IJMM
International Journal of Microbiology and Mycology
Website: www.innspub.net

TYPE: RESEARCH PAPER
Int. J. Microbiol. & Mycol.
Email: info@innspub.net

| ARTICLE INFORMATIONS |

OPEN ACCESS

Dieye *et al.*, 2026

Accepted: January 03, 2026
Published: January 09, 2026

Int. J. Microbiol. & Mycol.
Vol. 22, Issue: 1, p. 1-11.

Corresponding author:
Baïdy Dieye
Email: baidy.dieye@yahoo.fr

Phenotypic characterization of bacteria isolated from blood cultures at the Albert Royer National Children's Hospital (CHNEAR) in 2023

B. Dieye[*1,3], A. Diop[1,3], A. A. Niang[1,4], F. Diallo[1,4], M. A. Sonko[3], F. Thiam[3], S. S. Mbacke[3], C. B. Fall[1,3], M. Der[4], A. T. M. Diallo[5], A. Gaye[4], A. Dieng[1,6], R. Ka[2], M. L. Dia[1,4]

[1]Université Cheikh Anta Diop de Dakar, Senegal
[2]Université Iba Der Thiam de Thiès, Senegal
[3]Centre Hospitalier National d'Enfants Albert Royer, Dakar, Senegal
[4]Centre Hospitalier National de Fann, Dakar, Senegal
[5]Hôpital Dalal Jamm, Dakar, Senegal
[6]Hôpital Aristic Le Dantec, Dakar, Senegal

DOI: https://dx.doi.org/10.12692/ijmm/22.1.1-11

ABSTRACT

Septicemia remains a major cause of morbidity and mortality in pediatric populations and poses a significant global public health challenge due to antimicrobial resistance (AMR). Blood culture is the gold standard for diagnosis and provides essential data for guiding empirical antibiotic therapy. In Senegal, limited data are available on the bacteriological profile of bloodstream infections at the Centre Hospitalier National d'Enfants Albert Royer (CHNEAR), the national pediatric referral center. This retrospective descriptive study with analytical components examined bacteria isolated from blood cultures between January 1 and December 31, 2023. Patient and laboratory data were retrieved from registers and a local database (FileMaker Pro Advanced 11.0 v1). Blood cultures were processed using the BACT/ALERT system. Antibiotic susceptibility testing was performed using the Kirby–Bauer method and analyzed with the ADAGIO system. Data were extracted into Microsoft Excel 2013 and analyzed using STATA version 14.0. A total of 1,104 blood culture bottles were analyzed, primarily from the emergency department. The mean patient age was 17.67 years, with a male-to-female ratio of 1.32. The overall positivity rate was 26.81%, yielding 296 bacterial isolates. The predominant organisms were *Staphylococcus* spp. (43.77%), *Klebsiella* spp. (13.47%), *Pseudomonas* spp. (10.77%), and *Escherichia* spp. (10.10%). Extended-spectrum beta-lactamase (ESBL)-producing strains accounted for 38 isolates, mainly *Klebsiella pneumoniae* (47.37%), while 40.68% of *Staphylococcus aureus* isolates were methicillin-resistant (MRSA). These findings highlight moderate but concerning levels of antibiotic resistance. Strengthening local AMR surveillance and implementing targeted interventions aligned with the One Health approach are essential to improving septicemia management and reducing mortality.

Keywords: Septicemia, Blood cultures, Antibiotics, Antimicrobial resistance

INTRODUCTION

Septicemia remains a significant cause of morbidity and mortality in hospitalized patients, particularly in pediatric settings where clinical deterioration may occur rapidly. It reflects the presence of pathogenic microorganisms in the bloodstream and is often accompanied by a dysregulated host immune response that can progress to severe sepsis or septic shock. Despite improvements in diagnostic tools and antimicrobial therapy, mortality associated with severe bloodstream infections remains substantial, especially in resource-limited contexts. Early identification of the causative organism and timely initiation of appropriate antimicrobial therapy are therefore central to patient management.

Blood culture continues to represent the cornerstone of microbiological diagnosis in suspected septicemia. Beyond confirming the presence of bacteremia, it provides essential information on pathogen identification and antimicrobial susceptibility, allowing clinicians to adjust empirical therapy in a rational manner (Vinclair *et al.*, 2020; Ndiaye, 2024). However, the relevance of empirical antibiotic regimens depends heavily on knowledge of the prevailing local bacterial ecology. Resistance patterns are not static; they evolve under antibiotic pressure and vary between institutions, departments, and patient populations.

