

PERVELANCE OF *erm(C)* RESISTANCE GENES EXPRESSION IN *Staphylococcus aureus* IN COMPARISON TO *Lactobacilli*

Shahrukh Samson¹, Wafa Majeed¹, Muhammad Naeem Faisal¹, Nabeeha Shahab^{1*}, Maria Daud¹, Hafsa Iqbal¹, Mahnoor Syed¹ and Ambreen Mahmood Awan¹

¹Institute of Pharmacy, Physiology and Pharmacology, University of Agriculture, Faisalabad, Pakistan

Antimicrobial resistance is an alarming health problem all over the world. Antibiotic resistant bacterial strains are pathogenic and are becoming immune modulator. Studies revealed that antibiotic-resistant strains are concerned with massive and irrational use of antibiotics. Studies also revealed that increase in resistant bacterial strains have become “nightmare bacteria” so as to “pose a disastrous threat” all over the world. *Lactobacilli* are the key player in transferring the virulence factors and equally contributing in spreading the resistant genes to other bacterial population through horizontal gene transfer (HGT). In this study we identified the function of *lactobacilli* in shifting the *erm(C)* genes to *Staphylococcus aureus*. The population of the study consist of the patients those who made excessive use of antibiotics. Clinical samples were collected from human patient and cultured on mannitol salt agar medium and sensitivity assay was performed through disc method. Samples were subjected to isolation of g-DNA and amplification of bacterial DNA through PCR followed by Gel electrophoresis and q-RT-PCR for gene expression analysis. *erm(C)* is the resistant gene against erythromycin and high expression of this gene ($P \leq 0.03$) found in *Staphylococcus aureus* with comparison to *lactobacillus*. It indicates that erythromycin becomes resistant in *Staphylococcus aureus* and therapeutic response reduced.

Notes: