Original Paper

Detection of phospholipase and type IV pili genes in clinical isolates of multidrug-resistant *Pseudomonas aeruginosa*

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Abstract

Background and Objective: *Pseudomonas aeruginosa* is an opportunistic pathogen with numerous virulence factors such as phospholipase and type IV pili. The emergence of multidrug resistant *Pseudomonas aeruginosa* has become a serious public health threat worldwide. This study was done to determine the frequency of plcH, plcN, pilA and pilB genes in multi-drug resistant *Pseudomonas aeruginosa* isolated from clinical samples.

Methods: In this cross-sectional study, 93 isolates of *Pseudomonas aeruginosa* collected from different clinical samples from hospitals of Zanjan, Iran during 2013-14. After identification of isolates by biochemical tests, antibiotic susceptibility testing (Kirby-Bauer) was performed according to CLSI guidelines. Total DNA extracted and PCR was done to detect of plcH, plcN, pilA and pilB genes.

Results: Among 93 of *Pseudomonas aeruginosa* isolates, the highest antibiotic resistance related to Erythromycin and Cefoxitin (95.6%) and the lowest resistance related to Amikacin (26.8%). 80.6% of isolates were multidrug resistant (MDR). Out of 75 MDR isolates, the frequency of plcH, plcN, pilA and pilB genes was 97.4%, 49.3%, 26.6% and 17.3%, respectively.

Conclusion: According to high frequency of phospholipase C gene (plcH) in MDR *Pseudomonas aeruginosa* isolates which isolated from different clinical samples, presumably this virulence factor plays an important role in pathogenesis of this bacterium.

Keywords: *Pseudomonas aeruginosa*, Antibiotic resistance, Phospholipase C, Type IV Pili

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