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High Burden of Antimicrobial Resistance among Major Bacterial Pathogens in Bangui, Central African Republic: A Study Based on Data from a National Laboratory, 2013-2019

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Abstract

Introduction: Antimicrobial resistance (AMR) is now one of the major threats to global public health, with a particularly significant impact in resource-limited countries. The availability of reliable local data is essential to guide treatment and surveillance policies. The objective of this study was to describe the bacteriological and antibiotic resistance profiles observed at the National Laboratory of Clinical Biology and Public Health (LNBCSP) in Bangui. **Patients and Methods:** This is a descriptive study based on the analysis of aggregated microbiological data from the LNBCSP's routine tables covering the period 2013–2019. The results were analyzed in terms of the distribution of bacterial species and overall antibiotic susceptibility and resistance profiles. **Results:** A total of 3,020 bacterial isolates were analyzed. *Staphylococcus aureus* was the most frequently isolated species, followed by *Escherichia coli* and *Klebsiella pneumoniae*. High levels of resistance were observed for several commonly used antibiotics, including cotrimoxazole, penicillins, and fluoroquinolones. **Conclusion:** The results indicate a high burden of antimicrobial resistance in Bangui and highlight the urgent need to strengthen microbiological surveillance and the proper use of antibiotics.

Keywords

Resistance, Antibiotic, LNBCSP, Central African Republic

1. Introduction

Antimicrobial resistance (AMR) is now a major challenge for global public health. According to recent estimates, AMR is associated with several million deaths each year, a significant proportion of which are directly attributable to antibiotic resistance [1]. Since 2019, AMR has been responsible for 4.95 million deaths each year, including 1.27 million deaths attributed to antibiotic resistance. If no effective measures are implemented, this burden could increase further in the coming decades, reaching 10 million deaths by 2050 [1] [2].

One of the most worrying aspects of AMR is the emergence and spread of multidrug-resistant or highly resistant bacteria, including carbapenemase-producing Enterobacteriaceae and certain Gram-positive cocci resistant to last-resort antibiotics [2]-[5]. These pathogens, due to their epidemic potential and the limited treatment options available, pose a major threat to health systems [6] [7].

In sub-Saharan African countries, the situation is exacerbated by unregulated access to antibiotics, self-medication, prolonged empirical use of antimicrobial treatments, and the circulation of substandard or counterfeit drugs [8] [9]. Added to this are environmental factors, such as poor wastewater management and the use of antibiotics in animal production, which promote the spread of resistant bacteria [2] [10] [11].

In Central African Republic, national data on AMR remain limited [12]-[14]. The National Laboratory of Clinical Biology and Public Health (LNBCSP) plays a central role in microbiological surveillance and is an essential source of information for documenting the evolution of AMR in the country [15] [16]. The present study aims to analyze the available data in depth in order to describe the bacteriological profile and trends in antibiotic resistance observed in Bangui.

2. Patients and Methods

This was a retrospective descriptive study conducted in the bacteriology and emergency departments of the National Laboratory of Clinical Biology and Public Health (LNBCSP) in Bangui. The study covered the period from 2013 to 2019 and was based on the analysis of laboratory records and results tables.

The study population consisted of patients who had undergone bacteriological analysis with a positive culture and interpretable antibiogram. Patients with incomplete data were excluded from the analysis. Due to the lack of a structured individual database, no deduplication of isolates at the patient level could be performed.

The specimens collected included urine, stool, genital samples, sputum, and various aspirated body fluids (including synovial fluid from the knee, cerebrospinal fluid, pleural fluid, and pus).

For liquid specimens such as urine, a minimum volume of 5 mL was required, and all samples were collected in accordance with the recommended procedures outlined in the *Référentiel en Microbiologie* (*REMIC*). Specimens were transported promptly to the laboratory, typically within two hours of collection, to preserve sample integrity and ensure the reliability of microbiological analyses.

Genital samples were collected either on-site at the laboratory or, for hospitalized patients, within specialized healthcare facilities by trained personnel. Aspirated body fluids were generally obtained in hospital settings by qualified medical or surgical staff. These samples were collected in sterile containers that met appropriate transport and biosafety standards, as provided by the laboratory.

