

**An-Najah National University**

**Faculty of Graduate Studies**

**Resistance of Staphylococcal and Streptococcal Clinical  
Isolates to Macrolides and Functionally Related Antibiotics in  
Nablus District**

**By**

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**This Thesis is Submitted in Partial Fulfillment of the Requirements for  
the Degree of Master in Life Sciences (Biology), Faculty of Graduate  
Studies, An-Najah University, Nablus- Palestine.**

**2014**

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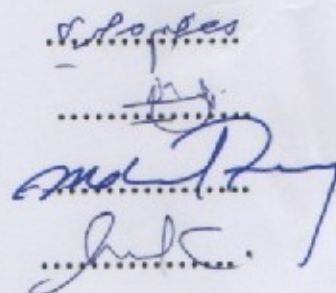
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## **Dedication**

**To My Family and Friends with Respect and Love**

## **Acknowledgments**

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Finally, special thanks are extended to my dear husband for his support. Similar thanks are extended to my beloved parents, daughter, brothers, sisters and relatives.

## الإقرار

أنا الموقعة ادناه مقدم الرسالة التي تحمل العنوان:

### **Resistance of Staphylococcal and Streptococcal Clinical Isolates to Macrolides and Functionally Related Antibiotics in Nablus District**

دراسة حول مقاومة بعض الأنواع البكتيرية للمضادات الحيوية من النوع (Macrolides)  
والمشابهة لها وظيفيا في منطقة نابلس

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## **Declaration**

The work provided in this thesis, unless otherwise referenced, is the  
researcher's own work, and has not been submitted elsewhere for any other  
degree or qualification.

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اسم الطالب:

**Signature:**

التوقيع:

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# **Resistance of Staphylococcal and Streptococcal Clinical Isolates to Macrolides and Functionally Related Antibiotics In Nablus District**

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## **Abstract**

A total of 200 Staphylococcal and 52 Streptococcal clinical bacterial isolates were collected from January 2012 to April 2013 from different clinical centers in Nablus district. Minimal inhibitory concentration (MIC) values of erythromycin and clindamycin were determined using agar dilution method. Micro-broth dilution method was only applied for *S. pneumoniae* isolates. A representative 47 isolates of erythromycin resistant strains were examined for antibiotic resistance genes (*ermA*, *ermB*, *ermC*, *msr*, *mef*, and *ere*) by PCR. MIC values of erythromycin and clindamycin, erythromycin-clindamycin induction test and data on resistant genes were combined to predict the most probable mode of resistance among the studied isolates. Relatively high frequencies of erythromycin resistance were found among Streptococci (63.5%) and Staphylococci (65.5%) isolates. The frequency of erythromycin resistance among coagulase negative Staphylococci (CONS) was 76.9%, which was higher than that among *S. aureus* (64.7%). With respect to clindamycin resistance, 48.1% of Streptococci and 20.5% of Staphylococci isolates were resistant. Resistance of Staphylococci isolates to erythromycin appears to be mediated by efflux mechanism (MS phenotype, 50.4%) and target site

modification (MLS<sub>B</sub> phenotypes, 49.6%). Expression of MLS<sub>B</sub> phenotype in staphylococci was constitutive in 61.5% and inducible in 38.5% of the isolates. Among Streptococci isolates, resistance to erythromycin was most commonly (75.8%) mediated by target modification (MLS<sub>B</sub>). However, efflux mechanism of resistance (M phenotype) was detected in 24.2% of the isolates. Among the 36 Staphylococcal isolates analyzed by PCR, *msr* gene was detected in 20 (55.6%), *ermC* in 11 (30.6%) and *ermA* in 9 (25%). On the other hand, among examined Streptococcal isolates (11), *ermB* gene was detected in 9 (81.8%) of isolates, *mef* in 3 (27.3%), *ere* in 1 (9.1%) and *ermC* in 1 (9.1%).

The percentage of erythromycin resistant Staphylococci was highest among infants 0-2 years old (74.5%) and older age group >65 years (75%). Similarly, clindamycin resistance among Staphylococci was highest in bacteria isolated from patients >65 years (50%). This was significantly higher than that among 3-14 year age group (3.5%,  $P=0$ ). Staphylococci isolates recovered from gynecology department showed the highest erythromycin resistance when compared to isolates from other departments and variations in resistance rates were significant ( $P=0.000$ ). Erythromycin resistance among Staphylococci bacteria isolated from blood and nasal swab were significantly higher than that among wound swabs ( $P=0.000$ ).

# **Chapter One**

## **Introduction**

## 1.1 Introduction

Results of national and global surveillance studies indicate that the incidence of isolation of antimicrobial-resistant pathogens in healthcare institutions is increasing and becoming common (1, 2, 3, 4, 5, 6, 7, 8, 9). Bacterial resistance often results in treatment failure, which can have serious consequences, especially in critically ill patients. Ineffective empiric antibiotic therapy, has resulted in increased mortality rates in patients with bloodstream infections caused by resistant *Pseudomonas aeruginosa*, *Staphylococci* spp., *Klebsiella pneumoniae*, *Escherichia coli*, *Enterobacter* spp., and enterococci (10, 11, 12, 13, 14). The challenge of isolation of resistant bacteria is not only within healthcare institutions but may also spread in communities as well (5, 15).

Surveillance studies carried out on antimicrobial agents were essential for establishing trends in antimicrobial resistance of pathogens and for recognition of emerging pathogens at different levels, i.e., national and global. Such studies helped in the development of targeted approaches to control antimicrobial resistance (16).

## 1.2 General characteristics of Staphylococci

The genus *Staphylococcus* is composed of several species, many of which may be encountered in human clinical specimens (17). Staphylococci are spherical cells arranged in irregular clusters similar to grape appearance. However, single cocci, pairs, tetrads, and chains are also seen (18, 17). Staphylococci bacteria are nonmotile, non-spore-forming, catalase-positive and gram-positive cocci (18, 17). The organisms are generally found on the skin and mucous membranes of humans. In humans, some of these pathogens produce the enzyme coagulase, which is used for laboratory identification for these organisms (17, 18).

## 1.3 Clinical significance of Staphylococci

Among the genus staphylococcus, the three main species of clinical importance are *S. aureus*, *S. epidermidis*, and *S. saprophyticus* (18). *S. aureus* is coagulase positive and is a major pathogen for human (18, 17). It is found in the external environment and the anterior nares of 20-40% of healthy adults. Other sites of colonization include intertriginous skin folds, the perineum, and the vagina. Although this organism is frequently a part of the normal human microflora, it can cause significant opportunistic infections under the appropriate conditions (17). *S. aureus* is the most virulent encountered Staphylococcus species. It produces exotoxins causing diseases such as toxic shock and Staphylococcal scalded skin syndromes. In addition, *S. aureus* can make direct invasion and

systemic dissemination resulting in diseases like bacteremia, septic shock syndrome, skin infection and abscesses (19, 20).

Coagulase-negative Staphylococci (CONS) are increasing in importance as cause of hospital-acquired infections, particularly nosocomial bacteremias (21), and neonatal sepsis (22). The National Nosocomial Infection Survey (NNIS) reported that the incidence of CONS as a cause of nosocomial bacteremias increased from 9 to 27% during the period 1980 to 1989, to become the most common single cause of these infections (21). It was reported that there is an association between the dramatic increase in CONS as a cause of nosocomial bacteremias and the increase rate of resistance of these pathogens to antimicrobial agents (23).

Among coagulase negative staphylococci, *S. epidermidus* and *S. saprophyticus* are frequently reported in human infections (17). *S. epidermidis* is widely recognized as one of the etiologic agents of bacteremia, postoperative cardiac infections endocarditis, osteomyelitis, urinary tract infections with a frequent association with colonization of intravascular catheters and orthopedic devices (12, 14). *S. saprophyticus* is known to causes urinary tract infections in young women (18).

## **1.4 General characteristics of Streptococci**

Streptococci bacteria represent a large group of gram-positive microorganisms of remarkable heterogeneity. Most Streptococci are

facultative anaerobes, nonmotile, and tend to grow in chains of variable length, especially during cultivation in vitro (24, 18). Some Streptococci produce a capsular polysaccharide (18).

## 1.5 Clinical significance of Streptococci

*Streptococcus pneumoniae* (*S. pneumoniae*) is an etiological agent of pneumonia. It's a major killer of humans, albeit its lethality frequently arises as a complication of a preceding debilitating illness (24). *S. pneumoniae* may also cause complications such as meningitis, endocarditis and septic arthritis (18). *Streptococcus pyogenes* is the most frequent bacterial cause of pharyngitis; this bacterium also causes impetigo, rheumatic fever and glomerulonephritis (25, 18). Viridans Streptococci are identified to cause systemic diseases such as bacteraemia, bacterial endocarditis, especially in patients with decreased white blood cells counts or patients with pneumonia (26, 27).

*Streptococcus agalactiae* is a pathogen of growing importance in human pathology. It is the most important cause of neonatal sepsis (28, 29) and meningitis in newborn infants (30, 31).

## 1.6 Macrolides, Lincosamides and Streptogramin B (MLS<sub>B</sub>) Antibiotics

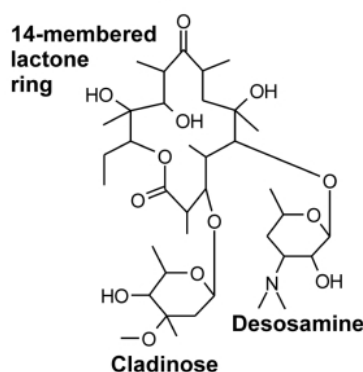
MLS<sub>B</sub> antibiotics are chemically distinct, but have similar mode of action against bacterial cells (32, 33, 34, 35), therefore, common characteristics will be discussed together.



## 1.6.1 Structures of antibiotics

### 1.6.1.1 Macrolides

Macrolides antibiotics consist of a macrocyclic lactone ring containing 14, 15 or 16 atoms with neutral or amino sugars linked via glycosidic bonds (Figure 1) ( 36, 37).

