Incidence and bacteriological profile of surgical site infections at Ouakam Military Hospital

Abstract

Introduction: Surgical site infection (SSI) is the 3rd most common healthcare-associated infection. In sub-Saharan Africa, treatment is often probabilistic. The aim of this study was to determine the incidence of this type of infection at the Ouakam Military Hospital and to determine the antibiotic resistance profile of the bacteria isolated.

Methodology: A prospective, analytical and descriptive study was carried out over 2 years in the medical analysis laboratory department and the surgical departments operating in the same operating theatre. Identification and antibiotic susceptibility testing of isolated bacteria were performed using the VITEK® 2 COMPACT (BioMérieux) automated system, and statistical analysis was performed using Epi info software (version 7.2.6.0).

Results: The incidence of SSIs was 4.6%. A total of 129 bacterial strains were isolated, including 41.1% *Staphylococcus aureus*, 24.0% *Escherichia coli* and 12.4% *Pseudomonas aeruginosa.* 26.4% of the *S. aureus* strains were resistant to methicillin and none were resistant to vancomycin. Production of extended-spectrum beta-lactamase was noted in 41.9% of *E. coli* strains, 50.0% of *Klebsiella pneumoniae* strains and 100.0% of *Enterobacter cloacae* strains. Only these three bacteria developed carbapénèmases at rates of 3.2%, 10.0% and 66.7% respectively. The rate of *P. aeruginosa* strains resistant to ceftazidime was 37.5%.

Conclusion: The incidence of SSI is relatively low. However, the alarming rates of resistance suggest rigorous monitoring of antibiotic resistance.

Keywords: surgical site infection; bacterial species; antibiotic resistance; Dakar

1. Introduction

Surgical site infection (SSI) is the 3rd most common healthcare-associated infection after urinary tract and respiratory infections(Fournel, 2017). It is defined as an infection occurring within 30 days of the surgical procedure, or within one year in the case of implants or prostheses (Thiolet et al., 2007). It is an infection that occurs when several events occur at the same time: contamination of the surgicalsite, bacterial colonisation of the surgical site, growth and development of microorganisms implicated in the infection, and the host's immune defences being overwhelmed by the infectious agent (Fournel, 2017). In developed countries, the incidence of this type of infection is estimated at between 1.2 and 5.2%, while in low- and middle-income countries it ranges from 1.2 to 23.6%(World Health Organization, 2011). In sub-Saharan Africa, it varies between 6.8% and 26% (Ngaroua et al., 2016). Because of its frequency and its considerable economic and therapeutic consequences, SSI is a major public health problem. Itnot only increases the cost of treatment, but also considerably lengthens hospital stays (Anderson et al., 2007).Infected patients are therefore at greater risk of undergoing further surgery, and the risk of death is unfortunately doubled in the post-operative period (Bercion et al., 2007).The treatment of these infections is complex and represents a major challenge, particularly in developing countries where financial resources

are limited. In these countries, treatment is most often based on empirical antibiotic therapy, sometimes without first accurately identifying the pathogen responsible for the infection. This practice compromises the efficacy of treatment for these infections by encouraging the emergence of resistant bacterial strains through the selection of resistant mutants(Ouedraogo et al., 2011). Antimicrobial resistance (AMR) is a threat to global health and to the development of societies. It has been declared by the World Health Organisation (WHO) as one of the top 10 global public health threats facing humanity(World Health Organization, 2020). As part of the response to AMR, biological diagnostics occupy an important place in the global action plan. Accurate identification of pathogens and determination of their susceptibility to anti-infectives play an essential role in the fight against this scourge. The aim of this study was to determine the incidence of surgical site infections at Ouakam Military Hospital, to identify their bacterial ecology and to determine the resistance profile of these germs to the various antibiotics commonly used in medical practice in our context.

2. Methodology

2.1. Setting and study population

We conducted a prospective, analytical and descriptive study at the Ouakam military hospital over a 2-year period (April 2021 - March 2023). It was carried out jointly in the medical biology laboratory and the various surgical specialities operating in the same operating theatre (orthopaedic surgery, general surgery, gynaecological and obstetric surgery, ear, nose and throat surgery and neurosurgery). Our study population consisted of all patients who developed SSI after undergoing surgery in this operating theatre during the study period.

2.2. Sampling

The samples analysed consisted of pus samples. Pus from deep areas was collected by aspiration or puncture through the skin or mucosa, and pus from superficial areas was collected by syringe or swab.

2.3. Bacteriological diagnosis

On each pus sample, we performed:

-macroscopic examination: determination of the colour, consistency and odour of the pus.

-microscopic examination in the fresh state: assessment of bacterial mobility, shape and grouping patterns, leucocyte and red cell counts.