Overall, standardized collection and transport procedures were implemented to minimize pre-analytical variability and ensure the quality and reproducibility of microbiological results.

Bacterial identification was based on standard microbiological techniques, including culture on standard and enriched agar media, biochemical and immunological tests, and the use of API galleries (bioMérieux, Marcy-l'Étoile, France). Antibiograms were performed by agar diffusion in accordance with current EUCAST/CASFM (2013,2014, 2015, 1016, 2017, 2018 and 2019). A total of fifteen antibiotics (Biorad, Marnes-la-coquette, France) were tested: Cefepime (FEP 30 µg), Cefotaxime (CTX: 30 µg), Ceftriaxone (CRO: 30 µg), Cefixime (CFM: 5 µg); Cefoxitin (FOX: 30 µg): Amoxicillin + clavulanic acid (AMC: 20 - 10 µg), Ampicillin (AM: 30 µg), Ciprofloxacin (CIP: 5 µg), Ofloxacin (OFX: 5 µg), Pefloxacin (PEF: 5 µg), Amykacin (AK: 30 µg), Kanamycin (K: 30 IU), Tobramycin (TOB: 10 µg), Chloramphenicol (C: 30 µg), Tetracycline (TE: 30 µg), Imipeneme (IMP: 10 µg).

Recommendations: When necessary, minimum inhibitory concentration tests using E-test® strips were used to confirm certain resistance profiles.

The data were entered and analyzed using Epi Info software version 3.3.2. The results are presented as frequencies and percentages.

3. Results

A total of 3,020 patients were included in the analysis. The mean age of patients was 33.3 years, with a predominance of young adults aged 21 to 30 years. The overall distribution of isolated bacterial species is shown in Table 1 and Table 2.

The analysis of antimicrobial resistance revealed substantial variability across pathogen–antibiotic combinations, with generally high resistance rates observed for commonly used antibiotics (Table 3).

Among Gram-negative bacteria, *Escherichia coli* exhibited high resistance to ampicillin, with 50.39% (n = 391) of isolates resistant. Similarly, resistance to amoxicillin–clavulanic acid reached 38.25% (n = 166), and to nalidixic acid 38.25% (n = 166). Resistance to third-generation cephalosporins was also notable, with ceftriaxone resistance observed in 46.03% (n = 145) of isolates and cefotaxime in 36.15% (n = 47). In contrast, lower resistance rates were observed for ciprofloxacin (21.55%, n = 131) and gentamicin (21.97%, n = 76), suggesting relatively preserved activity.

Klebsiella pneumoniae demonstrated considerable resistance, particularly to ceftriaxone (20.95%, n = 66) and ampicillin (14.18%, n = 110), highlighting the burden of resistance among Enterobacteriaceae. Resistance to cefotaxime was 13.08% (n = 17), consistent with the presence of extended-spectrum beta-lactamase (ESBL)-producing strains.

Table 1. Distribution of bacterial species isolated by sex.

Bacteria	Male (n, %)	Female (n, %)	Total (n, %)
E. coli	167 (8.1%)	461 (22.5%)	628 (30.6%)
Klebsiella pneumoniae	43 (2.1%)	116 (5.7%)	159 (7.8%)
Staphylococcus aureus	477 (23.3%)	1574 (76.7%)	2051 (100.0%)
Streptococcus pneumoniae	50 (2.4%)	49 (2.4%)	99 (4.8%)

Table 2. Distribution of bacterial species isolated by age group.

Age Group	Bacterial infection number (Percentage)	Interpretation
0 - 11 months	32 (1%)	Low prevalence
1 - 5 years	112 (3.7%)	Moderate prevalence
>5 years	2877(95.3%)	Higher prevalence
Total	3020 (100%)	

Table 3. Resistance profile of the main bacterial isolates.

