

Profile of Bacterial Infections and Antibiotic Resistance at the Infectious and Tropical Diseases Clinic in Fann Hospital, Dakar, Senegal, 2019 – 2020

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Abstract: Antibiotic resistance is a growing public health problem worldwide. Gram-positive bacteria, such as methicillin-resistant *Staphylococcus aureus* (MRSA), used to be the biggest concern in the world of antibiotic resistance. More recently, gram-negative bacteria resistant to antibiotics are on the increase worldwide. The aim of this study was to determine the infection and antibiotic resistance profiles of bacterial isolates in the Infectious and Tropical Diseases Department (SMIT) at Fann University Hospital. We carried out a descriptive and retrospective study reviewing medical records for infectious diseases, collected over a 24-month period from January 1, 2019, to December 31, 2020. All the patients, diagnosed with bacterial infection with bacterial proof were included in this study. During the study period, 230 cases of bacterial infections were identified from 643 hospitalized patients, a proportion of 35.76%. The study population was predominantly male (56.5%). The main comorbidities were HIV infection (60.43%) and hypertension (7.40%). The main infections diagnosed were bacteremia (63%) and urinary tract infections (36%). Respiratory tract infections were found in 15.2% of patients. Isolated *Escherichia*, *Enterobacter* and *Klebsiella* strains showed high resistance to aminoglycosides, cotrimoxazole, ciprofloxacin and third generation cephalosporins (C3G). *Salmonella* strains were sensitive to all most all the antibiotics tested except lincomycin. Finally, the resistance of enterobacterial strains isolated to imipenem were low for *Klebsiella* and high for *Pseudomonas*.

Keywords: Bacterial Infections, Antibiotic Resistance, Senegal

1. Introduction

Antibiotic resistance is a growing public health problem worldwide [1]. Gram-positive bacteria, such as methicillin-resistant *Staphylococcus aureus* (MRSA), used to be the biggest concern in the world of antibiotic resistance.

More recently, gram-negative bacteria resistant to antibiotics are on the increase worldwide [1]. The patients at high risk for these infections are those already hospitalized with invasive devices or taking extended courses of antibiotics [2]. The causes of the rising trends in antimicrobial resistance are multi-factorial. A key factor in emerging resistance is a lack of

good antibiotic stewardship leading to overuse of antimicrobials. In addition, the inappropriate empiric coverage, delays in accurate diagnoses, as well as de-escalation of therapy are factors implicated in antibiotic resistance. As time goes on, there are fewer and fewer antimicrobials available that are effective in treating these infections, therefore, the problem further escalates [3-5]. In Senegal, few studies have addressed bacterial infection with bacterial proof, particularly at the Fann clinic of Infectious and Tropical Diseases (SMIT). Our study was carried out within this context and the main objective was to assess the bacterial infection diagnosed at SMIT. The specific objectives were to describe epidemiological, clinical, and bacteriological profile of these infections and to determine the antibiotic resistance patterns of bacterial isolates.

2. Methods

Our study was conducted at the SMIT of the Fann University Hospital (CHNU) in Dakar. This was a descriptive and retrospective study reviewing medical records of patients diagnosed with bacterial infections, collected over a 24-month period from January 1, 2019, to December 31, 2020. All the patients, regardless of sex or age, diagnosed with bacterial infection with bacterial proof (except tuberculosis and tetanus) were included in this study. To facilitate the retrospective collection of data from patient's files, the following definitions were used:

1. Bacteremia: presence of pathogenic bacteria in the circulating blood, confirmed by positive blood cultures.
2. Lower respiratory tract infection (LRI) is defined by respiratory symptoms with a positive cytobacteriological examination of sputum.
3. The diagnosis of urinary tract infection (UTI) was made through the cytobacteriological examination of urine (ECBU) followed by an antibiogram.
4. Genital infections: all infections (discharge, ulcerations, pelvic pain) affecting all organs of the genital tract, with isolation of germs.

