Mintage Journal of Pharmaceutical & Medical Sciences
REVIEW ARTICLE
ISSN 2320 –3315

EVALUATION OF MACROLIDE RESISTANCE AND DISTRIBUTION OF RESISTANT GENES IN STAPHYLOCOCCUS AUREUS BETWEEN, 2010 – 2013; A SYSTEMATIC REVIEW

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Received -15-12-14; Reviewed and accepted -31-12-14

ABSTRACT

Objective: Staphylococci aureus and Coagulase-negative staphylococci (CoNS) are a major source of infections associated with indwelling medical devices. Macrolide antimicrobial agents are widely used across the world to protect against bacterial infection.
Methods: This is a systematic review study valuating all pubmed, science direct, Scopus and Google scholar articles about the Evaluation of macrolide resistance in Staphylococcus aureus between 2010 – 2013 using analytical statistical analysis. Data were collected and the related information extracted and put in statistical package and analyzed.
Results: According the result of this study prevalence of macrolide resistant in some of region was more than other region and it caused by different conditions. The most common genes in macrolide resistant was erm(A) but could not be found in regulatory region of the isolates.
Conclusion: We should try to reduce the resistant to antimicrobial drug by set the healthy plane and reduce using of antimicrobial drug.

Keywords: Staphylococcus aureus, macrolide, resistance.

INTRODUCTION

Staphylococcus aureus is a leading cause of diseases such as skin and soft tissue infections, pneumonia, bloodstream infections, osteomyelitis and endocarditis, as well as toxin-mediated syndromes like toxic shock and food poisoning [1, 2]. Macrolides are antibiotics widely used for the treatment of human and animal infections. The use of these antibiotics has been accompanied by selection of resistant bacteria, e.g. staphylococci (Schlegelova et al., 2002). Macrolide resistance of frequently colonizing pathogens is clearly associated with prescription of macrolide antibiotics [3, 4]. It has developed resistance to a wide range of antimicrobial drugs, which complicates the treatment of infections [5]. Resistance to macrolides in staphylococci may be due to target site modification, active efflux (encoded by msrA) of the antibiotic, and by drug inactivation [6]. Numerous groups previously reported a very high rate of macrolide-resistant Staphylococcus aureus colonization in CF and other infections patients on long-term azithromycin and other macrolides therapy [5, 7, 8, 9]. S. aureus strains have been observed for resistance against different antibiotics viz. beta-lactam, aminoglycosides, fluoroquinolones, lincosamides and macrolides. The erm genes confer cross-resistance to macrolides, lincosamides and streptogramin B (MLSB) antibiotics and can be expressed constitutively or inducibly [10, 11]. Numerous antibiotic-resistant genes have been identified and characterized in S. aureus strains. Moreover, the antibiotic-resistant genes: mecA (methicillin), aacA-D (aminoglycosides), tetK, tetM (tetracyclines), ermA, ermB, ermC (macrolide lincosamide– streptogramin B), msrA (macrolides) and linA (lincosamides resistance) have been reported in last decade among isolates of S. aureus [12, 13, 14, 15]. Resistance to macrolides in staphylococci may be based on the active efflux mechanism encoded by the msrA gene or on 23S rRNA methylation, which is encoded by erythromycin resistance genes ermA, ermB, ermC [16, 17].

REVIEW PROCESS

A systematic review on relevant studies published in Web of Science, Pub Med and Google scholar between 2010 and 2013 reporting the macrolide resistant Staphylococcus aureus. The review was restricted to studies carried out on Staphylococcus aureus and macrolides subjects and written in the English language. Results were evaluated according to the date and subject and the subject and the report was written accordingly.

Macrolides and functions

The macrolides are widespread bactriostatic antibiotics that more of negative gram bacteria are resistant to them. Erythromycin known as celebrated antibiotic of this group and product from streptomycin erytrose. Main structure of these antibiotics is a lacton macro cyclic cycle joined to two glucose (desosamin and cladinose). azithromysin and claritromycin are produced from change in macrolide structure. Azithromysin and claritromysin commonly used for treatment of mycobacterium infections. Macrolides caused to inhibition of product of polypeptides chain by joined to 32rRNA of 50s sub unit of ribosome.

Macrolides resistant

Methylation of 32rRNA caused to disorder in joining of drug to ribosome and finally caused to resistant of bacteria to the macrolide. Furthermore other ways exist to create resistant to the antibiotic such as inactivation of macrolides by enzyme (phohsphorilas and golicolidase) and mutation in ribosomal protein and 32rRNA.