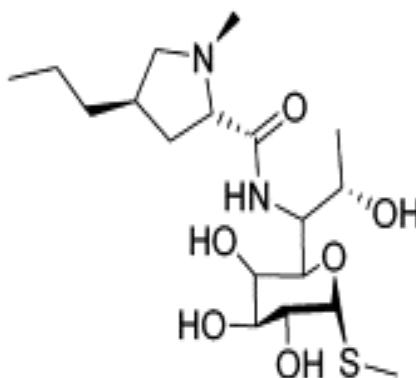


**Figure 1.1** Chemical structure of macrolides (erythromycin) (36).

According to the number of atoms in the lactone nucleus, macrolide antibiotics can be categorized into three groups. Macrolides possessing 14-membered lactone ring includes erythromycins, oleandomycin, roxithromycin, dirithromycin, clarithromycin and flurithromycin, whereas 15-membered antibiotics include azithromycin. Examples of 16-membered macrolides include josamycin, rosaramicin, rokitamycin, kitasamycin, mirosamycin, spiramycin and tylosin. Both of spiramycin and tylosin antibiotics are used almost exclusively in treatment of animals (38).

### 1.6.1.2 Lincosamide

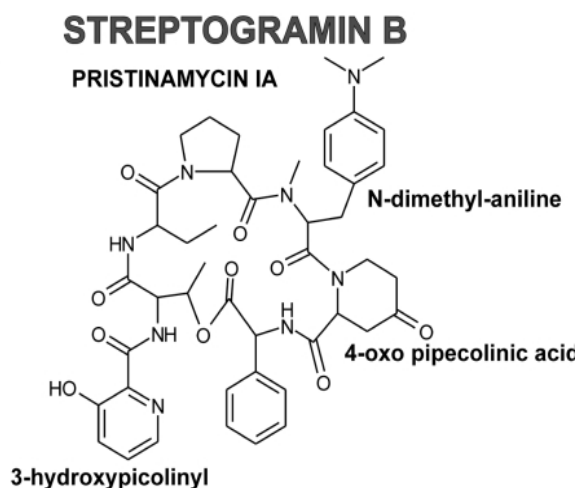
Lincosamide class of antibacterial agents originates from a natural product, lincomycin (Figure 2) and includes semisynthetic derivatives, clindamycin and pirlimycin (39). Lincomycin is composed of an amino acid (propylhygric acid) (40), linked via a peptide bond to a sugar moiety (methylthiolincosamide) (41, 42).



**Figure 1.2** Chemical structure of lincomycin (40, 41, 42).

### 1.6.1.3 Streptogramin B

The streptogramin family is subdivided into A and B groups or alternatively into M and S groups, respectively. Streptogramin B consists of several modified amino acids as shown in Figure 1.3 (43, 44).



**Figure 1.3** Chemical structure of a Streptogramin B (43).

### 1.6.2 Mechanism of action and applications of MLS<sub>B</sub> Antibiotics

All MLS<sub>B</sub> antibiotics inhibit protein synthesis. MLS<sub>B</sub> antibiotics bind to the large 50S ribosomal subunit, close to the peptidyl transferase center (45, 46, 47, 48, 49, 50, 51, 52). This binding was reported to block peptide bond formation and/or peptidyl-tRNA translocation from the A to the P site of the ribosome (50, 51, 52). This center is composed entirely of RNA (53, 54, 55, 56). Several alterations in 23 S ribosomal RNA, give resistance against all members of the MLS<sub>B</sub> group (57).

MLS<sub>B</sub> antibiotics are widely used in the treatment of Staphylococcal and Streptococcal infections (58, 59). MLS<sub>B</sub> drugs are recommended as alternative treatment of patients, who are allergic to *B*-lactam antibiotics (60, 61, 58). Moreover, erythromycin and other macrolides are considered alternative treatment for Streptococcal pharyngitis and other non-serious infections caused by *S. pyogenes* (62,

63, 64). MLS<sub>B</sub> drugs are recommended for penicillin-resistant Viridians Streptococci (60, 61, 58). Macrolides has been used as therapy in severe cases of acne. It is also the agent of choice in treating whooping cough, Campylobacter and Mycoplasma infections, and legionnaires disease (65). Although, lincosamide are mostly active against gram-positive organisms it's also used against selected gram-negative anaerobes and protozoa (66, 67).

### **1.6.3 Resistance mechanisms to MLS<sub>B</sub> antibiotics**

Although macrolide, lincosamide and streptogramin B antibiotics possess different chemical structures, they are functionally overlapping. Thus, a discussion of the mode of resistance to macrolide antibiotics must include lincosamide and streptogramin B families (44). The expanded therapeutic application of macrolide, lincosamide and streptogramin antibiotics to different infection types has been associated with increased numbers of resistant strains among Staphylococci and Streptococci (32, 33, 34, 35, 68). Bacterial resistance to MLS antibiotics may be expressed through different mechanisms including target site modification, efflux pump and enzymatic inactivation of antibiotic (69, 70, 71, 57, 72, 73, 74).

#### **1.6.3.1 Target modification**

Target modification occurs at the level of the ribosomes via a 23S rRNA methylase enzyme. This enzyme is encoded by erythromycin resistance methylase (*erm*) gene (69, 71, 57). There are several classes of

*erm* genes distinguishable by hybridization criteria (69, 71, 57). Examples of *erm*s include *ermA*, *ermB*, and *ermC* (75, 69, 35), *ermF* (76), *ermY* (77). Methylases enzyme adds one or two methyl residues to a highly conserved adenine residue in domain V (the peptidyl transferase center) of 23S rRNA (78, 57, 69). This ribosomal modification makes the bacterial strain resistant to most macrolides, lincosamides, and streptogramin B compounds; phenotypically, this resistance pattern is known as MLS<sub>B</sub> resistance (79, 78, 69). Expression of MLS<sub>B</sub> resistance can be inducible or constitutive and is unrelated to the class of an *erm* determinant (80, 81, 69, 82, 83). In Staphylococci and Streptococci bacteria, constitutive expression of MLS<sub>B</sub> resistance can lead to cross-resistance to macrolides, lincosamides and streptogramin B (cMLS<sub>B</sub>) (resistance includes 16-membered ring macrolides) (84, 72). In Staphylococcal bacteria, inducible MLS<sub>B</sub> resistance strains possess resistance to 14- and 15-membered ring macrolides and susceptibility to 16-membered ring macrolides (84). Staphylococcal isolates with inducible resistance phenotype show in vitro resistance to erythromycin and susceptibility to clindamycin (85, 86, 87, 88). Such bacterial strains possess *erm* genes, which require an inducing agent to express resistance to clindamycin. For example erythromycin antibiotic can act as a strong inducer of methylase enzyme production (89). Clindamycin therapy of infections caused by bacteria with inducible resistance phenotype can lead to development of clindamycin resistance and consequently clinical failure (85, 86, 87, 88).

In Streptococcal isolates, a variety of phenotypes are produced by expression of inducible resistance. Phenotypes include high or low level of erythromycin resistance, with susceptibility or resistance to clindamycin (72, 90).

#### **1.6.3.2 Efflux mechanism**

Staphylococci appear to have an efflux system (91, 92, 70, 93, 94, 95, 96, 84, 97, 98) which is specific for 14- and 15-membered macrolides and streptogramin B antibiotics. Lincosamide antibiotics are not pumped by this staphylococcal efflux system. The resulting resistance pattern is called MS phenotype. The efflux system appears to be multi-component (84, 97). The gene *msrA* (84, 97) encodes ATP-binding proteins that are involved in transport (99, 100, 101). It is clear that *msrA* must be present to confer the macrolide and streptogramin B resistance i.e. MS phenotype (96). In Streptococci, active efflux pump is encoded by *mef* (macrolide efflux) gene (102, 103, 104). The *mef(A/E)* gene causes resistance to 14- and 15-membered macrolides compounds only, and the encoding phenotype is designed M (74). Two subclasses of the *mef* gene have been described, *mef(A)* gene (102), originally found in *S. pyogenes*, and *mef(E)* gene originally found in *S. pneumoniae* (103). The subclass *mef(A)* and *mef(E)* are 90% identical at the nucleotide level but they are endowed with important genetic differences (105).

### 1.6.3.3 Enzymatic inactivation

Resistance caused by bacterial production of enzymes that inactivate MLS<sub>B</sub> antibiotics has been described for a number of clinically important organisms such as *S. aureus* (106, 107, 108, 109, 110, 98) *S. haemolyticus* (106, 108), and *Escherichia coli* (111, 112, 113, 114, 115, 116, 117, 118, 119). Lactone ring of the macrocyclic nucleus can be hydrolysed by certain enzymes such as *EreA* and *EreB*. In addition, macrolides can be inactivated by phosphotransferases, which were reported in *S. aureus* (98). However, enzymatic inactivation in gram-positive bacteria is rarely reported (120).

## 1.7 Aims of the study

Little information is known about the prevalence of the resistance to macrolides and functionally related antibiotics among Staphylococci and Streptococci clinical isolates in the Palestinian territories, thus, the current study aims at:

1. Determine the prevalence of resistance to macrolides and lincosamides among Staphylococci and Streptococci clinical isolates in northern Palestine, mainly in Nablus district.
2. Determine the phenotypes of resistance to macrolides using Minimum Inhibitory Concentrations (MIC) values of erythromycin and clindamycin, and from induction tests (erythromycin-clindamycin).

3. Detect the molecular mechanism of resistance to macrolide by polymerase chain reaction (PCR) using representative isolates.



## **Chapter Two**

# **Materials and Methods**

## **2.1 Collection of bacterial isolates**

Bacterial isolates were collected from January 2012 to April 2013 from different clinical centers in Nablus district. These centers included Rafedia, Nablus, Al-Arabi and Al-Watani hospitals and New Technology and Medicare medical laboratories (isolate collection from Medicare started at February 2013). Patient demographic data were obtained from laboratory records for each isolate. The information included: name, age, sex, specimen type, clinical center, hospital wards, date of hospital admission and date of specimen collection. Each isolate was given an identity number and stored in 20% glycerol Nutrient Broth at -70 °C. Hospital associated infection was defined as occurrence of infection 48 hours or more after hospital admission.

