Bacteriological Profile and Antibiotic Resistance Pattern at the Yaounde University Teaching Hospital: A Retrospective Study

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Original Research Article

ABSTRACT

Aims: Over the decades, antibiotic resistance has become a cross-border public health problem. This calls for the profiling of microorganisms, particularly bacteria implicated in antibiotic resistance, in order to improve clinical practice and reduce the incidence of therapeutic failure in the treatment of infectious diseases.
Study Design: We conducted a retrospective cross-sectional study.
Place and Duration of the Study: The study was made at the bacteriology laboratory at the Yaounde University Teaching Hospital, Cameroon during the period between January 2016 and June 2021.

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18/53 (34.0%) of Haemophilus influenza isolates were resistant to amoxicillin. Multidrug resistance of *Escherichia coli* to amoxicillin, trimethoprim and gentamicin was 88.1%, 80.7% and 29.8% respectively. In contrast, resistance to ciprofloxacin in *Salmonella typhi* was rare [3].

Low-income countries are most affected by antimicrobial resistance related infections, such as community-acquired infections [9,18–22]. A study by Lonchel and al in Yaounde on 358 faecal samples, showed *Escherichia coli* as the most frequently isolated ESBL producer in ambulatory patients (66.7%) and student volunteers (90%). Isolates showed additional resistance to gentamicin, ciprofloxacin and trimethoprim/sulfamethoxazole [23]. Studies conducted at the Douala General Hospital in Cameroon reported high resistance of *Escherichia coli* and *Klebsiella* spp to third-generation cephalosporins, penicillins and cotrimoxazole, as well as *Staphylococcus aureus and coagulase-negative staphylococci* showing more than 50% resistance to meticillin, respectively [24,25]. In 2016, hospitals in Cameroon reported a total of 25,975 cases of tuberculosis, including 175 (0.7%) cases of multidrug resistance [26].

In view of the challenge posed by this scourge to date, and the ever-increasing prevalence of AMR, we proposed to take stock of the situation based on recent epidemiological data on antimicrobial resistance. In the framework of our study, we will evaluate the antimicrobial resistance profile in the laboratory of the University Teaching Hospital in Cameroon over a period of 04 years and 06 months. More precisely, we will proceed with a census of the bacteria isolated in the Yaounde University Teaching Hospital (YUTH) laboratory during the study period. Then we will establish the antibiotic resistance profile by year and finally we will show the evolution of the resistance profile of the main strains found by year.

2. METHODOLOGY

2.1 Design

We have conducted a retrospective study with a descriptive aim. Our study has taken place over a total period of 04 years and 06 months from January 2016 to June 2021. Our study has been conducted at the Yaounde University Teaching Hospital (YUTH) in Cameroon. The YUTH was created in 1978 in order to offer students of the Faculty of Medicine and Biomedical Sciences a better practical and adapted training. It is both a teaching hospital guaranteeing rigorous care and quality training for future health professionals, and a sentinel site for the emerging antimicrobial surveillance in Cameroon. Our source population consisted of bacterial strains considered to be resistant bacteria and which have been isolated from diagnostic samples taken from people of all ages and sexes. All bacterial strains from the following biological fluids were included: blood, stool, urine, suppurations, probe tip and catheter tip. We have carried out exhaustive sampling during the entire recruitment period.

2.2 Procedure

2.2.1 Search of archives and registers

After obtaining the agreement of the Director of the YUTH, we collected the data based on the archived records, we selected the results that met the inclusion criteria at the bacteriology laboratory of the YUTH Hospital.

2.2.2 Selection of results

A pre-established and pre-tested data collection form was conceived. The information collected were place of hospitalisation, age, sex, nature of the bacteria, date of isolation, sampling site, department concerned, antibiotic sensitivity profile tested for each antibiotic, percentage of resistance in each species.

2.3 Research for Resistant Bacteria

This part of the procedure is intended as an indication of the technique used in the laboratory to obtain the results.

2.3.1 Sampling

Biological products were collected from the various departments of the YUTH. After the preliminary verifications in the laboratory, the macroscopic analysis of the samples was performed. This was followed by the culture phase, which depended on the biological fluid taken. Different specific culture media were used [27,28].

2.3.2 Morphological characteristics

2.3.2.1 Fresh state

A drop of bacterial suspension was observed under a light microscope with a 10X and then

40X objective. This was done to determine the shape, arrangement and especially the mobility of the bacteria.

2.3.2.2 Quantitative cytology

Urine cytology was used with the Kova cell. This analysis consisted of counting the number of red blood cells and white blood cells in a given volume of pathological products [28].