-microscopic examination after Gram staining: 2 groups of bacteria are obtained: Gram-positive bacteria and Gram-negative bacteria; assessment of the bacterial flora.

-culture: pus samples were inoculated on selective media: Chapman's medium, Eosin Methylen Blue (EMB) medium and non-selective media: Blood Agar, Cystine Lactose Electrolyte Deficient Medium (CLED), then incubated at 37 degrees Celsius for 24 to 48 hours. Bacteria were identified and susceptibility-tested using the VITEK® 2 COMPACT (BioMérieux) automated system.

2.4. Data collection and statistical analysis

Data were collected using the hospital's FileMaker Pro and LabManager software. Age was divided into four groups: < 20 years, 20 - 40 years, 40 - 60 years and > 60 years.

Statistical analysis was carried out using Epi info software (version 7.2.6.0).

2.5. Ethical consideration: Respect for individuals and the confidentiality of the information in the files were guaranteed during the course of this study.

3. Results

3.1. Socio-demographic results

A total of 3413 patients underwent surgery in the shared operating theatre during the study period. Of these, 157 presented with an SSI, corresponding to an incidence rate of 4.6% (Table 1). Within this study population, men were more represented at 61.1% (96/157) compared with 38.9% for women (61/157), corresponding to a sex ratio of 1.57. The mean age of the patients was 39.9 years, ranging from 5 to 77 years. The age group 20 to 40 years with a percentage of 40.8% (64/157) was the most represented in our series. In terms of surgical specialities, SSIs were more frequent in orthopaedic surgery and general surgery with 51.6% (81/157) and 40.8% (64/157) respectively. They were less frequent in neurosurgery with only 1 case of SSI noted (0.6%).

Table 1: General characteristics of the study population (N = 157)

Variables	Number (n)	Percentage (%)
Age groups (years), mean age = 39.9 years		
≤ 20	23	14.6
]20-40]	64	40.8
]40-60]	48	30.6
> 60	22	14
Gender		
Male	96	61.1
Female	61	38.9
Surgical specialties		
Orthopaedic and trauma surgery	81	51.6
General surgery	64	40.8
Ear, nose and throat surgery	6	3.8

Gynaecological and obstetric surgery	5	3.2
Neurosurgery	1	0.6
Type of pus		
Superficial	92	58.6
Deep	65	41.4

3.2. Positivity rate of pus cultures and distribution of bacterial strains

Of the 157 pus samples analysed, 120 cultures were positive, corresponding to a positivity rate of 76.4%. They were monomicrobial in 92.5% (111/120) and bi-microbial in 7.5% (9/120), giving a total of 129 bacterial strains isolated. Of all the bacteria isolated, *S. aureus* was the most frequent at 41.1% (53/129), followed by *E. coli* and *P. aeruginosa* at 24.0% (31/129) and 12.4% (16/129) respectively (Figure 1).

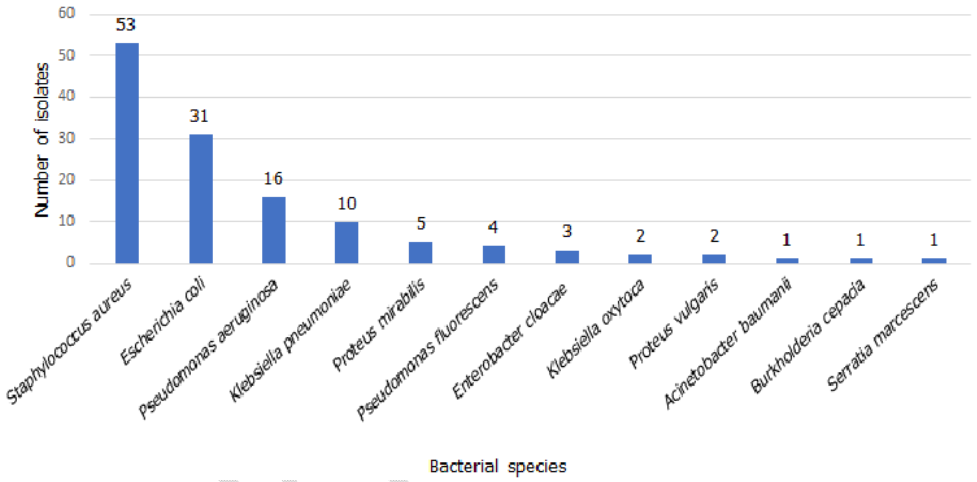

Figure 1: Frequency of isolation of bacterial species

With regard to the distribution of bacterial isolates according to surgical speciality (Table 2), *E. coli* with 44.4% (24/54) was the germ most isolated in general surgery, followed by *S. aureus* with 25.9% (14/54). In orthopaedic surgery, more than half (54.3%) of the bacterial isolates were *S. aureus* strains, with 38 isolates out of 70. No bacteria were isolated from pus samples from neurosurgery.