In recent years, antimicrobial resistance (AMR) has increasingly complicated the management of bloodstream infections. The emergence and spread of extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae, carbapenemase-producing organisms, and methicillin-resistant *Staphylococcus aureus* (MRSA) have progressively narrowed therapeutic options. This challenge is particularly pronounced in low- and middle-income countries, where diagnostic delays, prior antibiotic exposure, and limited surveillance infrastructure may facilitate the selection and dissemination of multidrug-resistant strains (Kone, 2010) .

In Senegal, several studies have described blood culture findings and resistance patterns in selected hospital settings (Sonko, 2013; Ndiaye, 2024).

Nevertheless, microbiological surveillance remains uneven, and up-to-date, institution-specific data are often lacking. At the Albert Royer National Children's Hospital (CHNEAR), the national pediatric referral center, septicemia continues to represent a frequent indication for hospitalization and laboratory investigation. While earlier work documented invasive infections in this institution, recent comprehensive data describing the current spectrum of isolated pathogens and their phenotypic resistance profiles are limited. Given the dynamic nature of AMR and the evolving use of antimicrobial agents, the absence of updated local data may result in a mismatch between empirical therapeutic strategies and circulating pathogens, potentially affecting treatment outcomes and contributing to further resistance selection.

Against this background, the present study was undertaken to characterize, at the phenotypic level, the bacteria isolated from blood cultures performed at CHNEAR over a one-year period (January 1 to December 31, 2023), to describe the distribution of the principal pathogens according to clinical context and hospital department, to analyze their antimicrobial susceptibility patterns, and to document the prevalence of multidrug-resistant organisms, particularly ESBL-producing Enterobacteriaceae and MRSA. By providing updated local epidemiological evidence, this work seeks to support more informed empirical antibiotic choices and to contribute to ongoing efforts aimed at strengthening antimicrobial stewardship within the framework of national AMR control initiatives.

MATERIALS AND METHODS

Study design and setting

We conducted a retrospective descriptive study with an analytical component at the microbiology laboratory of the Albert Royer National Children's

Vol. 22, Issue. 1, p. 1-11, 2026
Website: https://innspub.net

Hospital (CHNEAR), Dakar, Senegal. CHNEAR is a level III national pediatric referral center with approximately 140 inpatient beds and multiple specialized departments, including emergency care, neonatology, pulmonology, endocrinology, pediatric surgery, and intensive care.

The microbiology unit operates within a multipurpose laboratory platform and routinely performs blood culture processing and antimicrobial susceptibility testing for hospitalized patients. The study period extended from January 1 to December 31, 2023.

Study population and eligibility criteria

All blood culture bottles processed during the study period were screened for inclusion. Blood cultures were requested by treating physicians based on clinical suspicion of septicemia or severe infection.

We included all blood cultures with complete demographic and microbiological data. Cultures were excluded if patient demographic information (age, sex, hospital department) or antimicrobial susceptibility data were incomplete.

Because this study relied exclusively on routinely collected laboratory data, no additional sampling or intervention was performed.

Blood culture procedures

Blood samples were collected under aseptic conditions by trained healthcare personnel according to institutional standard operating procedures. Specimens were inoculated into aerobic and/or anaerobic blood culture bottles and processed using the automated BACT/ALERT® 3D system (bioMérieux, France), which continuously monitors microbial growth.

Positive bottles were subjected to immediate Gram staining followed by subculture onto appropriate solid media. Organism identification was performed using conventional phenotypic methods routinely applied in the laboratory, including colony morphology assessment and standard biochemical identification techniques.

A blood culture was considered negative if no growth was detected after the manufacturer-recommended incubation period.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing (AST) was performed using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar. Zone diameters were measured and interpreted using the ADAGIO® automated reading system (Bio-Rad, France) to enhance standardization and reduce observer variability.

Interpretation of susceptibility categories (susceptible, intermediate, resistant) followed the European Committee on Antimicrobial Susceptibility Testing (EUCAST) 2023 clinical breakpoints.

Phenotypic definitions were applied as follows:

1. Extended-spectrum beta-lactamase (ESBL) production was confirmed by demonstration of synergy between third-generation cephalosporins and clavulanic acid, in accordance with EUCAST recommendations.
2. Methicillin-resistant *Staphylococcus aureus* (MRSA) was defined by resistance to cefoxitin.
3. Carbapenem resistance was defined as resistance to at least one tested carbapenem agent according to EUCAST breakpoints.