2.3.3 Gram staining

Gram staining was performed to identify bacterial morphologies. This stain classifies bacteria according to their ability to bind crystal violet. After staining, we observed the bacteria under a microscope at high magnification (under a 100X objective). We could have: Gram-positive bacilli, Gram-negative bacilli, Gram-positive cocci, Gram-negative cocci and Yeast [28].

2.3.4 Identification and typing of bacteria

After the Gram staining, we made an inoculum which we enmeshed in an API gallery. API 20NE galleries were used for non-fermentative bacteria and API 20E galleries for fermentative bacteria. Based on the biochemical factors found in the gallery we were able to make a 90% identification of the genus and species [28].

2.3.5 Antibiotic susceptibility

The disk diffusion method used for the antimicrobial susceptibility testing (AST) was Kirby Bauer, according to the Antibiogram Committee of the French Microbiology Society. The medium used for the majority of bacterial species is Mueller-Hinton. The cell suspension was prepared in sterile physiological water from a young and pure culture on appropriate isolation medium with a suspension calibrated to 0.5 Mac Farland [27].

2.3.6 Plating of the antibiogram

This should be done 15 minutes after preparation of the inoculum. It is done by swabbing so that after incubation we obtain distinct but joined colonies. The swab was dipped into the suspension and the excess liquid was removed by turning the swab on the walls of the tube. To ensure good uniformity, we rubbed the entire surface of the agar dish three times, rotating the dish about 60°C between the streaks.

2.3.7 Application of the discs

The discs were applied manually with light pressure on the agar surface with sterile forceps to ensure complete contact of the disc with the agar, respecting the recommended distances between the discs [27].

2.3.8 Incubation of the antibiogram

The plates were then turned upside down and incubated ideally within 15 min of disc deposition, but not exceeding 30 min.

2.3.9 Reading of the antibiogram

After 16-18 hours of incubation, each plate was examined. The diameters of the resulting zones of inhibition were measured according to the Antibiogram Committee of the French Microbiology Society protocol.

2.4 Ethical Considerations

Before starting our research, a clearance from the Institutional Research Ethics Committee (IREC) of the Faculty of Medicine and Biomedical Sciences has been obtained and a research authorization from the Director of the Yaounde University Teaching Hospital has been obtained.

2.5 Data Analysis

All data collection forms were stored in a database designed under the Censuses and Survey Procession software (CSPro) version 7.3. The data were then analysed using Statistical Package for Social Science (SPSS) version 25.0. Graphs were done in Excel 2016. The categorical variables were presented in frequency and percentage. The antibacterial resistance rate was calculated by taking the number of times the study strain was resistant, divided by the number of times the strain was resistant and susceptible. The intermediate level of resistance was not considered for the calculation.

3. RESULTS

3.1 Sociodemographic and Bacteriologic Profile

During our study period, 1071 strains were isolated from 955 individuals during the period from January 2016 to June 2021. The sex ratio

M:F was 1:1 with 502 (52,6%) male and 453 (47,4%). The most represented referral service was the Paediatric Department followed by the Emergency Department as shown in the Fig. 2. The most represented age groups were 0-5 years and 60-65 years, respectively 34.6% and 5.8% (Table 1).