Table 2: Distribution of bacterial isolates by surgical specialty

Bacterial species	General surgery (N=54)	Gynaecological and obstetric surgery (N=3)	Ear, nose and throat surgery (N=2)	Orthopaedic and trauma surgery (N=70)	Neurosurgery (N=0)
A. baumanii	1 (1.9%)	-	-	-	-
B. cepacia	-	-	-	1 (1.4%)	-
E. cloacae	1 (1.9%)	1 (33.3%)	-	1 (1.4%)	-
E. coli	24 (44.4%)	-	-	7 (10.0%)	-
K. oxytoca	2 (3.7%)	-	-	-	-
K. pneumoniae	4 (7.4%)	-	2 (100%)	4 (5.7%)	-
P. aeruginosa	6 (11.1%)	1 (33.3%)	-	9 (12.9%)	-

P. fluorescens	1 (1.9%)	-	-	3 (4.3%)	-
P. mirabilis	-	-	-	5 (7.1%)	-
P. vulgaris	-	-	-	2 (2.9%)	-
S. aureus	14 (25.9%)	1 (33.3%)	-	38 (54.3%)	-
S. marcescens	1 (1.9%)	-	-	-	-

3.3. Resistance profile of *S. aureus* isolates

For *S. aureus* strains, the highest rates of resistance were recorded against benzylpenicllline with 92.3% (48/52). The proportion of methicillin-resistant *S. aureus* (MRSA) was 26.4% (14/53) and all the strains isolated were sensitive to vancomycin (Table 3).

Table 3: Resistance profile of *S. aureus* isolates

Antibiotics	***S. aureus* (T=53)**	
	n(N)	**R (%)**
BPEN	48(52)	92.3
OXA	14(53)	26.4
AMX	48(52)	92.3
TIC	48(52)	92.3
AMC	5(24)	20.8
CF	14(32)	43.7
FOX	14(53)	26.4
IPM	14(29)	48.2
GM	10(53)	18.8
KAN	21(53)	39.6
AMK	21(53)	39.6
TOB	13(53)	24.5
CIP	12(44)	27.2
OFX	8(39)	20.5
FEP	6(33)	18.1
NOR	12(38)	31.5
LEV	5(34)	14.7
ERY	13(33)	39.3
CM	5(40)	12.5
L	5(38)	13.1
PR	4(30)	13.3
DOX	12 (30)	40
RIF	1(16)	6.2
SXT	15(32)	46.8
CHL	2(11)	18.1

FA	1(7)	14.2
VA	0(34)	0
FOS	3(38)	7.9

T=total number of isolates, n=number of resistant isolates, N=number of isolates tested, R (%) = resistance rate, BPEN = Benzylpenicillin, OXA = Oxacillin, AMX = Amoxicillin, TIC = Ticarcillin, AMC = Amoxicillin/Clavulanic Acid, CF = Cefazolin, FOX = Cefoxitin, IPM = Imipenem, GM = Gentamicin, KAN = Kanamycin, AMK = Amikacin, TOB = Tobramycin, CIP = Ciprofloxacin, OFX = Ofloxacin, FEP = Pefloxacin, NOR = Norfloxacin, LEV = Levofloxacin, ERY = Erythromycin, CM = Clindamycin, L = Lincomycin, PR = Pristinamycin, DOX = Doxycycline, RIF = Rifampicin, SXT = Cotrimoxazole, CHL = Chloramphenicol, FA = Fusidic acid, VA = Vancomycin, FOS = Fosfomycin.

3.4. Resistance profile of enterobacterial isolates

The Enterobacteriaceae isolated showed significant resistance to amoxicillin and ticarcillin, with rates of at least 60%. Overall high levels of resistance were observed against all antibiotic families with the exception of carbapenems. Gentamycin was the least effective aminoglycoside on these strains and ciprofloxacin was the most effective fluoroquinolone (Table 4).

