

Non-Tuberculous Bacterial Infections among Hospitalized People Living with HIV in a Senegalese Referral Centre: Clinical Presentation, Bacterial Spectrum, Resistance Patterns and Outcomes

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Abstract

Introduction: People living with HIV (PLHIV), particularly those with advanced immunosuppression, remain vulnerable to severe non-tuberculous bacterial infections. This study described the clinical presentation, bacterial isolates, antimicrobial susceptibility patterns, resistance phenotypes, and outcome profile of microbiologically documented non-tuberculous bacterial infections among PLHIV hospitalized at the Infectious and Tropical Diseases Department (SMIT) of Fann hospital in Dakar, Senegal. **Patients and Methods:** A retrospective descriptive study was conducted in the SMIT of Fann hospital, from March 2019 to December 2022. Demographic, clinical, laboratory, microbiological, antimicrobial susceptibility and outcome data were extracted. **Results:** Thirty-six patients were included after screening bacteriology-linked HIV inpatient records. Median age was 44.5 years (IQR: 36.0 - 53.0) and 55.6% were female. CD4 count was available for 10 patients, of whom 90.0% had less than 200 cells/ μ L. Prior hospitalization within six months was recorded in 22/36 patients (61.1%; 22/28 documented responses), and prior antibiotic exposure in 13/36 (36.1%; 13/14 documented responses). Median symptom duration before admission was 30 days and median hospital stay was 23 days. Urine and blood cultures were the main positive specimens.

Overall, 90 specimens yielded 57 isolates and 16 species/taxa. Gram-negative bacteria represented 59.6% of isolates. Leading pathogens were *Escherichia coli* (26.3%), *Klebsiella pneumoniae* (21.1%) and *Staphylococcus aureus* (19.3%). ESBL production was detected in 61.3% of *Enterobacterales*. MRSA represented 36.4% of *S. aureus* isolates. Resistance was high to amoxicillin-clavulanate (90.0%), cotrimoxazole (83.3%), ceftriaxone (71.4%) and ciprofloxacin (63.4%); imipenem resistance was 7.4%. Antibiotic reassessment was recorded in 27/33 documented cases (81.8%). In-hospital case fatality was 33.3%. **Conclusion:** In this referral centre, microbiologically documented non-tuberculous bacterial infections in PLHIV were marked by urinary and bloodstream predominance, ESBL-producing *Enterobacterales*, resistant staphylococci and high case fatality. The findings support early bacteriological documentation, therapeutic reassessment, antimicrobial stewardship and strengthened infection prevention and control.

Keywords

HIV, Bacterial Infections, Antimicrobial Resistance, Extended-Spectrum Beta-Lactamase, Dakar

1. Introduction

HIV infection remains a major contributor to infectious morbidity and mortality worldwide despite major progress in the scale-up of antiretroviral therapy (ART). In 2024, approximately 630,000 people died from AIDS-related illnesses globally, underscoring persistent gaps in early diagnosis, treatment initiation, retention in care, and the management of advanced HIV disease [1] [2]. People living with HIV (PLHIV) who are admitted to hospital frequently present with advanced HIV disease and multiple infectious complications [3]-[6]. Among these, severe bacterial infections remain leading causes of severe illness and death in patients with advanced HIV disease [3] [4].

Non-tuberculous bacterial infections (NTBIs), particularly severe bacterial infections, represent an important but often under-characterized component of HIV-related morbidity in hospital settings. They may present as bloodstream infections, pneumonia, urinary tract infections, neuromeningeal infections, gastrointestinal infections, or skin and soft-tissue infections [3] [4] [7]. Compared with immunocompetent individuals, they occur at higher incidence, present with atypical features, progress more severely, and recur more frequently [3]. Their occurrence is favoured by impaired cellular and humoral immunity, mucosal barrier dysfunction, malnutrition, repeated healthcare exposure, prior antibiotic use, invasive procedures and delayed presentation to care [8]. In hospitalized PLHIV, these infections mimic tuberculosis, fungal infections, viral diseases or non-infectious inflammatory conditions [4] [9]. This diagnostic uncertainty frequently leads to broad-spectrum empirical antibiotic therapy [6] [10] [11]. This treatment

may be lifesaving when appropriately targeted but may also increase antimicrobial selection pressure when microbiological confirmation is delayed or unavailable [6] [10].

The burden of these infections is further complicated by antimicrobial resistance (AMR), globally recognized as a major threat to patient survival. Sub-Saharan Africa is carrying one of the highest estimated burdens and western sub-Saharan Africa is showing the highest all-age death rate attributable to resistance in the 2019 global analysis [12]. The 2025 WHO Global Antibiotic Resistance Surveillance Report showed that approximately one in six laboratory-confirmed bacterial infections worldwide in 2023 were resistant to antibiotics, rising to nearly one in five in the African Region [13]. In PLHIV, available evidence suggests an increased risk of antimicrobial-resistant bacterial infections, including infections caused by extended-spectrum beta-lactamase (ESBL)-producing *Enterobacterales* [14] and methicillin-resistant *Staphylococcus aureus* [15]. These resistance patterns have direct implications for empirical antibiotic choices, antibiotic stewardship, infection prevention and control, and hospital outcomes [6] [13] [16].

In sub-Saharan Africa, the interplay between HIV, severe bacterial infections and AMR is amplified by late presentation to care, advanced immunosuppression at admission, limited access to rapid diagnostics, constrained microbiology laboratory capacity and restricted availability of last-line antibiotics [5] [17]. In this context, local microbiological surveillance is essential to guide rational empirical therapy and improve patient outcomes [13]. However, data describing the clinical presentation, biological profile, bacterial spectrum, antimicrobial susceptibility patterns, resistance phenotypes and outcomes of non-tuberculous bacterial infections among hospitalized PLHIV remain limited in many West African tertiary hospitals.

In Senegal, HIV prevalence is relatively low compared with several countries in sub-Saharan Africa [1]. However, referral hospitals continue to manage patients with advanced HIV disease and severe infectious complications [4] [18]. Previous studies from the Infectious and Tropical Diseases Department (Service des Maladies Infectieuses et Tropicales, SMIT) of Fann National University Hospital in Dakar have reported bacterial bloodstream infections among HIV-infected hospitalized patients, including Gram-positive and Gram-negative pathogens such as *Escherichia coli*, *Klebsiella pneumoniae* and *Staphylococcus aureus*, with documented methicillin resistance and ESBL production [19]. Other local data have also shown that PLHIV admitted to this department frequently present with advanced disease and severe infectious conditions, including bacterial pneumonia and septicemia [18] [20]. Earlier work on enterobacterial infections at Fann Hospital documented high levels of resistance to third-generation cephalosporins, aminoglycosides, ciprofloxacin and cotrimoxazole [21]. Nevertheless, these data remain fragmented and have generally focused on specific syndromes or bacterial groups rather than providing an integrated assessment of non-tuberculous bacterial infections in hospitalized PLHIV.

Therefore, this study aimed to describe the clinical presentation, to identify the bacterial species isolated, determine antimicrobial susceptibility patterns and resistance phenotypes, and estimate in-hospital case fatality of microbiologically documented non-tuberculous bacterial infections among PLHIV hospitalized in the Infectious and Tropical Diseases Department of Fann National University Hospital in Dakar, Senegal.

2. Patients and Methods

2.1. Study Design, Period and Setting

We conducted a retrospective descriptive study over a 46-month period, from March 2019 to December 2022, in the Department of Infectious and Tropical Diseases (SMIT) of the Fann National University Hospital Centre, Dakar, Senegal. This department is a national tertiary referral centre for the management of infectious diseases, including HIV infection, opportunistic infections, severe bacterial infections and antimicrobial-resistant infections.

2.2. Study Population

The study population included hospitalized PLHIV in the Department of Infectious and Tropical Diseases for whom at least one non-tuberculous bacterial infection was microbiologically documented during the study period and for whom minimum clinical, microbiological, therapeutic and outcome data were available.

HIV infection was defined by documented HIV serology or by a known diagnosis recorded in the medical file. Patients infected with HIV-1, HIV-2, or dual HIV-1/HIV-2 infection were eligible.

A bacterial infection was considered microbiologically confirmed when a pathogenic bacterium was isolated from a clinically relevant biological specimen. These specimens included blood, urine, cerebrospinal fluid, respiratory samples, pus, wound swabs, stool or any other sterile or non-sterile specimen interpreted considering the clinical context.

Patients were included if they met all the following criteria:

- Hospitalization in the Department of Infectious and Tropical Diseases (SMIT) of Fann Hospital Centre between March 2019 and December 2022;
- Documented HIV infection;
- Diagnosis of at least one non-tuberculous bacterial infection during hospitalization;
- Availability of medical records containing the minimum information required for clinical, biological, microbiological and outcome analysis.

