and 2022 (1%). Only one species of *Shigella* was isolated from stool in 2021.

Antibiotic susceptibility patterns of priority pathogens

The susceptibility patterns for priority pathogens according to the WHO GLASS tool¹² are presented in Figures 1–3. Antibiotics are classified according to the WHO Access, Watch, Reserve (AWaRe) classification.¹³

Among the Access group of antibiotics, ampicillin and amoxicillin/clavulanic acid had the lowest susceptibility rates. The trimethoprim/sulfamethoxazole combination also showed low rates of susceptibility. The highest rates were found for nitrofurantoin and amikacin. For species isolated in urine, more than 50% of isolates were susceptible to nitrofurantoin and a slightly lower rate was observed for fosfomycin.

Within the Watch group, the lowest susceptibility rates were observed with third-generation cephalosporins. The highest susceptibility was observed with imipenem.

According to the 2022 GLASS report, surveillance of resistance for *E. coli* species focuses on third- and fourth-generation cephalosporins, quinolones, carbapenems, sulphonamides and polymyxins, especially colistin. Colistin is also classified within the Reserve group of the AWaRe classification, but it was not part of the antibiotics tested within the laboratory, as the recommended testing method is MIC determination.

E. coli showed high resistance rates to most of the antibiotics under surveillance, according to the GLASS report. Antibiotic resistance of *K. pneumoniae* are presented in Figure 2. The resistance profile for *K. pneumoniae* followed the same patterns as *E. coli*. Resistance patterns in *Staphylococcus* species were as follows: gentamicin showed the highest susceptibility rates for *S. aureus*, followed by fusidic acid. Trimethoprim/sulfamethoxazole showed the lowest susceptibility rates.

Discussion

Samples received and bacterial ecology

Although the total number of samples received increased from 2020 to 2022, concordant with a parallel increase in the

Table 3. Frequency of bacteria isolated from targeted specimens

Bacteria	Overall, n (%)	Blood, n (%)			Body fluid, n (%)			Catheter, n (%)			Pus, n (%)			Urine, n (%)		
		2020	2021	2022	2020	2021	2022	2020	2021	2022	2020	2021	2022	2020	2021	2022
Gram-negative isolates																
<i>Acinetobacter baumannii</i>	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.85)	0 (0.0)
<i>Citrobacter freundii</i>	18 (2.4)	2 (2.9)	1 (1.7)	2 (2.6)	0 (0.0)	1 (16.7)	0 (0.0)	0 (0.0)	0 (0.0)	2 (4.5)	0 (0.0)	4 (6.9)	0 (0.0)	1 (1.2)	1 (0.85)	1 (1.2)
<i>Citrobacter koseri</i>	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (20.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
<i>Enterobacter cloacae</i>	28 (3.6)	6 (8.8)	2 (3.4)	2 (2.6)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	3 (6.8)	0 (0.0)	5 (8.6)	0 (0.0)	8 (14)	0 (0.0)	3 (3.7)
<i>E. coli</i>	241 (30.5)	5 (7.4)	1 (1.7)	10 (12.8)	4 (40.0)	1 (16.7)	2 (40.0)	4 (26.7)	4 (40.0)	16 (36.4)	2 (8.3)	8 (13.8)	8 (14)	32 (39.5)	63 (53.8)	77 (48.1)
<i>Klebsiella aerogenes</i>	9 (1.1)	0 (0.0)	1 (1.7)	3 (3.8)	1 (10.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.9)	3 (3.7)
<i>Klebsiella oxytoca</i>	15 (1.9)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	5 (8.6)	2 (3.5)	4 (2.5)	1 (0.9)	3 (3.7)
<i>K. pneumoniae</i> subsp. <i>pneumoniae</i>	191 (24.2)	11 (16.2)	8 (13.6)	14 (17.9)	2 (20.0)	2 (33.2)	1 (20.0)	2 (13.3)	4 (40.0)	10 (22.7)	4 (16.7)	17 (29.3)	13 (22.8)	26 (32.1)	24 (20.5)	53 (33.1)
<i>Morganella morganii</i>	2 (0.2)	0 (0.0)	1 (1.7)	1 (1.3)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
<i>P. mirabilis</i>	8 (1.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	3 (5.2)	2 (3.5)	2 (2.5)	0 (0.0)	1 (0.6)
<i>P. aeruginosa</i>	50 (6.4)	1 (1.5)	7 (11.9)	4 (5.1)	0 (0.0)	1 (16.7)	0 (0.0)	1 (6.7)	0 (0.0)	3 (6.8)	10 (41.7)	7 (12.1)	7 (10.6)	5 (6.2)	2 (1.7)	2 (1.3)
<i>Salmonella</i> spp.	8 (1.0)	5 (7.4)	2 (3.4)	1 (1.3)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
<i>Serratia liquefaciens</i>	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (20.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
<i>Serratia marcescens</i>	32 (4.0)	2 (2.9)	3 (5.1)	2 (2.6)	0 (0.0)	0 (0.0)	0 (0.0)	1 (6.7)	1 (10.0)	3 (6.8)	0 (0.0)	1 (1.7)	6 (10.6)	5 (3.1)	6 (5.1)	2 (2.5)
Gram-positive isolates																
<i>Enterococcus</i> spp.	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
<i>S. aureus</i> subsp. <i>aureus</i>	157 (19.9)	27 (39.7)	28 (47.5)	34 (43.6)	3 (30.0)	1 (16.7)	0 (0.0)	7 (46.6)	1 (10.0)	6 (13.6)	6 (25)	8 (13.8)	10 (17.5)	4 (4.9)	18 (15.4)	4 (4.9)
CoNS	21 (2.7)	8 (11.8)	4 (6.8)	4 (5.1)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	5 (3.2)	0 (0.0)	0 (0.0)
<i>Streptococcus</i> spp.	6 (0.7)	1 (1.4)	1 (1.5)	1 (1.3)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (2.4)	2 (8.3)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)