Table 4: Resistance profile of Enterobacteriaceae isolates

Antibiotics	*E. cloacae* (T=3)		*E. coli*(T=31)		*K. oxytoca* (T=2)		*K. pneumoniae* (T=10)		*P. mirabilis* (T=5)		*P. vulgaris* (T=2)		*S. marcescens* (T=1)	
	n(N)	R(%)	n(N)	R(%)	n(N)	R(%)	n(N)	R(%)	n(N)	R(%)	n(N)	R(%)	n(N)	R(%)
AMX	NR	NR	27(31)	87.1	NR	NR	NR	NR	3(5)	60	NR	NR	NR	NR
TIC	3(3)	100	21(31)	67.7	NR	NR	NR	NR	3(5)	60	0(2)	0	1(1)	100
PIP/TAZ	2(3)	66.7	3(6)	50.0	-	-	3(4)	75	0(3)	0	-	-	0(1)	0
AMC	NR	NR	22(31)	71.0	0(2)	0	9(10)	90	3(5)	60	2(100)	100	NR	NR
CF	NR	NR	22(31)	71.0	0(2)	0	10(10)	100	3(5)	60	NR	NR	NR	NR
FOX	NR	NR	7(31)	22.6	0(2)	0	5(10)	50	1(5)	20	0(2)	0	NR	NR
CTX	3(3)	100	13(31)	41.9	0(2)	0	5(10)	50	2(5)	40	0(2)	0	1(1)	100
CRO	3(3)	100	13(31)	41.9	0(2)	0	5(10)	50	2(5)	40	0(2)	0	1(1)	100
CAZ	3(3)	100	13(31)	41.9	0(2)	0	5(10)	50	2(5)	40	0(2)	0	1(1)	100
CFM	3(3)	100	13(31)	41.9	0(2)	0	5(10)	50	2(5)	40	0(2)	0	1(1)	100
IPM	2(3)	66.7	2(31)	6.5	0(2)	0	2(10)	20	0(5)	0	0(2)	0	0(1)	0
ERT	1(3)	33.3	1(31)	3.2	0(2)	0	1(10)	10	0(5)	0	0(2)	0	0(1)	0
ATM	1(3)	33.3	8(21)	38.1	0(2)	0	3(6)	50	1(4)	25	0(2)	0	-	-
GM	2(3)	66.7	13(26)	50.0	0(2)	0	5(10)	50	3(5)	60	1(2)	50	0(1)	0
TOB	2(3)	66.7	10(26)	38.5	0(2)	0	4(9)	44.4	2(5)	40	0(0)	0	NR	NR
AMK	1(3)	33.3	7(30)	23.3	0(2)	0	1(10)	10	1(5)	20	0(2)	0	NR	NR
KAN	2(3)	66.7	2(13)	15.4	0(2)	0	0(3)	0	0(3)	0	0(2)	0	-	-
CIP	2(3)	66.7	17(31)	54.8	-	-	5(10)	50	1(5)	20	1(2)	50	1(1)	100
OFX	3(3)	100	21(24)	87.5	-	-	5(10)	50	1(3)	33.3	1(1)	100	1(1)	100
PEF	3(3)	100	22(31)	71.0	-	-	6(10)	60	2(3)	66.7	1(1)	100	1(1)	100
NAL	3(3)	100	22(24)	91.7	2(2)	100	8(9)	88.9	4(5)	80	2(2)	100	1(1)	100
NOR	3(3)	100	18(26)	69.2	0(2)	0	6(10)	60	2(5)	40	1(2)	50	1(1)	100

LEV	3(3)	100	18(22)	81.8		-	5(6)	83.3	1(1)	100	1(1)	100	1(1)	100
DOX	1(3)	33.3	15(19)	78.9	2(2)	100	6(10)	60	3(3)	100	2(2)	100	-	-
SXT	2(3)	66.7	24(31)	77.4	2(2)	100	7(10)	70	3(5)	60	1(2)	50	0(1)	0
CHL	-	-	2(5)	40.0	-	-	0(3)	0	-	-	-	-	-	-
FOS	1(3)	33.3	5(31)	16.1	0(2)	0	1(10)	10	0(5)	0	0(1)	0	0(1)	0

T=total number of isolates, n=number of resistant isolates, N=number of isolates tested, R(%) = resistance rate, NR=natural resistance,-=not tested, AMX = Amoxicillin, TIC = Ticarcillin, PIP/TAZ = Piperacillin/Tazobactam, AMC = Amoxicillin/Clavulanic Acid, CF = Cefazolin, FOX = Cefoxitin, CTX = Cefotaxime, CRO = Ceftriaxone, CAZ = Ceftazidime, CFM = Cefixime, IPM = Imipenem, ERT = Ertapenem, ATM = Aztreonam, GM = Gentamicin, KAN = Kanamycin, AMK = Amikacin, TOB = Tobramycin, CIP = Ciprofloxacin, OFX = Ofloxacin, PEF = Pefloxacin, NAL = Nalidixic acid, NOR = Norfloxacin, LEV = Levofloxacin, DOX = Doxycycline, SXT = Cotrimoxazole, CHL = Chloramphenicol, FOS = Fosfomycin.