The strains isolated were mainly from blood cultures 578 (54%) and pus 221 (20.6%) as described in Table 2. *Coagulase-negative staphylococci (CNS)* were represented at 18.5% followed by *Escherichia Coli* (17.7%), *Staphylococcus Aureus* (14%) and *Klebsiella Pneumoniae* (11.2%).
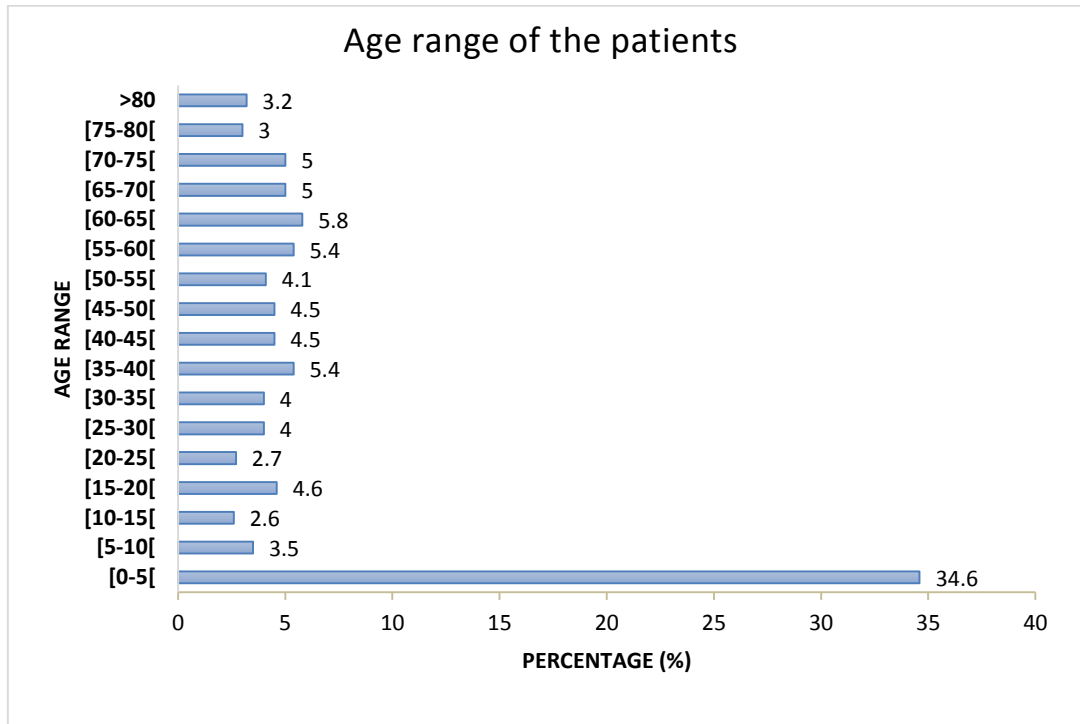
Fig. 1. Age range of patients
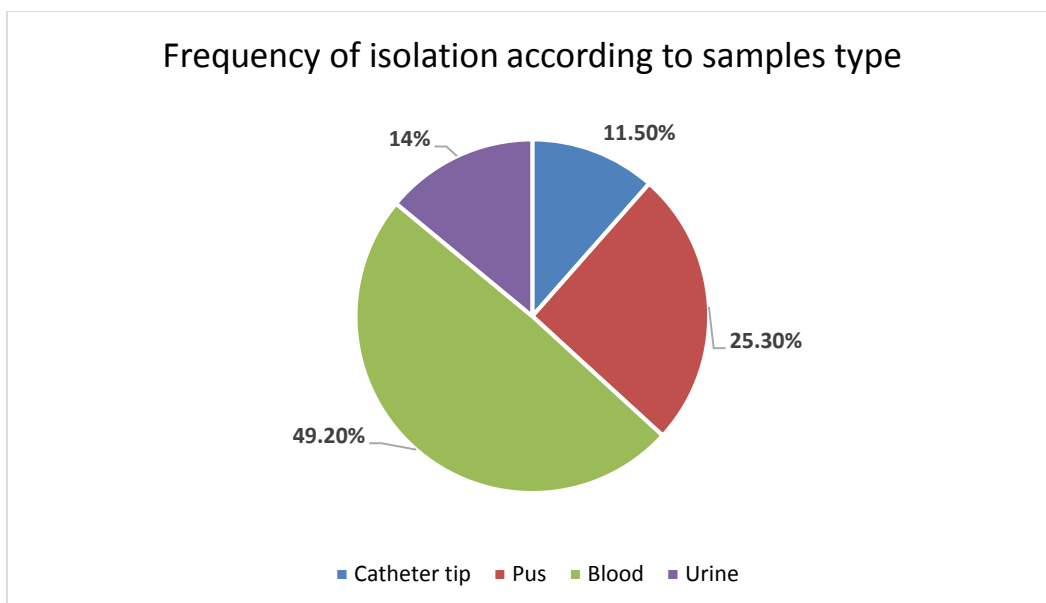
Fig. 2. Frequency of isolation according to samples type
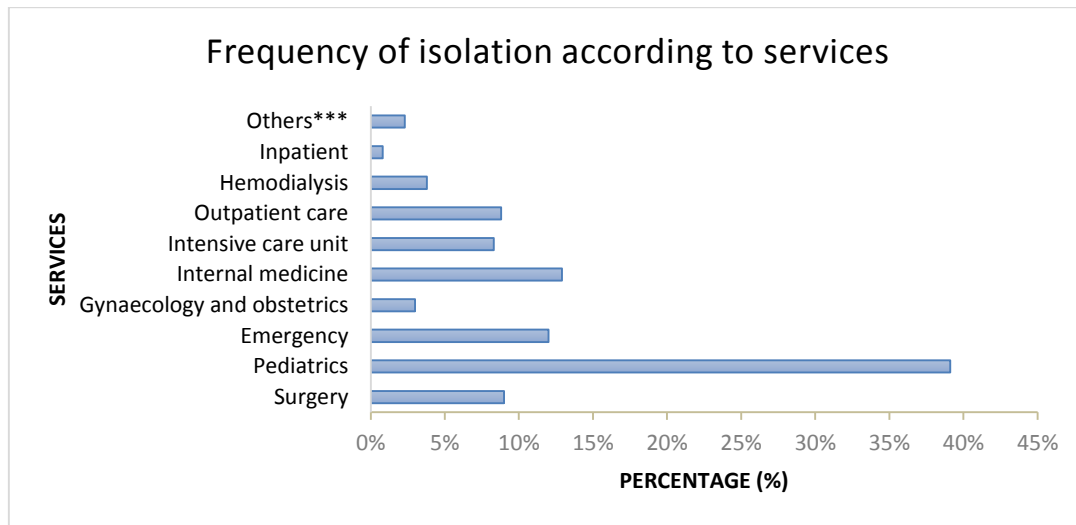
Fig. 3. Frequency of isolation according to services
*** Other includes those services: ENT, Operating Theatre, Odontostomatology, Physiotherapy*