Multidrug resistance (MDR) was defined according to the international expert proposal by Magiorakos *et al.* (2012) as acquired non-susceptibility to at least one agent in three or more antimicrobial categories.

Internal quality control procedures were routinely performed using reference control strains in accordance with laboratory quality assurance protocols.

Data collection

Laboratory and demographic data were extracted from laboratory registers and the electronic database

Vol. 22, Issue. 1, p. 1-11, 2026
Website: https://innspub.net

(FileMaker Pro Advanced 11.0 v1), where all blood culture results are routinely archived.

The following variables were collected:

1. Age
2. Sex
3. Hospital department
4. Clinical indication (when available)
5. Culture result (positive, negative, contaminated)
6. Gram stain classification
7. Identified organism
8. Antimicrobial susceptibility profile
9. Presence of ESBL, MRSA, or carbapenem resistance phenotype

Data were exported into Microsoft Excel 2013 for cleaning and verification before statistical analysis.

Statistical analysis

Statistical analyses were performed using STATA version 14.0 (StataCorp, USA). Continuous variables were summarized as means ± standard deviation when normally distributed. Categorical variables were presented as frequencies and percentages.

Primary outcome measures included:

1. Proportion of positive blood cultures
2. Distribution of bacterial species
3. Prevalence of multidrug-resistant phenotypes

Descriptive comparisons were performed according to Gram classification and hospital department. Given the retrospective and observational nature of the study, results were interpreted within the limitations inherent to descriptive hospital-based analyses.

Ethical considerations

The study was based exclusively on anonymized laboratory data collected during routine clinical care. No identifiable patient information was included in the analytical dataset. Institutional authorization was obtained from CHNEAR administration prior to data extraction. According to local regulations, formal individual informed consent was not required for retrospective analysis of anonymized data.

RESULTS

Overall blood culture activity and positivity rate

During the study period, a total of 1,104 blood culture bottles were processed at the CHNEAR microbiology laboratory. Of these, 296 yielded bacterial or fungal growth, corresponding to a positivity rate of 26.81%, while 806 (73.01%) remained sterile. Only two bottles (0.18%) were classified as contaminated (Table 1) .

Table 1. Distribution of the number of blood cultures according to culture results

Culture	Number	Percentage (%)
Negative	806	73,01
Positive	296	26,81
Culture contamination	2	0,18
Total	1104	100

The mean age of patients who underwent blood culture testing was 17.67 years. The distribution by sex showed a male predominance, with a sex ratio (male/female) of 1.32 (Fig. 1).

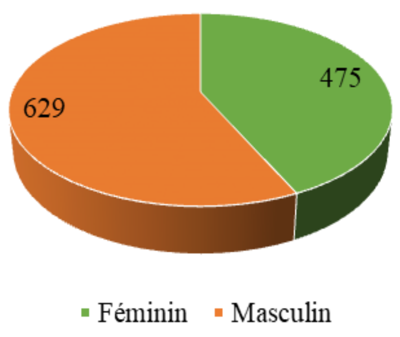

Fig. 1. Distribution of blood cultures by

Distribution by hospital department and clinical indication

Blood culture requests originated primarily from the emergency department (21.38%), followed by pulmonology (20.65%) and endocrinology (9.69%). Smaller proportions were contributed by neonatology, pediatric surgery, intensive care, and other internal services (Table 2) .

Table 2. Répartition du nombre d'hémocultures selon les services

Services	Number	Percentage (%)
SAU	236	21,38
PK	228	20,65
PM	107	9,69
PN	105	9,51
PO	134	12,14
Pediatric surgery	16	1,45
Pediatric resuscitation	45	4,08
Other internal services (USAD, Dermatology ...)	17	1,54
External services	32	2,90
Total	1104	100

Most of the blood cultures came from the SAU at CHNEAR.

Table 3. Distribution of the number of blood cultures according to diagnosis

Diagnostics	Number	Percentage (%)
Infectious syndrome	492	44,57
Fever/Febrile spikes/Sepsis/SIRS/Malaria/Hypothermia/Chills/Convulsions	166	15,04
Hemoglobinopathies	26	2,36
Respiratory disorders	47	4,26
Cardiac disorders	42	3,80
Meningitis	16	1,45
Abdominal disorders	6	0,54
INN, IMF, prematurity, IUGR	21	1,90
Skin disorders	10	0,91
Bone and joint disorders/Inflammatory disorders/Inflammatory trauma/Trauma	10	0,91
Kidney and urinary tract disorders	8	0,72
Metabolic disorders	2	0,18
Blood and blood vessel disorders	6	0,54
Shock	6	0,54
Examination/Control blood culture/Nosocomial infection	10	0,91
Other (Suppuration/Superinfection/Fistulas/Dehydration/Brain disorders /West syndrome	180	16,30
Unspecified	56	5,07
Total	1104	100

Infectious syndrome is the primary diagnosis that prompted the request for blood culture.