Extended-spectrum beta-lactamase (ESBL) production was noted in 41.9% of *E. coli* strains, 50% of *K. pneumoniae* strains and 40% of *P. mirabilis* strains. All *E. cloacae* strains were ESBL producers. With regard to resistance to carbapenems, only *E. cloacae, K. pneumoniae* and *E. coli* developed carbapénèmases at rates of 66.7%, 10.0% and 3.2% respectively (Table 5).

Table 5: Distribution of ESBL and carbapénèmase strains

	BLSE		Carbapénèmase	
Bacterial species	**n(N)**	**%**	**n(N)**	**%**
E. cloacae	3(3)	100	2(3)	66.7
E. coli	13(31)	41.9	1(31)	3.2
K. oxytoca	0(2)	0	0(2)	0
K. pneumoniae	5(10)	50	1(10)	10
P. mirabilis	2(5)	40	0(5)	0
P. vulgaris	0(2)	0	0(2)	0
S. marcescens	0(1)	0	0(1)	0

3.5. Resistance profile of no-fermenting Gram-negative Bacillus isolates

The no-fermenting gram-negative bacilli isolated during our study showed varying levels of resistance to the different families of antibiotics tested, ranging from 0% to 100% (Table 6). The percentage of *P. aeruginosa* strains resistant to ceftazidime was 37.5% (6/16).

Table 6: Resistance profile of no-fermentative Gram-negative Bacillus isolates

Antibiotics	***A. baumanii* (T=1)**		***B. cepacia* (T=1)**		***P. fluorescens* (T=4)**		***P. aeruginosa* (T=16)**	
	n(N)	**R(%)**	**n(N)**	**R(%)**	**n(N)**	**R(%)**	**n(N)**	**R(%)**
TIC	0(1)	0	NR	NR	1(4)	25.0	6(16)	37.5
PIP/TAZ	-	-	NR	NR	-	-	0(4)	0
CAZ	0(1)	0	0(1)	0	1(4)	25.0	6(16)	37.5

CFM	0(1)	0	0(1)	0	2(3)	66.7	4(6)	66.7
ATM	NR	NR	NR	NR	0(4)	0	7(16)	43.8
IPM	0(1)	0	0(1)	0	1(4)	25.0	2(16)	12.5
GM	0(1)	0	1(1)	100	1(3)	33.3	4(13)	30.8
KAN	0(1)	0	1(1)	100	2(3)	66.7	NR	NR
AMK	0(1)	0	1(1)	100	1(4)	25.0	3(16)	18.8
TOB	0(1)	0	1(1)	100	0(1)	0	0(8)	0
CIP	0(1)	0	NR	NR	0(2)	0	2(7)	28.6
AN	1(1)	100	-	-	-	-	10(16)	62.5
NOR	0(1)	0	0(1)	0	1(2)	50	6(16)	37.5
SXT	1(1)	100	0(1)	0	1(1)	100	NR	NR
CHL	1(1)	100	NR	NR	2(2)	100	NR	NR
CL	0(1)	0	NR	NR	0(2)	0	0(9)	0
FOS	NR	NR	NR	NR	1(2)	50	2(16)	12.5

T=total number of isolates, n=number of resistant isolates, N=number of isolates tested, R(%) = resistance rate, NR=natural resistance, -=nottested, TIC = Ticarcillin, PIP/TAZ = Piperacillin/Tazobactam, CAZ = Ceftazidime, CFM = Cefixime, IPM = Imipenem, ATM = Aztreonam, GM = Gentamicin, KAN = Kanamycin, AMK = Amikacin, TOB = Tobramycin, CIP = Ciprofloxacin, AN = Nalidixic acid, NOR = Norfloxacin, SXT = Cotrimoxazole, CHL = Chloramphenicol, CL = Colistin, FOS = Fosfomycin.

4. Discussion

Surgical site infection is the 3rd most frequent cause of healthcare-associated infections. The main risk factors involved are the pre-, per- and post-operative environment of the patient and the healthcare team, the host's immune defences and, above all, the level of cleanliness of the surgical procedure (Fournel, 2017). This study was carried out jointly by the medical biology laboratory and the various surgical specialities operating in the central operating theatre of the Ouakam Military Hospital. We recorded 157 cases of SSI in 3413 patients operated on over 2 years, corresponding to an incidence rate of 4.6%. The incidence of SSI found in our study is lower than most of the results reported in the African literature. This is illustrated by the meta-analysis published in 2016(Ngaroua et al., 2016), which showed an incidence of between 6.8% and 26% in sub-Saharan Africa. However, a study carried out in Burkina Faso (Abdoulaye et al., 2018) showed a much lower prevalence of 2.4%. This wide variability in SSI incidence rates between regions could be explained by the fact that this type of infection is highly dependent on the protocols and practices implemented,which are specific to each healthcare establishment. As found by other authors (Toure et al., 2020;Mukagendaneza et al., 2019), most (40.8%) of the patients with SSI in our series were adults aged between 20 and 40 years, with an average age of 39.9 years. Our study population was predominantly male, with a sex ratio (M/F) of 1.57. Although some studies(Abdurrahman et al., 2023; Bang et al., 2022) have shown a predominance of females in SSI, most authors, particularly Africans (Abdoulaye et al., 2018; Lakoh et al., 2022), have reported that males predominate in this type of infection. Some authors hypothesise that certain risk factors for these infections are more common in men (accidents on public roads due to speeding, knife fights, accidents on road or construction sites) than in women (Babokh et al., 2022). The majority of SSIs recorded during our study occurred after orthopaedic surgery (51.6%) or general and visceral surgery (40.8%). These two surgicalspecialities were also the most common SSIs in the 2016 meta-analysis (Ngaroua et