Patients were excluded if they had:

- Tuberculosis alone without evidence of another non-tuberculous bacterial infection;
- Viral, fungal or parasitic infection without documented bacterial infection;
- Incomplete records preventing confirmation of HIV status, bacterial infection

status or hospital outcome.

The screening process was reconstructed from hospital admission registers, laboratory records and the study extraction database.

2.3. Operational Definitions

A non-tuberculous bacterial infection was defined as any bacterial infection other than infection caused by *Mycobacterium tuberculosis* complex or atypical mycobacterial infections. Previous tuberculosis was recorded as a comorbidity when available.

Infections were classified according to documented site of infection as follows: bloodstream infection, urinary tract infection, pneumonia or lower respiratory tract infection, central nervous system infection, gastrointestinal infection, skin and soft tissue infection, ENT (ear, nose, throat) infection, genital infection, and other documented bacterial infections.

Bloodstream infection was defined by the isolation of a bacterial pathogen from at least one blood culture in a compatible clinical context. For organisms commonly considered potential contaminants, such as coagulase-negative staphylococci, clinical relevance was retained only when supported by repeated isolation, compatible clinical signs, presence of an intravascular device, or explicit interpretation by the treating team.

Urinary tract infection was defined by urinary symptoms or systemic signs compatible with infection, associated with significant bacteriuria according to laboratory thresholds used during the study period.

Pneumonia or lower respiratory tract infection was defined by compatible respiratory symptoms, clinical examination, radiological findings when available, and isolation of a bacterial pathogen from a respiratory sample.

Central nervous system infection was defined by clinical signs suggestive of meningitis, meningoencephalitis or cerebral infection, supported by cerebrospinal fluid abnormalities and bacterial identification.

Advanced HIV disease was defined, when CD4 count was available, as a CD4 lymphocyte count below 200 cells/mm³ or the presence of a WHO clinical stage 3 or 4 condition [4].

Admission-to-culture timing was not consistently documented. Therefore, episodes could not be reliably classified as community-onset or hospital-onset.

2.4. Data Source and Data Collection Tools and Techniques

Data were collected retrospectively from medical records, hospital admission registers, laboratory records and microbiology reports. The list of patient records was obtained from the medical informatics unit. A standardized Excel data extraction form was used to collect socio-demographic, clinical, hematological and biochemical, microbiological, therapeutic and outcome variables.

The following variables were extracted: age, sex, residence, HIV serotype, antiretroviral therapy status, CD4 lymphocyte count, comorbidities, previous hos-

pitalization, history of antibiotic exposure during the months preceding hospitalization, clinical presentation at admission, infection site, biological findings, microbiological specimens, isolated bacterial species, antimicrobial susceptibility results, antibiotic therapy administered during hospitalization, length of hospital stay and hospital outcome. Dates of specimen collection were not consistently available and were not used for onset classification.

2.5. Microbial Procedures

Microbiological specimens were collected as part of routine clinical care. These included blood cultures, urine cultures, cerebrospinal fluid cultures, respiratory samples, pus, wound swabs, stool cultures and other samples depending on the suspected site of infection.

Bacterial identification and antimicrobial susceptibility testing were performed by the hospital microbiology laboratory according to a routine procedure. Identification was based on conventional bacteriological methods (Api gallery) or automated techniques (Vitek2[®]) when available. Antimicrobial susceptibility testing was performed using disk diffusion or automated systems techniques according to the guidelines of the Antibigram Committee of the French Society of Microbiology (CASFM) applied during the study period.

2.6. Antimicrobial Resistance Definitions

Antimicrobial resistance profiles were described by bacterial species and by antimicrobial class. Extended-spectrum beta-lactamase-producing *Enterobacterales* were defined according to laboratory interpretation based on resistance phenotype and/or confirmatory testing when available. Carbapenem resistance was defined by non-susceptibility to at least one carbapenem tested. Methicillin-resistant *Staphylococcus aureus* (MRSA) was defined by resistance to ceftazidime or oxacillin, or by laboratory interpretation as MRSA. The unit of analysis was the bacterial isolate, not the patient, separately for each antibiotic; denominators therefore vary across antibiotics. Isolate counting followed a specimen-based approach consistent with GLASS principles. The same bacterial species recovered from different anatomical specimens in the same patient during the same hospitalization was counted separately for susceptibility analysis. Repeated isolates of the same species from the same specimen type within 14 days were de-duplicated by retaining the first isolate, in line with cumulative antibiogram guidance. In polymicrobial specimens, each distinct bacterial species was counted as one isolate. Resistance proportions were calculated using the number of isolates tested for each antibiotic as the denominator. Resistance phenotypes were reported separately for Gram-negative bacilli and Gram-positive cocci.

2.7. Data Entry and Analysis

The collected data were recorded in an Excel spreadsheet and analyzed using Stata SE version 15.1. Continuous variables were presented as mean $\pm$ standard deviation.

tion for normally distributed data, or as median and interquartile range for skewed distributions. Categorical variables were reported as frequencies and percentages. For variables with missing data, denominators were specified in the text or tables. Percentages were calculated using the total number of patients unless a documented-response or tested-isolate denominator was explicitly indicated. The distribution of bacterial species and antimicrobial resistance profiles was reported by specimen type and bacterial group.

2.8. Ethical Considerations

The study was conducted with the approval of the head of the department. The study was carried out in accordance with the principles outlined in the Declaration of Helsinki. It was based on routinely collected retrospective hospital data. The data collected in the study were de-identified to maintain the confidentiality and anonymity of the patient information and were entered into a secure database. Given the retrospective design and the use of anonymized routine clinical data, the requirement for individual informed consent was not required. No financial compensation was provided for use of the data.

3. Results

3.1. Socio-Demographic and HIV-Related Characteristics

During the study period, 451 admissions of people living with HIV (PLHIV) were recorded. Among them, 49 inpatient records had microbiological sampling with at least one positive non-mycobacterial bacterial culture. Thirty-three records were excluded because key clinical, microbiological, therapeutic or outcome data were incomplete. The final study population therefore included 36 hospitalized people living with HIV with microbiologically documented non-tuberculous bacterial infection. A total of 36 hospitalized people living with HIV with microbiologically documented non-tuberculous bacterial infection were included. The median age was 44.5 years (IQR: 36.0 - 53.0), with the 30 - 59 age group comprising 77.7% of the patients ($n = 28$). Women accounted for 55.6% (sex-ratio: 0.8).

Comorbidities other than HIV were documented in 17 patients (47.2%). Among them, the most frequent were hypertension (11.4%), diabetes mellitus, prior cerebrovascular accident and pulmonary/multifocal tuberculosis (8.3% each). A previous in-hospital stay within the preceding six months was reported by 22 patients (61.1% of the cohort; 78.6% of the 28 patients with documented information). Prior antibiotic exposure within the three months preceding the admissions was recorded in 13 patients (36.1% of all patients; 92.9% of the 14 patients with documented information) (36.1%). Ceftriaxone was the most frequently listed pre-admission antibiotic (30.8%), followed by imipenem (15.4%) and amoxicillin-clavulanate (15.4%).

HIV-1 was the predominant serotype, accounting for 88.9% of cases, while HIV-2 represented 11.1%. A baseline CD4 cell count was available for 10 patients (27.8%). Among these tested patients, the median CD4 count was 36 cells/ μ L

(IQR: 15 - 65; range 2 - 283), and 90.0% had CD4 counts below 200 cells/ μ L. CD4 count and WHO clinical stage were not available for all patients, therefore advanced HIV disease was not assumed for the entire cohort. At admission, 15 patients (41.7%) were receiving antiretroviral therapy (ART), while 21 (58.3%) were ART-naïve or off-treatment.

Sociodemographic characteristics, comorbidities, antibiotic exposure and HIV-related features are summarized in **Table 1**.

Table 1. Sociodemographic characteristics, comorbidities, antimicrobial exposure prior to admission and HIV-related features of patients with non-tuberculosis infections at the infectious diseases department of Fann hospital in Dakar, 2019-2022 (N = 36).

