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Antibiotics resistance patterns of Panton-Valentine leukocidin-positive methicillin-resistant staphylococci isolated from clinical samples in Abidjan, Côte d'Ivoire

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Methicillin-resistant staphylococci have emerged as significant pathogens which cause various infections and its multidrug resistance is a major concern. This study aimed to determine the prevalence of Panton-Valentine leukocidin (PVL) gene and antibiotic resistance patterns of staphylococci isolated from clinical infections in Abidjan. A total of 35 staphylococci strains was obtained from 35 clinical samples (pus, blood, pleural fluid, sputum, wound, and urine), then, characterized by polymerase chain reaction (PCR) to differentiate *S. aureus* from coagulase-negative staphylococci (CNS) and to detect the presence of PVL genes (*LukS*). The antimicrobial susceptibility was performed using disk diffusion method and the phenotype of resistance to macrolides-lincosamides-streptogramin B (MLSB) was detected. Out of 35 strains, 80% (28/35) were methicillin-resistant *Staphylococcus aureus* (MRSA) and 20% (7/35) were methicillin-resistant CNS (MR-CNS). *S. aureus* were isolated from 75% of outpatient samples and 84.2% of inpatient samples. However, CNS were isolated from 25% of outpatient samples and 15.8% of inpatient samples. *LukS* were detected in 68.6% of strains (20 MRSA and 4 MR-CNS) and both inpatients and outpatients. The highest resistance rates were observed for penicillin (100%), cefoxitin (100%), ciprofloxacin (66%), tobramycin (66%), tetracyclin (66%), sulphamethoxazole-trimethoprim (63%), erythromycin (60%), kanamycin (57%) and gentamicin (54%). In addition, *S. aureus* strains were subdivided into five antibiotics resistance phenotypes: 57.1% belonged to phenotype 1 (Methicillin-resistant and susceptible to Kanamycin-Tobramycin-Gentamicin) followed by 25% of phenotype 4 (Resistant to Methicillin-Kanamycin-Tobramycin-Gentamicin), 7.1% of phenotype 2 (MR with constitutive MLS_B), 7.1% of phenotype 5 (MR and resistant to Kanamycin-Tobramycin-Gentamicin with inducible MLSB) and 3.6% of phenotype 3 (MR with inducible MLS_B). CNS strains were grouped in three phenotypes (1, 4 and 5). 100% of *LukS* positive MRSA were multi-drug resistant, with 45% of strains resistant to 6 or more antibiotics. The high level of multi-drug resistance of clinical PVL positive staphylococci with inducible MLS_B, suggest increasing the monitoring of these pathogens in Côte d'Ivoire.

Key words: Methicillin-resistant *Staphylococcus aureus* (MRSA), Panton-Valentine Leukocidin, inducible MLS_B, multi-drug resistance.