al., 2016), with a different order of frequency (19.1% in general and visceral surgery and 14.8% in orthopaedic surgery). On the other hand, (Abdurrahman et al., 2023) reported in their study that SSI after obstetric and gynaecological surgery came 2nd after general and visceral surgery. This atypical result could be explained by the fact that more than half (61.2%) of the surgical procedures recorded in this study were performed in the gynaecology and obstetrics department. During our study, only one case of SSI was noted after an operation in neurosurgery, in contrast to aanother study (El-Kholy et al., 2018)where this speciality recorded 18.2% of SSIs. These observations confirm the significant heterogeneity in the incidence of SSI according to surgical speciality and region noted in the meta-analysis (Ngaroua et al., 2016).

In our study, the bacterial culture positivity rate was 76.4%. They were monomicrobial in 92.5% (111/120) and bimicrobial in 7.5% (9/120), equivalent to a total of 129 bacterial strains isolated. This high rate of positive pus cultures has also been reported by many other authors (Ouédraogo et al., 2011; Abdoulaye et al., 2018; Abdurrahman et al., 2023; Lakoh et al., 2022; Babokh et al., 2022), confirming the bacterial aetiology of SSI. In our series, *S. aureus* was the main germ involved, accounting for 41.1% of all isolates. This finding has been noted in most studies (Sievert et al., 2013; Koutsoumbelis et al., 2011). This germ is characterised by a cell wall that is very rich in murein, a substance that plays the most active role in attracting phagocytic cells, and by the presence of teichoic acids, which contribute to pus formation by recruiting neutrophils via chemokines (Fournier & Philpott, 2005).

S. aureus was followed by *E. coli*(24.0%), *P. aeruginosa*(12.4%) and *K. pneumoniae*(7.8%). Our results corroborate those in France (Daniau, 2020) with rates of 23.3% and 13.4% for *S. aureus* and *E. coli* respectively. The same trends were noted in the series in Ethiopia (Abdurrahman et al., 2023). Overall, these 4 germs are the most frequently incriminated in SSI found in the literature, with the order of frequency varying from one study to another. In Cotonou(Toure et al., 2020), *S. aureus* was the leading cause of SSI, followed by *P. aeruginosa.* In Marrakech(Babokh et al., 2022), *E. coli*(15.9%) was the leading cause, followed by *K.pneumonia*(12.3%) and *P. aeruginosa*(10.8%). On the other hand, different profiles were recorded in the study by Lubega *et al.*where *K. pneumoniae*(50%) and *S. aureus*(27.8%) dominated (Lubega et al., 2017) and that by El-Kholy *et al.*with *P. aeruginosa* as the leading germ (El-Kholy et al., 2018).

In general, and visceral surgery, *E. coli* with 24 isolates (44.4%) was the most isolated germ, followed by *S. aureus* with 14 isolates (25.9%. This result is in perfect agreement with most of the studies reported and confirms the predominance of enterobacteriaceae in infectionsfollowing abdominal surgery(Idrissi et al., 2020;Diarra et al., 2020), although Carvalho *et al.* reported more *S. aureus* than *E. coli* strains in their study(Carvalho et al., 2017).

In orthopaedic surgery, *S. aureus* dominated the epidemiological profile, accounting for more than half of bacterial isolates (54.3%). This is consistent with the results in Niamey(Abdoulaye et al., 2018) and in Cotonou (*Toure et al., 2020)*. However, it differs from another study carried out in Senegal in 2012 (Alioune Badara et al., 2017), which reported a predominance of enterobacteriaceae (*K. pneumoniae* and *E. coli*) in SSIs in this surgical specialty.

