

Molecular Detection of Virulence Factors Genes in *Pseudomonas aeruginosa* Isolated from Different Infections Cases in Al-Diwaniya Hospital

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Abstract:

Pseudomonas aeruginosa is the most important and dangerous organism in human infections due to production of several extracellular and cell-associated virulence factors that cause severe tissue damage, the most important virulence factors including (exoenzyme S, exotoxin A and lipoprotein), these factors were encoded by (exoS, toxA and oprI gene respectively). In this study we used polymerase chain reaction technique (PCR) for detection of virulence factor genes produced by *P. aeruginosa* that isolated from wound, burn and pulmonary tract infections patient swab samples. The PCR results show that all *P. aeruginosa* isolates carried virulence factor genes with difference in prevalence between them. The burn infection *P. aeruginosa* isolates show high prevalence of virulence factor genes more than wound and pulmonary tract infections isolates as well as the virulence factor gene (ToxA) shows high production in most isolates. In this study we concluded that the production of virulence factor genes in *P. aeruginosa* is important to human infection especially (ToxA) gene and the PCR technique is very specific and fast method in detection of virulence factor genes in *P. aeruginosa*.

Key words: *Pseudomonas aeruginosa* Virulence Factors Genes.

Natural history Classification QH 426-470

Introduction:

P. aeruginosa is an opportunistic pathogen that is capable of infecting humans⁽¹⁾. In humans it can cause severe infections in virtually all tissues. Pulmonary tract infection with *P. aeruginosa* is a major cause of morbidity and mortality in patients with cystic fibrosis⁽²⁾. *P. aeruginosa* infections in hospitals mainly affect patients in intensive care units with burn wound infections or chronic illnesses⁽³⁾.

P. aeruginosa possesses a large number of cell-associated and extracellular virulence factors, which are tightly regulated by cell-to-cell signaling systems⁽⁴⁾. Most virulence factors produced by this bacterium which are important in its pathogenicity are: Exotoxin, Exoenzyme S, L lipoprotein, las

B elastase and phospholipase C⁽⁵⁾. Among these virulence factors are a variety of secreted factors, such as proteases, phospholipases and the exotoxin A. *P. aeruginosa* strains also possess a type III secretion system that allows them to deliver toxins (effectors) directly into the cytoplasm of a host cell⁽⁶⁾. Exotoxin A, which is an important cause of tissue necrosis since it blocks protein synthesis⁽⁷⁾. Exotoxin A, encoded by the toxA gene, inhibits protein biosynthesis by transferring an ADP-ribosyl moiety to elongation factor 2 of eukaryotic cells. Exoenzyme S, encoded by the exoS gene, is also an ADP-ribosyltransferase that is secreted by a type-III secretion system into the cytosol of epithelial cells⁽⁸⁾. L and I lipoproteins are two outer membrane

proteins of *P. aeruginosa* responsible for inherent resistance of *P. aeruginosa* to

PCR has the potential for identifying microbial species rapidly by amplification of sequences unique to a particular organism ⁽¹⁰⁾. In this study, we examined detection of most virulence

antibiotics and antiseptics ⁽⁹⁾.

factors genes in *P. aeruginosa* isolates that isolated from wound, burn and pulmonary tract by using polymerase chain reaction technique.

Materials and Methods:

Sample collection: 100 swab samples were collected from wound, burn and pulmonary tract infection Al-Diwaniyacity. The samples placed in sterile transport media then transferred into microbiology laboratory College of Veterinary Medicine and store in refrigerator until bacterial isolation.

Bacterial isolation: *P. aeruginosa* was isolated from fecal samples by inoculation on brain heart infusion broth media at 37°C overnight for primary enrichment culture and then the bacterial growth were inoculated on chrome agar at 37°C overnight for selective isolation of pure culture *P. aeruginosa* isolates.

