ABSTRACT

EFFECTS OF *ermTR* GENE IN ERYTHROMYCIN SUSCEPTIBLE *Streptococcus pyogenes* NZ131 and *Staphylococcus aureus* RN4220

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ermTR is one of the most common gene that confers resistance to macrolides especially in *Streptococcus*. The effect of *ermTR* was never shown in isogenic conditions. The purpose of the present study was to show the effect of *ermTR* in isogenic conditions by cloning *ermTR* and transferring this gene to a Gram positive bacteria. Total DNA was extracted from *S. pyogenes* C1 and was used for amplification of *ermTR* gene. Modified primers with addition of restriction sites were used to simplify cloning. Amplicons as well as pUC18 were restricted than mixed and ligated. Transformants were selected after electrotransformation of *E. coli* DH10B and DB10 on selectif media. Recombinant plasmids were purified, restricted and subcloned in a shuttle plasmid pJIM2246 and were used for transformation of *E. coli* DH10B. Recombinant pJIM2246 plasmids with *ermTR* gene were introduced to *E. faecalis* JH2-2, *S. aureus* RN4220 and *S. pyogenes* NZ131by electroporation.

MICs for *E. coli* and *S. aureus* transformed with ermTR gene. The construct contained no regulatory region to see the effect of ErmTR methylase continuously synthesized.

This study showed two main differences between ErmTR and other methylases. i) Level of erythromycin resistance conferred by ErmTR remains low. ii) Lincomycin resistance level conferred by ErmTR methylation is higher than macrolide. Other methylases *ermA, ermB* confer high level of macrolide resistance and high level lincomycin resistance if the synthesis is permanent. These methylases methylates adenine at position 2058 of 23S rRNA. Also mutations at that position confer high level resistance. Further studies are necessary to determine methylation site of ErmTR. ErmTR may methylate an other site than A2058 at 23S rRNA.

Key words: *ermTR*, macrolide resistance, methilation, regulatory region, MIC, induction