

Original Research Article

Clindamycin Resistance among *Staphylococcus aureus* Clinical Isolates in Alexandria

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ABSTRACT

Background: Macrolides, lincosamides, streptogramins-B (MLS_B) resistance can be constitutive or inducible. Staphylococcal strains with constitutive MLS_B (cMLS_B) phenotype are easily detected using routine disk diffusion technique. Contrarily, inducible MLS_B (iMLS_B) phenotype needs a special double disk diffusion test, D-test to be detected. Misdiagnosis of iMLS_B can lead to therapy failure with clindamycin. The aim of this study was to detect the prevalence of erythromycin and clindamycin resistance among *Staphylococcus aureus* clinical isolates and to detect the resistance encoding genes *ermA* and *ermC*. **Materials and Methods:** One hundred non-repetitive *S. aureus* isolates were included in this study. Antimicrobial susceptibility was detected to all isolates. The molecular identification of *S. aureus* and methicillin resistance was performed by detecting *femA* and *mecA* genes respectively. iMLS_B was detected by D-test assay. The presence of *ermA* and *ermC* genes was detected by PCR. **Results:** Methicillin resistance was detected in 54% of isolates. Most of isolates (73%) were susceptible to erythromycin and clindamycin. Out of the 27 isolates resistant to erythromycin, 10(37%) showed cMLS_B phenotype. The remaining 17 (63%) isolates resistant to erythromycin but susceptible to clindamycin were classified into 14 (82%) iMLS_B resistance phenotype that showed positive D-test and 3 (18%) macrolide-streptogramin (MS_B) resistance phenotype that showed negative D-test. *ermA* and *ermC* were detected among the 27 *S. aureus* isolates resistant to clindamycin and/or erythromycin. Both genes were detected together in 2 isolates (7.5%), *ermA* was detected alone in 5 isolates (18.5%) and *ermC* was detected alone in 20 isolates (74%). **Conclusion:** From the previous results, we can conclude that D test is a simple, reliable method to detect clindamycin resistance in erythromycin resistant isolates. Nevertheless, the incidence of true susceptibility to clindamycin among erythromycin resistant *S. aureus* isolates is low.

INTRODUCTION

Staphylococcus aureus (*S. aureus*) is a common human pathogen. It is responsible for a wide range of community and hospital acquired infections including skin and soft tissue infections, respiratory tract infections, bacteremia and infective endocarditis [1]. Antibiotics of the classes Macrolides-Lincosamides-Streptogramin B (MLS_B) are interesting for treating such infections particularly with the increasing prevalence of methicillin resistance in staphylococci that renders the organism resistant to all cell wall inhibitors of the family β -lactams [2,3]. Macrolides like erythromycin, Lincosamides like clindamycin and

Streptogramin B like quipristin/daflopristin belongs to different chemical classes of antibiotics that inhibit protein synthesis via binding to 50S ribosomal subunit, thus hindering ribosomal translocation [4]. Because of its perfect pharmacokinetic properties, clindamycin has been frequently used to treat *S. aureus* particularly methicillin resistant *S. aureus* (MRSA). However, the persistent use of clindamycin increases the selection of MLS_B resistant staphylococcal strains [2,5-8].

Staphylococcal resistance to MLS_B can be induced via three molecular mechanisms: target site modification, efflux of the antibiotic and/or drug

modification [9]. In target site modification, methylation of the A2058 residue of the 23S rRNA occurs, which hinders the binding of the MLS_B antibiotics to their target. This resistance mechanism is encoded by erythromycin ribosome methylase (erm) genes and induces cross-resistance to these antibiotics. Among the 4 main types of erm genes (ermA, ermB, ermC and ermF) in different bacteria; ermA and ermC are the accused MLS_B resistance phenotype in *S. aureus* [9-11].

MLS_B resistance phenotype can be constitutive or inducible. Staphylococcal strains with constitutive MLS_B resistance (cMLS_B) phenotypes are easily detected using routine disk diffusion susceptibility testing [11,12]. On the other hand, strains are showing inducible MLS_B resistance (iMLS_B) phenotypes needs the presence of inducing agent for the production of the methylase and exhibit resistance to erythromycin and susceptibility to clindamycin [13]. This makes the detection of iMLS_B not a straight forward task. Nevertheless, a special double-disk diffusion protocol, the D-test, was established for the diagnosis of iMLS_B [14].