Table 4. Distribution of the number of blood cultures according to Gram stain results

Gram results	Number of germs	Percentage (%)
Gram-negative bacilli	156	52,52
Gram-negative bacilli + Gram-positive cocci in chains in chains	2	0,67
Gram-positive bacilli positif in clusters	129	43,43
Gram-positive bacilli in chains	8	2,69
Gram-positive diplococci	1	0.34
Yeasts	1	0.34
Total	297	100

With Gram staining, GNB are at the forefront, followed by GPC clusters.

Regarding clinical indications, infectious syndrome was the most frequent reason for requesting blood cultures, accounting for 44.57% of cases. Other indications included febrile syndromes (15.04%), respiratory disorders (4.26%), cardiac disorders (3.80%), and a variety of less frequent conditions (Table 3).

Gram stain distribution

Among the 297 microorganisms identified (including one instance of polymicrobial growth), Gram-negative bacilli (GNB) were predominant, representing 52.52% of isolates. Gram-positive cocci (GPC) in clusters accounted for 43.43%, while Gram-positive cocci in chains represented 2.69%. Gram-positive diplococci and yeasts were each observed in 0.34% of cases (Table 4).

Bacterial spectrum of isolates

A total of 297 microorganisms were identified from positive blood cultures. The most frequently isolated genus was *Staphylococcus*, accounting for 43.77% (n=130) of isolates. Within this genus, *Staphylococcus aureus* represented 59 isolates.

Gram-negative organisms collectively represented a substantial proportion of isolates. Among them, *Klebsiella* spp. accounted for 13.47% (n=40), predominantly *K. pneumoniae*. *Pseudomonas* spp. represented 10.77% (n=32), and *Escherichia coli* accounted for 10.10% (n=30). Other genera included *Enterobacter* (8.08%), *Salmonella* (5.39%), *Streptococcus* (3.03%), *Citrobacter* (1.35%), *Serratia* (1.01%), and rare isolates such as *Pantoea*, *Pasteurella*, and *Candida* species (Table 5).

Table 5. Distribution of the number of blood cultures according to isolated germs

Genres	Species	Number	Percentage (%)
Citrobacter	*C. freundii* : 3 *C.* spp : 1	4	1,35
Enterobacter	*E. cloacae* : 11 *E. sakazakii* : 4 *E. agglomerans* : 1 *E.* spp : 8	24	8,08
Klebsiella	*K. pneumoniae* : 38 *K. oxytoca* : 2	40	13,47
Pseudomonas	*P. aeruginosa* :12 *P.* spp : 20	32	10,77
Salmonella	*S. typhi* : 7 *S. paratyphi* ?: 1 *S.* spp : 8	16	5,39
Serratia	*S. marcecens* : 1 *S. odorifera* : 1 *S.* spp : 1	3	1,01
Staphylococcus	*S. haemolyticus* : 1 *S. hominis* : 2 *S.* spp : 46 *S. aureus* : 59 *S. xyloris* : 5 *S. capitis* : 4 *S. epidermidis* : 6 *S. auricularis* : 1 *S. warneri* : 2 *S. sciuri* : 1 *S. saprophyticus* : 3	130	43,77
Streptococcus	*S. pneumoniae* : 1 *S.* du groupe C : 1 *S.* spp : 7	9	3,03
Escherichia	*Escherichia coli*	30	10,10
Pantoea	*Pantoea* spp	1	0,34
Pasteurella	*P. pneumotropica*	2	0,67
Candida	*C. albicans*	1	0,34
Unidentified germs		5	1,68
Total		297	100

Antimicrobial susceptibility patterns

Enterobacteriaceae

Among Enterobacteriaceae, resistance patterns varied by genus. For *Klebsiella* spp., 18 isolates were identified as ESBL-producing strains, all belonging to *K. pneumoniae* (Fig. 2). Among *Escherichia coli*, 10 isolates demonstrated ESBL production (Fig. 3). For the *Enterobacter* genus, 9 isolates were classified as ESBL-producing (Fig. 4) , and overall resistance rates were comparatively higher than in other genera. *Salmonella* spp. isolates were generally susceptible; however, high resistance rates were observed for amoxicillin (80%),

Vol. 22, Issue. 1, p. 1-11, 2026
Website: https://innspub.net

nalidixic acid (66.66%), norfloxacin (54.55%), ticarcillin, and colistin (50%) (Fig. 5). The *Citrobacter* genus showed overall susceptibility, although resistance to several beta-lactam antibiotics, including carbapenems in selected strains, was observed (Fig. 6).