Variables	Frequency (n)	Percentage (%)
Sociodemographic characteristics		
<i>Age group</i>		
<18 years	1	2.8
18 - 29 years	1	2.8
30 - 44 years	16	44.4
45 - 59 years	12	33.3
≥ 60 years	6	16.7
<i>Gender</i>		
Female	20	55.6
Male	16	44.4
<i>Marital status</i>		
Married	23	63.9
Single	6	16.7
Widowed	6	16.7
Not recorded	1	2.8
Comorbidities other than HIV		
At least one non-HIV comorbidity	17	47.2
Hypertension	4	11.1
Diabetes mellitus	3	8.3
Prior stroke	3	8.3
Prior pulmonary/multifocal tuberculosis	3	8.3
Asthma	2	5.6
Cardiomyopathy/ischemic heart disease	2	5.6
Chronic kidney disease	1	2.8
Thermal burn	1	2.8

Continued

Hospitalization within the past 6 months		
Yes	22	61.1
No	6	16.7
Not recorded	8	22.2
Antibiotic exposure within the past 3 months		
Yes	13	36.1
No	1	2.8
Not recorded	22	61.1
Antibiotic classes used pre-admission		
Ceftriaxone	4	30.8
Imipenem	2	15.4
Amoxicillin/clavulanic acid	2	15.4
Benzathine penicillin (Extencillin)	1	7.7
Cotrimoxazole	1	7.7
Spiramycin	1	7.7
Cefixime	1	7.7
Ciprofloxacin	1	7.7
HIV-related features		
<i>HIV serotype</i>		
HIV-1	32	88.9
HIV-2	4	11.1
<i>CD4 cell count</i>		
Available (cells/ μ L)	10	27.8
CD4 < 200 cells/ μ L	9	90.0*
CD4 < 50 cells/ μ L (severe immunodeficiency)	6	60.0*
<i>Antiretroviral therapy (ART) status</i>		
On ART at admission	15	41.7
ART-naïve/not on ART	21	58.3
TLD (TDF/3TC/DTG)	10	66.7**
Other regimens	4	26.7**
<i>Other HIV-related factors</i>		
Concurrent opportunistic infection	5	13.9
Cotrimoxazole chemoprophylaxis at admission	2	5.6

*Percentage computed on the 10 patients with documented CD4 cell counts. **Percentage computed on the 15 patients on ART at admission. For variables with missing data, percentages in the table use the total study population denominator unless otherwise specified; documented-response denominators are provided in the Results text. Abbreviations: ART, antiretroviral therapy; DTG, dolutegravir; TDF, tenofovir disoproxil fumarate; 3TC, lamivudine.

3.2. Clinical Characteristics

The median duration of symptoms prior to admission was 30 days (IQR: 14 - 60). Fever was the most common clinical sign, observed in 80.6% of patients. Respiratory signs occurred in 58.3% (21 patients), including cough in 41.7% and dyspnea in 22.9%. Digestive signs were present in 44.4%, including diarrhea in 36.1% and vomiting in 27.8% of patients. Asthenia was recorded in one-third of patients, while weight loss, anorexia and neurological signs were each documented in 27.8%. Altered consciousness was noted in 22.9% of patients. A Glasgow Coma Scale < 15 was documented in 10 patients (27.8%). At admission, 9 patients (25.0%) had a quick Sequential Organ Failure Assessment (qSOFA) score ≥ 2 , and 4 (11.1%) had a CRB-65 score ≥ 2 among those with a respiratory presentation.

Anatomic sites of the bacterial infection showed a predominance of urinary tract involvement (n = 24; 66.7%), followed by bloodstream infection/bacteremia (n = 17; 47.2%), central nervous system infection (n = 6; 16.7%), genital tract infection (n = 7; 19.4%) and pulmonary infection (n = 4; 11.1%). Twenty-one (21) patients (58.3%) had bacteriological involvement of two or more anatomic sites.

Table 2 shows the patients' clinical profile of this study.

Table 2. Clinical features and anatomic sites of bacterial infection in HIV-infected patients at SMIT of Fann hospital in Dakar, Senegal, 2019-2022 (N = 36).

Variable	Frequency (n)	Percentage (%)
<i>Main presenting clinical symptoms</i>		
Fever	29	80.6
Cough	15	41.7
Diarrhea	13	36.1
Asthenia	12	33.3
Weight loss	10	27.8
Anorexia	10	27.8
Vomiting	10	27.8
Dyspnea	8	22.2
Altered consciousness	8	22.2
Chest pain	5	13.9
Headache	4	11.1
Abdominal pain	3	8.3
Motor deficit	3	8.3
Dysuria	1	2.8
Convulsion	1	2.8
Agitation	1	2.8

Continued

<i>Physical examination findings</i>		
Glasgow Coma Scale < 15	10	27.8
Respiratory signs	21	58.3
Lung consolidation	19	52.8
Neurological signs	10	27.8
Meningeal stiffness	3	8.3
Digestive signs	16	44.4
Urinary signs	3	8.3
<i>Severity scores at admission</i>		
qSOFA ≥ 2	9	25.0
CRB-65 ≥ 2 (in patients with respiratory presentation)	4	11.1
<i>Anatomic sites of bacterial infection</i>		
Urinary tract infection	24	66.7
Bloodstream infection/bacteremia	17	47.2
Genital tract infection	7	19.4
Central nervous system infection	6	16.7
Lower respiratory tract infection	4	11.1
Skin and soft tissue infection	2	5.6
ENT (ear, nose, throat) infection	2	5.6
Gastro-intestinal infection	1	2.8
Anatomic concomitant sites ≥ 2	21	58.3

3.3. Hematological and Biochemical Parameters

The median hemoglobin level was 8.2 g/dL (IQR: 6.9 - 9.6), and 80.0% of patients had hemoglobin below 10 g/dL. The median leukocyte count was 6300 cells/mm³ (IQR: 3700 - 8970). Leukopenia was present in 28.6%, while leukocytosis was observed in 17.1%. The median lymphocyte count was 800/mm³, with profound lymphopenia (<1500/mm³) recorded in 77.4% of tested patients (24/31). Thrombocytopenia below 150,000/mm³ was documented in 32.4% of tested patients. C-reactive protein was the most frequent inflammatory markers performed and procalcitonin was obtained in two patients. The median C-reactive protein concentration was 125.8 mg/L (IQR: 89.3 - 184.8), with CRP above 100 mg/L in 61.8% of patients. Serum creatinine values were available for 32 patients. The median value was 12.2 mg/L [IQR 7.1 - 15.7; range 3.5 - 114].

3.4. Bacteriological Profile and Antimicrobial Resistance

3.4.1. Bacterial Isolates and Specimens' Distribution

Across the 36 patients, 90 microbiological specimens were processed. Microbio-

logically confirmed infection sites were predominantly urinary and bloodstream infections. Urine culture was performed in 30 patients and was positive in 24 (80.0%). Blood culture was performed in 20 patients and was positive in 12 (60.0%). Other secretion or pus samples were positive in all nine patients tested, and vaginal/genital samples were positive in six of seven patients. Cerebrospinal fluid culture was performed in 15 patients but was positive in two (13.3%). Stool culture and respiratory specimens were infrequently tested, with one positive result each.

A total of 57 bacterial isolates and 16 bacterial species/taxa were identified. The isolate was the unit of microbiological analysis. Gram-negative bacteria predominated, representing 59.6% of isolates, while Gram-positive bacteria accounted for 40.4%. The most common species were *Escherichia coli* (26.3%), *Klebsiella pneumoniae* (21.1%), and *Staphylococcus aureus* (19.3%). *Staphylococcus saprophyticus* accounted for 7.0%.

The species distribution aligned with the predominance of urinary and bloodstream infections. *Escherichia coli* was primarily isolated from urine (19.3% of all isolates) and vaginal/genital samples (5.3%). *Klebsiella pneumoniae* was recovered mostly from urine (10.5%), blood culture and other secretion/pus (3.5% each). *Staphylococcus aureus* was mainly isolated from blood culture and other secretions or pus samples (7.0% each), and urine (3.5%).

The distribution of bacterial isolates by specimen type and by bacterial species are detailed in **Figure 1**.

3.4.2. Antimicrobial Susceptibility Testing Patterns and Resistance Phenotypes

The antimicrobial susceptibility profile showed a high burden of resistance across several major antibiotic classes. Resistance proportions were calculated using the number of tested isolates for each antibiotic as the denominator. Resistance was very high for amoxicillin (100.0%), amoxicillin-clavulanate (90.0%), cotrimoxazole (83.3%), and ceftriaxone (71.4%). Resistance to ciprofloxacin was also frequent (63.4%). Resistance to imipenem was 7.4%, and 24.2% to amikacin. No resistance was observed to vancomycin. The heatmap in **Figure 2** depicts the antimicrobial susceptibility testing results for the main isolated species.

The resistance phenotype analysis revealed a high burden of clinically relevant resistance among the main bacterial species isolated. Among *Staphylococci*, methicillin-resistant *Staphylococcus aureus* represented 36.4% of *S. aureus* isolates, while MLSb phenotype (macrolide-lincosamide-streptogramin B resistance phenotype), quinolone resistance, and cotrimoxazole resistance were each observed in 36.4%. *Staphylococcus saprophyticus* showed particularly high resistance proportions, with methicillin resistance in 75.0% of isolates. Cotrimoxazole, MLSb and KTG (kanamycin-tobramycin-gentamicin resistance phenotype) resistance were observed in all isolates.