Misdiagnosis of iMLS_B may result in therapy failure with clindamycin. However, considering all erythromycin resistant isolates as clindamycin resistant neglects the use of clindamycin to treat infections with truly clindamycin-susceptible staphylococcal isolates [15,16].

In this study we detected the prevalence of erythromycin and clindamycin resistance among *S. aureus* clinical isolates using disk diffusion technique according to the guidelines of the CLSI [17]. Additionally, the presence of resistance encoding genes ermA and ermC was detected using polymerase chain reaction (PCR).

MATERIALS AND METHODS

Bacterial isolates

A total of one hundred non-repetitive *S. aureus* isolates were included in this study. The isolates were obtained from different clinical specimens submitted to the Microbiology laboratory of the Medical Research Institute, Alexandria University. All isolates were identified as Gram positive cocci, catalase and coagulase positive and fermented mannitol in mannitol salt agar.

Antimicrobial susceptibility testing

According to clinical and laboratory standards institute (CLSI) guidelines [17], disk diffusion method was used for detection of antimicrobial susceptibility to 11 antimicrobial agents, namely penicillin (P), amoxicillin/clavulanate (AMC), cefoxitin (FOX), ciprofloxacin (CIP), fusidic acid (FD), co-trimoxazole (SXT), doxycycline (DO), gentamicin (CN), linzolid (LZD) clindamycin (DA) and erythromycin (E) with the exception of vancomycin which was detected by minimum inhibitory concentration (MIC) method. All culture media and antimicrobial disks were purchased from Oxoid[®].

D-test was performed according to the CLSI guidelines [17]. Briefly, erythromycin disk (E) was placed 15 mm (edge to edge) from clindamycin disk (DA) on a Müller Hinton agar plate inoculated with a cotton swab immersed in 0.5 McFarland standard staphylococcal suspension. After overnight incubation at 35°C, the formation of D-inhibition zone around clindamycin disk with flattening in the area between the two discs indicates iMLS_B phenotype (Figure 1).

Polymerase Chain Reactions (PCR)

DNA extraction was performed by boiling method. Briefly, 2 to 3 colonies from overnight cultured were suspended in TE buffer containing 0.1% triton X100. Bacterial suspensions were incubated in a boiling water bath for 15 minutes followed by rapid cooling on ice. After centrifugation for 15 minutes at 14,000 rpm in a microfuge, the supernatant was used as a source for bacterial DNA.

Molecular Identification of MRSA

Multiplex PCR for the detection of the presence of femA gene and mecA was used to confirm the identity of the isolates as *S. aureus* and its resistance to methicillin respectively.

Molecular detection of erythromycin ribosomal methylation (erm) genes

ermA and ermC genes that encode erythromycin ribosomal methylase enzyme were amplified using specific pair of primers (Table 1). All primers were purchased from Biosearch Technologies (Biosearch Technologies, California, USA).

PCR was performed in 25 µl final volume containing 12.5 µl MyTaq HS Red MixBioLine

(BioLine, London, UK), 10 pmole of each primer and 0.5 µl DNA extract. Amplifications were performed using Veriti Thermal Cycler (Applied Biosystems, California, USA) according to the following protocol, initial denaturation 95°C for 5 minutes followed by 35 cycles of 95°C for 15 seconds, annealing for 15 second and extension at 72°C for 40 seconds followed by final extension at 72°C for 5 minutes.

RESULTS

This study included 100 *S. aureus* isolates obtained from different clinical specimens (Figure 2). Most isolates were obtained from wound swabs (40%) followed by nasal swabs (24%).

Antimicrobial susceptibility testing

All isolates were resistant to penicillin but sensitive to linzeolide and vancomycin. According to susceptibility to cefoxitin, 54% of isolates were diagnosed as MRSA (Figure 3).

Molecular diagnosis of MRSA

Using multiplex PCR (Figure 4), all isolates included in the current study were diagnosed molecular as *S. aureus* via detection of femA gene. mecA was amplified in only 54% of isolates which was previously diagnosed as MRSA using cefoxitin disk diffusion (100% sensitivity and specificity). The remaining 46 isolates were methicillin susceptible *Staphylococcus aureus* (MSSA).