Negative samples were considered only for growth under aerobic conditions.

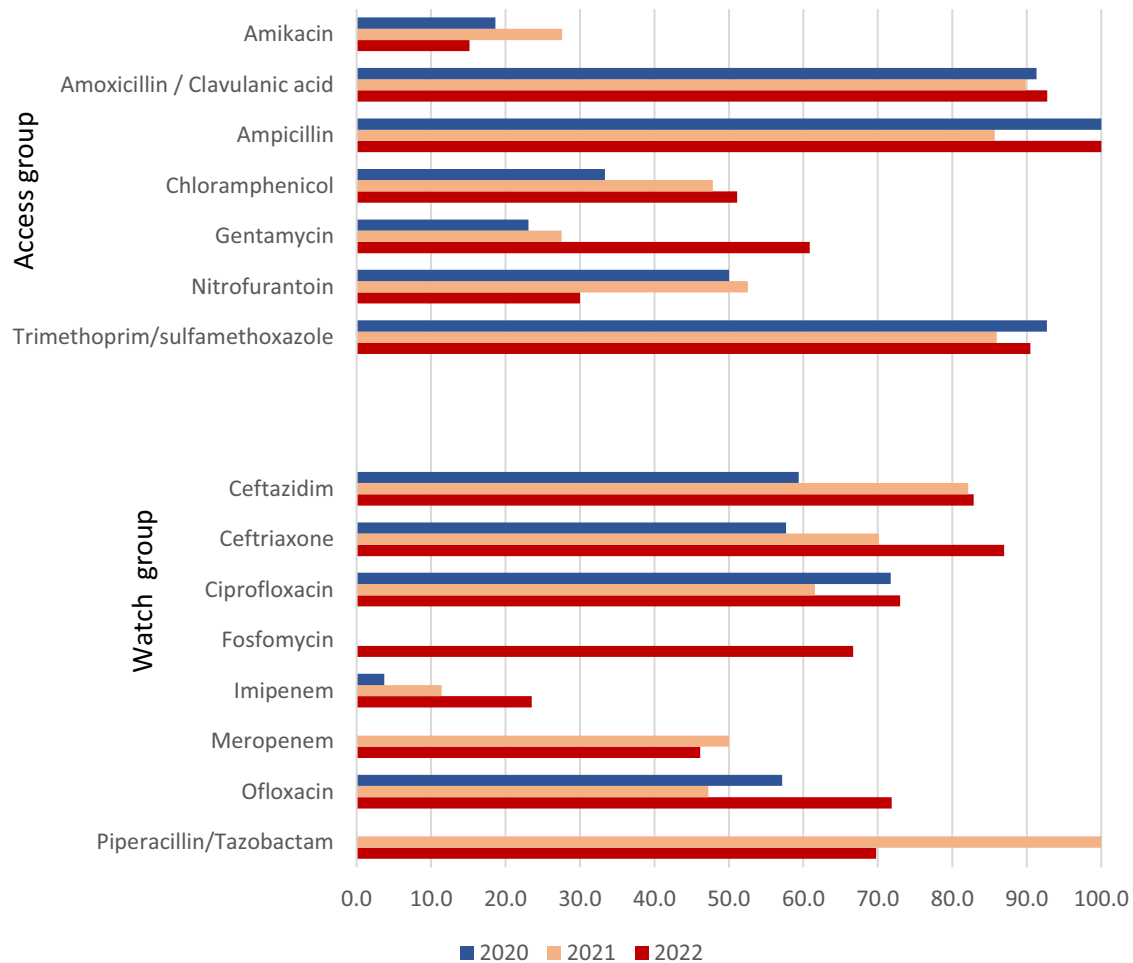
Antibiotic resistance profile of *E. coli* species 2020-2022

