**PCR based identification of exotoxin A-producing** *Pseudomonas aeroginosa* isolated from burn wound infection

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# Abstract

Exotoxin A (*exoA*) is a major pathogenic factor in *Pseudomonas aeruginosa*. This non-fermenting gram-negative bacillus causes a wide range of infections. *P. aeruginosa* is a major cause of hospital-acquired infections. With this view, this study was aimed to identify *P. aeruginosa* strains carrying the *exoA* gene isolated from burn wounds. As part of the cross-sectional study, 110 samples of burns were collected in several hospitals. After identification of bacterial strains by biochemical and microbiological tests, genomic DNA was extracted. PCR reaction was performed for screening for *exoA* gene. After examining DNA extracted using quantitative (Nano drop with  $OD_{260/280}=1.8-2nm$ ) and qualitative (electrophoresis on the 0.7% gel agarose) methods, 75.4% (n; 83 of 110) isolates carried the *exoA* gene. The high prevalence of the *exoA* gene in *P. aeruginosa* strains indicate the important role of this exoenzyme in the spread of infection in burn patients. Therefore, it is recommended that people with burn infections be screened for the *exoA* gene.

Keywords: Exotoxin A, Pseudomonas aeruginosa, Burn Wound.

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## 1. Introduction

*Pseudomonas aeruginosa* is a gram-negative, opportunistic pathogen that is widely distributed throughout the environment (1). It is a ubiquitous organism, especially in environments such as soil, food, water, and hospital settings (2). *P. aeruginosa* is the second most common pathogen in surgery and the third most frequent cause of hospital infections after *Escherichia coli* and *Staphylococcus aureus*, which represent approximately 10% of hospital infections (3).

*P. aeruginosa* is a typical hospital-acquired causative agent of respiratory and urinary tract infections, dermatitis, bacteremia, soft tissue infections, bony and articular infections, gastrointestinal and systemic infections, predominantly in patients with intense burns, bed ulcers, and in patients with cancer or AIDS who are immunosuppressed (4, 5). Burn sores are local cell-mediated reactions (6, 7). A variety of cellular and extracellular virulence factors, such as exotoxin A, flagella and elastases, are implicated in the pathogenesis of *P. aeruginosa*. Also, cell damage to the skin can reverse humoral pyocyanin, lipopolysaccharide, pili, and phospholipase (8).

Exotoxin A is the highest important virulence factor of most P. aeruginosa strains. This toxin is intended for highly toxic mammalian cells (9, 10). The toxA gene is located in the genetic sequence of the P. aeruginosa chromosome, which is responsible for regulating exotoxin A synthesis (9, 11). ExoA is a significant member of the Type II secretor system(T2SS), which inhibits the ADP-ribosylation protein synthesis of the eukaryotic elongation factor 2 (12-15). In addition, exoA converts nicotinamide dinucleotide to adenosine diphosphate ribosylate (16). ExoA has three components: Part I binds to host cellular receptors and establishes endocytosis, Part II transports the toxin into the cell cytoplasm, and Part III catalyzes adenosine diphosphate ribosylation of elongation factor 2 (17). In epidemiologic studies, the dissemination of resistant and extremely virulent pathogens

is also the chief problem worldwide. The current study aims to investigate the *exoA* gene among the clinically *P. aeruginosa* strains isolated from wound burn infections.

# 2. Materials and methods

## 2.1. Study plan and clinical samples.

In the cross-cutting study, a complete of 110 wounds burned samples were collected from several teaching hospitals (Tehran, Iran) during a period of one year from April 2015 to April 2016. Bacterial isolates were identified using biochemical and microbiological tests such as gram staining, oxidase, O/F test, Triple Sugar Iron Agar (TSI), and Sulfide-Indole-Motility (9), pyocyanin pigment production, growth at 42 °C and citrate utilization. All isolates were kept in brain heart infusion broth (Becton Dickinson, Franklin Lakes, NJ) containing 15% (v/v) glycerol (Merck Co., Germany) at -70 °C for further use. *P. aeruginosa*strain ATCC 27853 was used as quality control in this work.