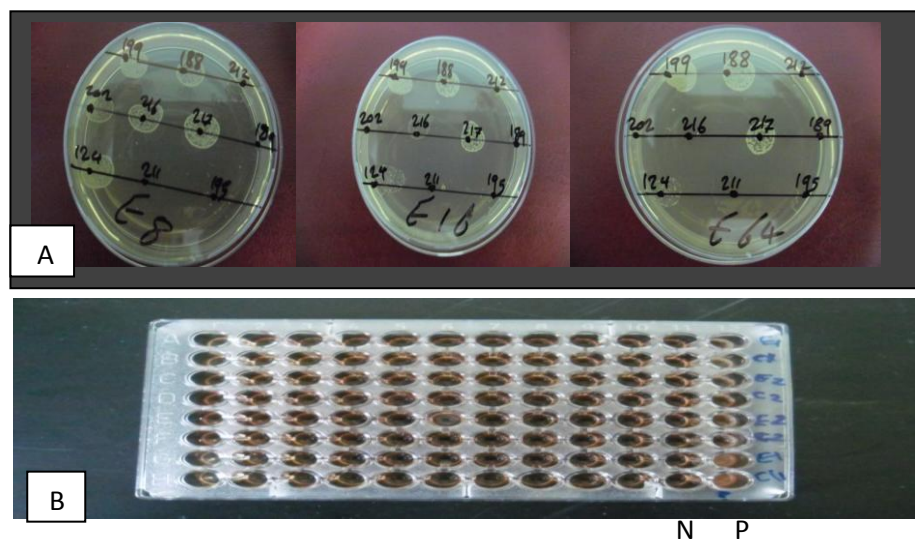
## **2.2. Identification of bacterial isolates**

Identification of bacterial isolates was confirmed by several biochemical tests as mentioned previously by Win et al and Forbes et al (121, 17). Gram stain and catalase tests were performed for all isolates. Identification of Staphylococcal bacteria was based on coagulase test, mannitol salt agar test, aerobical production of acid from maltose, and susceptibility to bacitracin, novobiocin, and polymyxin B. Identification schemes used for Streptococcal isolates included: growth on Blood Agar in absence of pyridoxal (vitamin B6); haemolysis type; growth at 6.5% NaCl supplemented blood agar; susceptibility to bacitracin, trimethoprim-sulfamethoxazole (SXT), optochin and vancomycin; growth at 10°C, and

chromogenic media Uriselect (Bio-Rad, France). All antibiotics were obtained from Oxoid (UK).

### 2.3 Determination of minimal inhibitory concentration (MIC)

MIC values of erythromycin and clindamycin were determined by agar dilution method for Staphylococcal and Streptococcal strains, while micro-broth dilution method was used for *S. pneumoniae* isolates (Figure 2.1). The applied procedures were according to Clinical Laboratory Standards Institute (CLSI) (121, 122). *S. aureus* ATCC 25923 was included in each run as control strain with susceptibility to both erythromycin and clindamycin antibiotics.



**Figure 2.1** Determination of MIC. **A.** Agar dilution method plates. **B.** Micro-broth dilution method.

N, negative growth control; P, positive growth control.

### **2.3.1 Media preparation**

In agar dilution method, flasks containing 50ml (or 47.5ml for Streptococci) of Mueller-Hinton (MH) agar (hy-labs, Israel) were sterilized and placed in water bath at 40 °C. To each flask a specific volume of antibiotic solution and for Streptococci 2.5ml blood was/were added, followed by well mixing and pouring into Petridishes. This resulted in MH agar plates with 0.03, 0.06, 0.125, 0.25, 0.5, 1, 2, 4, 8, 16, 32, 64, 128µg/ml concentrations of antibiotics. Plates without antibiotics were prepared to serve as positive control of bacterial growth.

In micro-broth dilution method, 100 µl of MH broth containing 5% lysed sheep blood (lysed by 5 freeze-thaw cycles and distilled water) was dispensed in each well of the microtitre tray. This was followed by the addition of 100 µl of 32µg/ml antibiotic in the first well. After mixing, a 100 µl of sample mixture was transferred to the next well and the process was repeated until well number 11. A 100µl sample was removed from this well after mixing. The last well (number 12) was antibiotic free and served as positive control of bacterial growth. This resulted in wells containing 0.03, 0.06, 0.125, 0.25, 0.5, 1, 2, 4, 8, 16 µg/ml concentrations of antibiotics.

### **2.3.2 Preparation of bacterial inoculum**

Four to five colonies of bacteria from fresh culture were placed in trypticase soy broth (TSB). The turbidity of broth was adjusted to be

equivalent to 0.5 Mcfarland standard ( $1.5 \times 10^8$  CFU/ml). In agar dilution method, the bacterial suspension was diluted 1:15 with TSB to achieve a concentration of  $1 \times 10^7$  CFU/ml. For micro-broth dilution method, the bacterial suspension was diluted 1:3 with TSB to achieve a concentration of  $5 \times 10^7$  CFU/ml.

### **2.3.3 Inoculation of bacterial isolates**

A 1 µl of bacterial suspension ( $10^4$  CFU/spot) was transferred to the MH agar plates containing different concentrations of antibiotics. Inoculum's spots were allowed to dry at room temperature before inverting the plates and the plates were then incubated at 35°C for 18 hours.

In micro-broth dilution method, 1 µl of bacterial suspension, possessing a concentration of  $5 \times 10^7$  CFU/ml, was transferred to each well except well number 11, which was used as a negative control of bacterial growth. Microtitre tray was covered and incubated at 35°C for 18 hours.

### **2.3.4 Interpretation of results**

The MIC was considered to be the lowest concentration of the agent that completely inhibits visible growth as judged by the naked eye (121). MIC break points of erythromycin and clindamycin were based on CLSI (122). Staphylococcal bacterial isolates were considered susceptible to erythromycin when MIC was  $\leq 0.5 \mu\text{g/ml}$ , intermediate 1-4  $\mu\text{g/ml}$ , and resistant when MIC  $\geq 8 \mu\text{g/ml}$ . Clindamycin break points for

Staphylococci isolates were as follows: susceptible,  $\leq 0.5 \mu\text{g/ml}$ ; resistant,  $\geq 4 \mu\text{g/ml}$ ; and intermediate 1-2  $\mu\text{g/ml}$ .

A Streptococci bacterial isolate (including *S. pneumoniae*) was considered susceptible to erythromycin or clindamycin when MIC was  $\leq 0.25 \mu\text{g/ml}$  and was considered resistant when MIC was  $\geq 1 \mu\text{g/ml}$ . An isolate with erythromycin MIC value of 0.5 was considered an intermediate resistant isolate.

## **2.4 Detection of inducible MLS<sub>B</sub> phenotype**

This test was performed for isolates that were resistant to erythromycin but susceptible to clindamycin. For detection of inducible MLS<sub>B</sub> phenotype, double disk diffusion method (D-test) was performed according to CLSI guidelines (123). A 24 hour old bacterial culture was used to prepare a suspension in normal saline equivalent to 0.5 McFarland. The Staphylococcal bacterial suspension was then inoculated onto a Mueller - Hinton agar (MH) plate, while Streptococcal suspension was inoculated onto MH supplemented with 5% blood. Erythromycin (15 $\mu\text{g}$ ) disk was placed 15 mm (edge to edge) apart from clindamycin (2 $\mu\text{g}$ ) disk on inoculated MH Plates. The plates were incubated for 18 hours at 35°C. Isolates with D-shape zone around the clindamycin, were interpreted as positive for inducible resistance (D-test positive) as shown in Figure 2.2.



**Figure 2.2** Inducible MLS<sub>B</sub> phenotype. E, erythromycin; DA, clindamycin;

## 2.5 Detection of methicillin resistance

This test was performed for *Staphylococci* isolates. Resistance to oxacillin antibiotic was detected by disk diffusion test. Preparation of bacterial suspension and plates was similar to that previously described for inducible MLS<sub>B</sub> phenotype; however, the media was supplemented with 5% NaCl when *S. aureus* isolates were examined. Oxacillin disk (1µg) was applied to inoculated media and the plates were then incubated at 30°C for 18 hours. A zone of inhibition  $\leq 10$  mm and  $\leq 17$  mm indicated *S. aureus* and CONS resistance to oxacillin, respectively (122).

## 2.6 Detection of Resistant Genes

### 2.6.1 DNA extraction

Bacterial isolates were grown on nutrient or blood agar for 24 hours. Colonies (2-3) were transferred to Eppendorf tube containing 600µl of Tris acetate - EDTA (TAE) buffer and mixed well to form a suspension. After one hour, Eppendorf tubes were centrifuged at 4000g

for 5 minutes and supernatant was discarded. A volume of 600µl distilled water was added to the pellet and tubes were placed in boiling water for 15 minutes and left to cool down at room temperature. An equal volume of chloroform was added and mixed followed by brief centrifugation. The upper layer containing DNA material was aspirated and placed in a new Eppendorf tube. Chloroform extraction step was repeated to ensure that DNA is protein free sample. Extracted DNA was stored at - 20°C.

### **2.6.2 Polymerase chain reaction (PCR)**

The reagents of PCR were obtained from SIGMA-ALDRICH (USA). The final reaction mixture (25µl) contained 1x PCR solution [1.5 units Taq DNA polymerase, 10mM Tris-HCl, 50 mM KCl, 1.5 MgCl<sub>2</sub>, 0.001% gelatin, 0.2mM deoxynucleoside triphosphate (dNTP)]. A concentration of 0.8pmole/µl was used for each of the used primers. With respect to MgCl<sub>2</sub> concentration it was 2mM for *ermA*, *ermB*, *ermC*, *msr* primers (4mM MgCl<sub>2</sub> concentration was used when each primer pair was applied alone) or 4mM MgCl<sub>2</sub> for the *ere* and *mef* primers (124).

The PCR assays were made using Tprofessional standard Thermocycler (Biometra GmbH, Germany). PCR mixtures were subjected to thermal cycling as follows: 5 minutes at 94°C and then 40 cycles of 1 minute at 94°C for the denaturation step and 1.5 minutes at 45°C for the annealing step and 2 minutes at 72°C for the extension step. This was followed by a final extension step at 72°C for 7 minutes. PCR products were detected by 1.5% agarose gel electrophoresis with ethidium



bromide staining. Primers, their corresponding sequences, expected size of PCR products, and their reference article are listed in Table 2.1.

## **2.7 Statistical Analysis**

Minitab version 15.0 was used by a statistical specialist. Chi-square and Fisher's exact tests were applied for comparison of the resistance frequencies among different groups and prevalence of resistance to antibiotics in different age groups. Independent *t*-test was applied for comparison of the mean values among different age groups. A *P*-value <0.01 was considered statistically significant.