Bacterial genomic DNA extraction: Bacterial genomic DNA was extracted from *P. aeruginosa* isolates by using (Presto™ Mini gDNA Bacteria Kit. Geneaid. USA). 1ml of overnight

bacterial growth on BHI broth was placed in 1.5ml microcentrifuge tubes and then transferred in centrifuge at 10000 rpm for 1 minute. After that, the supernatant was discarded and the bacterial cells pellets were used in genomic DNA extraction and the extraction was done according to company instruction. After that, the extracted gDNA was checked by Nano drop spectrophotometer, then store in -20°C in refrigerator until perform PCR assay.

Polymerase chain reaction (PCR): PCR assay was performed by using specific primer for detection evaluates *exoS* and *oprI* virulence factors genes according to method described by ⁽¹¹⁾. These primers were designed by using NCBI-Gene Bank and primer3 plus design online. As show in the following table:

Primer	Sequence		Size	Gene Bank code
exoS gene	F	GCTTCAGCAGAGTCCGTCTT	684bp	L27629.1
	R	GCCGATACTCTGCTGACCTC		
ToxA gene	F	GGCTATGTGTTTCGTCGGCTA	487	AF227424.1
	R	TGATCGCCTGTTCCCTTGTCG		
oprI gene	F	CGGCTGGGAGATTGCTGTTA	202bp	X58714.1
	R	CCTTGCGATAGGCTTCGTC		

These primers were provided by (Bioneer Company, Korea). Then PCR master mix was prepared by using (AccuPower® PCR PreMix kit. Bioneer. Korea). The PCR premix tube contains freeze-dried pellet of (Taq DNA polymerase 1U, dNTPs 250µM, Tris-HCl (pH 9.0) 10mM, KCl 30mM, MgCl₂ 1.5mM, stabilizer, and tracking dye) and the PCR master mix reaction was prepared according to kit instructions in 20µl total volume by added 5µl of purified genomic DNA and 1.5µl of 10pmole of forward primer and 1.5µl of 10pmole of reverse primer, then complete the PCR premix

tube by deionizer PCR water into 20µl and briefly mixed by Exispin vortex centrifuge (Bioneer. Korea). The reaction was performed in a thermocycler (Mygene Bioneer. Korea) by set up the following thermocycler conditions; initial denaturation temperature of 95 °C for 5 min; followed by 30 cycles at denaturation 95 °C for 30 s, annealing 58 °C for 30 s and extension 72 °C for 1min and then final extension at 72 °C for 10 min. The PCR products were examined by electrophoresis in a 1.5% agarose gel, stained with ethidium bromide and visualized under UV transilluminator.

Results and Discussion:

Bacterial isolation results of *P. aeruginosa* isolation results was show in the following table:

Sample type	Total samples	Positive isolate	Percent
Wound	35	18	51.4%
Burn	45	37	82.2%
Pulmonary tract	20	12	60%

PCR was appeared specific assay that used in detection of virulence factors genes (ToxA, exoS and OrpL) producing

P. aeruginosa isolates human infections patients' samples. Where, The PCR results were show in following table:

Virulence gene	Clinical isolates		
	Wound (18)	Burn (37)	Pulmonary tract (12)
ToxA	13 (72.2%)	35(94.5%)	9 (75%)
exoA	7 (38.8%)	25 (67.5%)	5 (41.6%)
oprL	9 (50%)	13 (56.7%)	6 (50%)

Ch-square statistical significant at (P < 0.05)