INTRODUCTION

Staphylococcus aureus and coagulase-negative staphylococci (CNS) are Gram-positive opportunistic pathogens that cause various diseases, ranging from localized mild infections to invasive life-threatening diseases (Pedroso et al., 2018; Tong et al., 2015). However, CNS have emerged as significant pathogens causing nosocomial infections (Lenart-Boron et al., 2016; Nanoukon et al., 2017). *S. aureus*, especially methicillin-resistant *S. aureus* (MRSA) strains increase the occurrence of serious infections (Skov et al., 2012) which are among the most frequent bacteria in healthcare-associated infections. Skin and soft tissue infections due to *S. aureus* are most common, whereas pneumonia, osteomyelitis, endocarditis, and sepsis, although less usual, account for greater morbidity and mortality (Tong et al., 2015; Dong et al., 2013). *S. aureus* possesses an arsenal of virulence factors that contribute to evasion of host defenses. These virulence factors, including toxins, exoenzymes, and adhesins, which are secreted or linked to cell membrane and fight against the action of antibiotics. Antibiotic resistance in both hospital-acquired methicillin resistant *S. aureus* and community-acquired MRSA strains has increased the difficulty to treat these infections (Messina et al., 2016; Shopsin et al., 2016). Most MRSA strains can also produce a leukotoxin as Panton-Valentine leukocidin (PVL), a bicomponent cytotoxin encoded by prophage that increases their virulence and can cause skin and soft tissue infection and necrotizing pneumonia (Shallcross et al., 2013; van der Meeren et al., 2014; Yanagihara et al., 2009). PVL is a member of pore forming toxins that targets host leukocytes. Two open reading frames are responsible for coding PVL, that is, LukS-PV and lukF-PV (Abdulgader et al., 2015). The MRSA strains are widely distributed around the world with quick evolution of antimicrobial resistance and it is a high priority according to WHO to found new antibiotics (Willyard, 2017). WHO global report on surveillance of antimicrobial resistance lacked information from the majority of the countries in sub-Saharan African countries or lacked data on priority pathogens such as MRSA (WHO, 2014). However, a recent retrospective review performed on wound infection between 2004 and 2016, had shown the prevalence of MRSA in Benin (34.6%), Congo (31.9%), Togo (14.3%) and Madagascar (14.5%) (Lai et al., 2018). *S. aureus* colonizes about one third of healthy humans and is most often found in the nose (Kaspar et al., 2016). A study in Burkina Faso, showed that the rate of *S.aureus* nasal carriage was 32.9% with 29% in healthy volunteers and 37% in hospital patients in Bobo Dioulasso. In addition, the percentage of MRSA strains isolated from hospital patients was very low (2.3%) with high prevalence of strains harboring PVL-encoding genes (45%) (Ouedraogo et al., 2016). Nosocomial infections are a major threat in most of the hospitals and as high as 19% in the developing countries, where number of direct contacts between the hands of Health Care Workers and the patient occurs, which mandates the strict adherence to infection control practices and standards (Maheshwari et al., 2014). In Ghana, Saba et al. (2017) isolated MRSA (17%) from handles and other points of contact in a public hospital environment. In the Burn Center of Korle Bu Teaching Hospital in Ghana, 50% of patients were infected with *S. aureus* including MRSA (Amissah et al., 2017). In Côte d'Ivoire, previous studies have reported the occurrence of *S. aureus* strains harboring PVL gene. During 2004 and 2005, two outbreaks caused by the same clone of doxycycline resistant, PVL-positive methicillin-susceptible *S. aureus* (MSSA) were characterized in two French military companies (Lesens et al., 2007). In the Cocody University Teaching Hospital, Kacou et al. (2011) have reported high rate of PVL positive *S. aureus* strains (67.7%) from clinical samples in hospitalized patients. However, Zinzendorf et al. (2012) showed a high rate (77.4%) of clinical *S. aureus* strains from patients expressed PVL gene in Abidjan Military Hospital. The increasing prevalence of staphylococcal virulence factor, PVL, and MRSA strains isolated from patients is a growing problem. Constant surveillance and adequate infection control measures for *S. aureus* may reduce their roles in the incidence of nosocomial diseases and other infections. Update data on *S. aureus* resistances are particularly important to know the type of antibiotic resistance for establishing adequate therapeutic approaches. The objective of this study was to deternine the prevalence of PVL gene and antibiotic resistance patterns of *Staphylococcus* species isolated from patients in Abidjan, Côte d'Ivoire.

MATERIALS AND METHODS

Sample collection

Pasteur Institute of Côte d'Ivoire is a laboratory where patients from different hospitals in Côte d'Ivoire are referred for medical tests. The clinical samples (n=35) were collected from 16 outpatients referred to Pasteur Institute and 19 inpatients of Cocody University Teaching Hospital., Samples of inpatients came from surgery (n=5), maternity/neonatal (n=2), neurology (n=1), obstetrics/gynecology (n= 2), pediatrics (n=3), pulmonology (n=2), emergency (n=3) and urology (n =1) services of Cocody University Teaching Hospital.

All samples were collected from Pasteur Institute between February and September, 2017 (Table 1).

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Table 1. The source of clinical samples.

Type of clinical samples	Outpatients clinical samples	Inpatients clinical samples
Pus (n=19)	10	9
Blood (n=11)	4	7
Pleural fluid (n=1)	0	1
Sputum (n=2),	0	2
Wound (n=1)	1	0
Urine (n=1)	1	0
Total (n=1)	16	19

Table 2. List of primers used in this study.