**Table 2.1 Primers used in the study.**

<b>Primer</b>	<b>Primer sequence</b>	<b>Expected size of PCR product (b.p*)</b>	<b>Reference</b>
<i>ermC1:</i>	5'GCTAATATTGTTTAAATCGTCAATTCC –3'		(125)
<i>ermC2:</i>	5' GGATCAGGAAAAGGACATTTTAC –3'	572	(125)
<i>ermB1</i>	5'-GAAAAGGTACTCAACCAAATA-3'		(124)
<i>ermB2</i>	5'- AGTAACGGTACTTAAATTGTTTAC-3'	639	(124)
<i>ermA1</i>	5'-TCTAAAAAGCATGTAAAAGAA-3'		(124)
<i>ermA2</i>	5'-CTTCGATAGTTTATTAATATTAGT-3'	645	(124)
<i>msrA1</i>	5'- GGCACAATAAGAGTGTTTAAAGG-3		(84)
<i>msrA2 :</i>	5'- AAGTTATATCATGAATAGATTGTCCTGTT-3'	399	(84)
<i>mefA/E1</i>	5'-AGTATCATTAATCACTAGTGC-3		(124)
<i>mefA/E2</i>	5'-TTCTTCTGGTACTAAAAGTGG-3	348	(124)
<i>ereA1</i>	5'-AACACCCTGAACCCAAGGGACG-3'		(119)
<i>ereA2</i>	5'-CTTCACATCCGGATTCGCTCGA-3'	420	(119)

\*base pair

## **Chapter Three**

### **Results**

### 3. 1 Bacterial isolates

A total of 252 bacterial isolates were collected from January 2012 to April 2013. Isolates were collected from different types of clinical specimens and one positive culture per patient was included. Bacterial isolates included 200 Staphylococci and 52 Streptococci isolates. Isolates were obtained from the following hospitals and private laboratories in the city of Nablus: Rafidia hospital (160), New Technology laboratory (35), Nablus Specialty Hospital (26), Al-Arabi Specialty Hospital (19), Al-Watani Hospital (7) and Medicare laboratory (5) as shown in Table 3.1. Staphylococci isolates comprised of 187 *S. aureus* and 13 coagulase negative Staphylococci (12 *S. epidermidis* and 1 *S. saprophyticus* isolates). Streptococci isolates included 33 *Streptococcus agalactiae*, 14 Viridans Streptococci, 3 *S. pneumoniae*, and 2 *S. pyogenes*.

Staphylococci isolates were recovered from various clinical materials of 56 outpatients and 144 patients hospitalized in 10 different departments. Among the hospitalized patients, the frequency of Staphylococcal bacterial isolation was highest in general surgery unit (32 isolates) and ranged from 6 to 17 isolates in the rest of units. The majority of Streptococci isolates were obtained from outpatients (Table 3.1).

**Table 3.1 Source of Staphylococci and Streptococci isolates.**

Variable	Total number	Staphylococci isolates No.	Streptococci isolates No.
<b>Source</b>			
Rafedia hospital	160	140	20
New Technology laboratory	35	9	26
Nablus Specialty hospital	26	21	5
Al-Arabi Specialty hospital	19	18	1
Al-Watani hospital	7	7	0
Medicare-laboratory	5	5	0
<b>Units</b>			
Outpatients	92	56	36
Inpatients	160	144	16
General surgery	37	32	5
Emergency	20	17	3
Pediatrics	18	16	2
Burns	16	16	0
Neonates	15	14	1
Urology	14	14	0
ICU*	11	9	2
Internal medicine	15	13	2
Orthopedic	7	7	0
Gynecology	7	6	1
<b>Specimen</b>			
Wound swab	143	126	17
Urine	42	23	19
Blood	10	8	2
Sputum	9	6	3
Nasal swab	8	8	0
Fluid	6	5	1
Throat swab	6	1	5
Vaginal swab	5	2	3
Umbilical swab	5	5	0
Ear swab	3	2	1
Semen	3	3	0
Skin	2	2	0
Burn swab	2	2	0
Tissue	2	2	0
C.V.P *	1	1	0
Chest swab	1	1	0
CSF*	1	0	1
Pus	1	1	0
Drain	1	1	0
Breast discharge	1	1	0
<b>Sex</b>			
Male	132	113	19
Female	120	87	33
<b>Total</b>	<b>252</b>	<b>200</b>	<b>52</b>

\* ICU, Intensive care unit; CVP, central venous catheter; CSF, Cerebrospinal fluid

Most of the Staphylococci isolates were recovered from wound swab (126 isolates) followed by urine (23), blood (8), nasal (8) and sputum (6) specimens (Table 3.1). Staphylococcal infections were more common among males (56.5%). Streptococci isolates were recovered predominantly from urine (19 isolates) and wound swabs (17) as shown in Table 3.1. The frequency of Streptococcal infection is higher among females (27.5%) compared to males (14.4%).

In the present study, patients were grouped into 6 age groups. Distribution of bacterial isolates among various age groups was as follows: 0-2 year (51 Staphylococci and 4 Streptococci), 3-14 (29 Staphylococci and 3 Streptococci), 15-39 (36 Staphylococci and 20 Streptococci), 40-65 (31 Staphylococci and 10 Streptococci), > 65 (12 Staphylococci and 2 Streptococci) and unknown age (41 Staphylococci and 13 Streptococci). Staphylococci and Streptococci isolates were recovered during all months of the year.

### **3.2 Susceptibility of Staphylococci and Streptococci isolates to erythromycin and clindamycin**

Table 3.2 shows the percentage of resistance to erythromycin and clindamycin among the bacterial isolates. A total of 131 (65.5%) Staphylococci isolates were resistant to erythromycin. A much lower frequency of resistance to clindamycin (20.5%) was found among Staphylococci isolates. Data presented in Figure 3.1 shows resistance percentages of major bacterial groups. The MIC for erythromycin resistant

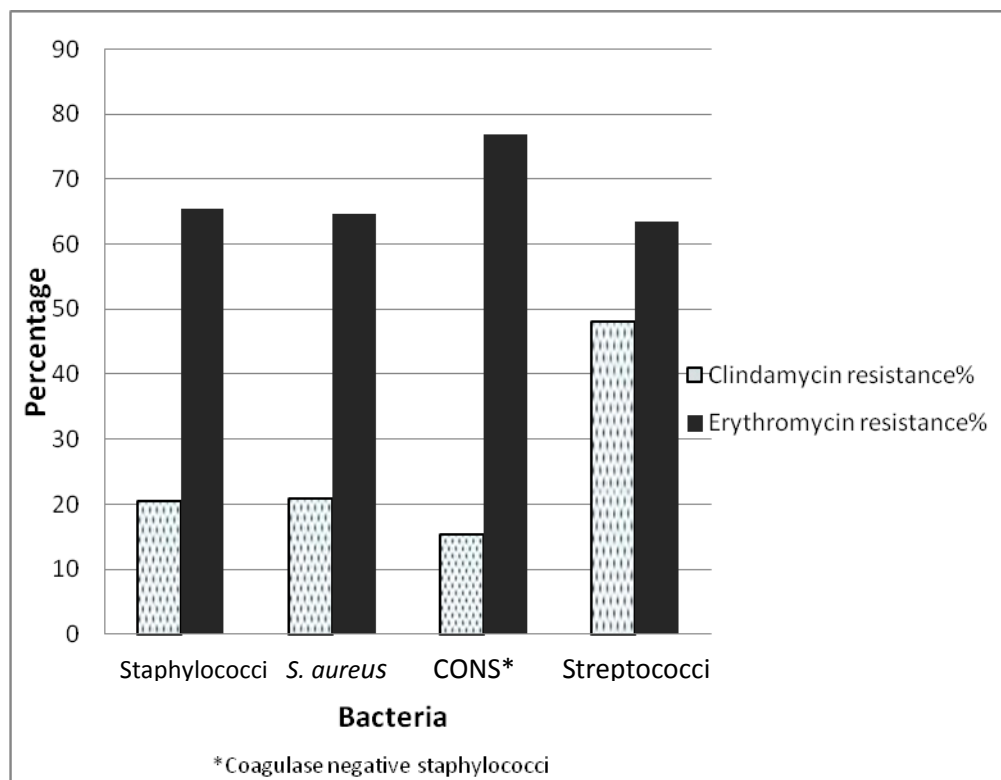
Staphylococci isolates ranged from 8 to  $\geq 128\mu\text{g/ml}$ . MIC of clindamycin resistant isolates ranged from 4 to  $\geq 128\mu\text{g/ml}$ . The frequency of erythromycin resistance among coagulase negative Staphylococci (CONS) was 76.9%, which was higher than that among *S. aureus* (64.7%). Differences between CONS and *S. aureus* were not significant ( $P= 0.317$ ). In contrary, higher clindamycin resistance rate was detected among *S. aureus* (20.9%) strains without significant deference ( $P= 0.600$ ) as shown in Table 3.2 and Figure 3.1.

**Table 3.2 Resistance of erythromycin and clindamycin in different bacterial species included in the study.**

Bacterial species	No	Erythromycin			Clindamycin		
		Resistant No* (%)	Intermediate No* (%)	Susceptible No* (%)	Resistant No (%)	Intermediate No (%)	Susceptible No (%)
Staphylococci	200	131(65.5)	6(3 )	63(31.5)	41 (20.5)	6(3)	153 (76.5)
<i>S. auerus</i>	187	121(64.7)	6(3.2)	60(32.1)	39(20.9)	5(2.7)	143(76.5)
CONS*	13	10(76.9)	0(0)	3(23.1)	2(15.4)	1(7.7)	10(76.9)
<i>S.epidermidis</i>	12	10(83.3)	0(0)	2(16.7)	2(16.7)	1(8.3)	9(75)
<i>S.saprophyticus</i>	1	0(0)	0(0)	1(100)	0(0)	0(0)	1(100)
Streptococci	52	33(63.5)	0(0)	19(36.5)	25(48.1)	0(0)	27(51.9)
<i>S. agalactiae</i>	33	26(78.8)	0(0)	7(21.2)	20(60.6)	0(0)	13(39.4)
Viridans <i>S.</i>	14	5(35.7)	0(0)	9(64.3)	3(21.4)	0(0)	11(78.6)
<i>S.pneumoniae</i>	3	0(0)	0(0)	3(100)	0(0)	0(0)	3(100)
<i>S.pyogenes</i>	2	2(100)	0(0)	0(0)	2(100)	0(0)	0(0)

\* No, number; CONS, coagulase negative Staphylococci.