Pathogen	Antibiotic	Resistance (%)	n (resistant)
Escherichia coli	Ampicillin	50.39	391
Escherichia coli	Amoxicillinclavulanic acid	38.25	166
Escherichia coli	Ceftriaxone	46.03	145
Escherichia coli	Ciprofloxacin	21.55	131
Klebsiella pneumoniae	Ampicillin	14.18	110
Klebsiella pneumoniae	Ceftriaxone	20.95	66
Staphylococcus aureus	Erythromycin	94.42	913
Staphylococcus aureus	Doxycycline	93.8	666
Staphylococcus aureus	Ciprofloxacin	68.91	419
Staphylococcus aureus	Gentamicin	64.45	223
Streptococcus pneumoniae	Doxycycline	5.07	36
Streptococcus pneumoniae	Erythromycin	4.45	43

Among Gram-positive bacteria, *Staphylococcus aureus* showed very high resistance rates to several antibiotics. Resistance to erythromycin reached 94.42% (n = 913) and to doxycycline 93.80% (n = 666). High resistance was also observed for ciprofloxacin (68.91%, n = 419) and gentamicin (64.45%, n = 223). Moderate resistance levels were found for amoxicillin–clavulanic acid (46.31%, n = 201) and chloramphenicol (44.77%, n = 227).

For *Streptococcus pneumoniae*, resistance remained comparatively lower but still notable, including 5.07% (n = 36) for doxycycline and 4.45% (n = 43) for erythromycin.

Overall, resistance across all isolates was highest for erythromycin (32.02%, n = 967), doxycycline (23.51%, n = 710), ciprofloxacin (20.13%, n = 608), and chloramphenicol (16.79%, n = 507). Lower overall resistance rates were observed for gentamicin (11.46%, n = 346) and ceftriaxone (10.43%, n = 315), indicating relatively better retained efficacy.

Staphylococcus aureus accounted for the majority of isolates, followed by *Escherichia coli* and *Klebsiella pneumoniae*. Resistance profiles varied significantly depending on the bacterial species and the classes of antibiotics tested. Figure 1 illustrates the levels of resistance observed in the main bacterial pathogens isolated.

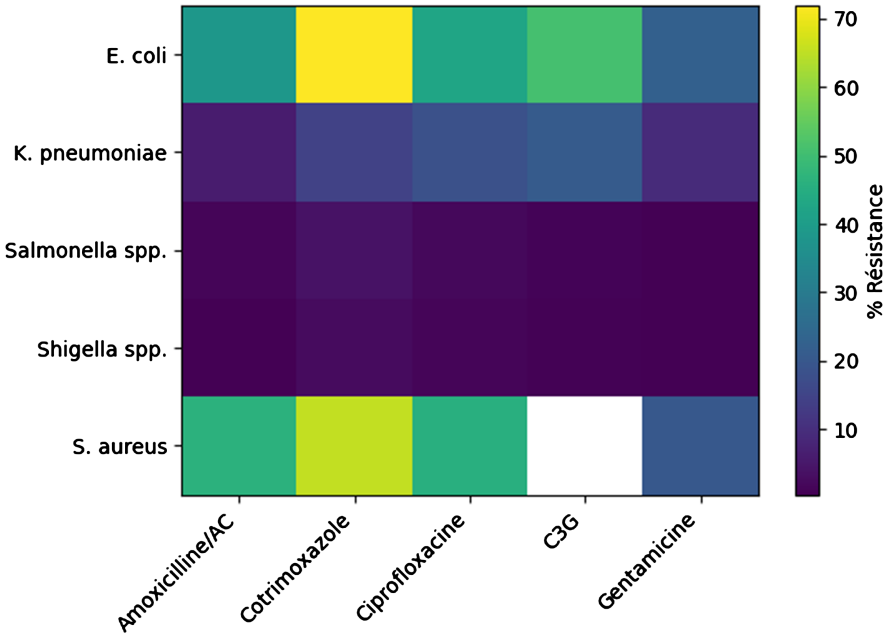

Figure 1. Resistance profile of the main bacteria isolated at the LNBCSP in Bangui from 2013 to 2019.