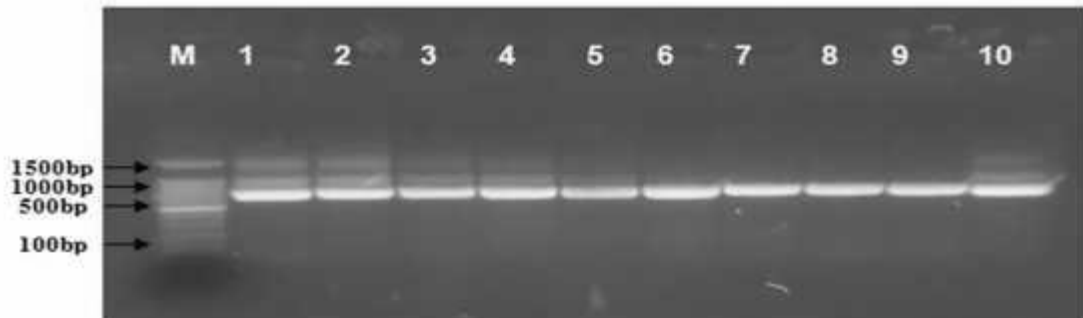


Figure (1): Agarose gel electrophoresis of PCR assay show the some positive results of exotoxinAtoxA gene in *P. aeruginosa*. Where, Lane (M) DNA marker (100bp), Lane (1-3) positive samples at 684 bp for exoS gene in *P. aeruginosa* isolate.

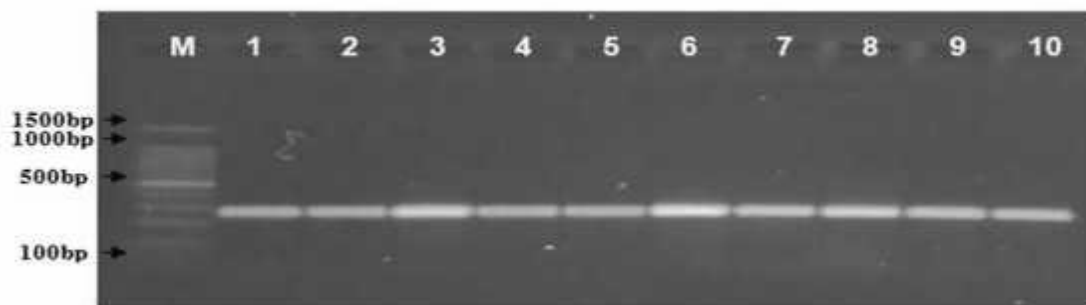


Figure (1): Agarose gel electrophoresis of PCR assay show the some positive results of exotoxin toxA gene in *P. aeruginosa*. Where, Lane (M) DNA marker (100bp), Lane (1-3) positive samples at 453bp for toxA gene in *P. aeruginosa* isolate.

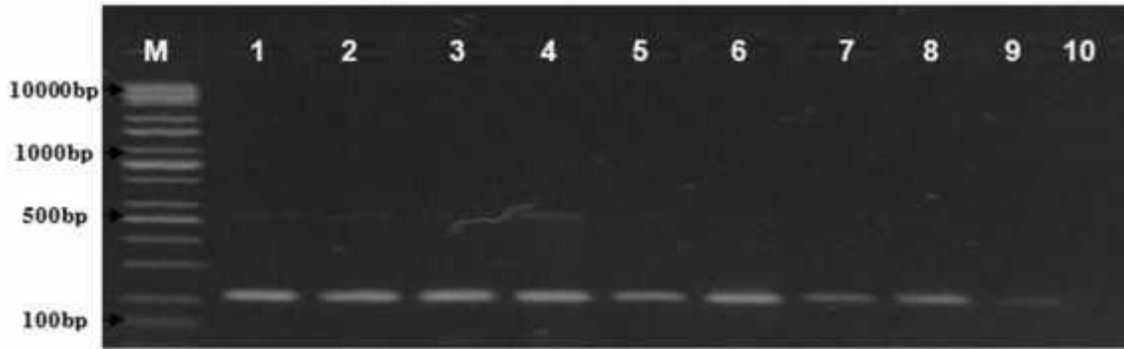


Figure (1): Agarose gel electrophoresis of PCR assay show the some positive results of Lipoprotein L gene in *P. aeruginosa*. Where, Lane (M) DNA marker (100bp), Lane (1-3) positive samples at 202bp for OrpL gene in *P. aeruginosa* isolate.