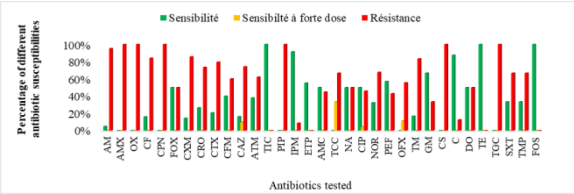

Fig. 2. Antibiotic susceptibility testing results for the genus *Klebsiella*

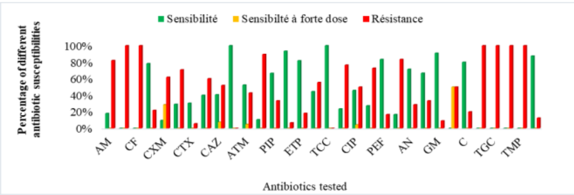

Fig. 3. Antibiotic susceptibility testing results for the genus *Escherichia*

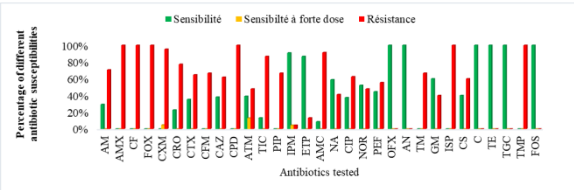

Fig. 4. Antibiotic susceptibility testing results for the genus *Enterobacter*

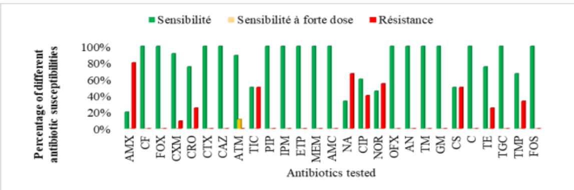

Fig. 5. Antibiotic susceptibility testing results for *Salmonella*

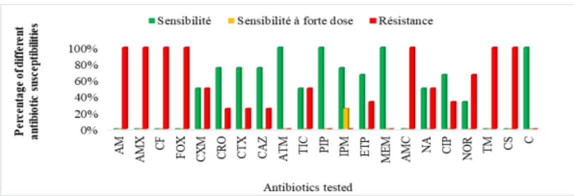

Fig. 6. Antibiotic susceptibility testing results for the genus *Citrobacter*

Non-fermenting Gram-negative bacilli

For *Pseudomonas* spp., resistance rates were moderate overall, with preserved susceptibility to several tested agents (Fig. 7).

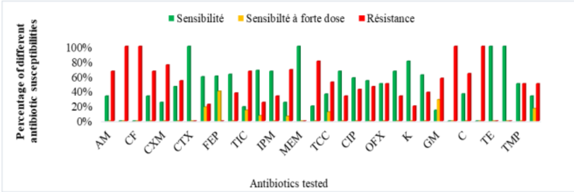

Fig. 7. Antibiotic susceptibility testing results for the genus *Pseudomonas*

Gram-positive cocci

Within the *Staphylococcus* genus, antimicrobial resistance was notable. Of the *S. aureus* isolates, 40.68% were resistant to methicillin, consistent with an MRSA phenotype (Fig. 8). Overall, *Staphylococcus* isolates demonstrated moderate resistance across several antibiotic classes. For the *Streptococcus* genus, isolates were generally susceptible to most tested antibiotics; however, resistance to gentamicin and cotrimoxazole reached 100%, and resistance to penicillin was observed in 75% of tested strains (Fig. 9).

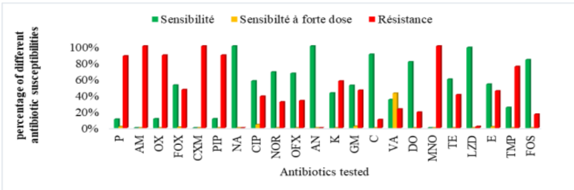

Fig. 8. Antibiotic susceptibility testing results for the genus *Staphylococcus*

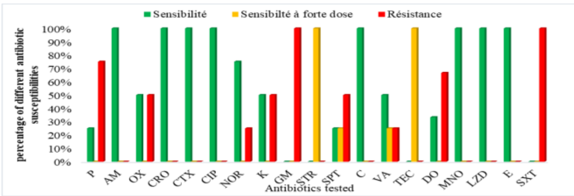

Fig. 9. Antibiotic susceptibility testing results for the genus *Streptococcus*

Less frequent isolates

Rare isolates included *Pantoea* spp., which exhibited marked resistance with susceptibility retained mainly to carbapenems and tetracycline (Fig. 10), and *Pasteurella pneumotropica*, which showed broad susceptibility to most tested antibiotics (Fig. 11). For the *Serratia* genus, moderate resistance was observed overall, with one isolate identified as ESBL-producing (Fig. 12) .