MLS_B Resistance profile

Most of isolates (73%) were susceptible to erythromycin and clindamycin. Out of the 27 isolates resistant to erythromycin, 10 (37%) were resistant to clindamycin, which was considered as cMLS_B phenotype. The remaining 17 (63%) isolates resistant to erythromycin but susceptible to clindamycin were classified into 14 (82%) iMLS_B resistance phenotype that showed positive D-test and 3 (18%) macrolide-streptogramin (MS^B) resistance phenotype that showed negative D-test (Table 2).

Molecular detection of ermA and ermC genes

ermA (Figure 5) and ermC (Figure 6) were detected among the 27 *S. aureus* isolates resistant to clindamycin and/or erythromycin. Both genes were detected together in 2 isolates (7.5%), ermA was

detected alone in 5 isolates (18.5 %) and ermC was detected alone in 20 isolates (74%) (Table 3).

DISCUSSION

Although about 30% of the populations are asymptomatic carriers of *S. aureus*, it is capable of generate a wide range of diseases varying from toxin-mediated illness to pyogenic community and hospital acquired infections [21].

S. aureus is known to acquire resistance to many classes of antimicrobials including penicillinase stable penicillins like methicillin. Isolates included in this study showed low level of resistance to many classes of antimicrobials including fluoroquinolones (21%), fusidic acid (55%), sulfonamides (12%) aminoglycosides (20%) and tetracyclines (30%). This low resistance levels may be associated with community acquired nature of infection in outpatients presented to the Microbiology department of the Medical Research Institute.

MRSA develops from MSSA upon the acquisition of staphylococcal chromosomal cassette mec (SCCmec) which is known as de novo MRSA [22]. Community acquired MRSA can develop de novo or via person-to-person carriage of hospital strains into the community [23,24]. However, de novo MRSA have generally been characterized as being susceptible to most non-β-lactam agents (other than erythromycin) while those that have spread from the hospital environment into the community often display the multi-drug resistant phenotype dominating among most of hospital-acquired strains [25,26].

Detection of MRSA is achieved via phenotypic and genotypic examination of bacterial isolates. In most cases, phenotypic methods are more feasible than genotypic methods, while genotypic methods usually provide better precision and accuracy [27].

Cefoxitin disk diffusion method was recommended by CLSI for the detection of methicillin resistance [28]. Being a potent inducer of the mecA regulatory system, cefoxitin was shown to be superior to oxacillin in detecting low levels of Methicillin resistance [29]. It shows high degree of sensitivity and specificity in foreseeing the presence of mecA in *S. aureus* [29,30]. In the current study, 54% of isolates were diagnosed as MRSA using both

phenotypic susceptibility testing to ceftazidime and genotypic detection of *mecA* gene.

Similar results were reported by Kumar et al., who found that the prevalence of MRSA was 53.74%. The majority of their Indian MRSA were isolated from pus (37.70%) followed by wound swabs (30.40%) and surgical wound swabs (7.60%). [31] Mansour et al., reported MRSA prevalence of 44.71%. The majority of their Pakistani MRSA isolates were from pus (36.8%) followed by wound Swabs (10.6%) [32]. Dilnessa et al., reported the major source of their Ethiopian MRSA was also pus (20.3%) [33].

femA is a chromosomally encoded factor, occurring naturally in *S. aureus* [34], that is indispensable for the development of high-level methicillin resistance. However, *femA* does not influence the synthesis of PBP2a [35]. It was shown that *S. aureus* strain with inactivated *femA* lost the methicillin-resistance trait, and the transduction of *femA* gene restored the resistance [36,37]. In the current study, *femA* was detected in all our isolates confirming its identity as *S. aureus*.

Drug selection is important in the treatment of *S. aureus* infections particularly MRSA. Clindamycin is a good choice recommended for treatment of community acquired MRSA. It is a semi-synthetic derivative of Lincosamine, with superb tissue penetration in lung, pleural fluid and bile. It distributes well into bones and considered an effective antibiotic in treatment of Osteomyelitis [38].

Although some *S. aureus* isolates are susceptible to clindamycin in vitro, they may not be effective in vivo particularly when the strain is resistant to erythromycin. This may be attributed to the presence of *iMLS_B* phenotype. Strains with *iMLS_B* resistance demonstrate resistance in vitro to 14- and 15-member macrolides, while showing susceptibility to lincosamides, and streptogramins. On the other hand, strains with *cMLS_B* resistance phenotype exhibit in vitro resistance to all of these agents [39].