#### 2.2. DNA extraction

Genomic DNA was extracted from *P. aeruginosa* pure colonies using a G- spin Genomic DNA Extraction Kit (Fermentas, Germany) and then kept at -20 °C until used. The concentration and quality of the template DNA were evaluated by a Nano Drop<sup>TM</sup> 1000 Spectrophotometer (Thermos Scientific, Wilmington, DE, USA). DNA isolates with a concentration of 0.1 ng/µl were used as the templates for polymerase chain reaction (PCR) assay.

#### 2.3. Polymerase Chain Reaction

The oligonucleotide primer sequences used for amplification of the *exoA* gene are listed in Table 1. The PCR reaction was carried out in a total volume of 25  $\mu$ l, including 1.0  $\mu$ l of bacterial DNA; 2  $\mu$ l of 10×PCR buffer; 1.5 mmol/l of MgCl<sub>2</sub>; 0.7  $\mu$ l (each) of dATP, dGTP, dCTP, and dTTP; 0.5  $\mu$ l of each primer; 1.0  $\mu$ l of Taq DNA

Table 1. Primers used to identify *exoA* genes in *P. aeruginosa*.

Gene	Primer sequences $(5' \rightarrow 3')$	PCR-products (bp)
exoA	F=5'- TGCTGCACTACTCCATGGTC-3'	396 bp
	R=5'- ATCGGTACCAGCCAGTTCAG-3'	
•••••••••••••••••••••••••••••••••••••••		

	Table 2. Percent of female and male participantsin the study ( <i>P. aeruginosa</i> positive).				
•••	Group	N	Percentage %		
	Female	42	66.67		
	Male	21	33.33		

Table 3. The distribution of gene detected from			
P. aeruginosa.			

19.62

63

Group	N Percentage %	
exoA	83	75.4
no-exoA	27	24.59
Total	110	100

polymerase (5 U/µl; Amplicon Co., Denmark); and 15.7 µl of ddH2O. The target gene was amplified in a Techne TC-512 thermocycler (Eppendorf, Hamburg-Nord, Germany), as follows: initial denaturation at 94 °C for 5 min, 30 cycles of denaturation for 30 s at 94 °C, annealing for 40 s at 55 °C, and extension for 45 s at 72 °C, as well as a final extension for 5 min at 72 °C. The amplified PCR products were visualized by standard gel electrophoresis in a 1.5% agarose gel painted by ethidium bromide (5 µg/mL) for 30 min. The gels were recorded under ultraviolet light using the Gel-Doc.

## 2.4. Statistical Analysis

Total

SPSS software version 23 (SPSS, Inc., Chicago, IL, USA) was employed for statistical analysis. Descriptive statistics and Pearson's chi-square tests were used to assess the relationship between the presence of the *exo-A* gene and gender. The statistical significance was defined as

lower than 0.05 (*p*<0.005).

#### 3. Results

In total, 110 non-duplicative clinically *P. aeruginosa* isolates were collected from 75.5% (n; 83) male and 65.5% (n; 72) female. The average age of the patients studied was  $58.5\pm18.2$  years, with a range between 16 and 85 years (Table 2). Molecular distribution showed that 75.4% (n;83) of isolates were carried the exoA gene (Table 3). The results showed that there was no meaningful relationship between the genus and the frequency of the *exoA* gene (*P* value=0.1). Multiplex PCR reaction with specific primers for the *exoA* gene showed that a high percentage of the samples contained the *exoA* gene (Figure 1).

#### 4. Discussion

Invasive burn wound infection is an important cause of septicemia, septic shock and multiple malfunction syndrome (MODS) in persons suffering from severe burns (18, 19). Burn injury causes a mechanical disturbance in the skin's defense mechanism. The skin's natural barrier against microorganisms is replaced by a protein-rich moist, bloodless scar, which ultimately increases microbial growth. The gram-positive microbial population is not increased immediately after burn, but over a period of 7-10 days after burn, gram-negative replace gram-positive organisms (20).