Table 1. Bacteria found of our study population

	Number (strains)	Percentage (%)
BACTERIA		
Acinetobacter spp	34	3,2%
Citrobacter	18	1,7%
Escherichia coli	190	17,7%
Enterobacter	29	2,7%
Enterococcus spp	25	2,3%
Klebsielles		
Klebsiella oxytyca	13	1,2%
Klebsiella ozaenae	27	2,5%
Klebsiella pneumoiae	120	11,2%
Klebsiella rhinoscleromaticis	20	1,9%
Other Klebsiella	5	0,5%
Proteus		
Proteus mirabilis	13	1,2%
Proteus vulgaris	6	0,6%
Other Proteus	4	0,4%
Pseudomonas		
Pseudomonas aeruginosa	12	1,1%
Pseudomonas cepacia	7	0,7%
Pseudomonas of the fluorescens group	23	2,1%
Other Pseudomonas	6	0,6%
Staphylococci		
Staphylococcus aureus	150	14,0%
Staphylococcus epidermitis	44	4,1%
Staphylococcus saprophiticus	15	1,4%
Coagulase negative staphylococci	198	18,5%
Other staphylococci	2	0,2%
Streptococci		
Streptococcus milleri	7	0,7%
Streptococcus sanguis	4	0,4%
Other streptococcus (non identified)	18	1,7%
Other bacterial strains		
Providencia spp	4	0,4%

	Number (strains)	Percentage (%)
BACTERIA		
Salmonella spp	8	0,7%
Serratia spp	11	1,0%
Other bacteria (weakly represented)	28	2,7%
Non-fermentative gram negative bacilli	25	2,3%
Others gram negative bacilli	5	0,5%
TOTAL	1071	100%

3.2 Evolution of Bacterial Resistance of the Main Germs Found (2016-2020)

The report on the evolution of antibiotic resistance shows that in 2016 *Escherichia coli* strains were 78% resistant to penicillins, 44% to cephalosporins, 43% to quinolones and 6% to aminoglycosides. By the year 2020, the resistance of Escherichia Coli strains to penicillins has increased from 78% to 83%. Resistance to cephalosporins has increased from 44% to 61% and resistance to aminoglycosides has increased from 6% to 25%.

The report on the evolution of antibiotic resistance shows that in 2016, 68% of *Staphylococcus aureus* strains were resistant to penicillins, 67% to cephalosporins, 31% to quinolones, 20% to aminoglycosides, 36% to macrolides and 42% to tetracyclines. By the year 2020, the resistance of *Staphylococcus aureus* strains to penicillins has increased from 68% to 77%. Resistance to cephalosporins increased from 44% to 61%, resistance to aminoglycosides decreased from 20% to 11% and resistance to tetracyclines decreased from 42% to 30%.

Klebsiella Pneumoniae accounted for 72% of the *Klesiella* found. Some species were not specified (26.2%). Other species such as *Klebsiella Ozaenae* (1.8%) were poorly recorded. The report on the evolution of antibiotic resistance shows that in 2016, 97% of *Klebsiella Pneumoniae* strains were resistant to penicillins, 63% to cephalosporins, 36% to quinolones and 11% to aminoglycosides. Resistance to penicillins increased from 97% to 85%, to cephalosporins from 63% to 54%, to aminoglycosides from 11% to 19% and to quinolones from 36% to 17%.

3.3 Trends of Antibiotic Resistance

We note that all the mains bacteria studied that are: *E. coli, Staphylococci aureus* and *Klebsiella pneumonia*, show a resistance varying between 50% and 100% in general for the penicillin group as shown in the Fig. 3.