Among *Enterobacterales*, extended-spectrum β -lactamase (ESBL) production accounted for 19 of 31 isolates (61.3%). This was mainly driven by *Escherichia*

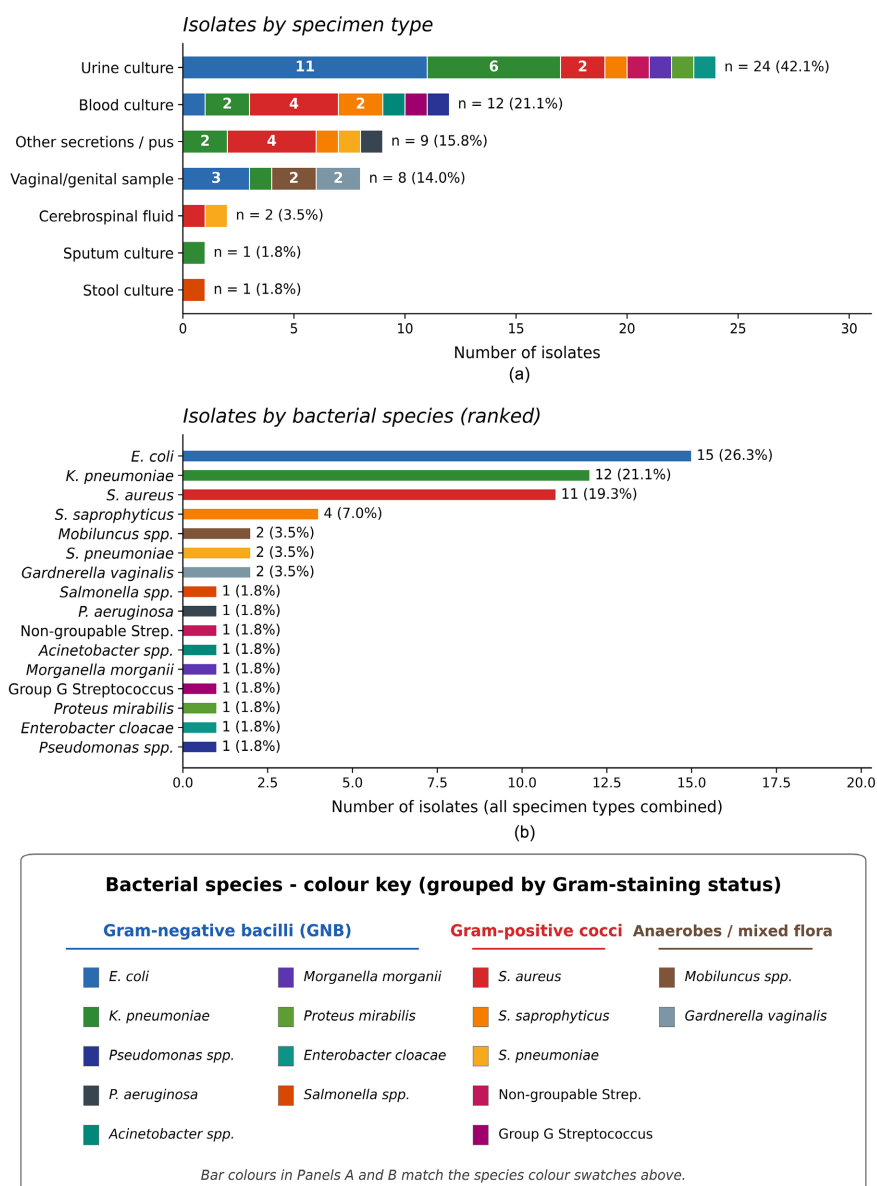


Figure 1. Distribution of bacterial isolates (N = 57) by specimen type (a) and by bacterial species (b) in HIV-infected inpatients hospitalized for a non-tuberculous bacterial infection at the Department of Infectious and Tropical Diseases, Fann University Hospital, Dakar, Senegal, 2019-2022. (a) Stacked horizontal bar chart showing the composition of bacterial isolates per specimen type. Numbers inside bar segments indicate the count of isolates for that species from the corresponding specimen (displayed when ≥ 2 isolates). Values to the right of each bar indicate the total number and percentage of all isolates contributed by the specimen type. (b) Ranked horizontal bar chart showing total isolates per bacterial taxon across all specimen types combined, presented in descending order. Values to the right indicate the absolute count and percentage of total isolates. Species names are in italic in accordance with current bacteriological nomenclature. Abbreviations: *E. coli*, *Escherichia coli*; *K. pneumoniae*, *Klebsiella pneumoniae*; *S. aureus*, *Staphylococcus aureus*; *S. saprophyticus*, *Staphylococcus saprophyticus*; *S. pneumoniae*, *Streptococcus pneumoniae*; *P. aeruginosa*, *Pseudomonas aeruginosa*; Non-groupable Strep., non-groupable *Streptococcus* spp.; *E. cloacae*, *Enterobacter cloacae*; GNB, Gram-negative bacilli; GPC, Gram-positive cocci; n, number; %, percentage of total isolates.

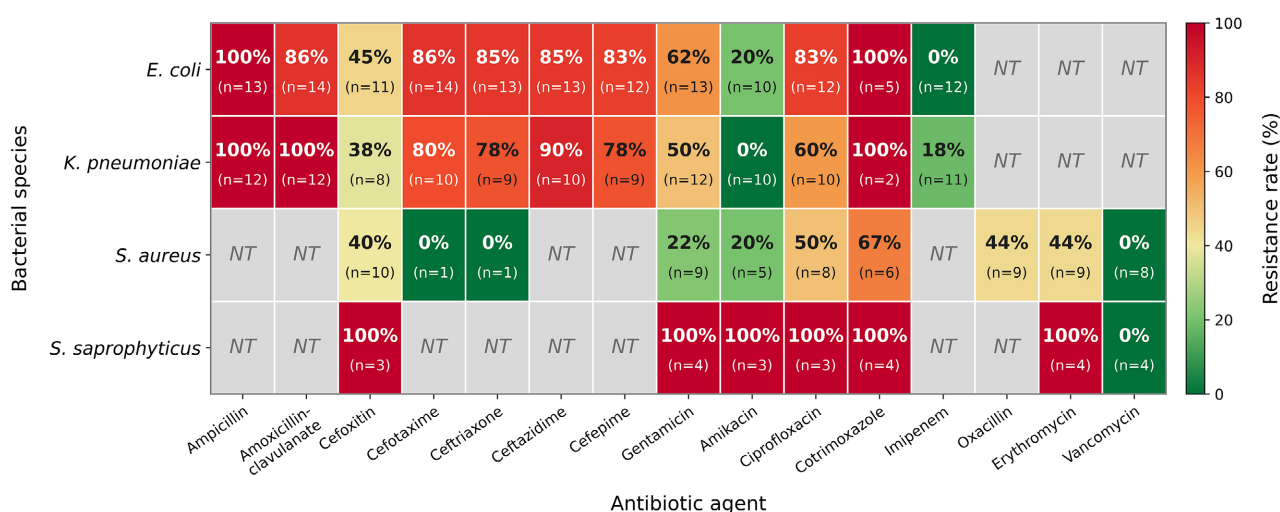


Figure 2. Antimicrobial resistance profile of the four predominant bacterial species isolated from HIV-infected inpatients hospitalized for a non-tuberculous bacterial infection at the Department of Infectious and Tropical Diseases (SMIT), Fann University Hospital, Dakar, Senegal, 2019-2022. The heatmap shows the proportion of resistant isolates for each antibiotic-species combination. Principal isolates were defined as bacterial species recovered at least three times in the study population. Each cell displays the percentage of resistant isolates among tested isolates, together with the corresponding number of tested isolates. The color gradient ranges from green, indicating low resistance, to dark red, indicating high resistance. Grey cells indicate antibiotics that were not tested (NT). Species names are shown in italics.

coli (66.7%) and *Klebsiella pneumoniae* isolates (58.3%). Quinolone resistance was also common in these two species, reaching 73.3% in *E. coli* and 66.7% in *K. pneumoniae*. Resistance to carbapenem was limited to *K. pneumoniae* isolates (16.7%). Non-fermenting Gram-negative bacilli were rare. No resistance was identified among *Pseudomonas* isolates, while the single *Acinetobacter spp.* isolate showed quinolone resistance. These findings highlight the predominance of ESBL-producing *Enterobacterales* and resistant *Staphylococci* among bacterial isolates.

Figure 3 summarizes the distribution of major antimicrobial resistance phenotypes by bacterial species.