Figure 1. Antibiotic resistance profile of *E. coli* 2020–22.

frequency of patients attending the health facility, data showed a progressive decrease in the proportion of positive samples over the years. This was particularly noticeable for urine samples, which dropped from 34.6% in 2020 to 11.4% in 2022. This global decrease may have been impacted by two key factors. From 2020, the laboratory was selected as part of the national network for surveillance of AMR. Being part of this network, it involved re-training of laboratory staff and capacity building for improvement of procedures and AST. It also involved more rigorous screening of sample collection procedures, which would have decreased the number of samples contaminated. The decrease may have also been influenced by an improved collaboration between clinicians and biologists, as cases with less significant bacteriuria were discussed before taking the decision to pursue with AST, depending on the patient's condition and symptoms.¹⁴

Stool culture presented the lowest percentages of positivity. As literature suggests that the presence of *Salmonella* and *Shigella* species is associated with age, especially children.^{15,16} The low positivity rates observed may partially be linked to our observed population which were mainly adults. The level of the

health facility, which is a reference hospital, could also explain these findings, as people with acute diarrhoea would preferably consult in peripheral health structures rather than reference hospitals or would have performed self-medication.

Catheters had the highest percentages of positivity but the yearly number of samples tested remained quite low. This suggests that the indication for such cultures was guided by strong evidence of these catheters being the source of the infection.

E. coli, *K. pneumoniae* and *S. aureus* were globally the most frequent bacteria isolated from urine in our study. If the first two are clearly described as main causes of urinary tract infections, *S. aureus* has been reported in lower frequencies.¹⁷ The relatively higher frequency of *S. aureus* was observed in patients with cancer and this may probably be the same in our setting,^{18,19,20} the Yaoundé General Hospital being a reference centre for cancer treatment in the country. Globally, authors have acknowledged great variations in the bacterial ecology in urine, depending on age, patient's status and region, thus highlighting the importance of having local epidemiology data available.¹⁷