Failure of therapy with clindamycin in *iMLS_B* phenotype may be due to selection of constitutive resistant bacteria under antibiotic pressure or due to conversion of inducible isolate to a constitutive one. Therefore accurate, susceptibility results are

essential for convenient therapy decisions. The presence of *iMLS_B* can be detected in erythromycin resistant strains by D-test that is simple and reliable [14,40,41]. D-test can distinguish strains that have the genetic potential to develop resistance during therapy from surely susceptible strains to clindamycin. Treating clindamycin susceptible strain without checking their D-test results may result in therapy failure. Contrarily, considering all erythromycin resistant strains as clindamycin resistant would reject a possibly safe and effective treatment [42].

From the results of antimicrobial susceptibility testing to erythromycin and clindamycin as well as the results of the D-test, *cMLS_B* phenotype was detected in 37% of erythromycin-resistant isolates. *iMLS_B* resistance phenotype were detected in 82% of erythromycin-resistant clindamycin-susceptible isolates. The remaining 18% were considered *MS_B* resistance phenotypes that were resistant to erythromycin but truly sensitive to clindamycin with a negative D-test.

Previous studies reported the pattern of the *MLS_B* resistance among staphylococci; some reports indicated a high frequency of the *iMLS_B* phenotype, while the others showed increasing prevalence of the *cMLS_B* phenotype. The true incidence relies on the studied patient population, the geographical region, the hospital characteristics and methicillin susceptibility [43,44].

In this study, it was found that *cMLS_B* was seen in significantly greater proportion among MRSA as compared to MSSA isolates ($p < 0.001$). Studies in India have reported 30% to 64% of the MRSA isolates to be of the *iMLS_B* phenotype (45). In the present study, 8 (15%) and 6 (11%) out of the 54 MRSA isolates were of *cMLS_B* and *iMLS_B* phenotypes respectively. Previous studies showed discrepancies in the incidence of *iMLS_B* among staphylococci. While some studies showed low incidences ranging from 5.4-19.2% [2,46], others showed higher ratios ranging from 27-74% [11,47].

The occurrence rate of *iMLS_B* shown by D-test results was 11% in MRSA and 13% in MSSA. In concordance with our results, an earlier study during 2004 reported 19% *iMLS_B* in MRSA and 19.2% in MSSA [46].

erm genes encode ribosome methylases that confer inducible or constitutive resistance to MLS_B, drugs by reducing binding by MLS_B agents to the ribosome [39]. Previous study proved the sensitivity of D-test performed at 15-20mm disk spacing was 100% when correlated with detection of erm and msr genes by PCR [48]. Additionally, it was found that ermC and ermA genes predominated within MLS_B phenotypes [49]. However, some of previous reports demonstrated prevalence of ermA genes [50], other, similar to our study, showed that the ermC gene was more common among *S. aureus* strains [51]. In the present study, most of erythromycin resistant isolates 74% harbored ermC gene, 18.5% harbored ermA gene and 7.5% harbored both genes. Most (60%) of ermC harboring isolates exhibited iMLS_B phenotype.

CONCLUSION

From the previous results, we can conclude that D-test is a straightforward, decisive method to detect clindamycin resistance in erythromycin resistant isolates which can enable us guiding the use of clindamycin in treating skin and soft tissue infections. Nevertheless, the incidence of true susceptibility to clindamycin among erythromycin resistant *S. aureus* isolates is low.

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Table 1: Sequence and characteristics of PCR primers included in this study

Gene	Primer	Sequence 5'-3'	Ta °C*	Amplicon size(BP)	reference
<i>femA</i>	Fem A F	CTTACTTACTGCTGTACCTG	52	686	[18]
	Fem A R	ATCTCGCTTGTTATGTGC			
<i>mecA</i>	mecA F	TGGCTATCGTGCACAATCG	52	304	[18]
	mecA R	CTGGAACCTTGTTGAGCAGAG			
<i>ermA</i>	<i>ermA</i> F	5'ACGATATTCACGGTTTACCCACTTA3'	51	610	[19]
	<i>ermA</i> R	5'AACCAGAAAAACCCTAAAGACACG3'			
<i>ermC</i>	<i>ermC</i> F	5'AGTACAGAGGTGTAATTTTCG3'	54	520	[20]
	<i>ermC</i> R	5'AATTCCTGCATGTTTAAAGG3'			

*Ta → annealing temperature

Table 2:MLS_B resistance profile using antimicrobial susceptibility with D-test results.