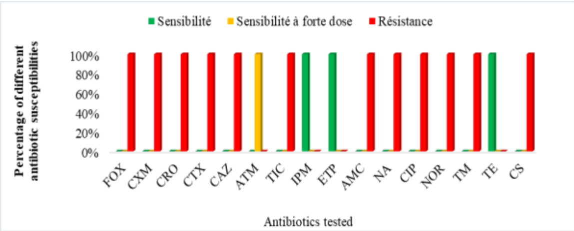

Fig. 10. Antibiotic susceptibility testing results for the genus *Pantoea*

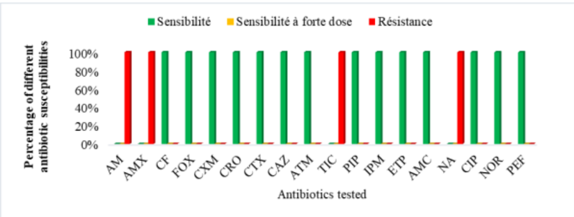

Fig. 11. Antibiotic susceptibility testing results for the genus *Pasteurella*

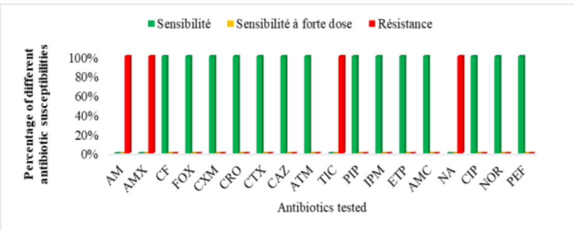

Fig. 12. Antibiotic susceptibility testing results for the genus *Serratia*

DISCUSSION

This study provides an updated overview of bloodstream infections diagnosed at CHNEAR over a one-year period, with particular attention to the phenotypic characteristics and antimicrobial susceptibility profiles of isolated pathogens. The overall blood culture positivity rate of 26.81% falls within the range reported in comparable hospital-based studies, although variability across settings is substantial and influenced by prior antibiotic exposure, sampling practices, and patient selection criteria. In pediatric populations, lower positivity rates have sometimes been reported, particularly when strict contamination control and shorter incubation times are applied (Yeung *et al.*, 2024). The relatively moderate positivity rate observed in our setting may reflect both genuine bacteremia and the clinical threshold for ordering blood cultures in a referral hospital.

The predominance of Gram-negative bacilli (52.52%) aligns with patterns increasingly reported in sub-Saharan Africa, where Enterobacteriaceae and non-fermenting Gram-negative organisms frequently account for a substantial proportion of bloodstream infections. However, *Staphylococcus* species represented the single most common genus isolated (43.77%), with *Staphylococcus aureus* accounting for nearly half of these isolates. This dual predominance of Gram-negative bacilli overall and *Staphylococcus* at the genus level underscores the mixed bacterial ecology typical of tertiary-care hospitals managing both community-acquired and healthcare-associated infections.

The proportion of methicillin-resistant *S. aureus* (MRSA) observed in this study (40.68% of *S. aureus* isolates) is clinically significant. Although MRSA has long been recognized as a major pathogen in hospital settings, its prevalence varies considerably across regions. A recent multicenter analysis demonstrated that methicillin resistance in *S. aureus* bacteremia is associated with increased intensive care admissions, even when mortality differences are less consistent (Arango-Gil *et al.*, 2025). In our context, the relatively high proportion of MRSA highlights the need for continuous surveillance and reinforces the importance of infection prevention strategies and rational empirical antibiotic selection.

Among Gram-negative organisms, ESBL production was particularly notable in *Klebsiella pneumoniae* (18 isolates), followed by *Escherichia coli* (10 isolates) and Enterobacter species (9 isolates). These findings are consistent with regional reports describing the growing burden of ESBL-producing Enterobacteriaceae in

Senegal and neighboring countries (Ndiaye *et al.*, 2023; Ondo N'Nang, 2023; Sarr *et al.*, 2024) . The predominance of ESBL-positive *K. pneumoniae* in our study mirrors patterns described in healthcare-associated infections, where this organism frequently exhibits multidrug resistance and contributes to prolonged hospitalization and therapeutic complexity (Vance *et al.*, 2023) .

