

## Abstract

*Pseudomonas aeruginosa* is an opportunistic pathogen and one of the most frequent pathogens in nosocomial infections. It causes different types of infections including urinary tract infections and Bacteremiae. This bacterium has many pathogenic factors including; exotoxin A, lipopolysaccharide, phospholipase C, flagella, elastase and alkaline protease. In this study, frequency of *fli C* and *alg D* genes from clinical *Pseudomonas aeruginosa* strains isolated were analysed. The isolates were identified by biochemical methods, DNAs were extracted. Next, special primers were utilized of flagellin and alginate genes. PCR was applied to detect the presence or non-presence of the related genes.

**Conclusion:** Our results demonstrate that 85% of the isolated clinical samples have a *fli C* gene and 95% of the clinical samples show to have a *alg D* gene. the results of our study confirm that flagellin and alginate genes presence is considered an important virulence factor of *pseudomonas aeruginosa*.

Key words: *Pseudomonas aeruginosa*, *Fli C*, *Alg D*, PCR

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**Frequency of *fli C*, *alg D* genes from clinical *Pseudomonas aeruginosa* Strains isolated in Zabol**

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