Once the identification of the germs was done according to conventional techniques, each isolated strain was subjected to a standard antibiogram. This involved diffusion of the antibiotic discs in agar medium Mueller Hinton (MH) in accordance with the recommendations of the Antibiogram Committee of the French Society of Microbiology (CASFM). To simplify the interpretation of resistance phenotypes, intermediate categorized strains were considered as resistant. The MRSA (methicillin-resistant *Staphylococcus aureus*) profile was assigned to *Staphylococcus aureus* isolates not susceptible to oxacillin and/or ceftioxin. And ESBL (bacterium secreting extended spectrum beta-lactamases), was assigned to strains resistant to penicillins, cephalosporins and aztreonam, but susceptible to amoxicillin-clavulanic acid (ticarcillin-clavulanic acid for *Pseudomonas* sp and enterobacter sp). Resistance to carbapenems, in case of resistance to imipenem.

We recorded demographic data (age, sex, geographical

origin, occupation, marital status); clinical data (HIV status, comorbidities, reasons for admission, infections sites); bacteriological data (isolated germs, bacterial resistance, mono or poly microbial culture); biological data (Complete Blood counts, CRP, glycemia); therapeutic data (antibiotics used, duration of treatment, association of antibiotics or not); prognostic data (time and duration of hospitalization, evolutionary modalities) from patients' records using a standard survey form. Data entry was done using Epi-Data software version 3.5.1. and their analysis was performed with Epi-info software version 7.1.5.

3. Results

3.1. Epidemiological and Clinical Data

During the study period, 230 cases of bacterial infections were identified from 643 hospitalized patients, representing a proportion of 35.76%. The study population was predominantly male (56.5%), with a sex ratio (M/F) of 1.3. The distribution according to age had shown that bacterial infections was more common in the age groups 40-59 years and 20-39 years, representing 41.30% and 39.13% respectively. Most of the study population (70%) came from urban areas and 22.18% from the suburban areas. Regarding marital status, most of patients were married (59%) and singles accounted for 23.04% of the patients. Most of patients (75.21%) had a comorbidity. The main comorbidities were HIV infection (60.43%) and hypertension (7.40%) (table 1). The most common reasons for hospitalization were fever (49.13%), neurological signs (34.78%) and signs of clinical immunosuppression (33.04%). The main infections diagnosed were bacteremia (63%) and urinary tract infections (36%). Respiratory tract infections were found in 15.2% of patients (table 2).

3.2. Paraclinical and Bacteriological Data

The white blood cell count was normal in 51.80% and hyperleukocytosis was noted in 30.40%. The C-Reactive Protein (CRP) was performed in 62 patients and was greater than 96 mg/l in 89.8% of the patients. In just over half of the patients (56.5%) the fasting blood sugar was normal. The bacteriological samples isolated 294 strains. Infections were mostly mono-microbial (89%). The most frequently isolated bacteria were *Staphylococcus* (27.8%), *Klebsiella* (23.3%), *Escherichia* (20.0%) and *Pseudomonas* (17.8%) (Table 3). Gram-negative bacilli accounted for 83.14% of germs isolated during urinary tract infections. Among these bacteria responsible for urinary tract infections, *Klebsiella* (25.30%), *Escherichia* (20.48%) and *Pseudomonas* (16.87%) predominated (table 4). In bacteremia, the most frequently isolated bacteria were *Staphylococcus* and *Pseudomonas* 33.10% and 14.48% respectively (table 4). Respiratory samples were taken from 35 patients (15.2%); *Klebsiella* (42.86%), *Pseudomonas* (17.14%) and *Staphylococcus* (14.29%) were the most frequent germs responsible for respiratory tract infections (table 4). For genital infections, the

most frequently isolated germs were *Escherichia* (48.39%) and *Klebsiella* (22.58%) (table 4).

Table 1. Patients' distribution according to epidemiological characteristics.