Gene	Primers	Sequence of primers (5'-3')	Size of amplified product (bp)	Reference
16S rRNA	16S rRNA-F 16S rRNA-R	GCAAGCGTTATCCGGATTT CTTAATGATGGCAACTAAGC	597	
FemA	FemA-F FemA-R	CGATCCATATTTACCATATCA ATCACGCTCTTCGTTTAGTT	450	Al-Talib et al. (2009)
LukS	LukS-F LukS-R	CAGGAGGTAATGGTTCATTT ATGTCCAGACATTTTACCTAA	151	

Staphylococci isolation

Bacteria were isolated and identified in the Department of Bacteriology at Pasteur Institute of Côte d'Ivoire. The phenotypic identification of staphylococci species was carried out by standard microbiology methods including Gram staining, catalase activity, mannitol fermentation and the ability to coagulate rabbit plasma (Kateete et al., 2010; Amini et al., 2012). Molecular characterisation of strains was carried out in the Molecular Biology Laboratory at Pasteur Institute of Côte d'Ivoire.

Molecular characterization of strains

DNA extraction

Bacterial DNA was extracted by boiling method (Kacou et al., 2011; Oliveira et al., 2014). An overnight culture of staphylococci strains in Brain-Heart Infusion (1.5 mL) was centrifuged (12000 rpm, 5 min) and the supernatant was discarded. The pellet was dissolved in 400 µL deionized water and the suspension was heated at 100°C for 10 min and then immediatly frozen at -20°C for 10 min. Finally, after centrifugation for 10 min at 12000 rpm, the supernatant containing bacterial DNA was stored at -20°C for further analysis.

Detection of staphylococcal genes

All strains were screened for the presence of three *Staphylococcus* genes by modified method of PCR amplification previously described by Kacou et al. (2011). DNA extracts were used as template in the PCR. The multiplex PCR was performed to identify the *Staphylococcus* genus (*16S rRNA* gene), to differentiate *S. aureus* from CNS (*FemA* gene), and to detect PVL toxin (*LukS*) genes simultaneously. The PCR was performed in a final volume reaction of 25 µL containing 9.75 µL nuclease-free water (Ambion), 5 µL PCR buffer (5X), 1.5 µL magnesium chloride ($MgCl_2$, 25 mM) (Promega Corporation, Madison, USA), 0.5 µL Deoxynucleotide Triphosphates (dNTPs; 10 mM), 0.5 µL of each primer (20 mM) (Table 2), 0.25 µL Go Tag®G2 Flexi DNA polymerase 5 U/µL (Promega Corporation, Madison, USA) and 5 µL of template DNA. The PCR method was performed according to the following program: initial denaturation (94°C, 5 min), 35 cycles each composed of initial denaturation (94°C, 30 s), primer annealing (60°C, 1 min) and extension (72°C, 1 min) and a final extension (72°C, 5 min). Primers used in this PCR were previously reported by Al-Talib et al. (2009) (Table 2). A previously known (Kacou et al., 2011) *LukS* gene positive *S. aureus* strain was used as a control strain. PCR amplification products were revealed on a gel Doc EZ® imager (Bio-Rad) after electrophoresis in 2% agarose gel containing Syber safe (Invitrogen).

Antimicrobial susceptibility

Susceptibilities were determined using the disk diffusion method in accordance with the performance standards for antimicrobial susceptibility testing, recommended by the Committee of Antibiogram of French Society of Microbiology (CA-SFM/EUCAST, 2016). The susceptibility testing was carried out by culturing strains on Mueller-Hinton agar (Bio-rad, Marne-la- coquette, France). Antibiotics used for susceptibility testing included penicillin 6 µg, cefoxitin 30 µg, ciprofloxacin 5 µg, norfloxacin 5 µg, gentamicin 10 µg, kanamycin 30 µg, tobramycin 10 µg, netilmicin 10 µg,

Table 3. *Staphylococci* strains isolated in clinical samples.

Type of clinical samples	Number of strains from outpatients		Number of strains from inpatients	
	S. aureus	**CNS**	***S. aureus***	**CNS**
Pus (n=19)	9	1	9	0
Blood (n=11)	1	3	4	3
Pleural fluid (n=1)	0	0	1	0
Sputum (n=2)	0	0	2	0
Wound (n=1)	1	0	0	0
Urine (n=1)	1	0	0	0
Total (n=35)	12	4	16	3

CNS: Coagulase-negative staphylococci.

