ABSTRACT

Background: *Staphylococcus aureus* can cause a range of illnesses, from minor skin infections to life-threatening diseases of respiratory tract, CNS and bones toxic shock syndrome, bacteremia, and sepsis. As we approach the halfway point of the second decade of fluoroquinolone use, resistance has already emerged in some species of bacteria and some clinical settings. This study has been undertaken to examine the mechanisms of fluoroquinolone resistance and discuss epidemiologic factors that may have contributed to the prevalence of antibiotic resistance in clinical settings.

Materials And Methods: 120 clinical isolates of *Staphylococcus aureus* from various clinical samples were cultured on blood agar. Following biochemical confirmation, fluoroquinolone resistance was tested by disc diffusion and agar dilution methods. Genotypic detection of gyrase genes (gyrA, gyrB, topoisomerase IV, grlA, grlB) were done by PCR.

Results: The resistance to fluoroquinolones among the total isolates of *Staphylococcus aureus* was 14%. High level of ciprofloxacin resistance was noted among majority of the isolates tested (MIC: 32 to 64 µg ml). Real time PCR for detection of fluoroquinolone resistance showed grlA and gyrA to be the most predominant genes expressed (72%) mostly in MRSA.

Conclusion: Injudicious use of antibiotics has led to widespread emergence of resistant organisms. The strict implementation of antibiotic policy tailor made to the individual hospital needs and prompt regular audits of compliance to the same are the only means of saving the populations from newer pathogens and multi drug resistant bugs.
**Keywords:** *Staphylococcus aureus*, Fluoroquinolones, gyrase genes, agar dilution, MRSA