



MOLECULAR STUDY OF ERYTHROMYCIN RESISTANCE FACTORS IN GRAM POSITIVE COCCI ISOLATED FROM IN SHAHID RAJAEI TEACHING HOSPITAL, QAZVIN

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Background: Gram positive cocci organisms show many molecular important resistance factors to erythromycin which would be important nosocomial infections agents. This study was conducted to determine the molecular factors for resistance to erythromycin, in gram positive cocci isolated from laryngoscope in Shahid Rajaei teaching hospital, Qazvin.

Methods: This molecular descriptive study was carried on the samples collected from the laryngoscope in 1392. In aseptic conditions; samples were transferred to microbiology laboratory. Bacterial identification was performed using the standard laboratory methods. Antibiotic sensitivity was carried out using usual disk diffusion agar method according to CLSI recommendation. PCR assay was performed and the products of it was sequenced to check the presence of *mef*, *msrA*, *ermA*, *ermB*, *ermC* genes.

Results: 21 isolates (41/1%) out of 51 were resistance to erythromycin. In Coagulase -ve Staphylococci (CONS) were positive for *ermC* (4-19.5%) and *mef* (1-4.76%), respectively. Alpha hemolytic Streptococci were also positive for both *ermA* and *ermB* (2-9.52%) and gamma hemolytic Streptococci carried *ermB* (4-19.5%), *ermA* and *mef* (1-4.76%).

Conclusion: The most important finding in this study is the presence of the erythromycin resistance genes for the *mef*, *msrA*, *ermA*, *ermB*, *ermC* in collected isolates from laryngoscope in our hospital. Since laryngoscope can potentially be carried in resistant isolates, disinfection and control the infection is essential before using this device in patients.

Keywords: Laryngoscope, Gram Positive Cocci, Erythromycin, Resistant Genes

PLASMID-MEDIATED QUINOLONE RESISTANCE DETERMINANTS QNR AND AAC(6)-IB-CR IN FLUOROQUINOLONE-RESISTANT ENTEROBACTERIACEAE IN HAMADAN, Iran

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Background: The quinolone group is an important class of broad-spectrum antimicrobial agents. Plasmid mediated quinolone resistance (PMQR) determinants have emerged as a significant concern in recent years. This study reports the screening of resistant-isolates to Fluoroquinolone antimicrobial agents for PMQR determinants and detection of *Qnr* and *aac(6)-Ib-cr* genes.

Methods: Total of 100 fluoroquinolone-resistant Enterobacteriaceae were isolated from 3 hospitals in Hamadan from October 2012 to June 2013. The isolates were identified by biochemical tests and confirmed by PCR. Antimicrobial susceptibility to 14 antimicrobial agents including levofloxacin and ciprofloxacin was determined by Clinical Laboratory Standards Institute (CLSI). Disk diffusion methods and ciprofloxacin MIC were obtained by broth microdilution. Then the isolates were screened for the presence of *qnrA*, *qnrB*, *qnrS* and *aac(6)-Ib-cr* genes using PCR assay.

Results: Among the screened isolates, 64 strains (64%) of *Escherichia coli*, 23 strains (23%) of *Klebsiella pneumoniae*, 13 strains (13%) of *Proteus mirabilis* were collected as quinolone-resistant isolates. Out of 100 isolates, two (2%) isolates were positive for *qnrS*, seventeen (17%) isolates were positive for *qnrB* and we did not find the *qnrA* gene in any of the isolates. There were also 32 positive isolates for *aac(6)-Ib-cr* gene.

Conclusion: In this study we describe the prevalence of *qnr* and *aac(6)-Ib-cr* genes in Fluoroquinolone-resistant Enterobacteriaceae in Hamadan. The carriage rate of multidrug-resistant Enterobacteriaceae in healthy people in Hamadan City is extremely high. Moreover, genes encoding transferable quinolones, in particular *aac(6)-Ib-cr*, are highly prevalent in these strains.

Keywords: Enterobacteriaceae, Antibiotic Resistance, Fluoroquinolone.

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