In the same line, all the mains bacteria studied, show a resistance varying between 30% and 100% in general for the cephalosporin (Fig. 5).

Also we observed that, all the mains bacteria studied, show a resistance varying between 10% and 100% in general for the quinolone (fig. 6).

4. DISCUSSIONS

Antimicrobial resistance has progressively become a public health problem of global concern. Increasing antibiotic resistance to certain pathogens will make it difficult to control and treat infectious diseases [29].

Men (53%) outnumbered women (47%) in this study. Although the margin is not significant, it is different from a study by Metchim and Madouni where women (61%) outnumbered men (39%). This could be explained by the difference in sample size between this 955 study and their 141 study [30].

The most isolated collection sites were blood (49%) and pus (25%) respectively. However, the other sites were urine (14%) and catheter tips (12%). This result is different from that of Alemayehu and Saravanan where the most represented sites of collection were urine, pus and blood. This could be explained by the difference in sample size, where our study counted 955 versus 693 [31]. Most of the samples were isolated in the age group 0-5 years, which is similar to Alemayehu and al.

Coagulase-negative staphylococcus (CoNS) was the most common bacterium, followed by *E. coli* in this study. This could be explained by the fact that the majority of the samples in this study were from the paediatric unit. *Coagulase-negative staphylococcus* and *E. coli*, among others, have been identified as major bacteria in neonatal sepsis [32].

Table 2. Evolution of *Escherichia Coli* resistance

	2016	2017	2018	2019	2020
Penicillins	78%	83%	92%	76%	83%
Amoxicillin+Clavulanic acid	82%	90%	77%	81%	80%
Amoxicillin	75%	96%	86%	83%	100%
Piperacillin	67%	79%	100%	73%	71%
Ticarcillin	67%	67%	95%	0%	88%
Piperacillin+tazobactam	-	11%	100%	0%	0%
Ticarcillin+tazobactam	-	100%	100%	50%	0%
Ticarcillin+Clavulanic acid	-	100%	100%	78%	88%
Ampicillin	-	0%	100%	0%	100%
Oxacillin	-	-	-	-	100%
Cephalosporins	44%	52%	66%	30%	61%
Cefalotin	64%	81%	89%	63%	80%
Cefepime	75%	58%	100%	23%	-
Cefixime	50%	75%	80%	-	-
Cefotaxime	45%	11%	100%	100%	100%
Cefoxitin	33%	30%	40%	17%	0%
Ceftazidime	28%	29%	63%	39%	67%
Ceftriaxone	55%	100%	79%	5%	67%
Cefuroxime	33%	50%	58%	40%	80%
Ceftpodoxime	-	-	100%	-	-
Quinolones	43%	50%	58%	12%	100%
Ciprofloxacin	29%	54%	56%	17%	100%
Levofloxacin	36%	55%	25%	0%	-
Norfloxacin	54%	22%	65%	0%	-
Ofloxacin	44%	50%	61%	0%	100%
Pefoxacin	-	-	-	43%	-
Aminosides	6%	20%	8%	15%	25%
Amikacin	0%	5%	0%	13%	13%
Gentamycin	9%	32%	18%	29%	50%
Netilmicin	0%	75%	33%	13%	-
Tobramycin	9%	10%	0%	0%	-
Carbapenemes	0%	6%	11%	9%	0%
Imipeneme	0%	0%	4%	0%	0%
Ertapeneme	0%	0%	33%	0%	0%
Meropeneme	-	50%	16%	22%	0%
Other					
Nalixidic acid	50%	73%	71%	65%	100%
Colistin	0%	71%	100%	21%	100%
Cotrimoxazole	92%	71%	81%	20%	40%
Fosfomycin	0%	8%	6%	17%	0%
Nitrofurantoin	20%	72%	0%	3%	0%
TOTAL (strains)	**24**	**43**	**43**	**54**	**14**