**Figure 3.1** Percentages of erythromycin and clindamycin resistance among Staphylococci and Streptococci isolates.

The frequency of erythromycin resistance among Streptococci isolates (63.5%) was similar to that of Staphylococci (65.5%) as shown in Table 3.2 and Figure 3.1. However, higher percentage of clindamycin resistant isolates was found among Streptococci (48.1%) in comparison with Staphylococci (20.5%). Difference in clindamycin resistant between the Staphylococci and Streptococci were of no significant value ( $P= 0.499$ ). MIC values for both erythromycin and clindamycin among resistant Streptococci isolates ranged from 1 to  $\geq 128\mu\text{g/ml}$ . *S. pyogenes* showed 100% rate of resistant to erythromycin and clindamycin while none of *S. pneumoniae* isolates showed resistance to both antibiotics.

Frequency of erythromycin resistance (70.6%) among methecillin resistant *Staphylococci* isolates was insignificantly ( $P= 0.095$ ) higher than that among methecillin susceptible isolates (59.3%) as shown in Table 3.3. Similarly, clindamycin resistance among methecillin resistant *Staphylococci* (23.9%) was higher than that among methecillin susceptible isolates (16.5%,  $P= 0.199$ ).

**Table 3.3. Erythromycin and clindamycin resistance among methecillin resistant and susceptible Staphylococci.**

Bacterial species	Total No	Methecillin resistant			Methecillin susceptible		
		Isolates No	Erythromycin resistant (%)	Clindamycin resistant (%)	Isolates No	Erythromycin resistant (%)	Clindamycin resistant (%)
Staphylococci	200	109	77(70.6)	26(23.9)	91	54(59.3)	15(16.5)
<i>S. auerus</i>	187	102	73(71.6)	25(24.5)	85	48(56.5)	14(16.5)
CONS*	13	7	4 (57.1)	1(14.3)	6	6(100)	1(16.7)
<i>S.epidermidis</i>	12	6	4(66.7)	1(16.7)	6	6(100)	1(16.7)
<i>S.saprophyticus</i>	1	1	0(0)	0(0)	0	-	-

\*CONS, coagulase negative Staphylococci

Relatively high percentages of erythromycin resistance were found among Staphylococci and Streptococci isolates obtained from hospitals and private laboratories included in the present study (Table 3.4). Staphylococci isolates from Al-Watani hospital showed the highest resistance rate (85.7%) for both erythromycin and clindamycin. This rate was significantly higher than that found among isolates collected from Rafedia hospital ( $P=0.000$ ). On the other hand, clindamycin resistance among Streptococci isolates obtained from the New Technology laboratory was the highest (61.5%). The differences were without significant value.

**Table 3.4: Clinical data of erythromycin and/or clindamycin resistant Staphylococci and Streptococci isolates.**

Variable	Staphylococci			Streptococci		
	No. isolates*	E R* (%)	DA R* (%)	No. isolates	E R (%)	DA R (%)
<b>Source</b>						
Rafidia hospital	140	90 (64.3)	22(15.7)	20	8(40)	7(35)
New Technology laboratory	9	5 (55.6)	2(22.2)	26	20 (76.9)	16(61.5)
Nablus Specialty hospital	21	12 (57.1)	6(28.6)	5	4(80)	2(40)
Al-Arabi Specialty hospital	18	14 (77.8)	3(16.7)	1	1(100)	0(0)
Al-Watani hospital	7	6 (85.7)	6(85.7)	0	0(0)	0(0)
Medicare-laboratory	5	4 (80)	2(40)	0	0(0)	0(0)
<b>Units</b>						
Out patients	56	41(73.2)	14(25)	36	26 (72.2)	22(61.1)
Inpatients	144	90(62.5)	27(18.8)	16	7(43.8)	3(18.8)
General surgery	32	12 (37.5)	1(3.1)	5	1(20)	1(20)
Emergency	17	9(52.9)	0(0)	3	2(66.7)	2(66.7)
Pediatrics	16	11(68.8)	4(25)	2	1(50)	0(0)
Burns	16	10(62.5)	3(18.8)	0	0(0)	0(0)
Neonates	14	12(85.7)	5(35.7)	1	0(0)	0(0)
Urology	14	8(57.1)	3(21.4)	0	0(0)	0(0)
ICU*	9	6(66.7)	4(44.4)	2	0(0)	0(0)
Internal medicine	13	10(76.9)	4(30.8)	2	2(100)	0(0)
Orthopedic	7	6(85.7)	1(14.3)	0	0(0)	0(0)
Gynecology	6	6(100)	2(33.3)	1	1(100)	0(0)
<b>Specimen</b>						
Wound swab	126	75(59.5)	19(15.1)	17	10(58.8)	10(58.8)
Urine	23	18(78.3)	7(30.4)	19	15(79)	12(63.2)
Blood	8	8(100)	2(25)	2	1(50)	0(0)
Sputum	6	4(66.7)	4(66.7)	3	2(66.7)	0(0)
Nasal swab	8	8(100)	2(25)	0	0(0)	0(0)
Fluid	5	2(40)	2(40)	1	1(100)	1(100)
Throat swab	1	1(100)	0(0)	5	2(40)	0(0)
Vaginal swab	2	2(100)	1(50)	3	2(66.7)	2(66.7)
Umbilical swab	5	4(80)	2(40)	0	0(0)	0(0)
Ear swab	2	0(0)	0(0)	1	0(0)	0(0)
Semen	3	2(66.7)	0(0)	0	0(0)	0(0)
Skin	2	1(50)	0(0)	0	0(0)	0(0)
Burn swab	2	1(50)	0(0)	0	0(0)	0(0)
Tissue	2	1(50)	1(50)	0	0(0)	0(0)
CVP*	1	1(100)	0(0)	0	0(0)	0(0)
Chest swab	1	1(100)	0(0)	0	0(0)	0(0)

**Table 3.4 (continued)**

Variable	Staphylococci			Streptococci		
	No. isolates*	E R* (%)	DA R* (%)	No. isolates	E R (%)	DA R (%)
CSF*	0	0(0)	0(0)	1	0(0)	0(0)
Pus	1	0(0)	0(0)	0	0(0)	0(0)
Drain	1	1(100)	1(100)	0	0(0)	0(0)
Breast discharge	1	1(100)	0(0)	0	0(0)	0(0)
<b>Sex</b>						
Male	113	78(69.9)	26(26.5)	19	12(63.2)	9(47.4)
Female	87	53(60.9)	15(18.4)	33	21(63.6)	16(48.5)
<b>Total</b>	200	131(65.5)	41 (20.5)	52	33(63.5)	25(48.1)

\* No. isolates, number of isolates; E R, Erythromycin resistant; DA R, Clindamycin resistant; CVP, central venous catheter; CSF, Cerebrospinal Fluid.

With respect to erythromycin resistance, Staphylococcal strains isolated from gynecology unit were with the highest frequency (100%) compared to isolates from other departments as well as outpatients' isolates. Frequency differences were significant in comparison with those isolates obtained from outpatients and patients of general surgery, emergency, pediatrics and burns units ( $P=0.000$ ). On the other hand, clindamycin highest frequency of resistance was found in intensive care unit (44.4%), which was also significantly higher than that of emergency department ( $P= 0.001$ ).

Pronounced resistance against erythromycin and clindamycin was found among Streptococcal bacteria isolated from outpatients (Table 3.4).

Among the most commonly encountered specimens in the present study, resistance to erythromycin was highest in Staphylococci bacteria isolates of blood and nasal swabs (100% both) followed by urine isolates (78%). The resistance of bacterial isolates of blood and nasal swabs, were significantly higher than that found among wound swabs ( $P=0.000$ ).

Resistance to clindamycin was highest in Staphylococci bacteria isolated from sputum (66.7%) followed by urine (30.4%). It was also found that out of 19 Streptococci bacteria isolated from urine specimen, 15 (79%) and 12 (63%) were resistant to erythromycin and clindamycin, respectively. Among Streptococci, no significance association between specimen type and resistance rate was detected.

Analysis of antibiotic resistance for Staphylococci isolates obtained from males and females showed that erythromycin resistance is slightly higher among male isolates (69.9%) compared to females (60.9 %) and the frequency of resistance were very similar in both genders in the case of Streptococci isolates (Table 3.4). It was also found that clindamycin resistance among Staphylococci was slightly higher in male's isolates (26.5%), while Streptococci bacteria showed slightly higher resistance in isolates obtained from females (48.5%) as shown in Table 3.4.

The mean age of patients infected by erythromycin resistant Staphylococci (23 years) and Streptococci (23.7 years) isolates was slightly different from that of patients with erythromycin susceptible Staphylococci (25.1 year) and Streptococci (20 years) isolates. No significant association was found. However, variation of clindamycin resistance was clear with respect to mean age of patients. Clindamycin resistant Staphylococci strains were isolated from patients with mean age (31.9 year), higher than that of clindamycin susceptible Staphylococci isolates (21.6 year). In addition, clindamycin resistant Streptococci isolates were isolated from

patients with mean age higher (31.3 year) than that of clindamycin susceptible Streptococci isolates (25.5 year). Such differences were of no significance for the tested antibiotics.