The Enterobacter genus demonstrated comparatively high resistance levels, with several ESBL-producing strains identified. This observation is consistent with the intrinsic and acquired resistance mechanisms characteristic of Enterobacter species, including inducible AmpC beta-lactamase production, which complicates treatment options (StatPearls, 2025; Ninteretse, 2024; Mbodj, 2023). The clinical implications are significant, particularly in settings where access to carbapenems or advanced combination therapies may be limited.

Salmonella isolates were generally susceptible, although resistance to commonly used agents such as amoxicillin and nalidixic acid was substantial. Similar resistance trends have been reported in long-term surveillance studies from other African settings (Tack *et al.*, 2019). These findings emphasize the ongoing need for vaccination strategies and periodic reassessment of first-line therapies for invasive *Salmonella* infections.

Non-fermenting Gram-negative bacilli, particularly *Pseudomonas* species, showed moderate resistance patterns overall. While not as prominently resistant as ESBL-producing Enterobacteriaceae in our series, these organisms remain clinically relevant due to their intrinsic resistance profiles and association with healthcare-associated infections.

Rare isolates such as *Pantoea* and *Pasteurella* species were identified in small numbers. Although their clinical significance is often context-dependent, emerging literature suggests that such organisms may occasionally cause bloodstream infections with variable resistance profiles (Casale *et al.*, 2023; Soto-Vega *et al.*, 2025) . Their detection underscores the diversity of pathogens encountered in a tertiary pediatric setting.

Several considerations should be acknowledged when interpreting these findings. First, the retrospective design limits the ability to assess clinical outcomes, prior antibiotic exposure, and infection source. Second, the inclusion of both pediatric and older patients may influence the observed microbial distribution. Third, molecular characterization of resistance mechanisms was not performed; therefore, ESBL and carbapenem resistance were defined phenotypically. Despite these limitations, the study provides valuable institution-specific data that contribute to local epidemiological mapping of bloodstream infections.

Overall, our findings highlight a substantial burden of multidrug-resistant organisms, particularly ESBL-producing Enterobacteriaceae and MRSA, in this national pediatric referral center. These results reinforce the importance of continuous microbiological surveillance, antibiotic stewardship programs, and infection prevention strategies. In resource-limited settings, such institution-level data are essential to inform empirical therapy guidelines and to align clinical practice with evolving resistance patterns within the broader "One Health" framework.

CONCLUSION

This study provides an updated phenotypic overview of bacteria isolated from blood cultures at the Albert Royer National Children's Hospital over a one-year period. Bloodstream infections in this tertiary pediatric setting were characterized by a mixed bacterial ecology, with a predominance of Gram-negative bacilli overall and a high representation of *Staphylococcus* species at the genus level. Of particular concern is the substantial presence of multidrug-resistant organisms, notably ESBL-producing Enterobacteriaceae and methicillin-resistant *Staphylococcus aureus*.

The observed resistance patterns reflect the evolving antimicrobial landscape and highlight the growing therapeutic challenges faced in resource-limited hospital environments. The frequency of ESBL-producing *Klebsiella pneumoniae* and *Escherichia coli,* as well as the considerable proportion of MRSA, underscores the need for continuous microbiological surveillance and evidence-based adaptation of empirical antibiotic protocols.

Although limited by its retrospective design and the absence of molecular characterization, this work provides institution-specific data that are essential for guiding antimicrobial stewardship efforts. Regular updating of local resistance profiles, reinforcement of infection prevention and control measures, and integration of laboratory data into national AMR monitoring frameworks remain critical priorities.

Strengthening surveillance capacity and promoting rational antibiotic use will be central to preserving therapeutic efficacy and improving outcomes for pediatric patients with suspected septicemia. Continued research, including prospective and molecular investigations, will further clarify resistance dynamics and support targeted interventions within the broader "One Health" strategy.

REFERENCES

Arango-Gil IS, Sandoval-Parra DA, Montoya-Jaramillo S, Ardila-Gil A, González-Tapias I, Urrego-Ramírez AS. 2025. Impact of methicillin-resistance on clinical outcomes in patients with *Staphylococcus aureus* bacteremia. International Journal of Infectious Diseases **161**, 108155. https://doi.org/10.1016/j.ijid.2025.108155

Casale R, Boattini M, Bianco G, Comini S, Corcione S, Garazzino St. 2023. Bloodstream infections by *Pantoea* species: clinical and microbiological findings from a retrospective study, Italy, 2018–2023. Antibiotics (Basel) **12**(12), 1723.