Table 3. Evolution of *Staphylococcus aureus* resistance

	2016	2017	2018	2019	2020
Penicillins	68%	57%	72%	52%	77%
Amoxicillin+clavulanic acid	65%	27%	66%	48%	100%
Amoxicillin	100%	100%	94%	73%	100%
Ampicillin	-	-	-	10%	-
Oxacillin	64%	80%	50%	21%	55%
Piperacillin	-	-	-	-	100%
Penicillin G	-	-	-	100%	-
Ticarcillin+Clavulanic acid	-	-	-	-	100%
Cephalosporins	67%	100%	62%	60%	43%
Cefalotin	100%	-	0%	-	-
Cefixime	100%	-	-	-	-
Cefuroxime	100%	-	60%	47%	-
Cefotaxime	0%	-	-	-	-
Ceftazidime	-	-	0%	100%	100%
Ceftriaxone	-	-	-	100%	0%
Cefoxitin	-	100%	68%	67%	42%
Quinolones	31%	40%	57%	60%	31%
Ciprofloxacin	0%	-	-	67%	38%
Ofloxacin	100%	25%	44%	50%	14%
Levofloxacin	0%	100%	100%	60%	100%
Norfloxacin	0%	-	100%	-	-
Aminosides	20%	54%	46%	40%	11%
tobramycin	8%	53%	57%	43%	20%
Gentamycin	43%	57%	30%	38%	0%
Netilmicin	-	-	100%	-	-
Kanamycin	-	-	-	0%	-
Macrolides	36%	32%	28%	43%	28%
Erythromycin	0%	0%	44%	47%	23%
Clindamycin	45%	53%	14%	36%	40%
Tetracycline	42%	65%	58%	60%	30%
Tetracycline	73%	77%	56%	58%	50%
Minocycline	15%	50%	59%	22%	0%
Carbapenemes	0%	-	-	100%	100%
Ertapeneme	-	-	-	-	100%
Imipenem	0%	-	-	100%	-
Meropeneme	-	-	-	-	100%
Other					
Fusidic acid	45%	11%	11%	17%	17%
Vancomycin	31%	29%	32%	3%	100%
Pristinamycin	50%	50%	23%	-	0%
Lincomycin	25%	0%	-	0%	18%
Cotrimoxazole	43%	30%	50%	50%	-
Rifamycin	0%	25%	8%	15%	22%
TOTAL (strains)	**19**	**20**	**45**	**44**	**15**