erythromycin 15 µg, clindamycin 2 µg, tetracyclin 30 µg, minocyclin 30 µg, tigecyclin 15 µg, chloramphenicol 30 µg, fusidic acid 10 µg, sulphamethoxazole-trimethoprim 25 µg, rifampicin 30 µg, vancomycin 30 µg, and teicoplanin 30 µg. Susceptibility to methicillin was screened with the cefoxitin disk diffusion result. All antibiotics were obtained from Bio-rad. It should be indicated that the reference strain *S. aureus* ATCC 29213 were used as positive-control and provided by the National Reference Center for Antibiotics, Pasteur Institute of Côte d'Ivoire. The macrolide-lincosamide-streptogramin B (MLS_B) group of antibiotics can be used to treat less severe skin and soft tissue infections (Liu et al., 2011). Strains resistant to both erythromycin and clindamycin in routine antibiotic susceptibility testing were considered constitutive MLS_B phenotypes. Inducible MLS_B phenotypes were identified using a double-disk diffusion test (D-test). Erythromycin 15 µg and clindamycin 2 µg disks were placed on a Mueller-Hinton agar plate containing a lawn culture of the test isolate at a distance of 15 mm edge to edge. After incubation at 35°C for 16 to 18 h, strains that showed no flattening of the inhibition zone around the clindamycin disk were reported as susceptible to clindamycin (negative D test); strains that showed flattening of the inhibition zone around the clindamycin disk adjacent to erythromycin disk (D zone) indicated inducible clindamycin resistance (positive D test). Strains with a D-shaped zone of inhibition were considered $iMLS_B$ Phenotype (resistant to erythromycin and susceptible to clindamycin) (Kumari et al., 2016; Pereira et al., 2016). Multidrug resistance (MDR) was defined as resistance to at least three distinct antimicrobial classes or being MRSA (Magiorakos et al., 2011).

RESULTS

Clinical specimens and staphylococci strains

In this study, a total of 35 staphylococci were isolated from 35 patient samples. Patients were 7 days to 62 years old and 17 patients were female and 18 were male. *S. aureus* strains isolated from patients samples were identified by Gram-positive cocci, catalase positivity, mannitol fermentation, and coagulase production. However, strains that were Gram-positive cocci, catalase positive, and coagulase negative were considered as CNS. This phenotypic identification was confirmed by PCR results. Among 35 bacteria tested, 28 (80%) were *S. aureus* (*16S rRNA* positive and *femA* positive) and 7 (20%) were CNS (*16S rRNA* positive and *femA* negative).

S. aureus strains were recovered from 75% of outpatients samples (12/16) and 84.2% of inpatients samples (16/19). However, CNS were isolated from 25% of outpatients samples (4/16) and 15.8% of inpatients samples (3/19). *S. aureus* was reported in all type of clinical specimens but CNS were isolated only in blood (54.5%; 6/11) and pus (5.3%; 1/19) (Table 3). CNS strains were isolated from hospitalized patients provided from maternity/neonatal and pediatrics.

Detection of PVL gene

PVL-encoding gene (*LukS*) was detected in 24 (68.6%) of the 35 strains. The PVL gene was present in all type of clinical samples (blood, pus, pleural fluid, sputum, wound, and urine). Among all *S. aureus* strains (28), 71.4% carried the *LukS* gene (20/28) (Figure 1). In addition, the *LukS* gene was present in 57.1% (4/7) of CNS. *LukS* positive CNS (*LukS*+CNS) strains were only detected from blood samples of inpatients and outpatients. In contrast, *LukS* positive *S. aureus* strains were detected from blood (4/11), pus (12/19), pleural fluid (1/1), sputum (1/2), wound (1/1) and urine (1/1) samples.

Antibiotic susceptibility of bacteria isolated

Antibiotic susceptibility tests were performed on the 35 *Staphylococcus* spp. isolated from clinical samples. The highest resistance rates were observed for penicillin (100%) andcefoxitin (100%). Resistance rates of 50 70% were recorded for the antibiotics ciprofloxacin (66%), tobramycin (66%), tetracyclin (66%), sulphamethoxazole-trimethoprim (63%), erythromycin (60%), kanamycin (57%) and gentamicin (54%). The lower resistance rate <50% were observed for rifampicin (26%), netilmicin (26%), fusidic acid (23%), norfloxacin (14%), minocyclin (11%), clindamycin (11%) and chloramphenicol (11%). All the strains were susceptible to tigecyclin tgc (100%), vancomycin (100%) and teicoplanin (100%) (Table 4). The strains resistant to cefoxitin were classified as those