3.5. Therapeutic Management and Outcomes

Empirical antibiotic therapy was dominated by ceftriaxone, which accounted for 29.4% of all empirical antibiotic molecules prescribed. Amoxicillin-clavulanate and spiramycin were each used in 7.4% of cases, followed by gentamicin (5.9%) and metronidazole (2.9%). The median duration of empirical treatment prior to availability of antimicrobial susceptibility testing results was 9 days (IQR: 7 - 11). After microbiological documentation and susceptibility testing, antibiotic reassessment or treatment modification was recorded in 27 of 33 of documented cases (81.8%); information was missing for 3 patients. When susceptibility-guided treatment was implemented, the main prescribed antibiotics were imipenem (33.3%), ciprofloxacin (19.4%), amikacin (16.7%), gentamicin (16.7%), and vancomycin (13.9%). The median length of hospital stay was 23 days (IQR: 18 - 36). Overall, clinical recovery was observed in 22 patients (61.1%). Twelve patients

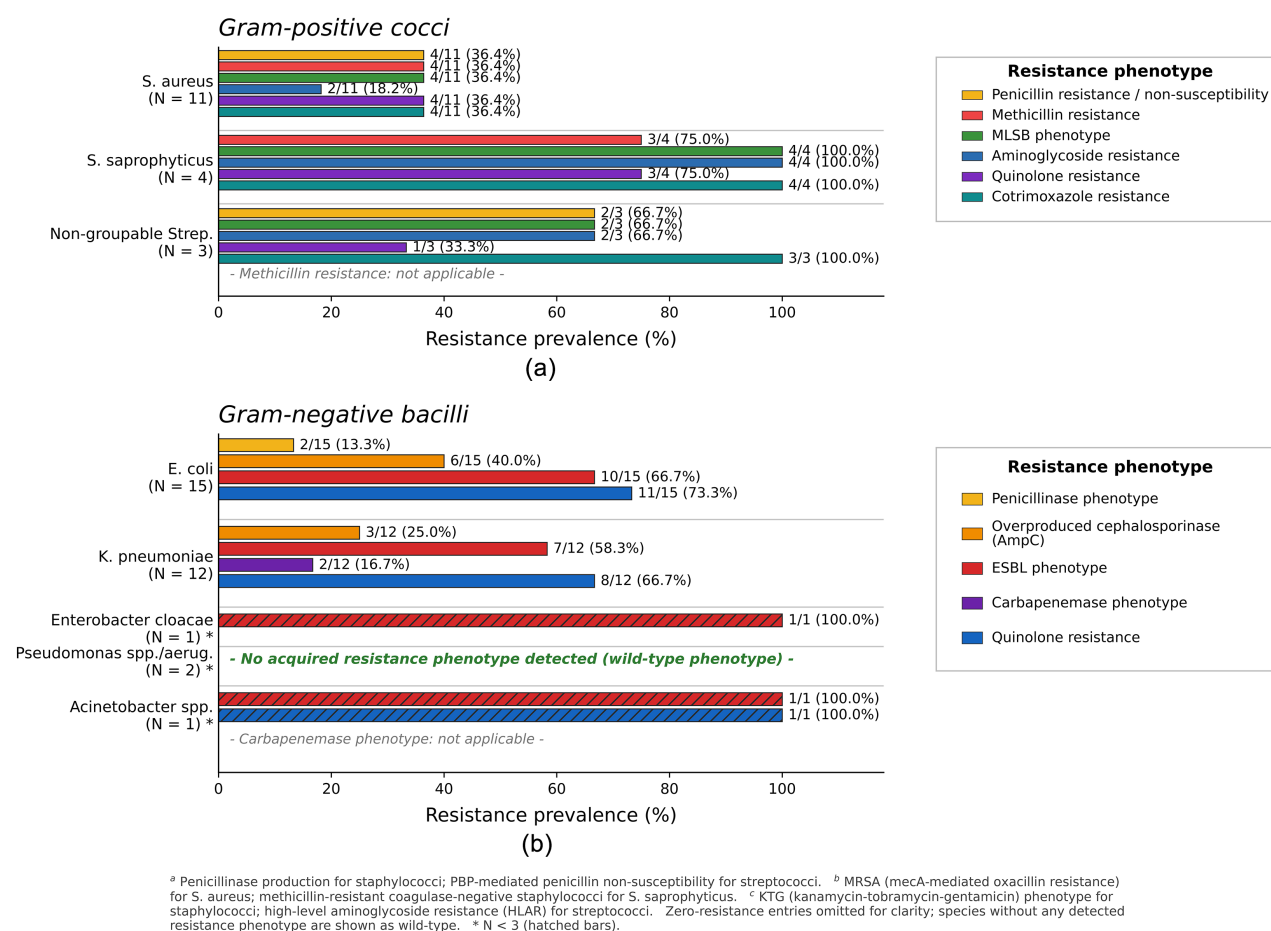


Figure 3. Antimicrobial resistance phenotype profile of the bacterial species recovered from HIV-infected patients hospitalized for a non-tuberculous bacterial infection at the Department of Infectious and Tropical Diseases (SMIT), Fann University Hospital, Dakar, Senegal, 2019-2022. (a) Resistance phenotype profile of the three predominant Gram-positive cocci. (b) Resistance phenotype profile of the five Gram-negative bacilli. Bars represent resistance prevalence; n/N labels indicate the number of resistant isolates and total tested. Zero-resistance phenotypes are omitted to enhance clarity; species without any detected acquired resistance are shown as wild-type. Hatched bars and asterisks indicate species with N < 3, for which percentages should be interpreted cautiously.

died, corresponding to an in-hospital case fatality proportion of 33.3%; two were transferred to another facility or service (5.6%). Among deceased patients, the median time from admission to death was 20 days (IQR: 11.0 - 39.2). Documented complications included renal disease or nephropathy (8.3%) and septic shock (5.6%).

4. Discussion

Non-tuberculous bacterial infections in hospitalized people living with HIV represent a major clinical challenge at the interface of advanced immunosuppression, delayed care, antimicrobial exposure and hospital-associated vulnerability. This study provides a focused description of non-tuberculous bacterial infections among hospitalized people living with HIV in a tertiary infectious diseases' referral centre in Dakar, Senegal. Understanding the clinical spectrum, bacterial ecology, antimicrobial resistance patterns and outcomes is essential to inform empir-

ical treatment strategies, optimize antimicrobial stewardship, and strengthen infection prevention practices in tertiary infectious diseases settings.

The clinical profile of this cohort strongly suggests that microbiologically documented non-tuberculous bacterial infections (NTBIs) frequently occurred in a context compatible with advanced HIV disease. CD4 count was available in only 10 patients (27.8%), among these tested patients, 90.0% of had CD4 counts below 200 cells/ μ L are highly consistent with advanced immunosuppression. This interpretation is aligned with the WHO definition of advanced HIV disease [4], and with WHO's recognition that severe bacterial infections are among the common causes of severe illness and death in advanced HIV disease [3] [22]. In practical terms, these data argue that bacterial infection in hospitalized PLHIV should not be viewed as an isolated infectious event, but as a potential marker of delayed diagnosis, treatment interruption, disengagement from HIV care, or insufficient screening for advanced HIV disease [4] [23].

The long median duration of symptoms before admission, reaching 30 days, is clinically important. It suggests delayed consultation, delayed referral, or possible under-recognition of bacterial infection in immunocompromised patients. In advanced or poorly controlled HIV disease, bacterial infections may present with non-specific manifestations, overlapping with tuberculosis, fungal infections, viral reactivation, malignancy, or drug-related complications. The high frequency of fever, respiratory symptoms, digestive symptoms, asthenia, weight loss and altered consciousness in this cohort illustrates this diagnostic complexity [24]. However, the predominance of urinary and bloodstream infections indicates that systematic microbiological sampling remains essential, even when symptoms are not site-specific [11] [24]. This is particularly relevant in settings where tuberculosis may dominate the diagnostic reasoning in PLHIV and potentially delay investigation for non-tuberculous bacterial infections [4].

Urinary tract infection was the leading documented site, and urine cultures had a high positivity rate among sampled patients. This urinary predominance is noteworthy, because much of the sub-Saharan African literature on severe bacterial infections among hospitalized PLHIV has historically focused on bloodstream and invasive bacterial infections, which are common and associated with substantial mortality [19] [25]. Our finding may therefore reflect a true burden of urinary infection among hospitalized PLHIV, consistent with recent African data showing a high prevalence of UTI among PLHIV, particularly in patients with low CD4 cell counts [7]. However, it may also be influenced by sampling practices, catheter exposure, prior hospitalization, and the difficulty of distinguishing infection from colonization in some patients [26] [27].

In our study, 58.3% of patients had bacteriological involvement of at least two anatomical sites. The high frequency of microbiological documentation should be interpreted cautiously. In immunocompromised patients, multiple positive cultures may reflect true concomitant infections, secondary bacterial dissemination, or colonization of non-sterile sites. Current guidance on advanced HIV disease

and microbiology utilization emphasizes that bacterial culture results must be interpreted within the clinical syndrome and the quality and anatomical relevance of the specimen [4] [28]. Therefore, isolates in this study were interpreted in relation to clinical presentation, anatomical plausibility, inflammatory markers and therapeutic decision-making, rather than culture positivity alone. However, given the retrospective design, residual misclassification between infection, colonization and contamination cannot be fully excluded [29].