Table 4. Evolution of *Klebsiella pneumonia* resistance

|	2016	2017	2018	2019	2020
Penicillins	97%	91%	90%	92%	85%
Amoxicillin+clavulanic acid	100%	100%	90%	85%	67%
Amoxicillin	92%	100%	100%	100%	100%
Ampicillin	-	-	-	-	100%
Piperacillin	100%	88%	73%	87%	80%
Piperacillin+tazobactam	-	0%	80%	100%	-
Ticarcillin	100%	100%	94%	100%	88%
Ticarcillin+clavulanic acid	-	100%	90%	100%	100%
Ticarcillin+tazobactam	-	100%	100%	50%	-
Cephalosporins	63%	83%	76%	77%	54%
Cefalotin	71%	92%	83%	77%	50%
Cefepime	80%	75%	100%	83%	-
Cefixime	25%	75%	50%	-	-
Cefotaxime	63%	100%	-	100%	60%
Cefoxitin	50%	20%	54%	40%	50%
Ceftazidime	67%	100%	73%	90%	50%
Ceftriaxone	100%	100%	93%	85%	50%
Cefuroxime	53%	100%	73%	75%	60%
Quinolones	36%	61%	66%	72%	17%
Ciprofloxacin	27%	64%	55%	54%	14%
Pefoxacin	-	-	-	89%	-
Levofloxacin	33%	33%	100%	75%	-
Norfloxacin	47%	100%	79%	82%	0%
Ofloxacin	33%	55%	67%	67%	33%
Aminosides	11%	41%	11%	37%	19%
Amikacin	0%	25%	10%	20%	11%
Gentamycin	22%	20%	13%	45%	0%
Netilmicin	13%	-	-	75%	33%
Tobramycin	100%	100%	-	-	100%
Tetracyclines	36%	-	100%	-	-
Minocycline	0%	-	-	-	-
Tetracycline	50%	-	100%	-	-
Other					
Nalixidic acid	38%	62%	55%	50%	38%
Fusidic acid	0%	-	-	-	-
Aztreonam	50%	100%	69%	81%	50%
Chloramphenicol	100%		50%	-	-
Colistin	100%	80%	100%	41%	33%
Cotrimoxazole	91%	50%	100%	92%	100%
Fosfomycin	0%	0%	58%	60%	60%
Nitrofurantoin	27%	75%	16%	38%	50%
Rifamycin	-	-	-	-	-
Vancomycin	50%	-	-	-	-
Teicoplanin	-	-	-	-	100%
TOTAL (strains)	**28**	**16**	**32**	**30**	**10**
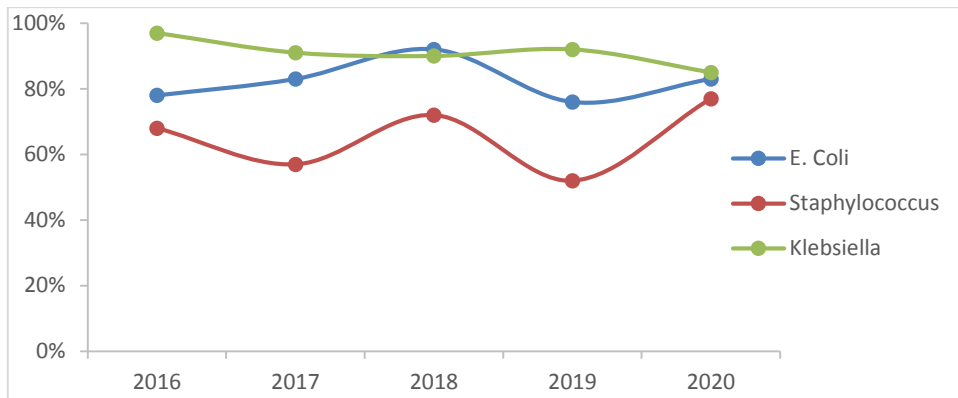
Fig. 4. Evolution of penicillin resistance
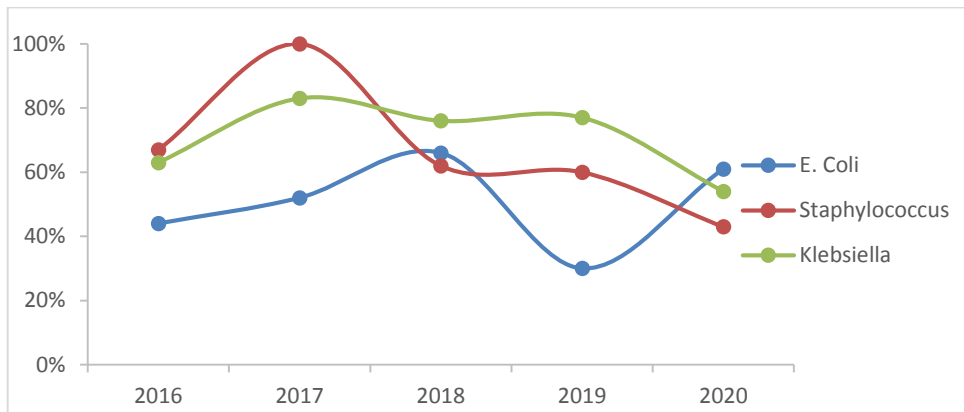
Fig. 5. Evolution of cephalosporin resistance (excluding nalixidic acid)
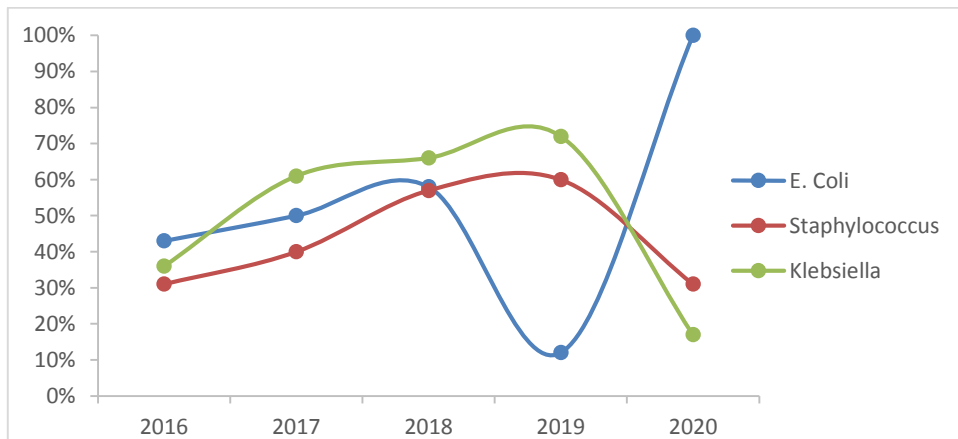
Fig. 6. Evolution of quinolone resistance

Resistance of *Staphylococcus aureus* to aminopenicillins, cephalosporins and aminoglycosides was identified in this study at 77%, 43% and 11% respectively in 2020. These results are similar to those of the study conducted by Rağbetli et al [33]. We observed a steady increase in *Staphylococcus aureus* resistance to aminopenecillins between 2016 and 2020, with a peak in 2020. Amoxicillin and amoxicillin/clavulanic acid showed full resistance to Staphylococcus aureus (100%). This result is quite similar to that of Andrianarivelo et al. in Madagascar [34].

Staphylococcus aureus was fully resistant (100%) in 2019 and less resistant (0%) to

ceftriaxone in 2020. This could be explained by the fact that the number of samples that were tested for ceftriaxone in 2020 was lower than those tested in previous years.