Molecular methods is better than the phenotypic methods that used in identification of *P. aeruginosa* more over biochemical testing takes long time to perform and requires extensive hands-on working the technologist⁽¹²⁾. The most important factor in the pathogenicity of *P. aeruginosa* is extracellular protein (exotoxin) that encoded by ToxA gene. This toxin can causes necrosis of liver, pulmonary edema, hemorrhage, and tubular necrosis of kidneys⁽¹³⁾. The percent study was designed singleplex PCR technique detection of virulence factor genes in *P. aeruginosa* isolated from different infection cases in Al-Diwaniya hospital.

The result show that burn infection *P. aeruginosa* isolates were show high prevalence of virulence factors genes more than wound and pulmonary tract infections isolates as well as the virulence factor gene (ToxA) was show high production in most isolates. This finding was agreed with⁽¹³⁾ who study different virulence genes as markers in *P. aeruginosa* that isolated from urinary tract infections and show high prevalence of virulence factor

gene (exotoxin A) at 100%. Other Study⁽¹⁴⁾ who developed PCR assay to detect *P. aeruginosa* by amplifying the toxA gene, they reported that of 130 *P. aeruginosa* isolates, 125 (96%) contained the toxA gene (sensitivity 96%) and (specificity 100%). These studies indicate that high specificity of toxA gene is unlike other virulence factors genes such as oprI and oprL genes that show a low sensitivity⁽¹⁵⁾. *P. aeruginosa* isolates generally producing cytotoxicity or invasion phenotypes which is correlated with presence of (exotoxin A) that encoding exoA gene. Our study by PCR technique was show difference in production of virulence factors genes (ToxA, exoS and orpL) according to clinical source of *P. aeruginosa* isolates were the burn infection isolates were show more prevalence more than pulmonary tract and wound infection at statistically significant ($P < 0.05$) (Table 1). In this study, we examined detection of most virulence factors genes in *P. aeruginosa* isolates that isolated from wound, burn and pulmonary tract by using polymerase chain reaction technique.

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الكشف الجزيئي عن جينات عوامل الضراوة في الزائفة الزنجارية المعزولة من حالات إصابات مختلفة في مستشفى الديوانية

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الخلاصة:

الزائفة الزنجارية هي الكائن الأكثر أهمية وخطورة في الإصابات البشرية نتيجة لإنتاجها عوامل ضراوة عدة خارج الخلية والخلايا المرتبطة التي تسبب التلف الشديد للأنسجة، ومن أهم تلك العوامل المتضمنة (S) exoenzyme و exotoxinA والبروتين الدهني)، وهذه العوامل تكون مشفرة بواسطة جينات (toxA و oprI على التوالي). استخدمت في هذه الدراسة تقنية سلسلة إنزيم البلمرة (PCR) للكشف عن جينات عوامل الضراوة المنتجة بواسطة بكتريا الزائفة الزنجارية *P. aeruginosa* التي عزلت بواسطة مسحات أخذت من مرضى الجروح والحروق وإصابات المسالك الرئوية. وبينت نتائج الـ PCR أن جميع عزلات *P. aeruginosa* كانت حاملة لجينات عوامل الضراوة مع وجود فرق في الانتشار فيما بينهما.

عزلات *P. aeruginosa* من إصابات الحروق أظهرت ارتفاع معدل الانتشار لجينات عوامل الضراوة أكثر من الجرح وعزلات إصابات المسالك الرئوية وكذلك جين عامل الضراوة (ToxA) الذي أظهر أعلى إنتاج في غالبية العزلات. وإستنتج من هذه الدراسة أن إنتاج جينات عوامل الضراوة في *P. aeruginosa* هو مهم بالنسبة للإصابات البشرية خاصة جين (ToxA). وتقنية PCR هي طريقة سريعة جداً ومحددة في الكشف عن جينات عامل الضراوة في *P. aeruginosa*.

كلمات مفتاحية: الزائفة الزنجارية، جينات عوامل الضراوة.