Antimicrobial resistance (AMR) is a major public health problem and remains a real challenge throughout the world. In our context, the emergence and spread of multi-resistant bacterial strains is thought to be linked to a number of factors: unfavourable socio-economic conditions, inadequate staffing levels,lack of infrastructure for aetiological diagnosis and

antibiotic resistance assessment, inadequate national and regional resistance surveillance networks, and inadequate regulation of antibiotic procurement and antibiotic quality (Da et al., 2023).

A high rate of resistance (92.3%) of *S. aureus* strains to penicillin G was noted during our study. Other authors have also reported similar results. For example, in Northeast Ethiopia and in Northeast India (Abdurrahman et al., 2023; Deka et al., 2020),authors reported *S. aureus*resistance to penicillin G of 100% and 85-96% respectively. The rate of methicillin-resistant *S. aureus*(MRSA) isolated in our study was 26.4%. According to the review on the state of antibiotic resistance in sub-Saharan Africapublished in 2023(Da et al., 2023), the prevalence of MRSA is increasing markedly in this region and varies between 11% and 35.7% depending on the type and study population. For MRSA strains isolated from SSIs, a prevalence of 14.8% was found in Morocco between 2018 and 2020 (Babokh et al., 2022). It was 15% in Egypt (El-Kholy et al., 2018) and Ghana(Bediako-Bowan et al., 2020) respectively in 2015 and between 2017 and 2019. However, in Ethiopia (Tadesse et al., 2018),authors found in 2014 a higher MRSA prevalence of 68.4%. This prevalence of MRSA is much lower in developed countries. In Europe, a retrospective cohort of surgical patients from 14 centres in 2016 showed an MRSA prevalence of 14% (Mellinghoff et al., 2023). These wide variations in the prevalence of MRSA are linked in particular to the great variability in the spread of community MRSA clones between countries and over time (Da et al., 2023). This resistance of *S. aureus* to methicillin is due to a gene called *mecA,* which codes for a protein called PLP2a, causing cross-resistance between Mpenicillins (methicillin, oxacillin) and other beta-lactamins. This *mecA* gene is carried by a chromosomal element that also contains other genes for resistance to heavy metals and other antibiotics, which explains the multi-resistance profile of MRSA (Dumitrescu et al., 2010), thus limiting therapeutic options. Glycopeptides, in particular vancomycin, are therefore an alternative of last resort in the treatment of MRSA infections. In this study, no strain of *S. aureus* showed resistance to vancomycin. Other authors (Doutchi et al., 2020; Marwam M. Badawi, 2017; Biradar et al., 2016)have found results identical to ours. However, the emergence of vancomycin-resistant strains of *S. aureus* has been reported by some African authors. In Niger (Abdoulaye et al., 2018)found a vancomycin resistance rate of 37.5% in *S. aureus* strains. In 2023, a systematic review and meta-analysis carried out in Ethiopia and including 31 studies (Belete et al., 2023)showed an overall prevalence of vancomycin-resistant *S. aureus* strains of 14.5%. Resistance of *S. aureus* to vancomycin is a major public health problem because it compromises the efficacy of treatment for MRSA infections. Compared with other families of antibiotics, the *S. aureus* strains in our series showed moderate levels of resistance overall, not exceeding 50%, except for tetracycline (53.8%). Similar results have been reported in others studies(Bediako-Bowan et al., 2020; Doutchi et al., 2020).

The strains of enterobacteria in our study showed overall high rates of resistance to penicillins (amoxicillin and ticarcillin), reaching a minimum of 60%. Our study therefore confirms the worrying level of resistance to penicillins in enterobacteria, as described by several authors (Ouédraogo et al., 2020; Abdurrahman et al., 2023; Seyoum Asres et al., 2017). ESBL production was observed in 41.9% of *E. coli* strains, 50% of *K. pneumoniae* strains and 40% of *P. mirabilis* strains. All 3 *E. cloacae*strain isolated were ESBL producers. Similar results were also documented in Niger in 2022 in a meta-analysis (Abdoulaye et al., 2022). This meta-analysis showed a prevalence of E-BLSE of 42%. Our results are also similar to those found in Ethiopia by (Abdurrahman et al., 2023) with 66.6% of *E. coli* and 28.5% of *K. pneumoniae* respectively producing ESBL. These results show that the prevalence of EBLSE