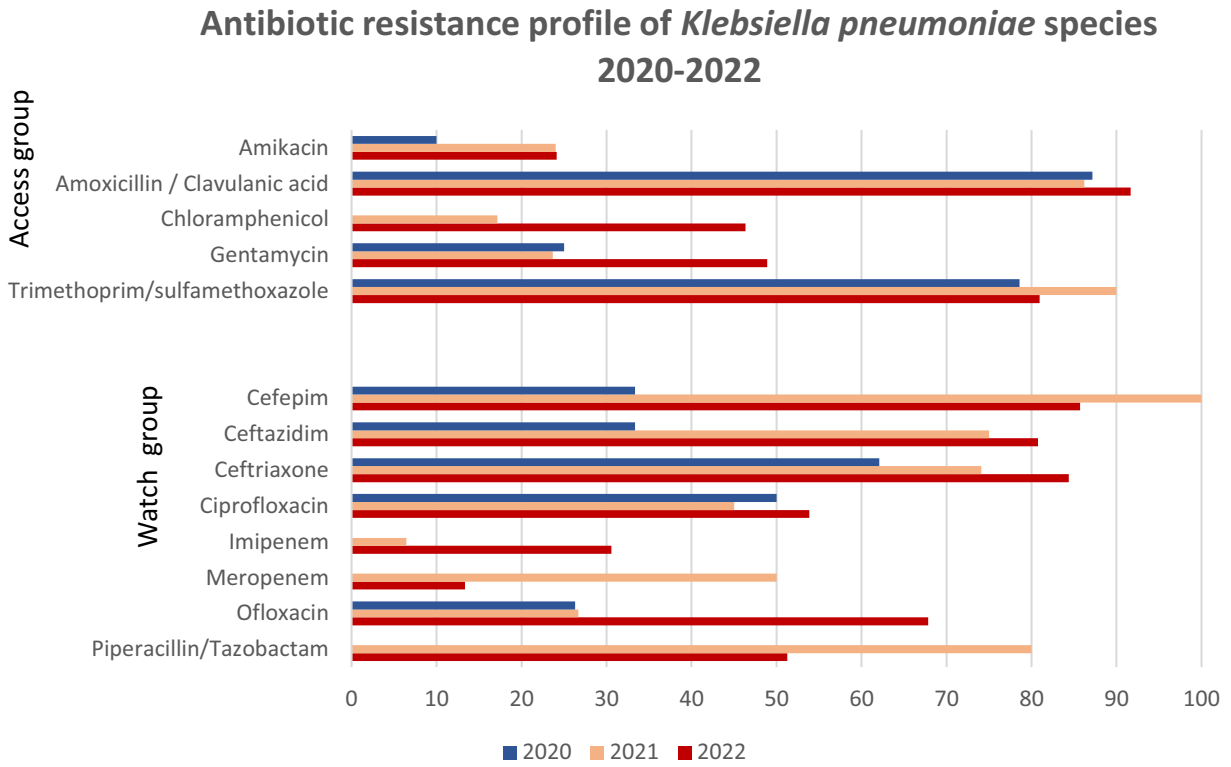


Figure 2. Antibiotic resistance profile of *K. pneumoniae* 2020–22.

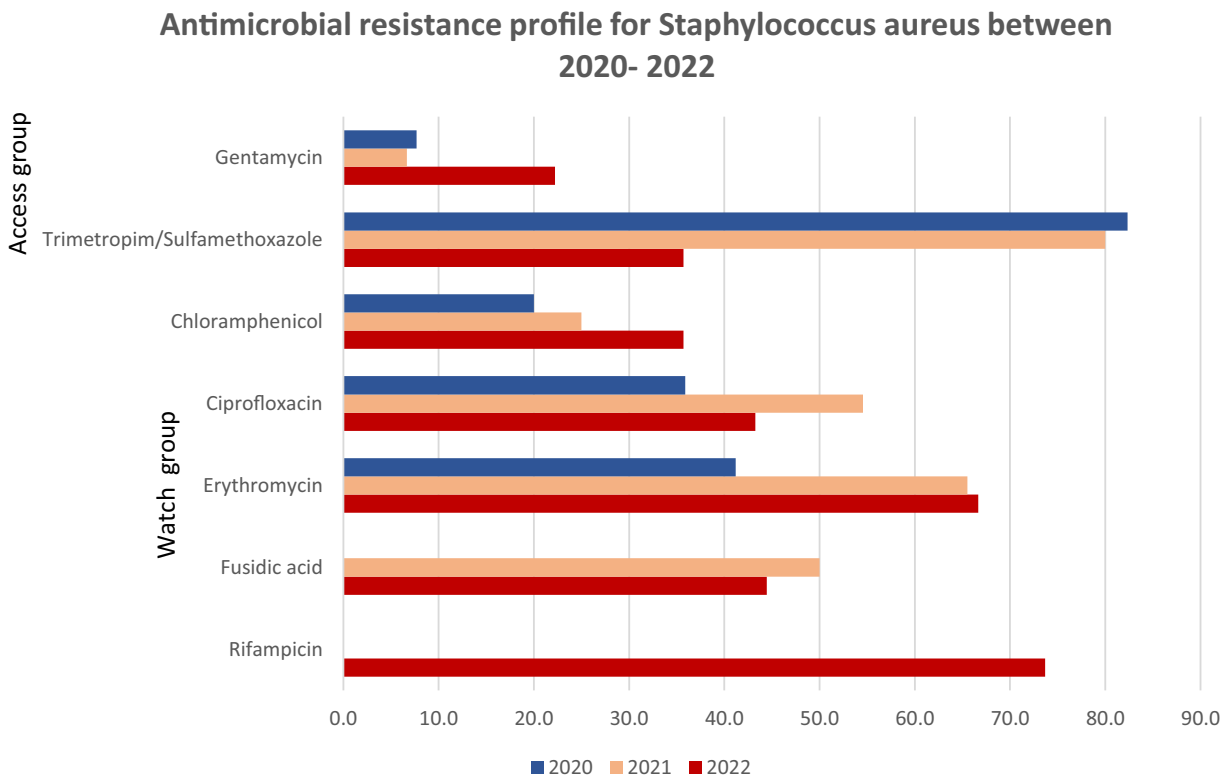


Figure 3. Antimicrobial resistance profile of *S. aureus* 2020–22.