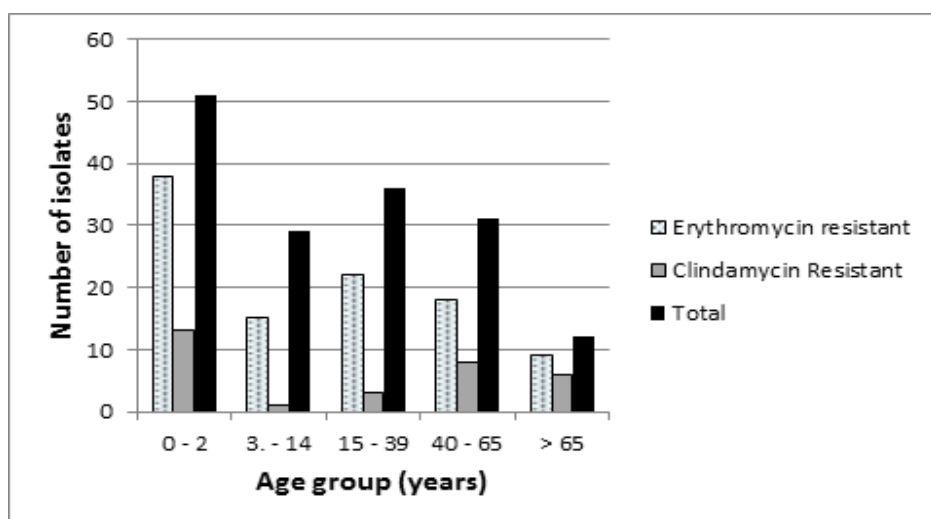
Table 3.5 below displays frequencies of antibiotics resistance of both Staphylococci and Streptococci isolates among different age groups. In Staphylococci bacterial isolates, erythromycin resistance was relatively high in all age groups (Figure 3.2), however, it was highest among age groups 0-2 years (74.5%) and age group >65 years (75%). In a similar manner, clindamycin resistance among Staphylococci was highest in bacteria isolated from patients >65 years (50%), which was also significantly higher than that of 3-14 year age group ( $P= 0.007$ ). Among age groups with abundant Streptococcal isolates, erythromycin (80%) and clindamycin (60%) resistance were found in age group 40-65 years.



**Table 3.5 Distribution of erythromycin and clindamycin resistant isolates among different age groups.**

Age (years)	Total	Staphylococci			Streptococci		
		No*	Er R*(%)	DA R* (%)	No	Er R(%)	DA R(%)
0-2	55	51	38 (74.5)	13(25.5)	4	2(50)	0(0)
3-14	32	29	15 (51.7)	1(3.5)	3	1(33.3)	1(33.3)
15-39	56	36	22 (61.1)	3(8.3)	20	15(75)	12(60)
40-65	41	31	18 (58.1)	8(25.8)	10	8(80)	6(60)
>65	14	12	9 (75)	6(50)	2	2(100)	1(50)
un known	54	41	29 (70.7)	10(24.4)	13	5(38.5)	5(38.5)

\*No, number; Er R, Erythromycin resistant; DA R, Clindamycin resistant.



**Figure 3.2** Distribution of resistant Staphylococcal isolates in different age groups.

### 3.3 Mechanisms of resistance to $MLS_B$

MIC values for erythromycin and clindamycin, erythromycin-clindamycin induction test and detection of resistance genes by PCR were combined to predict the most probable mechanism of resistance. The results indicate that resistance of Staphylococci isolates against erythromycin appear to be mediated by efflux mechanism (MS phenotype, 50.4%) and target site modification ( $MLS_B$  phenotypes, 49.6%) as shown in Table 3.6. Enzymatic inactivation of macrolides appears to have limited participation in the erythromycin resistance as predicted by the absence of enzymatic inactivating gene (*ere*) in all representative Staphylococci isolates examined for this purpose. In addition, detection of efflux gene (*msr*) in all examined isolates possessing resistance to erythromycin and susceptibility to clindamycin and negative for the induction test, indirectly confirms that enzymatic inactivation is rare in Gram-positive bacteria. Staphylococci isolates with target modification mode of resistance

expressed MLS<sub>B</sub> phenotype constitutively and inducible in 61.5% and 38.5% of the isolates, respectively. The above findings indicate that a considerable proportion of erythromycin resistant isolates (19.1%) exhibited inducible MLS<sub>B</sub>. In *S. aureus* MLS<sub>B</sub> phenotypes (51.2% of resistant isolates) was detected more frequently than CONS (30%) and the situation was reversed with respect to MS (Table 3.6). No significant association was found between bacterial type and phenotype of resistance.

**Table 3.6 Resistance phenotypes among Staphylococcal isolates.**

Isolate	Erythromycin resistant isolates	Phenotype of resistance		
		MLS <sub>B</sub> -con(%)*	MLS <sub>B</sub> -in(%)*	MS(%)*
Staphylococci	131	40 (30.5)	25 (19.1)	66 (50.4)
<i>s. aureus</i>	121	38 (31.4)	24 (19.8)	59 (48.8)
CONS*	10	2 (20)	1 (10)	7 (70)
<i>S. epidermidis</i>	10	2 (20)	1 (10)	7 (70)
<i>S.saprophyticus</i>	0	0 (0)	0 (0)	0 (0)

\*con, constitutive; in, inducible; CONS, Coagulase Negative Staphylococci

Data presented in Table 3.7 shows the phenotypes of resistance to erythromycin among Streptococci isolates. The finding of 75.8% of the studied isolates possessing MLS<sub>B</sub> resistance phenotype indicates that resistance to erythromycin is most commonly mediated by target modification. However, efflux mechanism of resistance (M phenotype) was detected in 8 (24.2%) of the isolates. No significant association was found between Streptococcal bacterial species and resistance's phenotype.

**Table 3.7 Phenotypes of resistance among Streptococcal isolates.**

Isolate type	Erythromycin resistant isolates	Phenotype of resistance	
		MLS <sub>B</sub> (Con or In)*%	M%
Streptococci	33	25(75.8)	8(24.2)
<i>S. agalactiae</i>	26	20**(76.9)	6(23.1)
<i>S. viridans</i>	5	3(60)	2(40)
<i>S. pneumoniae</i>	0	0(0)	0(0)
<i>S. pyogenes</i>	2	2(100)	0(0)

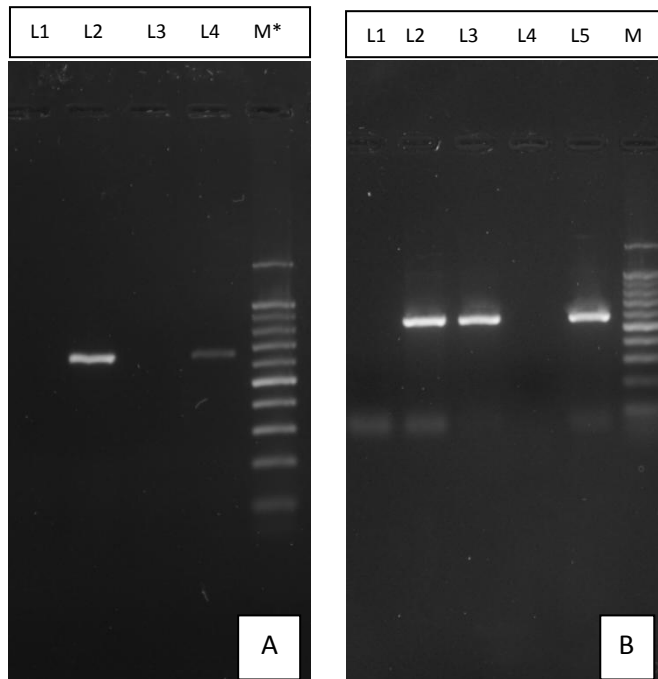
\*Con or In, constitutive or inducible

\*\*Including one isolate with positive induction test

### 3.4 Detection of resistant genes

A representative sample of erythromycin resistant isolates (47) was examined for presence of erythromycin resistance genes. Initially, multiplex- PCR was carried out with a reaction mixture containing more than 1 pair of primers (*ermB* and *ermA*; *ermB*, *ermA* and *msr*). Following this procedure did not yield good products. However, better sensitivity and product yield was obtained using single pair of primers in a reaction mix containing a higher MgCl<sub>2</sub> concentration (4mM). PCR products of representative samples are shown in Figures 3.3 and 3.4. The results showed that genes of *ermC* and *ermA* were detected in 11 and 9 Staphylococci isolates, respectively. On the other hand *ermB* was detected in 9 cases and *ermC* in only one case among Streptococci isolates (Table 3.8). It was also found that *ermA* and *ermC* were predominant among

Staphylococci isolates while *ermB* was predominant among Streptococci isolates.



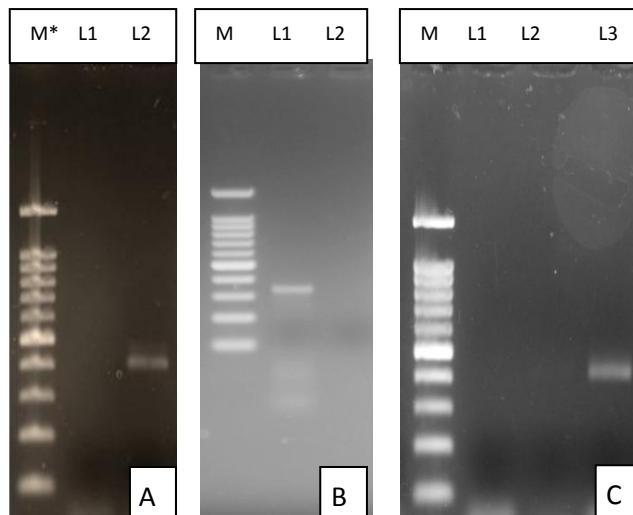
**Figure 3.3.** Amplified PCR products of *erm* genes.

**A. *ermA* and *ermB* separately:** Lane (L)1 is a negative *ermB* result; L2, *ermB* positive; L3, *ermA* negative; L4, *ermA* positive. **B. *ermC*:** L1 and L4, *ermC* negative; L2, L3 and L5, *ermC* positive; M: 100 bp ladder.

Efflux gene (*msr*) was detected in all 18 examined Staphylococci isolates exhibiting resistant to erythromycin, susceptible to clindamycin, and negative erythromycin-clindamycin induction test. All tested isolates were also negative with respect to the enzymatic inactivation *ere* gene. Such findings confirm that these isolates possess the MS phenotype. In addition, *msr* gene was detected in 2 isolates possessing the MLS<sub>B</sub> phenotype.

Efflux gene (*mef*) was detected in 2 streptococcus isolates exhibiting the M phenotype and in one isolates exhibiting the MLS<sub>B</sub> phenotype.

Enzymatic inactivating gene (*ere*) was only detected in 1 isolate exhibiting MLS<sub>B</sub> phenotype in association with other target modifying resistant genes (*ermC* and *ermB*).