A total of 57 bacterial isolates representing 16 species or taxa were recovered from 90 specimens. Gram-negative bacilli predominated (59.6%), driven by *E. coli* (26.3%) and *K. pneumoniae* (21.1%), while Gram-positive cocci accounted for 40.4%, led by *S. aureus* (19.3%) and *S. saprophyticus* (7.0%). This distribution is clinically relevant because *E. coli*, *S. aureus* and *K. pneumoniae* are among the leading bacterial pathogens contributing to the global burden of antimicrobial resistance [12]. This finding is also coherent with the WHO Bacterial Priority Pathogens List 2024, which places resistant *Enterobacterales*, including *E. coli* and *K. pneumoniae*, among critical-priority pathogens, and recognizes drug-resistant *S. aureus* as a high-priority pathogen [30]. The bacteriological distribution observed is also coherent with contemporary shifts in bacterial infections among PLHIV. Historically, invasive pneumococcal disease and non-typhoidal *Salmonella* were prominent in advanced HIV disease [31] [32]. However, more recent literature suggests that *Enterobacterales*, *S. aureus* and healthcare-associated pathogens are increasingly important, especially in patients with prior hospital exposure and antibiotic pressure [3] [4] [15]. A recent review on sepsis and antimicrobial resistance in advanced HIV disease emphasized that bacterial infections are frequently underestimated as causes of death [33]. This review also points out that PLHIV have a substantially increased risk of bacterial bloodstream infection, particularly at low CD4 counts [33]. In the present study, *E. coli* and *K. pneumoniae* together accounted for nearly half of all isolates, while *S. aureus* represented almost one-fifth. This profile is consistent with the predominance of urinary tract infections, bacteremia, skin/soft tissue or suppurative infections, and possible healthcare-associated acquisition.

The antimicrobial resistance profile is one of the strongest findings of the study. These resistance findings should be interpreted at the isolate level, as they reflect the susceptibility profiles of tested bacterial isolates rather than the prevalence of resistance among patients. The high resistance levels to amoxicillin, amoxicillin-clavulanate, cotrimoxazole, ceftriaxone and ciprofloxacin indicate that many commonly used empirical options may be unreliable in this population. This concern is especially relevant in settings where third-generation cephalosporins and fluoroquinolones remain widely used for empirical management of severe bacterial infections. The 61.3% ESBL rate among *Enterobacterales* is particularly alarming. This proportion exceeds the pooled ESBL prevalence reported in a recent systematic review among HIV-positive individuals, which estimated an overall prevalence of ESBL-producing *Enterobacterales* of approximately 20.3%, with marked

heterogeneity across regions and study populations [14]. It also aligns with Senegalese AMR surveillance data showing moderately high resistance to third-generation cephalosporins among *Enterobacterales* and high MRSA rates [16]. These findings are consistent with, and at the upper bound of, the ESBL prevalence recently reported across Senegalese clinical *Enterobacterales* isolates [34]. Our data thus are consistent with the general upward trend in ESBL and third-generation cephalosporin resistance documented across sub-Saharan Africa [35]. These results are also coherent with documented risk factors such as previous cephalosporin or carbapenem exposure, comorbidities, invasive devices and healthcare exposure [36].

The resistance profile has direct therapeutic implications. Ceftriaxone was the leading empirical antibiotic in this cohort, yet ceftriaxone resistance among tested isolates was 71.4%. This discrepancy is not simply a microbiological observation; it is a stewardship warning. In a setting where ESBL-producing *Enterobacterales* are frequent, empirical ceftriaxone may be inadequate for a substantial proportion of severely ill PLHIV, especially those with recent hospitalization, prior antibiotic exposure, severe sepsis, urinary source, or suspected bloodstream infection. This interpretation is consistent with IDSA guidance on the treatment of antimicrobial-resistant Gram-negative infections [37] and with Surviving Sepsis Campaign treatment recommendation for multidrug-resistant pathogens [11]. However, the solution is not indiscriminate escalation to carbapenems. Although carbapenems remain preferred agents for severe ESBL-producing *Enterobacterales* infections outside the urinary tract and for critically ill patients, unnecessary carbapenem exposure should be minimized to preserve their activity and reduce selection pressure for carbapenem-resistant organisms [37]. The rational approach is risk-stratified empirical therapy, systematic sampling before antibiotics, early reassessment at 48 - 72 hours, and strict de-escalation once susceptibility results are available [11] [38].

The observed use of imipenem after susceptibility testing reflects the microbiological pressure exerted by ESBL-producing *Enterobacterales*. Carbapenem resistance remained relatively limited overall, but its presence in *K. pneumoniae* is a serious signal. *K. pneumoniae* is a well-recognized hospital-adapted pathogen with strong epidemic potential, especially in high-risk wards, intensive care settings and immunocompromised patients [39]. The Senegal AMR report similarly observed lower rates of carbapenem resistance than third-generation cephalosporin resistance [16]. This report also emphasized the need for infection prevention measures, hand hygiene, standard and contact precautions, and minimization of invasive devices to limit spread of resistant *Enterobacterales* [16]. In this context, even a small number of carbapenem-resistant isolates should trigger institutional vigilance, because hospital transmission can rapidly transform a sporadic finding into an endemic problem.

The high cotrimoxazole resistance also requires a balanced interpretation. Cotrimoxazole remains clinically important in HIV care because of its preventive

role against several opportunistic and bacterial infections in eligible PLHIV. WHO guidance continues to recognize cotrimoxazole preventive therapy for adults with severe or advanced HIV disease as a survival-improving intervention [4]. However, high resistance among bacterial isolates limits its value as treatment for documented bacterial infections and may reflect cumulative selective pressure from prophylactic and therapeutic use. Studies in sub-Saharan Africa have reported very high cotrimoxazole resistance among *E. coli* isolates of 70.86% from people with HIV, including among those receiving cotrimoxazole prophylaxis [40]. Therefore, cotrimoxazole prophylaxis should not be interpreted as protection against all bacterial infections, and suspected severe bacterial infection in advanced HIV disease still requires microbiological documentation and locally adapted empirical treatment [37].

The Gram-positive findings are also clinically relevant. MRSA represented 36.4% of *S. aureus* isolates, and MLSB, quinolone and cotrimoxazole resistance were frequent. This proportion is broadly compatible with Senegalese surveillance estimates reporting MRSA rates between 28% and 42% in available datasets [16]. The absence of vancomycin resistance is reassuring, but it should not lead to complacency, particularly because national Senegalese AMR surveillance did not include estimates for vancomycin-resistant or vancomycin-intermediate staphylococci [16]. In resource-limited settings, vancomycin use is constrained by availability, renal monitoring requirements, therapeutic drug monitoring limitations and nephrotoxicity risks, especially in patients with anemia, renal dysfunction or severe sepsis. In practice, suspected invasive MRSA infection in PLHIV requires early source control, blood culture documentation, susceptibility-guided therapy and close renal monitoring [41] [42].

The high case fatality proportion, 33.3%, is one of the most important findings of this work. This mortality is higher than that reported in a recent Dakar tertiary-hospital study of bacterial infections in internal medicine and infectious diseases departments, where the death rate was 15% [43]. However, that study was not restricted to PLHIV with culture-documented bacterial infection and severe immunosuppression markers. The excess mortality in the present cohort is biologically plausible: patients combined delayed presentation, anemia, lymphopenia, frequent multi-site infection, bloodstream involvement, high inflammatory burden, prior hospitalization and high AMR pressure. These factors should be interpreted as a cluster of severity markers rather than as independent causal determinants, because the sample size does not allow robust multivariable modelling. The median interval from admission to death of 20 days suggests that mortality was not solely due to immediate fulminant sepsis. It may also reflect persistent infection, delayed effective therapy, complications or organ dysfunction, opportunistic coinfections, or underlying advanced HIV-related frailty. Recent Senegalese data identified anemia as strongly associated with death among hospitalized patients with bacterial infections [43]. More broadly, anemia is a recognized prognostic marker in HIV and is linked with poor outcomes [44] [45]. In the present study,

anemia and lymphopenia should be discussed as severity markers that may contribute to poor outcomes, even if the sample size does not allow robust multivariable modelling.

This study has several limitations. Its retrospective design exposes it to missing data, particularly for CD4 count, viral load, ART adherence, procalcitonin measures, prior microbiological colonization and timing of antibiotic exposure. The relatively small sample size also limited the statistical power and prevented reliable identification of mortality associated factors. The lack of admission-to-culture timing prevented classification of infections as community-onset or hospital-onset, limiting interpretation of the high antimicrobial resistance burden. In addition, prior antibiotic exposure may have reduced culture yield, especially for blood and cerebrospinal fluid cultures. Another limitation is the absence of molecular characterization of resistance mechanisms, which prevented confirmation of resistance genes. This study was conducted in a tertiary infectious diseases' referral centre, then the findings may not be generalizable to all PLHIV in Senegal, particularly outpatient populations or district-level hospitals.