Resistance Phenotype	Erythromycin susceptibility	Clindamycin susceptibility	D-test result	No of isolates
Susceptible	S	S	Not applicable	73
cMLS _B	R	R	Not applicable	10
iMLS _B	R	S	Positive	14
MS _B	R	S	Negative	3

Table 3: Association between methicillin resistance and MLS_B resistance phenotype among *S. aureus* isolates.

MLS _B resistance phenotype	MRSA	MSSA	Total
Susceptible	38	35	73
cMLS _B	8	2	10
iMLS _B	6	8	14
MS _B	2	1	3
Total	54	46	100

Table 4: Association between MLS_B resistance phenotypic and genotypic patterns.

Phenotypic resistance patterns	Molecular resistance patterns			Total
	ermA (%)	ermC(%)	ermA/ermC (%)	
cMLS _B	2 (7.5)	6 (22)	2 (7.5)	10 (37)
iMLS _B	2 (7.5)	12 (44.5)	0 (0)	14 (52)
MS _B	1 (3.5%)	2 (7.5)	0 (0)	3 (11)
Total	5 (18.5)	20 (74)	2 (7.5)	27 (100%)

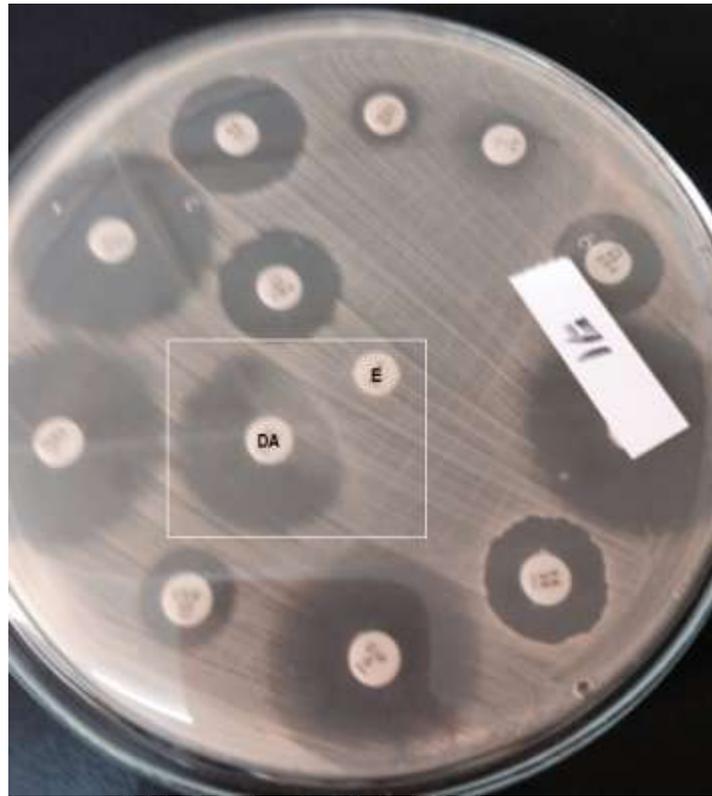


Figure 1: Antimicrobial susceptibility testing by disk diffusion method showing D-zone of inhibition around clindamycin (DA) with flattening side between DA and erythromycin (E) disk.