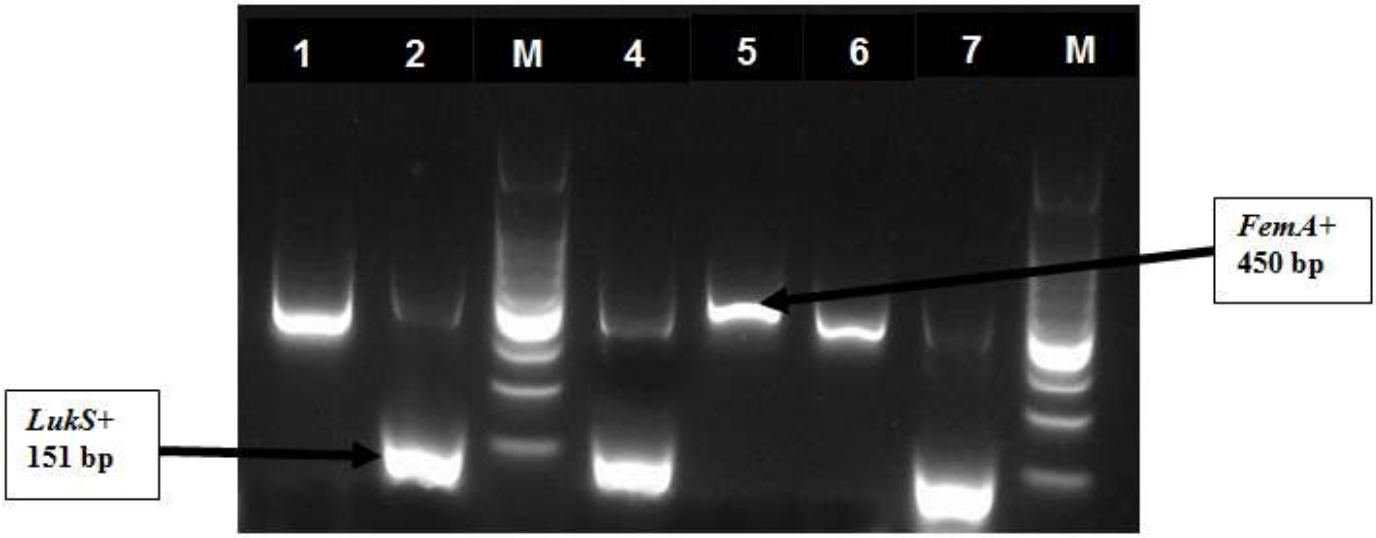

Figure 1. Electrophoresis result of *FemA* and *LukS* genes. Lane M: 100 bp DNA marker ; lane 2: Positive control (*LukS*+), lanes 1, 4, 5, 6, 7: clinical strains: *S. aureus FemA*+, lanes 4,7: clinical strains: *S. aureus LukS*+

Table 4. Percentage of antibiotics resistance in clinical *Staphylococci* strains

Antibiotics	Number (%) of resistant strains		
	Total clinical strains (n=35; %)	MRSA (n=28; %)	CNS (n=7; %)
Penicillin	35 (100)	28 (100)	7 (100)
Cefoxitin	35 (100)	28 (100)	7 (100)
Ciprofloxacin	23 (66)	17(61)	6 (88)
Norfloxacin	5 (14)	3 (11)	2 (28)
Gentamicin	19 (54)	14 (50)	5 (71)
Kanamycin	20 (57)	14 (50)	6 (88)
Netilmicin	9 (26)	5 (18)	4 (57)
Tobramycin	23 (66)	21 (75)	2 (28)
Erythromycin	21 (60)	15 (54)	6 (88)
Clindamycin	4 (11)	3 (11)	1 (14)
Tetracyclin	23 (66)	18 (64)	5 (71)
Minocyclin	4 (11)	3 (11)	1 (14)
Tigecyclin	0 (0)	0 (0)	0 (0)
Chloramphenicol	4 (11)	3 (11)	1 (14)
Fosfomycin	0 (0)	0 (0)	0 (0)
Fusidic acid	8 (23)	5 (18)	3 (43)
Sulphamethoxazole-trimethoprim	22 (63)	17 (60)	5 (72)
Trimethoprim	29 (83)	25 (89)	4 (57)
Rifampicin	9 (26)	7 (25)	2 (28)
Vancomycin	0 (0)	0 (0)	0 (0)
Teicoplanin	0 (0%)	0 (0%)	0 (0%)

strains methicillin-resistant staphylococci. In this study, 100% (35/35) of staphyloccocci strains were methicillin-resitant of which 80% were MRSA and 20% were methicillin-resistant CNS (Table 4).