Despite these limitations, the study has clear clinical and public health value. It documents a high-risk profile of hospitalized PLHIV with microbiologically documented NTBIs, combining delayed presentation, severe immunosuppression among tested patients, high ESBL burden, substantial MRSA prevalence, prolonged hospital stay and high mortality. These findings call for systematic advanced HIV disease assessment in PLHIV admitted with suspected severe infection. They also support the need to revise empirical antibiotic protocols in infectious diseases referral centres according to local AMR patterns and individual risk factors for ESBL-producing *Enterobacterales* and MRSA.

5. Conclusion

This study describes microbiologically documented non-tuberculous bacterial infections among hospitalized PLHIV in a Senegalese infectious diseases referral centre. These infections were marked by frequent urinary and bloodstream involvement, predominance of *Enterobacterales* and *Staphylococcus aureus*, high ESBL burden, clinically relevant MRSA and substantial multidrug resistance. These infections mainly affected severely immunocompromised patients, although advanced HIV disease could not be fully assessed across the cohort. The high in-hospital case-fatality proportion underscores the clinical consequences of the intersection between advanced immunosuppression, delayed presentation, severe bacterial infection and antimicrobial resistance. These findings support the need for systematic advanced HIV disease assessment, early microbiological documentation, locally adapted and risk-stratified empirical antibiotic protocols, timely de-escalation, antimicrobial stewardship and strengthened infection prevention and control. In West Africa, tertiary infectious disease units should be leveraged as sentinel platforms for surveillance of severe bacterial infections and antimicrobial

resistance among PLHIV.

Conflicts of Interest

The authors declare no conflicts of interest.

References

- [1] Joint United Nations Programme on HIV/AIDS(UNAIDS) (2025) Global HIV & AIDS Statistics—Fact Sheet [Internet]. UNAIDS, Geneva.
- [2] World Health Organization (WHO) (2025) HIV—Number of People Dying from HIV-Related Causes. Global Health Observatory. [Internet]. WHO, Geneva.
- [3] Burke, R.M., Sabet, N., Ellis, J., Rangaraj, A., Lawrence, D.S., Jarvis, J.N., *et al.* (2025) Causes of Hospitalisation among People Living with HIV Worldwide, 2014-23: A Systematic Review and Meta-Analysis. *The Lancet HIV*, **12**, e355-e366. [https://doi.org/10.1016/s2352-3018\(24\)00347-3](https://doi.org/10.1016/s2352-3018(24)00347-3)
- [4] World Health Organization (WHO) (2025) WHO Guidelines on the Management of Advanced HIV Disease [Internet]. WHO, Geneva.
- [5] Ousley, J., Niyibizi, A.A., Wanjala, S., Vandenbulcke, A., Kirubi, B., Omwoyo, W., *et al.* (2018) High Proportions of Patients with Advanced HIV Are Antiretroviral Therapy Experienced: Hospitalization Outcomes from 2 Sub-Saharan African Sites. *Clinical Infectious Diseases*, **66**, S126-S131. <https://doi.org/10.1093/cid/ciy103>
- [6] Langendorf, C., Bossard, C., Nackers, F., Comelli, A., Berghmans, M., Molay, G., *et al.* (2026) Community and Hospital-Acquired Invasive Bacterial Infections in Hospitalised Patients with Advanced HIV Disease: A Prospective Study in Kinshasa, DRC. *International Journal of Infectious Diseases*, **164**, Article 108383. <https://doi.org/10.1016/j.ijid.2026.108383>
- [7] Shabohurira, A., Eilu, E., Sankarapandian, V., Muhwezi, R. and Makeri, D. (2025) Prevalence, Bacterial Profile and Factors Associated with Urinary Tract Infections among People Living with HIV in Africa: A Systematic Review and Meta-Analysis. *Discover Public Health*, **22**, Article No. 50. <https://doi.org/10.1186/s12982-025-00433-9>
- [8] Zevin, A.S., McKinnon, L., Burgener, A. and Klatt, N.R. (2016) Microbial Translocation and Microbiome Dysbiosis in HIV-Associated Immune Activation. *Current Opinion in HIV and AIDS*, **11**, 182-190. <https://doi.org/10.1097/coh.0000000000000234>
- [9] Jacob, S.T., Pavlinac, P.B., Nakiyingi, L., Banura, P., Baeten, J.M., Morgan, K., *et al.* (2013) Mycobacterium Tuberculosis Bacteremia in a Cohort of HIV-Infected Patients Hospitalized with Severe Sepsis in Uganda-High Frequency, Low Clinical Sand Derivation of a Clinical Prediction Score. *PLOS ONE*, **8**, e70305. <https://doi.org/10.1371/journal.pone.0070305>
- [10] Africa Centre for Disease Control and Prevention and Center for Disease Dynamics, Economics & Policy (2021) African Antibiotic Treatment Guidelines for Common Bacterial Infections and Syndroms [Internet]. African Union, Africa CDC, Addis Ababa, Ethiopia.
- [11] Evans, L., Rhodes, A., Alhazzani, W., Antonelli, M., Coopersmith, C.M., French, C., *et al.* (2021) Surviving Sepsis Campaign: International Guidelines for Management of Sepsis and Septic Shock 2021. *Critical Care Medicine*, **49**, e1063.
- [12] Murray, C.J.L., Ikuta, K.S., Sharara, F., Swetschinski, L., Robles Aguilar, G., Gray, A.,

- et al.* (2022) Global Burden of Bacterial Antimicrobial Resistance in 2019: A Systematic Analysis. *The Lancet*, **399**, 629-655. [https://doi.org/10.1016/s0140-6736\(21\)02724-0](https://doi.org/10.1016/s0140-6736(21)02724-0)
- [13] World Health Organization (WHO), Antimicrobial Resistance Division (AMR) and Surveillance, Prevention and Control (SPC) (2025) Global Antibiotic Resistance Surveillance Report 2025 [Internet]. World Health Organization, Geneva.
- [14] Tigabie, M., Birhanu, A., Assefa, M., Girmay, G. and Tadesse, K. (2025) Extended-Spectrum β -Lactamase-Producing Enterobacterales among People Living with Human Immunodeficiency Virus across the Globe: A Systematic Review and Meta-Analysis. *PLOS ONE*, **20**, e0321873. <https://doi.org/10.1371/journal.pone.0321873>
- [15] Olaru, I.D., Tacconelli, E., Yeung, S., Ferrand, R.A., Stabler, R.A., Hopkins, H., *et al.* (2021) The Association between Antimicrobial Resistance and HIV Infection: A Systematic Review and Meta-Analysis. *Clinical Microbiology and Infection*, **27**, 846-853. <https://doi.org/10.1016/j.cmi.2021.03.026>
- [16] African Society for Laboratory Medicine, Africa CDC, WAHO and Center for Disease Dynamics, Economics and Policy (2022) Mapping Antimicrobial Resistance and Antimicrobial Use Partnership (MAAP). Senegal National Situation of Antimicrobial Resistance and Consumption Analysis from 2016-2018 [Internet]. Africa CDC.
- [17] Ondoa, P., Kapoor, G., Alimi, Y., Shumba, E., Osen, G., Maina, M., *et al.* (2025) Bacteriology Testing and Antimicrobial Resistance Detection Capacity of National Tiered Laboratory Networks in Sub-Saharan Africa: An Analysis from 14 Countries. *The Lancet Microbe*, **6**, Article 100976. <https://doi.org/10.1016/j.lanmic.2024.100976>
- [18] Cisse, V.M.P., Fall, N.M., Sarr, A., Mbaye, K.D., Bèye, H., Barro, K., *et al.* (2024) Opportunistic Infections among People Living with HIV in the Infectious Disease Department, the University Hospital of Fann in Dakar, Senegal. *Asian Journal of Research in Infectious Diseases*, **15**, 28-35. <https://doi.org/10.9734/ajrid/2024/v15i11389>
- [19] Wembulua, B.S., Lakhe, A., Diallo Mbaye, K., *et al.* (2021) Antibacterial Susceptibility Patterns of Bloodstream Isolates in 74 HIV-Infected Patients Hospitalized at the Clinic of Infectious and Tropical Diseases of Fann University Hospital, Dakar from 2013 to 2016. *Medecine Tropicale et Sante Internationale*, **1**, No. 2.
- [20] Fortes Déguénou, L., Manga, N.M., Diop, S.A., Dia Badiane, N.M., Seydi, M., Ndour, C.T., *et al.* (2011) Current Profile of HIV-Infected Patients Hospitalized in Dakar (Senegal). *Bulletin de La Société de Pathologie Exotique*, **104**, 366-370.
- [21] Thioub, D., Lakhe, N.A., Sarr, C., Lawson, A.T.D., Diouf, P.L.J., Sarr, A., *et al.* (2023) Profile of Bacterial Infections and Antibiotic Resistance at the Infectious and Tropical Diseases Clinic in Fann Hospital, Dakar, Senegal, 2019-2020. *International Journal of Infectious Diseases and Therapy*, **8**, 80-86.
- [22] World Health Organization (WHO) (2025) Severe Bacterial Infections. In: *WHO Guidelines on the Management of Advanced HIV Disease* [Internet]. World Health Organization, Geneva.
- [23] Ford, N., Meintjes, G., Calmy, A., Bygrave, H., Migone, C., Vitoria, M., *et al.* (2018) Managing Advanced HIV Disease in a Public Health Approach. *Clinical Infectious Diseases*, **66**, S106-S110. <https://doi.org/10.1093/cid/cix1139>
- [24] Unitaid (2023) Landscape of Rapid Diagnostic Tests for Severe Bacterial Infections in Advanced HIV Disease. Unitaid, Geneva.
- [25] Huson, M.A.M., Stolp, S.M., van der Poll, T. and Grobusch, M.P. (2014) Community-acquired Bacterial Bloodstream Infections in HIV-Infected Patients: A Systematic

