**ABSTRACT**

**Introduction:** Resistance to macrolides, lincosamides and streptogramins B (MLS$_B$ antibiotics) in *staphylococci* may be due to modification in ribosomal target methylase encoded by *erm* genes. The expression of MLS$_B$ resistance lead to three phenotypes, namely constitutive resistance (cMLS$_B$), inducible resistance (iMLS$_B$), and resistance only to macrolides and streptogramins B (MS$_B$). The iMLS$_B$ resistance is the most difficult to detect in the clinical laboratory. **Objective:** This study investigated the expression of MLS$_B$ resistance and the prevalence of the *erm* genes among 152 clinical isolates of *Staphylococcus aureus* and coagulase-negative *Staphylococcus* (CNS) from Hospital de Clínicas de Porto Alegre. **Methods:** Primary MLS$_B$ resistance was detected by the disk diffusion method. Isolates with iMLS$_B$ phenotype were tested by double-disk induction method. All isolates were tested by a genotypic assay, PCR with specific primers. **Results:** A total of 46.7% of *staphylococci* were positive for cMLS$_B$; 3.3% for iMLS$_B$ and 3.3% for MS$_B$. One or more *erm* genes were present in 50.1% of isolates. The gene *ermA* was detected in 49 isolates, *ermC* in 29 and *ermB* in 3. **Conclusion:** The prevalence of the *ermA*, *ermB* and *ermC* genes were 29.6%, 17.1% and 0.66% respectively, and constitutive resistance was the most frequent as compared to the other two phenotypes. **Keywords:** *Staphylococcus*; resistance; *erm* genes; macrolides.
reaction (PCR) with specific primers is a genotypic method used to confirm the presence of the MLS\(_B\) genes, \textit{erm}\(A\), \textit{erm}\(B\) e \textit{erm}\(C\).\textsuperscript{12} The risk for therapeutic failure is increased as constitutive resistance may raise from iMLSB during the course of clindamycin therapy in patients with severe \textit{staphylococci} infections.\textsuperscript{11}

The objective of this study was to determine the prevalence of the MLS\(_B\) genes in \textit{Staphylococcus aureus} and coagulase negative \textit{staphylococci} from patients attending the Hospital de Clínicas de Porto Alegre (HCPA).

MATERIALS AND METHODS

Bacterial isolates

Isolates of\textit{ S. aureus} and of CNS were collected from consecutive clinical specimens sent to the of microbiology laboratory of the HCPA. The period of the study was between September and October 2007. The bacterial identification was performed through Gram's technique and catalase and coagulase tests. Isolates were stored in glycerol broth at -20°C until use.

Susceptibility tests

The antimicrobial susceptibility test was performed by the disk diffusion method on Mueller Hinton Agar (bioMérieux, Marcy L’Etoile, France), according to the Clinical and Laboratory Standards Institute (CLSI 2008), with the following antibiotic (Oxoid\textsuperscript{®}): oxacillin (1 µg), cefoxitin (30 µg), vancomycin (30 µg), gentamicin (10 µg), clindamycin (2 µg), chloramphenicol (30 µg), doxycycline (30 µg), erythromycin (15 µg), levofloxacin (5 µg), rifampin (5 µg) and trimethoprim-sulfamethoxazole (25 µg). \textit{S. aureus} ATCC 25923 was used for quality control.

The standard CLSI double-disk diffusion (D test) test was performed using Mueller Hinton agar (bioMérieux, Marcy L’Etoile, France) with a 15 µg erythromycin disk and 2 µg clindamycin disk (Oxoid\textsuperscript{®}) placed at distances of 15 and 26 mm and incubated for 24 h at 35°C.\textsuperscript{11}