Antibiotic phenotypes of methicillin-resistant strains

In this study, staphylococci strains were subdivided into five phenotypes according to the antibiotics resistance

Table 5. Antibiotic profiles of Methicillin-resistant strains.

Antibiotic profiles	Number (%) of staphylococci strains	
	***S. aureus* (n=28; %)**	**CNS (n=7; %)**
MR + KTG S	16 (57.1)	3 (42.8)
MR + $cMLS_B$	2 (7.1)	0 (0)
MR + $iMLS_B$	1 (3.6)	0 (0)
MR + KTG R	7 (25)	2 (28.6)
MR + KTG R+ $iMLS_B$	2 (7.1)	2 (28.6)

MR: Methicillin-resistant; KTG S: Kanamycin-Tobramycin-Gentamicin Susceptible; KTG-R: Kanamycin-Tobramycin-Gentamicin Resistant; $cMLS_B$: Constitutive MLSB; $iMLS_B$: inducible MLSB.

pattern (Table 5): Phenotype 1 includes strains resistant to methicillin and susceptible to kanamycin, tobramycin, and gentamicin; Phenotype 2 includes strains resistant to methicillin with constitutive MLS_B ($cMLS_B$); Phenotype 3 includes strains resistant to methicillin with inducible MLS_B (iMLSB); Phenotype 4 includes strains resistant to methicillin, kanamycin, tobramycin, gentamicin; Phenotype 5 includes strains resistant to methicillin, kanamycin, tobramycin, gentamicin with inducible MLS_B ($iMLS_B$).

The *S. aureus* strains present five antibiotics phenotypes: 57.1% of *S. aureus* belonged to phenotype 1 followed by phenotype 4 (25%), phenotype 2 (7.1%), phenotype 5 (7.1%) and phenotype 3 (3.6%). However, CNS strains were characterised by three phenotypes (1, 4 and 5).

Antibiotics resistance pattern of positive PVL strains

Among the 24 *LukS* positive strains, 20 were MRSA with four different phenotypes of antibiotic resistance. The majority of *LukS* positive strains (70%) were phenotype 1. Two (2/20) of *LukS*+*S. aureus* strains were phenotype 2, also two strains (2/20) were phenotype 4 and two (2/20) other were phenotype 5 (Table 6). Of the four *LukS* positive CNS (LukS+CNS), phenotype 4 was observed in two (50%) strains and phenotype 5 in one (25%) strain and also one other (25%) isolate was phenotype 1. The highest prevalence of resistance of *LukS*+MRSA strains was for penicillin (100%), cefoxitin (100%) followed by tobramycin (60%), ciprofloxacin (57%), erythromycin (47%), tetracyclin (43%), sulphamethoxazole-trimethoprim (40%), gentamicin (36%) and kanamycin (37%). Lower percentage of resistance was observed for rifampicin (21%), norfloxacin (15%), chloramphénicol (10%), fusidic acid (11%), minocyclin (7%) and netilmicin (6%). All the *LukS*+MRSA strains were susceptible to tigecyclin (100%), fosfomycin (100%), vancomycin (100%) and teicoplanin (100%).

In addition, multi-drug resistant strains were classified as those resistant to three or more antibiotics classes. All *LukS*+MRSA were multi-drug resistant (100%; 20/20), of which 9 (45%) strains were resistant to 6 or more antibiotics, 2 (10%) strains were resistant to 5 antibiotics, 7 (35%) were resistant to 4 antibiotics and 2 (10%) were resistant to 3 antibiotics.