- Review. *Clinical Infectious Diseases*, **58**, 79-92. <https://doi.org/10.1093/cid/cit596>
- [26] Patel, P.K., Advani, S.D., Kofman, A.D., Lo, E., Maragakis, L.L., Pegues, D.A., *et al.* (2023) Strategies to Prevent Catheter-Associated Urinary Tract Infections in Acute-Care Hospitals: 2022 Update. *Infection Control & Hospital Epidemiology*, **44**, 1209-1231. <https://doi.org/10.1017/ice.2023.137>
- [27] Nicolle, L.E., Gupta, K., Bradley, S.F., Colgan, R., DeMuri, G.P., Drekonja, D., *et al.* (2019) Clinical Practice Guideline for the Management of Asymptomatic Bacteriuria: 2019 Update by the Infectious Diseases Society of America. *Clinical Infectious Diseases*, **68**, e83-e110. <https://doi.org/10.1093/cid/ciy1121>
- [28] Miller, J.M., Binnicker, M.J., Campbell, S., Carroll, K.C., Chapin, K.C., Gonzalez, M.D., *et al.* (2024) Guide to Utilization of the Microbiology Laboratory for Diagnosis of Infectious Diseases: 2024 Update by the Infectious Diseases Society of America (IDSA) and the American Society for Microbiology (ASM). *Clinical Infectious Diseases*, **2024**, ciae104. <https://doi.org/10.1093/cid/ciae104>
- [29] Vandembroucke, J.P., von Elm, E., Altman, D.G., Gøtzsche, P.C., Mulrow, C.D., Pocock, S.J., *et al.* (2007) Strengthening the Reporting of Observational Studies in Epidemiology (Strobe). *Epidemiology*, **18**, 805-835. <https://doi.org/10.1097/ede.0b013e3181577511>
- [30] World Health Organization (2024) WHO Bacterial Priority Pathogens List, 2024: Bacterial Pathogens of Public Health Importance to Guide Research, Development and Strategies to Prevent and Control Antimicrobial Resistance [Internet]. World Health Organization, Geneva.
- [31] Reddy, E.A., Shaw, A.V. and Crump, J.A. (2010) Community-Acquired Bloodstream Infections in Africa: A Systematic Review and Meta-Analysis. *The Lancet Infectious Diseases*, **10**, 417-432. [https://doi.org/10.1016/s1473-3099\(10\)70072-4](https://doi.org/10.1016/s1473-3099(10)70072-4)
- [32] Feasey, N.A., Dougan, G., Kingsley, R.A., Heyderman, R.S. and Gordon, M.A. (2012) Invasive Non-Typhoidal Salmonella Disease: An Emerging and Neglected Tropical Disease in Africa. *The Lancet*, **379**, 2489-2499. [https://doi.org/10.1016/s0140-6736\(11\)61752-2](https://doi.org/10.1016/s0140-6736(11)61752-2)
- [33] Wake, R.M. and Govender, N.P. (2025) mGem: Sepsis and Antimicrobial Resistance in the Context of Advanced HIV Disease. *mBio*, **16**, e00769-24. <https://doi.org/10.1128/mbio.00769-24>
- [34] Dossouvi, K.M., Cissé, A., Sow, O., Niang, E.H.A., Ndiaye, I., Sambe Ba, B., *et al.* (2026) Antimicrobial Resistance among Clinical Enterobacterales Isolated from Humans in Senegal: A Systematic Review and Meta-Analysis from 1987 to 2022. *BMC Infectious Diseases*, **26**, Article No. 478. <https://doi.org/10.1186/s12879-026-12742-8>
- [35] Guido, G., Frallonardo, L., Asaduzzaman, M., Farkas, F.B., De Vita, E., Seni, A., *et al.* (2025) Third-Generation Cephalosporin Resistance in Sub-Saharan Africa: A Systematic Review and Meta-Analysis. *Communications Medicine*, **6**, Article No. 10. <https://doi.org/10.1038/s43856-025-01243-5>
- [36] Larramendy, S., Deglaire, V., Dusollier, P., Fournier, J.P., Caillon, J., Beaudeau, F., *et al.* (2020) Risk Factors of Extended-Spectrum Beta-Lactamases-Producing *Escherichia coli* Community Acquired Urinary Tract Infections: A Systematic Review. *Infection and Drug Resistance*, **13**, 3945-3955. <https://doi.org/10.2147/idr.s269033>
- [37] Tamma, P.D., Heil, E.L., Justo, J.A., Mathers, A.J., Satlin, M.J. and Bonomo, R.A. (2024) Infectious Diseases Society of America 2024 Guidance on the Treatment of Antimicrobial-Resistant Gram-Negative Infections. *Clinical Infectious Diseases*, **2024**, ciae403. <https://doi.org/10.1093/cid/ciae403>

- [38] World Health Organization (WHO) (2022) The WHO AWaRe (Access, Watch, Reserve) Antibiotic Book [Internet]. World Health Organization, Geneva.
- [39] Asokan, S., Jacob, T., Jacob, J., AlSosowaa, A.A., Cherian, T., Peijnenburg, W.J.G.M., *et al.* (2025) *Klebsiella Pneumoniae*: A Growing Threat in the Era of Antimicrobial Resistance. *The Microbe*, **7**, Article 100333. <https://doi.org/10.1016/j.microb.2025.100333>
- [40] Assefa, M. and Girmay, G. (2024) Prevalence of Co-Trimoxazole Resistance among HIV-Infected Individuals in Ethiopia: A Systematic Review and Meta-Analysis. *Frontiers in Medicine*, **11**, Article 1418954. <https://doi.org/10.3389/fmed.2024.1418954>
- [41] Rybak, M.J., Le, J., Lodise, T.P., Levine, D.P., Bradley, J.S., Liu, C., *et al.* (2020) Therapeutic Monitoring of Vancomycin for Serious Methicillin-Resistant *Staphylococcus Aureus* Infections: A Revised Consensus Guideline and Review by the American Society of Health-System Pharmacists, the Infectious Diseases Society of America, the Pediatric Infectious Diseases Society, and the Society of Infectious Diseases Pharmacists. *Clinical Infectious Diseases*, **71**, 1361-1364. <https://doi.org/10.1093/cid/ciaa303>
- [42] Liu, C., Bayer, A., Cosgrove, S.E., Daum, R.S., Fridkin, S.K., Gorwitz, R.J., *et al.* (2011) Clinical Practice Guidelines by the Infectious Diseases Society of America for the Treatment of Methicillin-Resistant *Staphylococcus Aureus* Infections in Adults and Children. *Clinical Infectious Diseases*, **52**, e18-e55. <https://doi.org/10.1093/cid/ciq146>
- [43] Diop, M., Guitoula, C., Tamouh, A.G., Youbong, T., Daffé, S.M.M., Ndoye, M., *et al.* (2025) Prevalence of Bacterial Infections and Factors Associated with Death Related to These Infections in Two Medical Departments of a Tertiary Hospital in Dakar, Senegal. *IJID Regions*, **15**, Article 100623. <https://doi.org/10.1016/j.ijregi.2025.100623>
- [44] Kerkhoff, A.D., Lawn, S.D., Schutz, C., Burton, R., Boulle, A., Cobelens, F.J., *et al.* (2015) Anemia, Blood Transfusion Requirements and Mortality Risk in Human Immunodeficiency Virus-Infected Adults Requiring Acute Medical Admission to Hospital in South Africa. *Open Forum Infectious Diseases*, **2**, ofv173. <https://doi.org/10.1093/ofid/ofv173>
- [45] Abioye, A.I., Andersen, C.T., Sudfeld, C.R. and Fawzi, W.W. (2020) Anemia, Iron Status, and HIV: A Systematic Review of the Evidence. *Advances in Nutrition*, **11**, 1334-1363. <https://doi.org/10.1093/advances/nmaa037>