Epidemiological data	Frequency (n=230)	Percentage (%)
Sex		
Male	130	56.5
Female	100	43.5
Age group		
<20	8	3.48
20 to 40	90	39.13
40 to 60	95	41.30
60 to 80	31	13.48
> 80	6	2.60
Origin		
urban	161	70.00
suburban	51	22.18
Rural	18	7.82
Comorbidities		
HIV	139	60.43
HTA	17	7.39
Diabete	14	6.08

Table 2. Patients distribution by infection type.

Infections sites	Frequency (n=230)	Percentage (%)
Bactériemia	150	65.2
Urinary tract infections	123	53.5
Genital Infections	31	13.5%
Lower respiratory tract Infections	21	9.1%

Table 3. Patient distribution according to isolated bacterial.

Isolated Bacterial strains	Frequency (n=230)	Percentage (%)
Staphylococcus	64	27.8
Klebsiella	56	24.3
Escherichia	46	20.0%
Pseudomonas	41	17.8
Enterobacter	25	10.8
Acinetobacter	17	7.4
Streptococcus	14	6.0
Salmonella	7	3.0
Flavobacterium	6	2.6
Citrobacter	5	2.2
Treponema	3	1.3
Proteus	2	0.9
Xanthomonas	2	0.9
Serratia	2	2.9
Shigella	1	0.4
Enterococcus	1	0.4
Ureaplasma	1	0.4

Table 4. Distribution of bacterial strains isolated according to infection sites.

Bacteria	Culture			
	Urine (N=83; 36%) n (%)	Blood (N=145; 63%) n (%)	Sputum (N=35; 15.2%) n (%)	Vaginal swab (N=31; 13.5%) n (%)
Acinetobacter	5 (6.02)	7 (4,83)	3 (8,57)	2 (6,45)
Citrobacter	3 (3.61)	2 (1,38)	NA	NA
Enterobacter spp	5 (6.02)	14 (9,66)	3 (8,57)	3 (9,68)
Enterococcus	1 (1.20)	NA	NA	NA
Escherichia	17 (20.48)	12 (8,28)	2 (5,71)	15 (48,39)
Flavobacterium	1 (1.20)	5 (3,45)	NA	NA
Klebsiella	21 (25.30)	13 (8,97)	15 (42,86)	7 (22,58)
Pseudomonas	14 (16.87)	21 (15,17)	6 (17,14)	NA
Proteus	2 (2.41)	NA	NA	NA
Staphylococcus	8 (9.64)	48 (33,10)	5 (14,29)	3 (9,68)
Streptococcus	5 (6.02)	9 (6,21)	NA	NA
Salmonella	1 (1.20)	6 (4,14)	NA	NA

Bacteria	Culture			
	Urine (N=83; 36%) n (%)	Blood (N=145; 63%) n (%)	Sputum (N=35; 15.2%) n (%)	Vaginal swab (N=31; 13.5%) n (%)
Serratia	NA	1 (0,69)	1 (2,86)	NA
Shigella	NA	1 (0,69)	NA	NA
Xanthomonas	NA	2 (1,38)	NA	NA

NA* = not applicable

3.3. Antimicrobial Resistance Patterns of Tested Isolates

The strains of Staphylococci tested were methicillin-resistant in 50% of cases and resistant to penicillin in 80%. They were completely resistant to piperacillin and levofloxacin and had high level of resistance to ciprofloxacin and aminoglycosides. Escherichia strains tested were completely resistant to penicillins, cotrimoxazole, ciprofloxacin and showed a high level of resistance to third generation cephalosporins (C3G) but were fully susceptible to aminoglycosides and imipenem. There was total resistance of the Klebsiella strains tested to penicillin A, amox-clavulanic acid and ticarcillin. Resistance of the Klebsiella remained very high for third generation cephalosporins and piperacillin. Imipenem had good activity on the Klebsiella strains tested with a low resistance (16.66%). The Enterobacter strains tested had a very high-level of resistance to penicillins but were susceptible to aminoglycosides,