DISCUSSION

The present study reports the molecular characteristics and antibiotics resistance of staphycococci isolated from patients specimens in Abidjan, Côte d'Ivoire. A high prevalence of *S. aureus* was found in clinical samples (pus, blood, pleural fluid, sputum, wound, and urine) compared to the prevalence of CNS was lower. The strains of CNS was isolated in only 7 (20%) clinical samples. These prevalences were different than those reported in Nigeria where *S. aureus* and CNS were isolated at 56 and 43.9%, respectively in clinical infections (wounds, skin and soft tissue infections, osteomyelitis, burns, genitourinary tract infection, septicaemia, urinary tract infection, otitis media, and bronchitis) (Shittu et al., 2012). With regard to the virulence factors of these strains, PVL (a leukotoxin associated with human clinical diseases) encoding gene (*LukS*) was sought. This research showed that, the high rate of *LukS* gene prevalence in 68.6% of staphylococci strains was obtained from clinical infections of inpatients and outpatients. The *LukS* gene was detected at a high rate in *S. aureus* strains (71.4%) than in CNS strains (57%). The *LukS* positive CNS strains were detected only from blood. In the hospitalised patients, *LukS*+CNS strains were found in patients of neonatale and peditrics unit and maybe due to nosocomial infections. Indeed, CNS have emerged as one of the main microorganisms causing nosocomial infections and clinically (Nanoukon et al., 2017). The prevalence of PVL gene in *S. aureus* (71.4%) in the present study was high compared with the rate (67.8%) reported in a previous study conducted in Côte d'Ivoire in 2009 in clinical infections (Kacou et al., 2011). The prevalence of *LukS* carriage in *S. aureus* in clinical sample in Abidjan inceased from 67.8 to 71.4% between 2009 and 2017. The high frequency of PVL-positive *S. aureus* in patients provide important insights

Table 6. Antibiotic resistance phenotype of PVL gene positive strains.

Antibiotic profiles	Number (%) of *LukS* positive strains	
	LukS+ S. aureus (n=20; %)	*LukS*+CNS (n=4; %)
MR + KTG S	14 (70)	1 (25)
MR + $cMLS_B$	2 (10)	0 (0)
MR + $iMLS_B$	0 (0)	0 (0)
MR + KTG R	0 (10)	0 (50)
MR + KTG R + $iMLS_B$	2 (10)	1 (25)

MR: Methicillin-resistant; KTG S: Kanamycin-Tobramycin-Gentamicin Susceptible; KTG-R: Kanamycin-Tobramycin-Gentamicin Resistant; $cMLS_B$: Constitutive MLS_B; $iMLS_B$: inducible MLS_B; *LukS*+CNS*: LukS* Positive CNS; *LukS*+*S. aureus*: *LukS* Positive *S. aureus.*

to evaluate the risk of infection and dissemination of this bacteria in Abidjan, Côte d'Ivoire and in West Africa. In other sub-Saharan Africa countries, the frequency of PVL-positive *S. aureus* in clinical samples is high. In Ghana, PVL-encoding genes were detected in 75% (42/56) of *S. aureus* blood culture (Dekker et al., 2016) and in 27% (17/62) of carriage of PVL-positive *S. aureus* in burn patients (Amissah et al., 2017). This gene carriage rate was higher (90.7%; 68/75) in community-acquired-*S. aureus* isolated in Mozambique (van der Meeren et al., 2014), in the Democratic Republic of the Congo (49.1%) (Vandendriessche et al., 2017) and in Nigeria (33.3%; 17/51) in clinical infections (Shittu et al., 2012). The main findings of this study are a high prevalence of MRSA and PVL-positive gene strains. PVL is mostly associated with community-associated methicillin resistance in *S. aureus* infections. According the antibiotics resistance profile, 100% of staphylococci strains were methicillin-resistant, of which 80% were methicillin-resistant *S. aureus* (MRSA) and 20% were methicillin-resistant CNS. MRSA prevalence rate in the present study is very higher than MRSA prevalence rate (11.8%) obtained by Kacou et al. (2011) in 2009 in Abidjan. In addition, PVL gene (*LukS*) was detected only among methicillin-sensitive *S. aureus* (MSSA) strains. In contrast, in this present study, the PVL gene was commonly detected among MRSA as well as in methicillin-resistant CNS. The increase of prevalence of PVL-positive MRSA in Abidjan could present a significant challenge in disease management and infection control. The rate of PVL positive MRSA strains in Abidjan is higher than those reported from Ghana (63.8%) (Kpeli et al., 2016), Ouganda in pastoral communities (69.4%) (Asiimwe et al., 2017), Zambie (9.4%) (Samutela et al., 2017) and Nigeria (6.6%) (Shittu et al., 2012). However, the rate of PVL+MRSA was high than the rate (56.8%) reported by Bhatta et al. (2016) in MRSA isolated from clinical specimens in Nepal. The staphylococci isolated from patients in this study exhibit resistance to many antibiotics (Table 4). These results are in agreements with those reported by Chen et al. (2017) in China which the resistance rates of *S. aureus* to penicillin and cefoxitin were all 100%. However, all strains were susceptible (100%) to tigecyclin, vancomycin and teicoplanin. The MRSA strains collected from 13 different hospitals in Kuwait, were susceptible to vancomycin (100%), teicoplanin (100%) and linezolid (100%). Tigecyclin was not tested by the authors (Boswihi et al., 2018). The occurrence of MRSA is on the rise since the previous study (Kacou et al., 2011) in Abidjan. The threat posed by MRSA was vividly demonstrated in this study, as 100% of *LukS*+MRSA were multi-drug resistant and 45% of strains were resistant to 6 or more antibiotics tested. This might reflect the frequent and repeated administration of antibiotics, thus selecting for resistance and resulting in high frequencies of MDR. The MDR in staphylococci strains could lead to failure in treatment therapy, prolonged illnesses, increased expenses for health care, and in serious cases, risk of death (Tanwar et al., 2014). The prevalence of antimicrobial resistance in Abidjan clinical staphylococci strains was higher than those observed in other African countries. Indeed, the prevalence of antimicrobial resistance was below 5% for all antibiotics agents tested except for penicillin (97%), tetracycline (42%) and erythromycin (6%) in MRSA strains in Ghana (Egyir et al., 2014). Comparatively, the prevalence of MDR (9%) was lower than those reported in the present study. Bhatta et al. (2016) have reported overall 73% of MRSA from clinical specimens were multidrug reistant with 50% were PVL positive which indicates a lower prevalence than the present findings.