Table 1. Correlation between \textit{erm} genes and MLSB resistance phenotypes

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Phenotype</th>
<th>\textit{erm}A</th>
<th>\textit{erm}B</th>
<th>\textit{erm}C</th>
<th>\textit{erm}A/\textit{erm}C</th>
<th>\textit{erm}A/\textit{erm}B</th>
<th>\textit{erm}A/\textit{erm}B/\textit{erm}C</th>
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<tbody>
<tr>
<td>S. aureus</td>
<td>40 (cMLS(_S))</td>
<td>36</td>
<td>1</td>
<td>3</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>3 (iMLS(_S))</td>
<td>2</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>2 (MS(_S))</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>CNS</td>
<td>24 (cMLS(_S))</td>
<td>0</td>
<td>0</td>
<td>20</td>
<td>2</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>2 (iMLS(_S))</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>0</td>
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<tr>
<td></td>
<td>3 (MS(_S))</td>
<td>0</td>
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The inducible phenotype was characterized by a positive D test, a flattening of the inhibition zone around the clindamycin disk near to the erythromycin disk and indicates that erythromycin has induced clindamycin resistance (iMLSB). The phenotype cMLS\(_B\) was characterized by erythromycin and clindamycin resistance. Finally, the phenotype (MS\(_S\)) was characterized by clindamycin susceptibility and erythromycin resistance, with negative D test.

\textit{erm}A, \textit{erm}B and \textit{erm}C gene detection

A direct colony suspension of the culture equivalent to a 1.0 McFarland standard was prepared in 500 µL of 10 mM Tris-1 mM EDTA (pH 8.0), vortexed, and boiled for 10 min an aliquot of 5 µL of the suspension was used for each 25 µL reaction mixture.\textsuperscript{13}

PCR assays and primers specific from the \textit{erm}\(A\), \textit{erm}\(B\) and \textit{erm}\(C\) resistance genes used in this study have been previously described by Gerard, Lina \textit{et al.} (Table 1).\textsuperscript{14} Each reaction was carried out in a final volume of 25 µL and included 10 x PCR buffer (pht\textsuperscript{®}); 3 mM of MgCl\(_2\) (pht\textsuperscript{®}); 5 µM of each \textit{erm}\(A\), \textit{erm}\(B\) and \textit{erm}\(C\) forward and reverse primers (Invitrogen\textsuperscript{®}); RNAse and DNase free water; 1.25 U of Taq DNA polymerase (pht\textsuperscript{®}); 2.5 mM of each dATP, dTTP, dCTP, and dGTP (ABgene\textsuperscript{®}); and 5 µL of DNA. The PCR mixture was subjected to thermal cycle (30 cycles of 30 s at 94°C as the denaturation step, 30 s at 57°C as the annealing step, and of 5 min at 72°C as the extension step) with a JMR\textsuperscript{®} PTC-100. The PCR-amplified reaction mixture was resolved by electrophoresis through a 2% agarose gel containing ethidium bromide in Tris-borate-EDTA buffer at 12 V/cm for 30 min. The gel was visualized under UV light and the sizes of the amplification products were estimated by comparison with 100 bp molecular size standard ladder.

Three clinical samples with positives results for each of the three genes were submitted to sequencing and analyzed by BLAST and Chromas and DDBJ/EMBL/GenBank. These isolates were used as positive control in all experiments.
RESULTS

A total of 152 strains including 94 S. aureus and 58 CNS were included in this study. Eighty-one (53.3%) exhibited erythromycin resistance and were considered for evaluation of the three distinct MLS_b resistance phenotypes (cMLS_b, iMLS_b, MS_b). Among these 81 erythromycin-resistant strains, 10 showed clindamycin susceptibility and were tested by double-disk diffusion method. We found only five (6.2%) isolates with iMLS_b resistance phenotype (three S. aureus and two CNS) and five (6.2%) with MS_b resistance phenotype (two S. aureus and three CNS). The remaining 71 (87.7%) isolates were considered as cMLS_b resistance phenotype (46 S. aureus and 25 CNS).