levofloxacin, and imipenem. Acinetobacter strains isolated were resistant to piperacillin, ticarcillin, cefepime, imipenem. The strains showed 50% resistance for amikacin. Strains of Pseudomonas had a high resistance, at least 50% for levofloxacin, ticarcillin, cefepime and imipenem. Shigella strains tested showed complete resistance to ampicillin, amoxicillin, piperacillin and co-trimoxazole. They however, remained susceptible to aminoglycosides, levofloxacin, chloramphenicol. Salmonella strains were sensitive to all antibiotics tested except lincomycin.

Table 5 summarizes the cases of antibiotic resistance. Isolated strains of Escherichia, Enterobacter and Klebsiella showed strong resistance to aminoglycosides, C3G, ciprofloxacin and cotrimoxazole. Salmonella strains were sensitive to almost all the antibiotics tested, except for lincomycin. The resistance of isolated enterobacterial strains to imipenem was low.

Table 5. Antimicrobial resistance patterns of tested isolates.

Antimicrobial category	Antibiotics tested	Staphylococcus N=19 (%)	Escherichia N=26 (%)	Klebsiella N=19 (%)	Enterobacter N=9 (%)	Shigella N=7 (%)
Penicillin	Pénicilline G	80	100	100	100	NT
	Ampicilline	50	100	100	83.33	100
	Amoxicilline	100	100	100	85.7	100
	Amoxi- Aclav	16.6	100	100	100	NT
	Oxacilline	50.00	100	NT	100	NT
	Ticarcillin	66.66	100	100	100	NT
	Piperacillin	100	100	77.7	50	100
Carbapenem	Imipenem	100	00	16.66	00	NT
Aminoglycosides	Amikacine	57.14	00	12.5	00	NT
	Netilmicine	27.27	00	16.6	00	NT
	Kanamycine	77.7	00	25	00	00
	Gentamicine	54.5	00	11.1	00	00
	Tobramycine	NT	00	21.4	25	00
Cephalosporins	Céfaloine	00	100	73.3	100	00
	Céfotaxime	55.5	100	53.8	50	00
	Ceftriaxone	00	66.66	78.5	60	00
	Céfépime	100	00	70	100	70
Quinolones	Ciprofloxacin	50	100	44.4	28.5	NT
	Levofloxacin	100	00	00	00	00
MLSK	Erythromycine	60.0	NT	NT	NT	NT
	Lincomycine	33.33	NT	NT	NT	NT
Polymyxin	Fosfomycine	15.38	50	66.7	66.7	00
Sulfamides	Cotrimoxazole	55.5	100	63.6	50	100
Phenicol	Chloramphénicol	35.7	00	12.5	00	00
Cyclines	Tétracycline	66.6	NT	00	NT	NT

Table 5. Continued.

Antimicrobial category	Antibiotics tested	Salmonella N=2 (%)	Citrobacter N=2 (%)	Pseudomonas N=13 (%)	Acinetobacter N=2 (%)
Penicillin	Pénicilline G	00	NT	100	100
	Ampicilline	00	100	100	NT
	Amoxicilline	00	100	100	NT
	Amoxi- Aclav	NT	NT	100	NT