Result of macrolide resistant

Saribaş Z et al by research on total of 381 Staphylococcus aureus and 94 staphylococci (CNS) were tested by disc approximation method in 2010 shown that Of 381 isolates 112 (29.4%) S. aureus and 58 (61.7%) CNS were found to be resistant to erythromycin and inducible MLS(B) (iMLS(B)) resistance was the most prevalent pattern, being 56.2% and 41.4% among S. aureus and CNS isolates, respectively. The frequency of constitutive MLS (B) resistance (cMLS(B)) was 40.2% for S. aureus and 34.5% for staphylococci [18]. Karou SD et al by research on S. aureus, isolated from different pathologic sources were tested to determine their susceptibility to antibiotics in 2010 shown significant increase in resistance to beta-lactam antibiotics. Resistance to pristinamycin and erythromycin showed a tendency to increase while resistance to gentamicin and oleandomycin showed no statistically significant change [19]. Vandendriessche et al shown that Half of 314 MRSA isolates (n=157; 50.0%) were resistant to erythromycin [20]. Richter SS et al in 2011 shows that 90.9% of isolated MRSA was resistant to erythromycin [21]. In another study in 2011 Argudín MA et al indicated that 59 isolates of 100 isolated were resistant to four or more antimicrobial classes and 98 were methicillin resistant (mecA positive). In addition, 98%

were resistant to other antimicrobials, including macrolide-lincosamine-streptogramin B [22]. In another study twenty clinical were methicillin resistant Staphylococcus aureus strains were morphologically compared with 10 clinical macrolide sensitive strains. PCR amplification was performed to verify the presence of four known macrolide resistance genes and the result of this study indicated the ultrastructural characteristics were shared by all macrolide-resistant strains; they were not associated with the presence or absence of the known macrolide-resistance genes. Demonstrated that macrolide-resistant mutant strains derived in vitro from a macrolide-sensitive parent strain had thickened cell walls and did not harbor the known macrolide-resistance genes [23]. Patil NR et al study indicated Out of 250 isolates of Staphylococcus aureus, 90(36%) were found to be methicillin resistant Staphylococcus aureus. Among these, 46(51.11%) were Erythromycin resistant [25]. Shou-kui H et al in 2013 A totals of 205 samples collected and examined for S. aureus and resulted 62.5 % of samples resistance to erythromycin [26]. van der Donk CFM et al total of 245 S. aureus isolates were collected from NH residents and resulted Differences in the prevalence of resistance between the German and Dutch MSSA isolates were observed for the macrolides (15 % vs. 2 %, p = 0.003)[27].

Distribution of macrolide-resistance genes

First study indicated a total of 170 erythromycin resistant staphylococcal isolates were tested for the presence of erm and msrA genes. Among the S. aureus isolates with iMLS(B) and cMLS(B) phenoypes, the most common findings were the detection of ermA (44/63) and ermA + ermC (35/45) genes, respectively [18]. Another study indicated a clone specific to heterogenous macrolide resistant strains was not detected. Although all hMLSB strains had erm(A) gene, a specific and common genetic modification could not be found in regulatory region of the isolates [28]. One study in 2011 indicated from 314 methicillin resistant Staphylococcus aureus and 212 methicillin sensitive Staphylococcus aureus were collected and characterized by spa typing the gene erm(A) (n=112), erm(C) (n=41), erm(A)+erm(C) (n=3) or msr(A) (n=1). 35 of the 40 erythromycin-resistant methicillin sensitive Staphylococcus aureus (18.9%) carried the gene erm(A) (n=17), erm(C) (n=9) or msr(A) (n=9)[20]. Zmantar et al studies in 2011 indicated the frequency of erythromycin resistance genes in S. aureus was: ermA+ 7.7%, ermB+ 13.7%, ermC+ 6% and msrA+ 10.2%. In addition, the number of positive isolates in CoNS was respectively ermA+ (9.4%), ermB+ (11.1%), ermC+ (27.4%), and msrA+ (41%) [29]. Hyo Y et al in 2013 by research on Twenty clinical macrolide-resistant Staphylococcus aureus strains were morphologically compared with 10 clinical macrolide sensitive strains. PCR amplification was perform to verify the presence of four known macrolide resistance genes resulted the ultrastructural individuality were shared by all macrolide-resistant strains; they were not associated with the presence or absence of the known macrolide-resistance genes. Demonstrated that macrolide-resistant mutant strains derived in vitro from a macrolide-sensitive parent strain had thickened cell walls and did not harbor the known macrolide-resistance genes [23, 24]. Türkyılmaz S et al in 2010 indicated The susceptibility rates to antimicrobials tested were erythromycin 0 % among macrolide-resistant isolates, 9 of them had erm(A), and seven had both of genes [30]. In another study in 2011 Argudín MA et al showed that from 100 samples 70%, encoded by ermA, ermB, and ermC, alone or in combination [22].

DISCUSSION

Aims of this study is Evaluation of macrolide resistance and distribution of resistant genes in Staphylococcus aureus between “2010 – 2013”, result of this study indicated the prevalence macrolide-resistant Staphylococcus aureus are variety in different region and in some of region prevalence of macrolide- resistant was more than other region that this result may be affected by different condition such as widespread use of anti microbial drug, life style and the diet of nutrition. Result of studies about distributions of resistant gene showed that most common gene in all of study was emrA and all of study verifying this matter but could not be found in regulatory region of the isolates .emrB and emrC was in next steps. Probably these genes are caused of resistant to erythromycin and other macrolides. macrolid resistant probably created by widespread using of macrolides and by research about this gene and inhibition of this gene maybe can prevention of macrolide resistant.

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