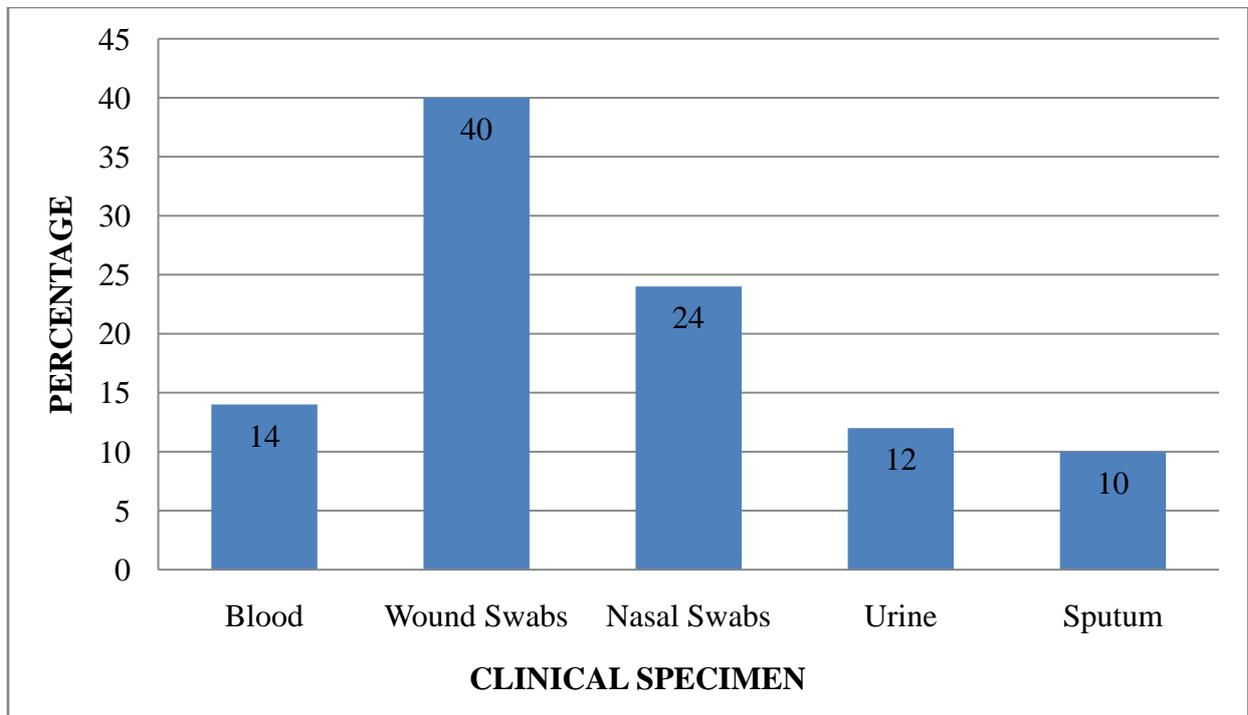


Figure 2: Distribution of *S. aureus* isolates among clinical specimen

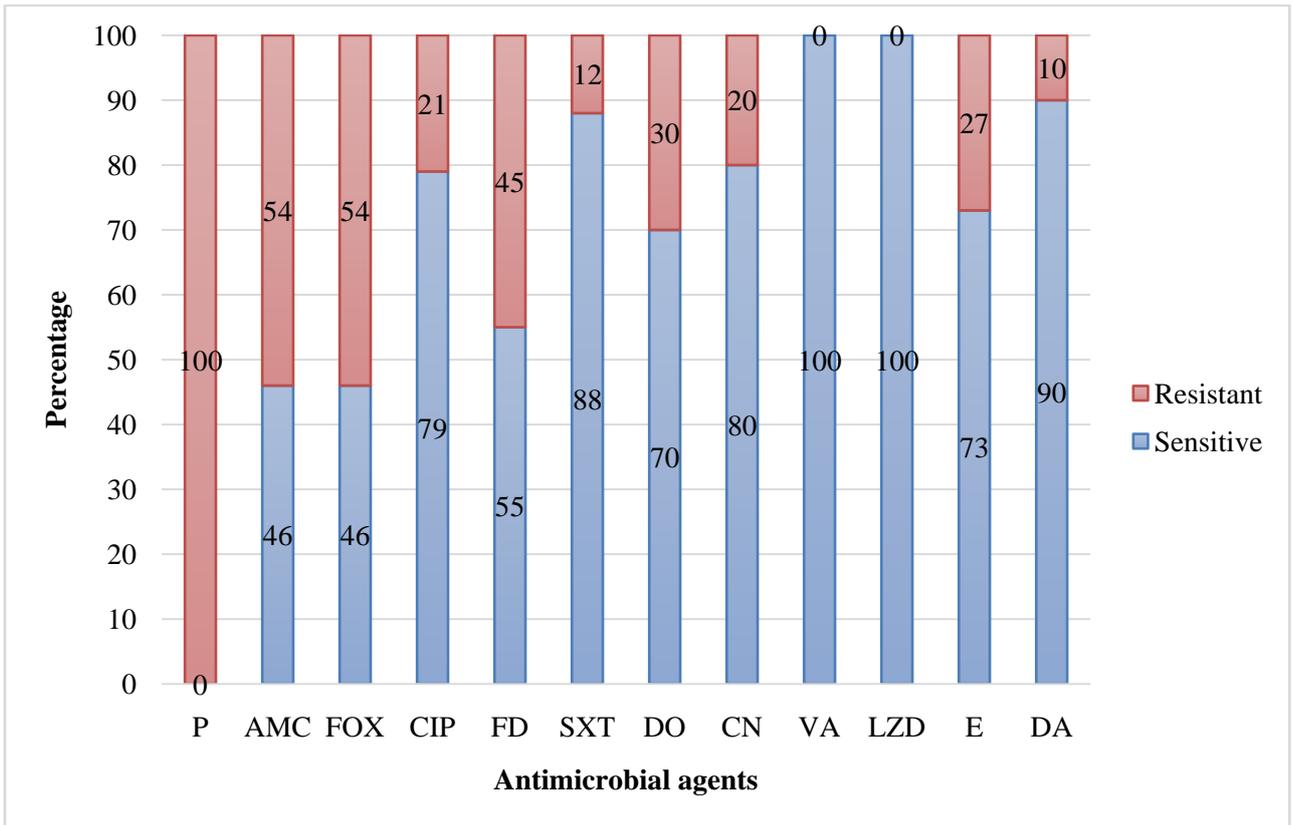


Figure 3: Antimicrobial susceptibility results

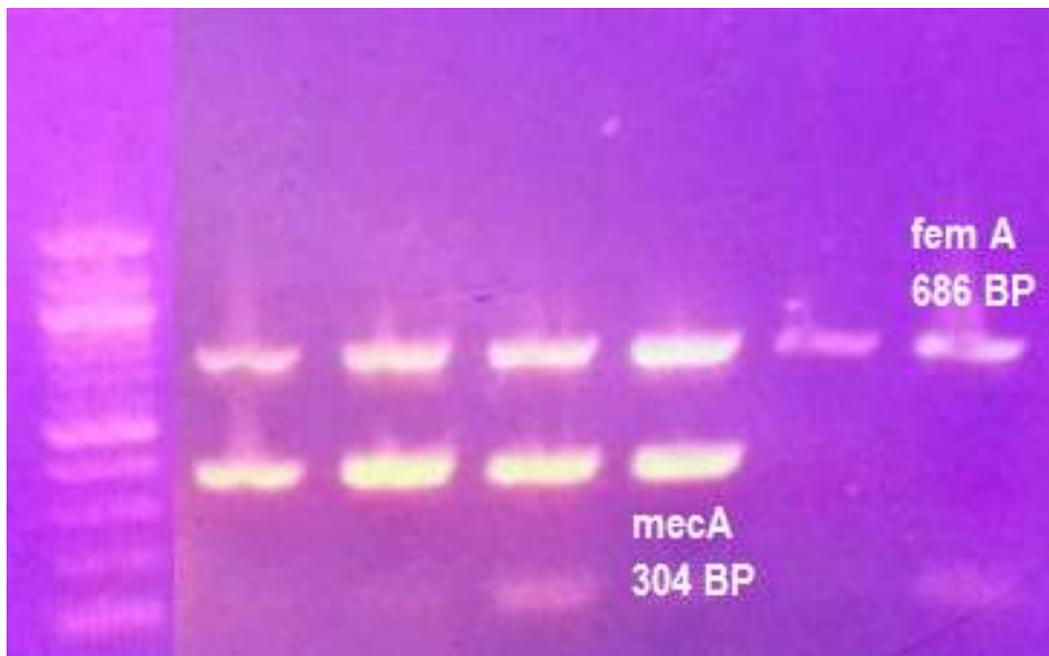


Figure 4: Ethidium bromide stained agarose gel showing the amplification bands of femA (686 BP) and mecA (304 BP)



Figure 5:Ethidium bromide stained agarose gel showing the amplification bands of ermA (610 BP)



Figure 6:Ethidium bromide stained agarose gel electrophoresis showing the amplification bands of ermC (520 BP)

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