Christaki E, Giamarellos-Bourboulis EJ. 2014. The complex pathogenesis of bacteremia: from antimicrobial clearance mechanisms to the genetic background of the host. Virulence **5**(1), 57–65. https://doi.org/10.4161/viru.26514

European Committee on Antimicrobial Susceptibility Testing (EUCAST). 2023. Breakpoint tables for interpretation of MICs and zone diameters. Version 13.0.

Kone MS. 2010. Bilan de sept ans d'hémocultures en milieu hospitalier pédiatrique de Bamako. Thèse de médecine, USTT de Bamako (Mali).

Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG. 2012. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions. Clinical Microbiology and Infection **18**(3), 268–281.

Mbodj M. 2023. Prévalence des entérobactéries productrices de carbapénémases isolées des prélèvements d'urines au laboratoire du CHR/Thiès de 2017 à 2021. Mémoire de diplôme d'études spécialisées en biologie clinique, UCAD.

Ndiaye I, Sambe BA, Thiam F, Boye MM, Sow O, Cissé A. 2023. Antibiotic resistance and virulence factors of extended-spectrum beta-lactamase-producing *Klebsiella pneumoniae* involved in healthcare-associated infections in Dakar, Senegal. Archives of Microbiology and Immunology. https://doi.org/10.26502/ami.936500105

Ndiaye M. 2024. Bilan des hémocultures positives au Centre Hospitalier National Dalal Jamm de juin 2020 à juin 2022 : profil de sensibilité aux antibiotiques des bactéries isolées. Thèse de doctorat en pharmacie, UCAD n° 36.

Ninteretse DBMR. 2024. Résistance aux carbapénémases des souches d'entérobactéries isolées au CHNU de Fann. Mémoire de diplôme d'études spécialisées en biologie clinique, UCAD.

Ondo N'Nang EG. 2023. Surveillance des *Escherichia coli* productrices de bêtalactamase à spectre élargi (*E. coli* BLSE) à l'Hôpital Principal de Dakar : projet tricycle OMS 2022. Thèse de doctorat en pharmacie, UCAD n° 210.

Sarr HH, Niang AA, Diop A, Diallo F, Dieye B, Diakhaby MEHB. 2024. Description of carbapenemase variants type OXA-181 and NDM-5 in clinical isolates of Enterobacteria in Senegal. African Journal of Bacteriology Research **16**(1), 1–6.

Sonko MA. 2013. Résultats des hémocultures dans les pathologies infectieuses invasives chez les enfants âgés de 0 à 59 mois hospitalisés du 1er janvier au 31 décembre 2012 à l'Hôpital d'Enfants Albert Royer. Thèse de doctorat en pharmacie, UCAD n° 103.

Soto-Vega E, Bello-Rossette E, Cabrera-Martínez MC, Arroyo Kuribreña JC. 2025. Rare urinary tract infection by *Rodentibacter pneumotropicus* (formerly *Pasteurella pneumotropica*) in an immunocompetent patient. American Journal of Case Reports **26**, e947344. https://doi.org/10.12659/AJCR.947344

StatPearls Publishing. 2025. Enterobacter infections.

Tack B, Phoba MF, Van Puyvelde S, Kalonji LM, Hardy L, Barbé B. 2019. Typhi from blood cultures in the Democratic Republic of the Congo: a 10-year surveillance. Clinical Infectious Diseases **68**(Suppl 2), S130–S137. https://doi.org/10.1093/cid/ciy1116

Vance MK, Cretella DA, Ward LM, Vijayvargiya P, Esquer Garrigos Z, Wingler MJB. 2023. Risk factors for bloodstream infections due to ESBL-producing *Escherichia coli*, *Klebsiella* spp., and Proteus mirabilis. Pharmacy (Basel) **11**(2), 74. https://doi.org/10.3390/pharmacy11020074

Vinclair C, Neuville M, Timsit J-F. 2020. Choc septique et septicémie. EMC-Maladies Infectieuses **37**(4), 1–14.

Yeung E, Sant N, Sucha E, Belaghi R, Le Saux N. 2024. Finding significant pathogens in blood cultures in children: should we set the timer to 36 hours? Journal of the Association of Medical Microbiology and Infectious Disease Canada **9**(1), 11–19. https://doi.org/10.3138/jammi-2023-0009