Antimicrobial category	Antibiotics tested	Salmonella N=2 (%)	Citrobacter N=2 (%)	Pseudomonas N=13 (%)	Acinetobacter N=2 (%)
Carbapenem Aminoglycosides	Oxacilline	NT	NT	NT	00
	Ticarcillin	NT	NT	66.7	100
	Piperacillin	00	100	00	100
	Imipenem	NT	00	50	100
	Amikacine	NT	00	12.5	50
	Netilmicine	NT	100	00	NT
	Kanamycine	00	NT	16.6	50
	Gentamicine	00	54.5	00	00
Cephalosporins	Tobramycine	00	NT	20	50
	Céfaloine	00	100	100	NT
	Céfotaxime	00	100	100	100
	Ceftriaxone	00	100	100	66,66
	Céfépime	00	100	62,5	100
Quinolones	Ciprofloxacin	00	100	25	100
	Levofloxacin	NT	NT	50	NT
MLSK	Erythromycine	NT	NT	NT	NT
	Lincomycine	100	NT	NT	NT
Polymyxin	Fosfomycine	NT	50	66.7	100
Sulfamides	Cotrimoxazole	NT	55.5	NT	100
Phenicol	Chloramphénicol	NT	00	NT	50
Cyclines	Tétracycline	NT	NT	NT	NT

NT* = not tested

3.4. Therapeutic and Evolutionary Data

Ceftriaxone was the most used antibiotic, either alone or in combination. The average duration of antibiotic treatment was 12.51 ± 8.31 days. Antibiotic treatment lasted less than 7 days in 35.13% of patients. The average length of hospitalization was 30.52 ± 37.77 days, and less than 10 days in 41% of patients. We found a lethality rate of 28%.

4. Discussion

In Africa, few studies have been conducted on bacterial infections with bacterial proof. In our study, infections were mainly the prerogative of young adults, mostly men. Most of our patients (69.9%) came from urban areas. This situation would probably be explained by the insalubrity which reigns in these urban communities, the high human density, the promiscuity, and the poor management of waste. Indeed, the combination of all these factors would promote the development of infectious pathologies, particularly bacterial ones. The SMIT is the referral center for management of infectious and tropical diseases in Senegal. Thus, most of our patients were HIV infected patients.

The main infections found in our study were bacteremia (63%). However, Aketi et al. mostly found urinary tract infections (39.4%) followed by pulmonary infections (12.8%) [6]. These differences could be explained by the fact that most of our patients were infected with HIV exposing them to invasive infections including bacteremia. Thus Lakhe et al., in a study carried out in the same department, found that 73% of bacteremia cases recorded were infected in HIV patients [7].

Urinary tract infections (UTI) are mainly caused by Gram-negative bacilli [8]. Our work supports this fact. The specific origin of these infections (healthcare-associated or community-acquired) was not specified in our study. The

strains most frequently isolated in urinary tract infections were *Klebsiella*, *Escherichia* and *Pseudomonas*. This observation was already made by Lakhe et al., who found *Klebsiella pneumoniae* (29.1%), *Escherichia coli* (28.2%) [9]. In addition, several other studies, conducted within Senegal and in other countries have reported similar trends in prevalence of these two germs in urinary tract infections [8, 10-12]. Our study is remarkable for the large number of *Klebsiella* strains isolated, making it the most frequent pathogen ahead of *Escherichia coli*. This may reflect the nosocomial origin of these infections. Other bacteria of nosocomial origin were also identified in our study, namely *Acinetobacter* and *Enterobacter*. All these elements indirectly show that healthcare-associated urinary tract infections (HATIs) represent a significant proportion of bacterial infections in our clinic.

During bacteremia, *Staphylococci* and *Pseudomonas* were the most isolated bacteria. Our results are like those of Lakhe et al, who in 2014, in the same department, found coagulase-negative staphylococci (23.1%), followed by *Pseudomonas aeruginosa* /spp (15.1%) and *Staphylococcus aureus* (10. 5%) [7]. The same observation was made in Bamako (Mali) by Maïga et al., who found a predominance of *Staphylococci* (30.13%) [13]. The frequency of staphylococci could be explained by the increase in invasive procedures such as the implantation of foreign material or the insertion of perfusion catheters, or by human contamination. *Pseudomonas*, especially the *aeruginosa* species, is the second most frequent germ in our study. It has already been proven that *Pseudomonas aeruginosa* is a frequent cause of bacteremia [14]. *Pseudomonas* bacteremia is essentially associated with health care, occurring preferentially in elderly, immunocompromised subjects, carriers of invasive devices or those pre-treated with antibiotics [14].