**Figure 3.4. Amplified PCR products for *msr*, *mef*, *ere* genes**

**A *msr* gene:** L1, *msr* negative; L2, *msr* positive

**B. *mef* gene:** L1, *mef* positive; L2, *mef* negative

**C. *ere* gene:** L1 and L2, *ere* negative; Lane 3, *ere* positive

\*M, 100 bp ladder

**Table 3.8 Genes of macrolide resistance found in examined Staphylococcal and Streptococcal isolates.**

Type of bacteria and resistance phenotype	Examined isolates	Detected Gene(%)					
		<i>mef</i> *	<i>ere</i> *	<i>ermC</i> *	<i>ermB</i> *	<i>ermA</i> *	<i>msr</i> *
Staphylococci	36	0(0)	0(0)	11(30.6)	0(0)	9(25)	20(55.6)
MLSb constitutive	7	0(0)	0(0)	7(100)	0(0)	0(0)	1(14.3)
MLSb inducible	11	0(0)	0(0)	4(36.4)	0(0)	8(72.7)	1(9.1)
MS	18	0(0)	0(0)	0(0)	0(0)	1(5.55)	18(100)
<i>S.aureus</i>	34	0(0)	0(0)	9(26.5)	0(0)	9(26.5)	19(55.9)
MLSb constitutive	5	0(0)	0(0)	5(100)	0(0)	0(0)	0(0)
MLSb inducible	11	0(0)	0(0)	4(36.4)	0(0)	8(72.7)	1(9.1)
MS	18	0(0)	0(0)	0(0)	0(0)	1(5.55)	18(100)
CONS	2	0(0)	0(0)	0(0)	0(0)	0(0)	0(0)
MLSb constitutive	2	0(0)	0(0)	2(100)	0(0)	0(0)	1(50)
Streptococci	11	3(27.3)	1(9.1)	1(9.1)	9(81.8)	0(0)	0(0)
MLS(C orI)	8	1(12.5)	1(12.5)	1(12.5)	8(100)	0(0)	0(0)
M	3	2(66.7)	0(0)	0(0)	1(33.3)	0(0)	0(0)

\* *erm*, erythromycin ribosome methylase; *msr*, macrolide-streptogramin B resistance gene; *mef*, macrolide efflux gene; CONS, coagulase negative Staphylococci.

In staphylococcal isolate, presence of multiple resistant determinant genes was found. The gene *msr* was found in combination with *ermC* in 2 isolates and with *ermA* in one isolate. In addition, both genes (*ermC* and *ermA*) were found in one isolate. On the other hand, among Streptococcal isolates, *ermB* gene was found in association with *mef* genes in a single isolate. *ermB* gene was also found in association with *ermC* and *ere* genes in another different isolate.

### **3.5 Nosocomial infection**

Evidence of nosocomial infection (concluded from isolation of bacteria after 48 hour of hospitalization) was found in 36 cases (24 were erythromycin resistant and 14 clindamycin resistant). Findings on resistant phenotypes and source of isolates for several samples (Rafidia hospital: pediatric 2, urology 2 and burns department 3) indicates relatedness of isolates and their role of nosocomial infections. To confirm this assumption, further molecular typing for these isolate is required.



## **Chapter Four**

### **Discussion**

Resistance to antimicrobial drugs is a worldwide problem and recognized as a threat to public health and patient safety. It reduces the available treatment options and causes increased morbidity and mortality as well as increased costs due to failure of empirical antimicrobial therapy. It is also accepted that improper use of antimicrobials is behind the increased selection pressure for antimicrobial resistance. Implementations of national programs, which monitor antimicrobial use and resistance have been shown to be an efficient approach for preserving the effectiveness of antimicrobial agents in many countries (126, 127).

In the current study, a relatively high frequency of erythromycin resistance among Staphylococci isolates (65.5%) was found. Resistance to erythromycin was more frequent in coagulase negative Staphylococci (CONS) than in coagulase positive Staphylococci (COPS), which were 76.9% and 64.7%, respectively. In a Turkish study (128), 59.2% of Staphylococci isolates collected during the period 2003 to 2005 were resistant to erythromycin. This study reported similar finding as they found that resistant rate to erythromycin in CONS (69.8%) was more than that observed among COPS isolates (49.6%). Other studies (129,130, 131, 132) also reported that, CONS were more likely to be erythromycin resistant than *S. aureus*. This may be explained by presence of CONS as normal flora in the patients before causing infection, a situation that allows longer exposure periods to antibiotics and consequently better condition for natural selection of resistance. Studies from Europe and USA, carried during the period 1996-1999 (133, 129, 134), reported an incidence of

resistance to erythromycin in *S. aureus* strains ranging from 13-30% in Europe and 20-50% in the USA. Lower resistant rates to erythromycin in these studies compared to our findings are most likely due to time factor. Such differences in resistance rates emphasize the importance of continuous monitoring of drug resistance development among bacterial strains.

In the present study, erythromycin resistance rate (70.6%) among methicillin resistant Staphylococci isolates was insignificantly higher than that among methicillin susceptible isolates (59.3%). Similar previous studies reported that 76.8% of methicillin resistant isolates were resistant to erythromycin and 28.6% of methicillin susceptible isolates were resistant to erythromycin (128). Higher erythromycin resistant rate among methicillin resistant Staphylococci has been linked to the presence of erythromycin resistant genes conserved in *mec* DNA (135). However, methicillin resistant Staphylococci strains that have susceptibility to erythromycin, as well as methicillin susceptible isolates with erythromycin resistance were reported (136, 128).

Frequency of erythromycin resistance among Streptococci strains in the current study was relatively high (63.5%). Among the most commonly encountered Streptococci species, resistance rates of *S. agalactiae* and viridians Streptococci were 78.8 and 35.7%, respectively. Lower resistance rate to erythromycin among *S. agalactiae* isolates (16.3%) was reported (137). However, erythromycin resistance among viridans

Streptococci in our study was very close to that (36%) reported by Helena Seppälä et al (138).

Prevalence of clindamycin resistance rate among Staphylococci in our study (20.5%) was lower than that of erythromycin (65.5%). This can be attributed to the induction capacity of erythromycin for methylase enzyme production that performs ribosomal modification as a mode of resistance. A higher rate of clindamycin resistance among Staphylococci (46.97%) was reported in India compared to our findings (139). Furthermore, in present study, Streptococci expressed higher resistance rate to clindamycin (48.1%) than Staphylococci. This can be explained by the fact that clindamycin is an inducer at different degree of *ermB* gene for methylase enzyme production in Streptococci but not in Staphylococci (90). Resistant to clindamycin in different species of Streptococci were reported to range from 0.8% to 30.6% (140, 137, 59).

The finding of 2 lincosamide resistant Staphylococci isolates that were not resistant to macrolides indicates the presence of other resistant phenotypes. Low prevalence of this phenotype was also reported by Leclereq et al (58).

In the present study, resistance of Staphylococci isolates to erythromycin appears to be mediated by both efflux (MS phenotype) and target site modification (MLS<sub>B</sub> phenotypes) mechanisms as they were detected in 50.4% and 49.6% of resistant strains, respectively. These mechanisms were also reported to be behind erythromycin resistance

among *Staphylococci* isolates in India, where 70.5% were  $MLS_B$  phenotype and 29.5% were of MS phenotype (139). The study also reported that among the erythromycin resistant isolates, constitutive  $MLS_B$  resistance was expressed in 46.97% while inducible clindamycin resistance  $MLS_B$  expressed only in 23.48% of the isolates. In erythromycin resistant isolates of the present study, 30.5% expressed  $MLS_B$  phenotype constitutively and 19.1% inducibly. Thus, a considerable proportion of erythromycin resistant isolates exhibited inducible  $MLS_B$  phenotype. These isolates will appear susceptible to clindamycin, in disk diffusion method, and will be at a high risk of conversion from inducible to constitutive  $MLS_B$  phenotype in vivo. As a result of conversion one should expect clindamycin medication failure (88, 85). Thus, simple laboratory testing (erythromycin-clindamycin induction test) can separate strains with genetic potential (i.e., the presence of *erm* genes) to become resistant during therapy from strains that are fully susceptible to clindamycin.

We found that most (75.8%) of erythromycin resistant *Streptococci* isolates possessed  $MLS_B$  phenotype. However, efflux mechanism of resistance (M phenotype) was detected in 24.2% of resistant isolates. Among the commonly isolated *Streptococcal* species, *streptococcus agalactiae* possessed  $MLS_B$  and M phenotype in 76.9% and 23.1% of erythromycin resistant isolates, respectively. Similar findings on phenotype frequency of *streptococcus agalactiae* isolates were reported (137). In the current study viridans *Streptococci* also predominantly expressed  $MLS_B$  phenotype (60%) and to lesser degree M phenotype (40%). This finding is

contradictory to that reported by Cerda Zolezzi et al (59) as M resistant phenotype was more prevalent (60%) than MLS<sub>B</sub> phenotype (40%). *S. pyogenes* represented by two isolates showed the MLS<sub>B</sub> phenotype. Among erythromycin resistant *S.pyogenes* isolates, M phenotype was more prominent compared to MLS<sub>B</sub> (140). Variations in erythromycin and clindamycin resistant frequencies as well as resistant phenotypes in different parts of the world are expected to occur due to time factor, compliance and use of antibiotics and outbreaks of a resistant strain in clinical settings during study periods.

The lack of outer membrane of cell-wall in Gram-positive bacteria (17, 65) causes diffusion of antibiotic modifying enzymes to surrounding media and prevents their concentration as in Gram-negative bacteria. Therefore, enzymatic inactivation is rarely reported as a mechanism of resistance in Gram-positive cocci (141, 120, 142, 143). Similarly, in the present study, enzymatic inactivation of macrolides was predicted to have limited participation in the erythromycin resistance. The absence of amplified PCR products for enzymatic inactivating gene (*ere*) in all 36 examined Staphylococci isolates is in support of the limited role of enzymatic participation. In Streptococci isolates, *ere* gene was detected in combination with *ermB* and *ermC* genes in one single isolate with MLS<sub>B</sub> phenotype of resistance (target modification). Such findings are in support that target modification is behind resistance in this isolate. In addition, detection of efflux (*msr*) gene in all examined Staphylococci isolates possessing resistance to erythromycin, susceptibility to clindamycin and

non-inducible resistance to clindamycin indirectly confirms that enzymatic inactivation is rare in Gram-positive bacteria.