All the 152 strains were tested for the presence of MLS_b resistance genes and 77 (50.1%) contained one or more erm genes (Figure 1). The ermA gene was detected in 44 isolates (41 S. aureus and three CNS), the ermB gene was found in only one isolate of S. aureus and the ermC gene was detected in 28 isolates (four S. aureus and 24 CNS). Combination of erm genes was detected in 4 CNS isolates (Graphics 1 and 2). For S. aureus isolates with cMLS_b resistance phenotype, 36 presented the ermA gene, only one exhibited the ermB gene and three had the ermC gene. Moreover, in three of the S. aureus isolates with iMLS_b resistance phenotype, two isolates were ermA positive and one was ermC positive. The ermC gene was identified in 20 isolates of CNS with cMLS_b resistance phenotype and in two isolates of CNS with iMLS_b resistance phenotype. Seven (six S. aureus and one CNS) isolates with cMLS_b resistance phenotype did not present any of the three erm genes (Table 1). Resistance to non-MLS_b antibiotics in S. aureus and CNS isolates with erm genes was higher in relation to the isolates without the erm genes: chloramphenicol (p = 0.004), doxycycline (p < 0.001), gentamicin (p < 0.001), levofloxacin (p < 0.001), oxacillin (p < 0.001), rifampin (p < 0.001) and, trimethoprim-sulfamethoxazole (p < 0.001). Of the 77 isolates who harbored erm genes, 65 (40 S. aureus and 25 CNS) were multidrug resistant (resistant to five or more antimicrobial class). The overall range of multiresistance among the staphylococci strains studied was 48.2%.

DISCUSSION

The incidence of constitutive and inducible MLS_b resistance may vary according to different geographic region and even from hospital to hospital or patient group. This variability is usually associated with the inconsistent use of erythromycin in different institutions; the origin of the isolate (nosocomial versus community acquired); patient age and clinical samples. In our study 53.3% of staphylococci presented one of three MLS_b resistance phenotypes. In fact, cMLS_b resistance phenotype was the most common (46.7%) and iMLS_b and MS_b phenotype were each detected in only 3.3% of the staphylococci.

In a study conducted in Texas by Fiebelkorn et al. the cMLS_b resistance phenotype was also the most prevalent phenotype (41.7% of staphylococci) but the iMLS_b was found in 25.2% of the isolates, indicating a difference in relation to MLS_b data of the present study. In Europe where the MLS_b resistance phenotype prevalence are somehow variable, in London Hamilton-Miller et al. detected staphylococci with iMLS_b as the predominant phenotype (43% of isolates) and the cMLS_b resistance phenotype was detected in only 24% of isolates. The D test is critical, in this scenario, to avoid therapeutic failure. On the other hand, CNS isolates studied in Sevilla demonstrated that the MS_b resistance phenotype was more common (11.2%) in relation to the other phenotypes (iMLS_b, cMLS_b, MS_b, and cMLS_a).

**Figure 1:** (A) Lanes 1 and 2 ermA positive in 421 bp; lane 3 negative control; lane 4 positive control; and lane 5 100 bp molecular size ladder. (B) Lane 1 ermB positive in 359 bp; lane 2 negative control; lane 3 positive control; and lane 4 100 bp molecular size ladder. (C) Lane 1 ermC positive in 572 bp; lane 2 negative control; lane 3 positive control; and lane 4 100 bp molecular size ladder.

**Graphic 1:** Frequency of *erm* genes in *S. aureus* isolates.

**Graphic 2:** Frequency of *erm* genes in SCN isolates.
7.4% and cMLS\textsubscript{S} 3.2%).\textsuperscript{20} In contrast, the cMLS\textsubscript{S} resistance phenotype was most frequent (46.9%) as compared to iMLS\textsubscript{S} (30.2%) in France.\textsuperscript{14}

In Turkey it was demonstrated that the prevalence of the cMLS\textsubscript{S} phenotype is higher than that of the iMLS\textsubscript{S} phenotype and the MS\textsubscript{S} phenotype is low, data similar to our study.\textsuperscript{15,18-20}

A previous study conducted in our city evaluated 200 CNS and showed that only 2.5% of isolates presented the iMLS\textsubscript{S} resistance phenotype.\textsuperscript{21} Therefore, one could speculate that the prevalence of the inducible phenotype is low in our city.