For blood cultures, the patterns observed were as described in several other studies.^{21, 22} Bacteria isolated throughout the years were also described among those who can be responsible for sepsis.²³

Besides knowing the bacteria's profile in our hospital setting, the data provided over these 3 years will also support accurate procurement for reagents and consumables.

AST

The global patterns of susceptibility for *E. coli* were comparable to data observed in other studies. This involved low susceptibility to aminopenicillins, third-generation cephalosporins and sulphonamides, medium susceptibility to quinolones and high susceptibility to aminoglycosides, especially amikacin, carbapenems and nitrofurantoin.^{24,25} However, the proportions observed from our data were consistently lower. Lower susceptibility of the amoxicillin/clavulanic acid combination may have been influenced by batch-to-batch variations and storage conditions. This observation has led to improvement of quality assurance for AST, which will be described in the upcoming sections. All this information guided specific improvement interventions at the level of the laboratory. When considering imipenem, we observed about 10% phenotypic resistance. Although some authors described the presence of phenotypic resistance patterns without the presence of resistance genes,²⁶ others near us have found the presence of resistance genes even though in a lower proportion compared with phenotypic resistance patterns.²⁷ This finding raised our concern to quickly set up additional tests for phenotypic carbapenemase detection, and also storage of strains for further genotypic assays. We also found low susceptibility to fosfomycin compared with other studies,²⁸ as the disc diffusion method for fosfomycin implies some additional specificity such as adding G6PD solution, which is ideal and more accurate in the determination of MIC. For nitrofurantoin, we recorded more than 60% susceptibility of the strains, rendering this antibiotic a potential good option for the treatment of uncomplicated urinary tract infections.

Improvement areas and ways forward

From the analysis of our data, we found that there were some gaps in terms of quality assurance, especially for AST and specifically preservation of the quality of the discs. If we confirmed the quality of the discs upon reception and before use, we observed that there was potentially a decrease of potency over time. Thus, we performed a global check of all the discs that were still in stock and those that presented with inappropriate results were discarded. We also systematically adopted keeping discs frozen, for those for whom the temperature storage ranged between 2°C and -20°C. Furthermore, rather than purchasing extremely high quantities of antibiotics to be stocked in order to avoid shortages, we decided to perform quarterly procurement based on our statistics from the past 3 years. Also, we systematically introduced quality control of discs every month.

As for some of the antibiotics tested, determination of MIC is reported to provide more effective results, considering the fact that manual measurement of inhibitory diameters was not repeatedly performed to minimize operator errors at the laboratory. Based on our findings, we got engaged in an advocacy

with the managers to quickly implement such methods in our laboratory.

We have also integrated procurement of reagents that will help in the systematic research of resistance patterns, ESBLs, MRSA or carbapenem-resistant strains.

Our data showed variable susceptibility to Access group antibiotics, which are considered as the first choice for antibiotic prescription. Molecules such as nitrofurantoin could be recommended for uncomplicated urinary tract infections based on our results. Based on the profile described per specimen and the antibiotic susceptibility profile, working groups between biologists and clinicians have been launched to define strategic antibiotic prescription guidelines for the health facility.

Improvement can also be planned for data collection, as for example, systematic recording of the specimen origin could lead to additional description of bacterial epidemiology depending on the units.

Conclusions

The review of the data from the bacteriology laboratory over the past 3 years provided a lot of information, from the trends in the number of samples received to the epidemiology of bacteria isolated and their susceptibility patterns. Use of such data is strongly dependent on good record-keeping, and software such as the WHONET® is helpful both for recording and data analysis. Analysis of results and comparison with other findings helped to detect potential gaps in quality control for AST and also raised several areas of improvement (internal control quality at reduced periodicity for AST, appropriate methods for AST). Furthermore, the process of exploitation of the data for general improvement of antibiotic prescription and use within the hospital enhanced more effective collaboration between clinicians and laboratory scientists. Overall, despite the numerous challenges that may be encountered in laboratories in low and middle-income settings, there is great interest to use AST data as part of the implementation of antimicrobial stewardship.

Funding

This study was carried out as part of our routine work.

Transparency declarations

None to declare.

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