In 2020, *Staphylococcus aureus* were resistant to levofloxacin and aminoglycosides at 100% and 0% respectively. This could be explained by the routine empirical prescription of oral forms of quinolones by practitioners for urinary tract and soft tissue infections. Whereas aminoglycosides are mainly found in intravenous solutions and usually require hospitalizations to be administered to patients.

Andrianarivelo et al. noted in their study a 75% resistance rate to tetracyclines, which is different from our study 30% (in 2020). This is probably due to the fact that their paper focused only on *Staphylococcus aureus*, whereas we had a variety of species in this study. Secondly, tetracyclines are not commonly prescribed on a daily basis in our context.

Despite an apparent steady but gradual decrease in *Staphylococcus aureus* resistance to the drug classes, namely aminopenicillins, cephalosporins and aminoglycosides in this study in 2020, this does not reflect the resistance of individual drugs by class.

We noted that *E. coli* resistance to penicillins, cephalosporins, quinolones and aminoglycosides increased over the years. These resistances almost doubled between 2016 and 2020; this has been reported in other studies by Saravanan and al, in Pondicherry and Ebongue and al, in Douala [24,31]. In 2020, there was 100% resistance to amoxicillin, ampicillin, oxacillin, cefotaxime, ciprofloxacillin and ofloxacin. During the study period 2018 - 2020, cefotaxime had an optimal resistance of 100%. This could be explained by the fact that most of our samples proven from the paediatric ward and that cefotaxime is routinely combined with other antibiotics in the treatment of neonatal infections in our setting.

Piperacillin + tazobactam and carbapenems had a higher sensitivity 0% (less resistant) between 2019 - 2020 respectively. This is probably due to the fact that these drug classes are not commonly prescribed by health practitioners.

In 2020, *Klebsiella pneumonia* showed resistance to penicillins in general (85%). This is because, according to the literature, *K. pneumoniae* is naturally resistant to penicillins,

especially amoxicillin and ticarcillin. We also noted a resistance to cephalosporins (54%), quinolones (17%) and aminoglycosides (19%). These results are similar to those of a study by Saravanan and al [31]. A study conducted in Cameroon reported less effective resistance of *K. pneumoniae* to Aminopenicillins [35].

Nevertheless, despite the recorded resistance of *Klebsiella pneumoniae* to Penicillins between 2016 and 2020, an overall increase in susceptibility of Penicillins, Cephalosporins, Quinolones and Aminoglycosides to *Klebsiella pneumoniae* was observed over the years in this study. We can observe from the 2020 data an excellent susceptibility of Tetracycline and Gentamycin to *Klebsiella pneumonia*, probably due to fewer prescriptions by physicians, but also due to the lack of routine resistance testing of *Klebsiella* species with these drug classes.

5. LIMITATION OF THE STUDY

The study did not determine if the resistance showed by the study was due to hospital-acquired or community acquired infection.

The study is retrospective and all the biological fluids were not included, so could not explain the trends of the bacteria concerning antibiotics.

6. CONCLUSION

This study aimed to determine the evolution of the antibiotic resistance profile of bacteria from January 2016 to June 2021 in the laboratory of the Yaounde University Teaching Hospital. The most represented department was the paediatric department and the most represented age group was 0-5 years. The most represented pathological product was blood. The most commonly identified strains were *coagulase negative staphylococci*, *Escherichia coli*, *Staphylococcus aureus* and *Klebsiella pneumonia*. The evolution of *Escherichia coli* resistance to penicillin, aminoglycosides, quinolones and cephalosporins increased between 2016 and 2020. For *Staphyloccocus aureus*, the evolution was increased between 2016 and 2020 for penicillin, constant for quinolones and reduced for cephalosporins, macrolides, tetracyclines and aminosides. For the *klebsiella Pneumoniae* strain, resistance was reduced for penicillins, cephalosporins and quinolones, but high for aminoglycosides. The magnitude of the challenge of antibiotic resistance in the medical world demonstrates the

urgency to act. It is important through multi-sectoral coordination that each sector, namely human, animal and environmental health, strengthens the surveillance of antibiotic resistance and raises awareness among both health professionals and the general population on the proper use and management of antibiotics and even antimicrobials in general.

ETHICAL APPROVAL

All authors hereby declare that the study has been be approved by an Institutional Ethical Review Board (IERB) of the Faculty of Medicine and Biomedical Sciences. The approval number is N° 121/UYI/FMSB/VDRC/DAASR/CSD.

ACKNOWLEDGEMENTS

We would like to thanks the staffs of the YUTH's laboratory unit for helping us during data collection and make our work more fluid.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle4.com/review-history/74753