Despite the fact that there is geographic variability among MLS\textsubscript{S} resistance phenotypes, the prevalence of \textit{erm} genes has been reported to be similar in various countries. According to our findings, the \textit{ermA} gene was the most prevalent among the \textit{S. aureus} isolates (43.6%) and the \textit{ermC} gene was the most prevalent among the SCN isolates (37.9%). Only three isolates of \textit{staphylococci} presented the \textit{ermB} gene (2.0%). The presence of more than one \textit{erm} gene was not detected in \textit{S. aureus} but it was observed in four SCN isolates. According to Martineau \textit{et al.}, in Canada, 20.9% of the \textit{S. aureus} were positive for the \textit{ermA} gene and 66% of CNS were positive for the \textit{ermC}gene, demonstrating that the prevalence of the \textit{ermA} gene in \textit{S. aureus} is slightly lower in comparison to other studies.\textsuperscript{22} A multicenter study in 24 European university hospitals confirmed the high prevalence of \textit{ermA} gene and the low prevalence of \textit{ermC} and \textit{ermB} genes among 851 \textit{S. aureus}.\textsuperscript{21} Lina \textit{et al.} found 63.2% of \textit{S. aureus} with \textit{ermA} gene positive and 44% of CNS strains \textit{ermC} gene positive, while the \textit{ermB} gene was present in only 1% of \textit{staphylococci}.\textsuperscript{14} The results reported by Westh \textit{et al.} in Denmark, also showed a high prevalence of the \textit{ermA} gene in \textit{S. aureus} isolates and the \textit{ermC} gene in CNS strains, as well as a low prevalence for the \textit{ermB} gene.\textsuperscript{14} In our study, the \textit{ermB} gene was also detected in a small percentage of \textit{staphylococci} isolates. This gene is generally found in animal \textit{staphylococci} strains.\textsuperscript{14,15,16}

In the present study, eight isolates (three \textit{S. aureus} and five SCN) susceptible to erythromycin proved to carry \textit{erm} genes (seven \textit{ermA} e one \textit{ermC}). The presence of \textit{erm} genes among isolates of \textit{staphylococci} susceptible to erythromycin had already been demonstrated in another study.\textsuperscript{21} This may be due to the lack of expression of \textit{erm} genes due to factors which down regulate the expression of this gene.\textsuperscript{21,23}

In our study we found six \textit{S. aureus} isolates and one CNS resistant to erythromycin and clindamycin but with negative genotypic test. These results were probably associated with the presence of other genes, such as \textit{msrA} and \textit{msrB}, with low frequency in \textit{Staphylococci} species isolated form humans,\textsuperscript{23} which were not evaluated in this study.

We detected three \textit{S. aureus} resistant to clindamycin and susceptible to erythromycin, which did not harbor \textit{erm} genes. In a study conducted by Lina \textit{et al.}, the only SCN sample that presented this susceptibility profile was positive for the genes \textit{linA} and \textit{linA}.'\textsuperscript{14} These genes confer lincomamides resistance only in \textit{S. hemolyticus} and \textit{S. aureus}. Incidence of \textit{staphylococci} with lincosamide resistance but without resistance to macrolides and streptograms is usually very low.\textsuperscript{14,26}

**CONCLUSION**

The aim of this study was to determine the prevalence of the MLS\textsubscript{S} phenotypes and genes in \textit{Staphylococcus aureus} and coagulase-negative \textit{staphylococci} from patients receiving care at our hospital. We found that constitutive MLS\textsubscript{S} resistance was the most prevalent phenotype in \textit{staphylococci}; \textit{ermA} was the most prevalent gene in \textit{S. aureus} strains, whereas \textit{ermC} was the most frequent gene in CNS isolates. Therefore, \textit{staphylococci} with resistance to MLS\textsubscript{S} are usually detected directly in routine susceptibility test and the “D test” is not required to be performed in most of our isolates. However, other regions in our country may not present the same resistance profile as ours and, therefore, surveillance studies are warranted in different institutions.

**REFERENCES**