The overall antibiotic susceptibility profile shows a low proportion of fully susceptible strains for most of the molecules tested. Gentamicin had the highest activity among the antibiotics analyzed, as illustrated in Figure 2.

4. Discussion

This study provides a detailed analysis of the bacteriological profile and antibiotic resistance observed at the LNBCSP in Bangui over an extended period. The predominance of *Staphylococcus aureus* and *Enterobacteriaceae,* particularly *Escherichia coli* and *Klebsiella pneumoniae*, is consistent with data reported in several sub-Saharan African countries [10] [17]-[20].

The high levels of resistance observed to first-line antibiotics, particularly co-

trimoxazole, penicillins, and fluoroquinolones, are a major warning sign for the empirical management of infections [8] [21]. These results suggest significant antibiotic pressure, both in the community and in hospitals [9] [22].

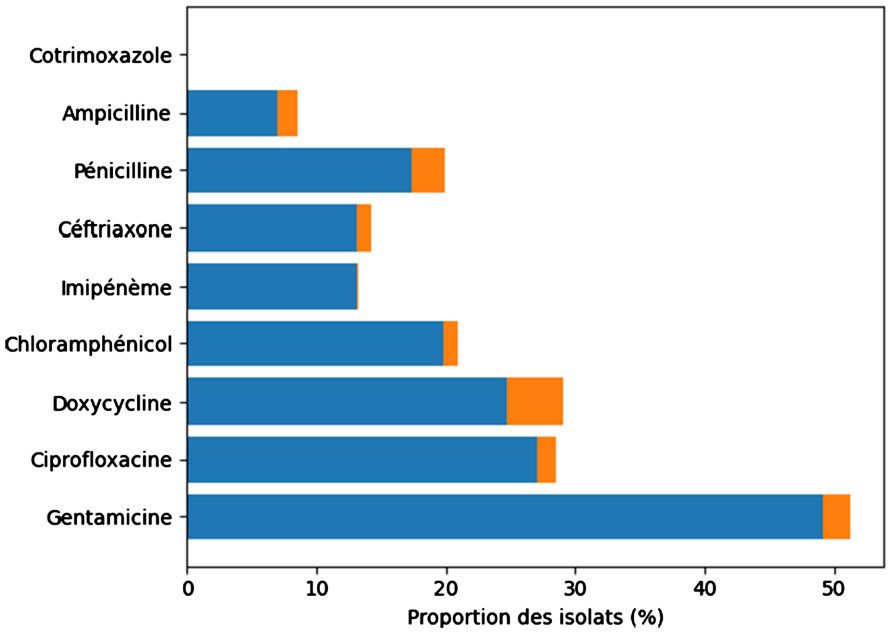

Figure 2. Proportions of susceptible and intermediate strains.

Conversely, certain antibiotics such as gentamicin retain relative activity, although their use must be regulated due to their potential toxicity and accessibility constraints [23]. The heterogeneity of resistance profiles among pathogens underscores the importance of continuous local microbiological surveillance to guide treatment policies [16] [24] [25].

5. Limitations of the Study

The main limitations of this study lie in the use of aggregated data from routine registries. The lack of individual data prevented the deduplication of isolates and detailed analysis of temporal trends. In addition, the lack of associated clinical information made it impossible to assess the direct clinical impact of the resistance observed.

6. Conclusion

In conclusion, this study highlights a high burden of antimicrobial resistance in Bangui. The predominance of *Staphylococcus aureus* and *Enterobacteriaceae*, combined with high rates of resistance to commonly used antibiotics, highlights a worrying reduction in treatment options [7]. These results call for urgent strengthening of microbiological surveillance, optimization of the proper use of antibiotics, and support for laboratory capacities in order to effectively combat antibiotic resistance in the Central African Republic [7] [26]-[30].

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Ethics

This study was conducted in accordance with the HELSINKI declarations on respect for human dignity.

Authors' Contribution

Database analyze: SO. Administrative and technical project management: KB, RCD. Laboratory technics and scientific writing: DHBLM, NGSL, AF, LE.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

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