*P. Aeruginosa* is a general destructive gram-negative organism. This is an opportunistic pathogen that causes rigid infections (21, 22).



Figure 1. Agarose gel electrophoresis of PCR amplification (m): 100 bp DNA size marker (Sinaclon), Positive control (*P. aeruginosa* ATCC) Lane 1-10; template DNA and negative control; distilled water.

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*P. aeruginosa* is a popular opportunistic and substantial agent in nosocomial infections as intense burns and Cystic fibrosis patients. This bacterium can motivate 30% of nosocomial infections due to its antibiotic resistance (23-25).

In the current study, we have used PCRbased diagnostic protocol for the identification of the *exoA* gene from *P. aeruginosa* isolated from wound burn infections. PCR showed that 75.4% of isolates were carried the *exo-A* gene.

*ExoA* is a major virulence factor produced by this organism. ExoA was first discovered by Liu and associates (26-28). Since then, ExoA has been toxic to a large variety of mammalian cells in vitro and is deadly to many animal species (29, 30). ExoA is a protein toxin that inhibits polypeptide synthesis by ribosylating the elongation factor ADP 2 and diphtheria toxin, which leads to cellular mortality (31, 32). Its cytotoxic activity covers a broad range of mammalian cells. It has been demonstrated that exoA inhibits the growth of human granulocytes and macrophages (33) and inhibits the production of interleukin-1 by peritoneal macrophages (20). These data demonstrate that *exoA*, as one of the most important virulence factors, can play a role in the physiopathology of sepsis of P. aeruginosa and death in burned patients (20, 21, 34, 35).

The *exoA* gene is more prevalent in wounds, burns, otitis media infection and, milk samples than others genes, and it is very important for *P. aeruginosa* because it hints to control damage in tissue and hence bacterial attack (36).

In the current study, from the 83 *P. ae-ruginosa* isolates, the *exoA* gene was detected in 83 (75.4%) PCR isolates. As well, Vasil and colleagues reported *exoA* production in close to 90% of 111 isolates of *P. aeruginosa* by analyzing for ADP ribosyl transferase activity (37, 38). Khan and Cerniglia introduced that the *exoA* gene was found in 93% of *P. aeruginosa* through PCR (26). Amini examined the catalytic locus of the *P. aeruginosa exoA* gene and showed that 90% of the iso-

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1. Rumbaugh KP, Griswold JA, Hamood AN. Pseudomonas aeruginosa strains obtained from patients with tracheal, urinary tract and wound infeclated bacteria had *exoA* gene, while in the present study 93.67% of the isolated bacteria had this gene (39). Some other studies have identified *P. aeruginosa* strains mediated by the *exoA* gene by PCR and reported the sensitivity of this method is the reliable diagnosis, which is similar to our results (11, 24, 27, 40). Hummel examined the sensitivity of the PCR-mediated *exoA* gene for the diagnosis of *P. aeruginosa* and reported the high sensitivity and speed of PCR in diagnosis (41, 42).

All of the above research and our findings suggest that *exoA* may play an important role in the onset of *P. aeruginosa* and its lethality. *ExoA* contributes to the dissemination of *P. aeruginosa* within the body of burned patients and its horizontal spread within the burned skin. In addition, it is responsible for the general virulence of *P. aeruginosa*. The results of this study may put us on the line for controlling serious wound burn infection caused by *P. aeruginosa* organisms and any sequelae or complications arising from it. In addition to these findings, we reported the application of PCR procedures that can be used promptly and specifically to detect *P. aeruginosa* strains.

## **5.** Conclusion

This study demonstrated that *P. aerugino*sa carrying the *exo-A* gene was the most prevalent in burn units. Therefore, due to the role of this enzyme in the development and spread of infection, especially in burned patients, attention to these strains and appropriate action for burn patients infected with these organisms, such as adequate treatment and, isolation is inevitable.

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# **Conflict of Interest**

The authors have no conflict of interest.

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