The high antimicrobial resistance in Abidjan is due to the overconsumption of antibiotics in the populations. Indeed, there is a huge prescription of antibiotics and because of poverty people turn to self-medication by sourcing from street drug sellers. It is important to note that there is a large informal market in Abidjan for medicines and antibiotics that are visible to everyone.

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have reported that overall 73% of MRSA from clinical specimens were multidrug reistant with 50% which were PVL positive indicating a lower prevalence than the present findings. Otherwise, according to resitance of antibiotics, clinical strains were grouped into 5 antibiotic phenotypes (Table 5). The frequency of $cMLS_B$ and $iMLS_B$ of the present study was lower than those found in previous studies. Two other previous Brazil studies (Bottega et al., 2014; Pereira et al., 2016) have documented the rate of $cMLS_B$ and $iMLS_B$ in clinical MRSA strains ranging from 14.3 to 37.9% and 2.1 to 4.9%, respectively; while the KTG-R phenotype was not detected. In India, the MLS_B phenotypes of MRSA in clinical samples were higher than those reported in this study. The $iMLS_B$ phenotype rate ranged from 19.1 to 35.2% and the $cMLS_B$ phenotype rate ranged from 11.4 to 31.9% in MRSA strains (Bhattacharya et al., 2015; Kumari et al., 2016). The antibiotic profile of CNS was not consitent with the results of Abdollahi et al. (2016) where 58.2% of 110 strains were methicillin resistant CNS to which 54.6% were $cMLS_B$ and 6.25% were $iMLS_B$ phenotype. It was important to know the type of MLS_B resistance for establishing adequate therapy. The vancomycin is used for the treatment of serious infections and MLS_B group are usually used to treat less severe skin and soft tissue infections (Liu et al., 2011). Reporting the susceptibility to clindamycin without verifying the presence of inducible resistance, may lead to inadequate therapy with this drug. In contrast, a negative result for inducible resistance to clindamycin, confirms the susceptibility of this antimicrobial, providing a very good therapeutic option (Pereira et al., 2016). Clindamycin is the preferred agent for the treatment of MRSA due to its excellent pharmacokinetic properties, such as optimal tissue penetration and accumulation in abscesses. However, the indiscriminate use of MLS_B antibiotics has led to an increase in the number of *Staphylococcus* spp. strains that are resistant to these drugs (Bottega et al., 2014).

Conclusion

The present analysis of *S. aureus* strains isolated from clinical specimens in Abidjan, showed a high level of multidrug resistance staphylococci strains both among inpatients than outpatients. These strains harboring a high rate of PVL gene with inducible resistance to MLS_B antibiotics. Therefore, frequent monitoring of this pathogen, its antibiotic susceptibility and determining their virulence factors is of great importance in control and treatment of infections. This study provides an important data to increase the country-wide monitoring of methicillin resistant staphylococci.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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