In the current study, out of 36 examined *Staphylococci* isolates, 9 isolates (25%) possessed *ermA*, 11 (30.6%) *ermC*, and 20 (55.6%) *msr*. Both *ermB* and *ere* were not detected. A low prevalence of *ermB* among *Staphylococci* was also recorded in earlier studies (144, 145). Absence of *ere* gene in *S. aureus* isolates was also reported by Schmitz et al (120),

Among the 11 examined erythromycin resistant *Streptococci* isolates, *ermB* gene was detected in 9 (81.8 % of examined strains); of which 7 were *S. agalactiae* and were 2 *viridans* isolates. In addition, *ermC* was detected in one *S. agalactiae* isolate. The efflux gene (*mef*) was detected in 3 streptococcus isolates (2 *agalactiae* and 1 in *viridans*) of which two were with M phenotype and 1 isolate with MLS<sub>B</sub> phenotype. Enzymatic inactivating gene (*ere*) was only detected in one isolate exhibiting MLS<sub>B</sub> phenotype in association with other resistant determinants (*ermC* and *ermB*). Zolezzi et (100), detected *ermB* in all erythromycin resistant *viridians* *Streptococci* strains possessing MLS<sub>B</sub> phenotype, either alone or in combination with *mef* gene. Among *S. agalactiae* *ermB* gene was detected 96% of isolates with MLS<sub>B</sub> (137). and *mef* gene was detected in all isolates with the M phenotype.

In the current study, variations in frequencies of antibiotic resistance among different studied centers seems to be attributed to hospital unit type. The finding of higher percentage of erythromycin and clindamycin

resistance among Staphylococci in Al-Watani hospital could be attributed to the fact that this hospital is specialized mostly for internal medicine where the patient could be suffering of severe infection, while Rafedia hospital is a surgical hospital and admitted patients most likely enrolled for sugary and not for treatment of infections.

The finding of significantly higher frequencies of erythromycin resistance among Staphylococci isolates recovered from gynecology unit in comparison to other units could be attributed to the fact that most of the women admitted to this department were pregnant or were admitted for delivery. This group of women are more sensitive to bacterial infection due to modulated immunity (146, 147), resulting in prolong bacterial infection periods allowing the possibility of development of resistance against different antibiotics.

Among the most commonly encountered specimens in the present study, resistance to erythromycin was highest in Staphylococci bacteria isolated from blood and nasal swabs (100% both), which were significantly higher than that of wound swabs ( $P=0.000$ ). In addition, resistance to clindamycin was highest in Staphylococci isolated from sputum (66.7%). Many of the cases of bacteremia and septicemia are complications after primary infection in sites other than blood circulation (148, 149). Usually a patient receives treatment before these complications. Therefore, the bacterial strains reaching blood is expected to be resistant to antibiotics used for the treatment of primary infections. The inside of the nasal cavity



and respiratory tract are known for their poor blood circulation. This is expected to decrease exposure of bacteria to immune system of the host and decrease in the exposure dose of antibiotic to bacteria. Under these conditions bacteria will have the advantage to develop antibiotic resistance. This might explain the high resistance rate to both studied antibiotics among Staphylococci strains isolated from nasal and sputum specimens. High prevalence of multidrug resistance (non-susceptibility to  $\geq$  four antimicrobial classes) in MRSA nasal isolates was also reported by Meghan et al (150). No Streptococci bacteria was found among nasal swabs and the number was limited among sputum isolates, thus, it was difficult to find similar relation between patterns of resistance and specimen types as in Staphylococci.

With respect to age groups, erythromycin resistance showed the highest rate among Staphylococci isolates recovered from 0-2 years and >65 years. This could be due to the capacity of the immune system in these age groups. The findings of very high resistant rates to erythromycin among Staphylococci isolated from neonates (90% of *S. epidermidis* and 100% of *S. haemolyticus* were resistant) are in agreement with our findings regarding 0-2 age group. (151). On the other hand, the findings of Adam et al (152) on resistance of *S. aureus*, *S. pneumoniae* and other pathogens to antibiotics (methicillin, clindamycin and claritromycin) are consistent with our findings among age group >65 years.

## **Recommendations and concluding remarks**

- The current study clearly indicates the presence of high macrolide resistant rates among bacterial isolates collected from various clinical settings. In addition, a considerable proportion of resistance was due to inducible phenotype, a situation that requires more attention by medical staff when deciding a suitable antibiotic. In our situation it seems to be essential to carry out the induction test before any decision for clindamycin prescription. It is also essential to have in mind variations of resistance rate among various age groups, specimen type and pregnant women in particular.
- In conclusion, it seems essential that the concerned governmental bodies pay more attention for monitoring resistance rates in the various clinical setting in the country in order to adopt the best treatment policy.

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جامعة النجاح الوطنية

كلية الدراسات العليا

دراسة حول مقاومة بعض الأنواع البكتيرية للمضادات الحيوية من النوع  
(Macrolides) والمثابهة وظيفيا لها في منطقة نابلس

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قدمت هذه الأطروحة استكمالا لمتطلبات الحصول على درجة الماجستير في العلوم الحياتية  
بكلية الدراسات العليا في جامعة النجاح الوطنية، نابلس - فلسطين.

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ب

## دراسة حول مقاومة بعض الأنواع البكتيرية للمضادات الحيوية من النوع (Macrolides) والمشابهة وظيفيا لها في منطقة نابلس

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### الملخص

تم جمع 200 عزلة بكتيرية من النوع Staphylococci و 52 النوع Streptococci من عدد من المراكز الصحية في محافظة نابلس خلال الفترة الممتدة من كانون ثاني من العام 2012 ولغاية شهر نيسان من العام 2013 م. شملت العزلات أنواع بكتيرية جمعت من عينات طبية مختلفة. تم استخدام طريقة agar dilution method لتحديد قيمة MIC للمضادات الحيوية من النوع اريثروميسين والنوع كلنداميسين لكل العزلات باستثناء العزلات من النوع S. pneumoniae و التي استخدم لفحصها طريقة Micro-broth dilution method. تم فحصت 47 عزلة مختلفة و مقاومة للمضاد الحيوي اريثروميسين باستخدام تقنية ال PCR بهدف الكشف عن الجينات المسؤولة عن المقاومة و المتمثلة بالجينات *ermA*, *ermB*, *ermC*, *msr*, *mef*, *ere*. استخدمت نتائج القيم لكل من MIC للمضادات الحيوية المستخدمة و فحص التحفيز على مقاومة المضاد الحيوي كلنداميسين وكذلك نتائج الكشف عن الجينات ذات العلاقة بمقاومة المضادات لغرض تحديد آلية المقاومة للمضادات الحيوية لدى الأنواع البكتيرية قيد الدراسة. لوحظ وجود نسب مقاومة عالية للمضاد الحيوي اريثروميسين لدى العزلات البكتيريا من النوع Streptococci (63%) وكذلك في النوع Staphylococci (65.5%) في حين كانت نسبة المقاومة لهذا المضاد الحيوي في النوع Coagulase negative staphylococci (76.9%) أعلى مما هي عليه في النوع S. aureus (64.7%). أما بالنسبة للمضاد الحيوي كلنداميسين كانت نسب المقاومة 48.1% في البكتيريا Streptococci و 20.5% في النوع Staphylococci. وبينت الدراسة أن مقاومة المضاد الحيوي من

النوع اريثروميسين في البكتيريا من النوع *Staphylococci* اعتمدت على آلية الضخ ( *efflux mechanism*) في % 50.4 من العزلات وعلى آلية تغير شكل هدف المضاد الحيوي في البكتيريا (Target modification) في % 49.6. وأما بالنسبة للبكتيريا *Streptococci* فاعتمدت على التغير في شكل الهدف في غالبية العزلات (% 75.8) لهذا المضاد الحيوي. كما تبين أن % 24.2 من هذا النوع البكتيري اعتمد على آلية ضخ المضاد الحيوي.

أما بالنسبة لنتائج الكشف عن الجينات ذات العلاقة بمقاومة المضادات الحيوية باستخدام تقنية ال PCR في 36 عزلة من النوع *Staphylococci* لوحظ وجود الجين *msr* و *ermC* و *ermA* بالنسب % 55.6 و % 30.6 و % 25 على التوالي. أما في ما يتعلق بدور هذه الجينات في العزلات البكتيرية من نوع *Streptococci* فقد لوحظ وجود الجينات *ermB* ، *mef* ، *ermC* ، *ere* موزعة على التوالي في 11 عزلة % 81.8، 27.3، 9.1 و % 9.1 .

أما في ما يتعلق بمقاومة المضاد الحيوي اريثروميسين في البكتيريا من النوع *Staphylococci* فقد كانت أعلى عند الأطفال الرضع في الفئة العمرية 0-2 سنة (% 74.5) والأشخاص كبار السن (% 75) وبالمثل كانت المقاومة للمضاد الحيوي كلنداميسين في البكتيريا من النوع *Staphylococci* مرتفعة عند الأشخاص كبار السن (% 50) وكانت هذه النسبة ذات دلالة إحصائية ( $P=0.000$ ) بالمقارنة بالفئة العمرية 3-14 سنة.

لقد كانت مقاومة البكتيريا *Staphylococci* للمضاد الحيوي اريثروميسين في قسم الأمراض النسائية الأعلى بالمقارنة مع باقي عزلات الأقسام الأخرى و كانت لهذه الفروقات دلالة إحصائية ( $P=0.000$ ). كما لوحظ ارتفاع في نسبة المقاومة للمضاد الحيوي اريثروميسين في البكتيريا المعزولة من عينات الدم و من التجويف الأنفي بنسب ذات دلالة إحصائية بالمقارنة مع تلك المعزولة من مسحات الجروح. أن وجود ما نسبة % 19.1 من العزلات البكتيرية من النوع *Staphylococci* المقاومة للمضاد الحيوي اريثروميسين و التي اعتمدت آلية الحث (Inducible  $MLS_B$  phenotype) في المقاومة لهي ظاهرة تستدعي انتباه الأطباء و المعنيين في اتخاذ سياسات استخدام هذه المضادات حيث أن الكشف عن المقاومة للمضاد

الحيوي كلنداميسين في هذه العزلات يحتاج إلى استخدام الفحص ألحثي ( Induction test ) لأن الطريقة التقليدية Disk diffusion وكذلك فحص ال MIC لا يمكنها الكشف عن نمط هذه المقاومة (Inducible mode). وأن العزلات ذات نمط التحفيز للمقاومة ( Inducible MLS<sub>B</sub> Phenotype) تمتلك الجين *erm* الذي يمكن أن يحول العزلة الحساسة للمضاد الحيوي كلنداميسين إلى عزلة مقاومة أثناء العلاج باستخدام هذا المضاد.