For patients in our study with Lower respiratory tract

infections, the most frequently isolated germs were *Klebsiella* (42.86%), *Pseudomonas* (17.14%) and *Staphylococcus* (14.29). The presence of these pathogens not only reflects the nosocomial origin of these infections but also their occurrence in specific patients, particularly the immunocompromised. On the other hand, existing literature shows that *Streptococcus pneumoniae* is the main cause of lower respiratory tract infections [15]. This discrepancy could be explained by the variability of the bacterial ecology between the departments.

The main bacteria responsible for genital infections in our work were *Escherichia* and *Klebsiella*. A study on vaginal colonization in diabetics also found *Escherichia coli* (21.6%) at the top of the list, followed by *Klebsiella* (8.1%) [16]. The prevalence of these germs could be linked to a possible contamination, of urinary or even digestive origin.

Our high lethality rate could be explained by the delay in seeking healthcare often noted in our patients, who arrive at the hospital after a rather complex therapeutic course. It could also be as a result of the inadequacy of our technical platform and the occurrence of these infections in immunocompromised subjects, often at the last stage of HIV infection.

Staphylococci strains tested were methicillin-resistant (MRSA) in 50% of cases. The increase in the prevalence of MRSA infections has affected all regions of the world [17]. It is reported that in people infected by MRSA, the risk of death was greater than 64% compared to people infected by MSSA [18]. This could partly explain the high lethality rate in our patients, in whom the same germ profile was responsible for most bacteremia. In addition, there was significant resistance to fluoroquinolones and aminoglycosides. Resistance to fluoroquinolones, particularly ciprofloxacin, may be linked to the availability of these antibiotics in IB (initiative de Bamako) pharmacies, thus exposing them to overuse and therefore to occurrence of resistance. The only guarantees of effective treatment were cefalotine and ceftriaxone.

We found a high prevalence of ESBL *E. coli* strain. Fortunately, no resistance to imipenem and aminoglycosides has been demonstrated for the strains of *Escherichia coli* identified. However, the rational use of carbapenems must be mandatory in order to avoid the emergence of carbapenemase-producing *E. coli* strains.

Klebsiella isolates were resistant to aminopenicillins, and more than 50% to third generation of cephalosporins. Antibiotic activity was complete for levofloxacin and high for imipenem. A few years prior, in the same department, Lakhe *et al.*, found that *Klebsiella* strains showed 100% resistance to amoxicillin-clavulanic acid, 80% resistance to cotrimoxazole and 60% resistance to C3G, gentamicin and ciprofloxacin [7]. WHO has pointed out that the resistance of *Klebsiella pneumoniae* strains to carbapenems has spread to all regions of the world. In some countries, these strains have become resistant to carbapenems in more than half of patients treated for *Klebsiella pneumoniae* infections [17].

The strains of *Pseudomonas* isolated in our study were multi-resistant with a high resistance to β -lactams. These resistance patterns are responsible for a reduction in therapeutic options, sometimes leading to a therapeutic

impasse. Controlling the spread of multi-resistant strains essentially involves hygiene measures, while preventing the emergence of resistant mutants involves optimizing individual antibiotic therapy.

5. Conclusion

The increasing prevalence of antibiotic resistance poses a threat to human health, particularly in resource-limited countries where a wide choice of antibiotics is not available. Bacteria such as *Staphylococcus*, *Escherichia*, *Pseudomonas* and *Klebsiella* have all been identified as pathogens with high rates of antibiotic resistance. Unfortunately, we found strains of *Pseudomonas* with a high level of resistance to carbapenems. Combating antibiotic resistance can be very complex in our context. It requires better use of antibiotics through a better understanding of the epidemiology of bacterial infections and resistance profiles to put in place appropriate treatment guidelines.

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