Molecular Detection of Extended Spectrum β-Lactamase (ESBL) Genes PER-1, GES-1 &CTX-M in Clinical Isolate of Pseudomonas aeruginosa

Fereshteh Satarian*[1]; Abbas Ali Imani Fooladi[2]; Seyed Fazlollah Mosavi[3]; Hamid Sedighian Rad[2]

1- Tehran Research and Science Branch, Islamic Azad University,Tehran, Iran

2-Applied Microbiology, Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran

3-Department of Bacteriology, Pasteur Institute of Iran,Tehran, Iran

f.satarian89@yahoo.com

Background & Objectives: Hospital-acquired infections caused by *Pseudomonas aeruginosa* are so intense and have a high mortality rate .Since that resistance to extended spectrum Cephalosporins in P. aeruginosa due to achieving the ESBLs genes being increasingly reported worldwide , this study aimed to consider molecular prevalence of ESBL genes blaPER-1 ,blaGES-1 &blaCTX-M in clinical isolate of *P. aeruginosa* strains.

Methods: Genome of 110 p. aeruginosa strains isolated from a variety of clinical samples such as sputum ,blood and urine were extracted then the presence of ESBLs genes blaPER-1 ,blaGES-1 & blaCTX-M were analyzed by polymerase chain reaction (PCR) with choosing three pairs primers.

Results: According to PCR result among 110 considered P. aeruginosa strains ,bla PER-1 was detected in 33.6%(37/110) ,blaGES-1 was detected in 39% (43/110) and bla CTX-M was detected in 65.4% (72/110) and among all strains 15.4%(17 /110) appeared to produce each three genes .

Conclusion: In the present study it was confirmed that a high spreading of ESBL genes exist in clinical P. aeruginosa strains , in addition bla CTX-M ESBLs gene is the most prevalent gene ,therefore performance of antibiogram test is necessary before using antibiotics.

Keywords: *Pseudomonas aeruginosa*; ESBL; PCR