is high overall in the West African region, although the absence of routine surveillance is an obstacle to the accurate estimation of the proportions of E-BLSE. In this region, the emergence and spread of these strains remains a real public health problem. As in the rest of the world, CTX-M-15 is the enzyme most commonly found in circulating strains in this region, although other enzymes have been described (Ouedraogo et al., 2017). The secretion of ESBLs by enterobacteria limits therapeutic choices because of the multi-drug resistance they induce (resistance in particular to cotrimoxazole, fluoroquinolones and aminoglycosides). This is because plasmids carrying the ESBL gene also carry other resistance genes (Cantón & Coque, 2006). This multi-resistance of EBLSE means that treatment choices should be directed towards carbapenems, which are antibiotics of last resort, used exclusively in hospitals and with a very broad spectrum of activity, particularly against enterobacteria. However, the massive and uncontrolled use of this class of antibiotics will result in the emergence of resistant bacterial strains. One of the mechanisms of bacterial resistance to carbapenems is linked to the expression of a beta-lactamase enzyme with high hydrolytic activity towards carbapenems: carbapénèmase(HCSP, 2013). During our study, this production of carbapénèmase, resulting in resistance to ertapenem, was noted in *E. cloacae, K. pneumoniae* and *E. coli* at rates of 33.3%, 10.0% and 3.2% respectively. In sub-Saharan Africa, the emergence of these enzymes, as described by certain authors(Leski et al., 2013; Motayo et al., 2013), isincreasing sharply. The emergence of carbapénèmases is of major clinical and therapeutic interest, as in the vast majority of cases they confer resistance to all beta-lactam antibiotics. What's more, it is stable and often associated with other mechanisms of resistance to other families of antibiotics (aminoglycosides, quinolones, etc). This is due to the plasmid localisation of the resistance genes (HCSP, 2013), which considerably limits the effectiveness of antibiotic therapy.

Of the other families of antibiotics tested, Enterobacteriaceae showed high overall resistance rates. In terms of aminoglycosides, amikacin was the most effective on these strains, with resistance rates of no more than 33.3%. Ciprofloxacin was the most effective fluoroquinolone, with a maximum resistance rate of 66.7% recorded for *E. cloacae.* This relatively high rate could be explained by co-resistance due to the high production of ESBLs by this germ. Furthermore, according to some authors(Hailaji et al., 2016), the emergence of resistance in enterobacteria to quinolones and fluoroquinolones is the main problem associated with their use. This resistance involves various mechanisms, the most common of which is modification of the targets, DNA gyrase and/or topoisomerase IV by point mutation of an amino acid. Our study revealed a high level of resistance in Enterobacteriaceae to the majority of antibiotics used in our context. This result is the consequence of selection pressure due to the massive prescription and often abusive use of broad-spectrum antibiotics in both hospital and community settings, as well as cross-transmission of acquired plasmid resistance (Fabre et al., 2010).

In the case of non-fermentative Gram-negative bacilli, we have observed resistance rates ranging from 0% to 100%. This group of opportunistic bacteria is characterised by natural resistance to several antibiotics, in particular beta-lactam antibiotics (aminopenicillins, 1st and 2nd generation cephalosporins, cefotaxime, ceftriaxone and ertapenem)(CASFM, 2023). In our study, the most isolated bacterium belonging to this group was *P. aeruginosa.*

P. aeruginosa naturally expresses an inducible cephalosporinase encoded by the *ampC* chromosomal gene. In wild strains, *ampC* is only weakly expressed due to repression by the products of its associated genes, *ampR* and *ampD*(Lister et al., 2009). However, induced and reversible hyper-expression in the form of resistance to ceftazidime confers resistance to all

penicillins, aztreonam and other cephalosporins active against *P. aeruginosa*(Barbier & Wolff, 2010). In our study, the number of *P. aeruginosa* strains resistant to ceftazidime was 37.5%. This result is intermediate to those in Ethiopia and Niger (Seyoum Asres et al., 2017; Abdoulaye et al., 2018)who reported rates of 12.5% and 90% respectively. *P. aeruginosa* is also naturally or acquired resistant to carbapenems. The main mechanism of resistance is impermeability through inactivating mutation of *oprD*, the gene encoding the D2 protein (Lister et al., 2009). Loss of this outer membrane porin confers a variable decrease in sensitivity to meropenem and doripenem, but also and above all a high level of resistance to imipenem (Barbier & Wolff, 2010). In our study, the rate of *P. aeruginosa* resistance to imipenem was 12.5%. These multi-resistant strains can represent a major problem for treatment, as they can lead to therapeutic impasse. In this case, the main treatment option is colistin, but its use is limited by its high nephrotoxicity (Barbier & Wolff, 2010).

5. Conclusion

This study shows a relatively low incidence rate of surgical site infections compared with most incidence rates reported in African countries. However, the alarmingly high rates of resistance among the various bacteria isolated during our work merit attention, with better surveillance and prevention of antimicrobial resistance.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

I declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

CONSENT AND ETHICAL APPROVAL

This study was hospital-based research conducted in normal conditions under the Declaration of Helsinki. Ethical permission was obtained from the hospital authorities. Information collected during the study was analysed using the participant's identification code to ensure confidentiality. Patient consent was also obtained prior to sample collection.

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