# Molecular Investigating Class I, Ii And Iii Integrons In Pseudomonas Aerginosae Isolated From Diabetic Foot Infection Patients In Najaf Province

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Abstract: The study aimed to isolate and diagnose Pseudomonas aerginosae from clinical specimens of diabetic foot infection patients, study the resistance of bacteria to antimicrobial agent and molecular detection of class 1, 2 and 3 integron-associated gene cassettes from Pseudomonas aeruginosa in Najaf province. Sensitivity test was examined via disk spread, method antibiotic, the insulated shows 100% resistance to cefepim, amoxiclave, ceftazidime, gentamicin, cefotaxime and cephalexine though the carry-on of the antibiotics showed various activity against the isolates. At molecular study, the investigated the presence of integrin's genes (intI, intII and intIII) using PCR technique and electrophoresis systems, PCR analysis showed that the integrin IntI, IntII and IntIII were detected in 12/30, 16/30 and 6/30 respectively in Pseudomonas aeruginosa isolates.

Keywords. Pseudomonas aerginosa, diabetic foot infection, Integrons gene

## **INTRODUCTION**

Pseudomonas aeruginosa is a significant human opportunistic bacterium in the diabetic foot. It is rod-shaped non-fermenting bacterium with unipolar motility consider a gram-negative aerobic [1]. P. aeruginosa is often first specifically through its pearlescent aspect and tortilla-like or grape-like odor. Have the accountable ability to display a wide of disease from surface colonization of ulcers to wide tissue spoilage, septic arthritis, count, osteomyelitis, and bacteremia [2]. Because the dangerous and dreaded pathogen therefore P. aeruginosa is commonly resistant to antibiotics. The clinical P. aeruginosa isolates display orientation to increase resistance towards many a high percentage and antimicrobial agents or multi-drug resistance (MDR) phenotype. A|minoglycosides, fluoroquinolones and anti-pseudomonal agents consider is the most effective beta-lactams, there's a technique of resistance to antimicrobial agents to the production of beta-lactamases, multidrug efflux pumps, presence of integrons, and downregulation of outer membrane porins. Found the large of antibiotic resistance genes found on transposons and plasmids that are located at a unique site named integron [3]. Carry these elements approximately 10% of the sequenced bacterial genomes, also on chromosomes about 90 distinct integrin Classes that most of them located. The primary of integrin's that include functional are Class 1, Class 2, and Class 3 that display a number of features not a model of the large numerically dominant chromosomal integrin Classes. Transposons can be carried utmost usually have on to 6 cassettes towed from a pool of on 100 cassettes and almost every of which encodes antibiotic confrontation determinants [4]. The most common integrons; Classe I found in P. aeruginosa bacteria while the others

integrons Class 2 and Class 3 amidst these pathogens are not commonly reported [5]. This study aimed to investigating class I, II and III Integrons in Pseudomonas aerginosae isolated from Diabetic Foot infection patients.

# MATERIALS AND METHODS

#### Specimens Collection and Bacterial Identification

In this Study can be collecting 30 samples swab specimens of diabetic foot infection ulcer, The samples were imparted through sterile transfer swabs to the bacteriology laboratory into culture on MacConkey agar and blood agar, through 24 hr. the plates was incubated at temp. 37°C after that then single isolate was transport to trypticase soya agar for diagnosis by biochemical tests and VITEK 2 compact system that proven the identification of isolates.

#### Plasmid DNA Extraction

Isolation of bacterial plasmid according to PureYield<sup>TM</sup> plasmid Miniprep Kit, the kit designed for isolation of plasmid DNA from cultures bacterial cells. The procedure of DNA extraction was done according to the manufacture instructions.

#### Identification

The PCR assay was performed to detect the integron genes for P. aerginoae shown in table (1), these primers were produced by Alpha DNA Company, Canada. The mixture of PCR for each primer with final volume 20 µl/reaction and the protocol used depending on Master Mix (AccuPower® PCR PreMix (Bioneer, Korea) instructions. Each monoplex PCR reaction mixture consisted of 2µl Forward Primer (10 picomole), 2µl Reverse Primer (10 picomole), 9µl De-ionized water, and 7µl the DNA of the isolates were added into the AccuPower® Taq PCR PreMix tubes that contain (Taq DNA polymerase, dNTPs, KCl, MgCl2, and buffer). All PCR components were assembled in a PCR tube then the PCR reactions for primers as shown in table 2. The PCR products were resolved by electrophoresis in a 0.9% agarose gel stained with Ethidium bromide staining 0.5% (BioBasic, Canda) and then visualized by Gel Documentation. The 100-bp DNA ladder (Bioneer, South Korea) used as a reference standard [6]. The positive results were distinguished [7]. Lastly, by using Biometra gel documentation system.

Type of Primer	Primer sequence (5'-3')	Amplicon size (bp)	Reference
IntI	F: CAGTGGACATAAGCCTGTTC R: CCCGAGGCATAGACTGTA	160	Zareei Y et al., 2014
IntII	F: CACGGATATGCGACAAAAAG R: GATGACAACGAGTGACGAAATG	787	Zareei Y et al., 2014
IntIII	F:GCCTCCGGCAGCGACTTTCAG R: ACGGATCTGCCAAACCTGACT	980	Odumosu BT et al., 2013

Gene	Initial denaturation	No. of cycles	Denaturation	Annealing	Extension	Last extension
IntI, II,	95°C at 6	35	95°C at 45	51°C at 45	72°C at 1	72°C at
III	min		Sec	Sec	Min	7Min

Table 2. PCR programs of primers that apply in the thermocycler

# **RESULTS AND DISCUSSION**

Diabetic individuals tend to evolve various complications like peripheral arterial disease and neuropathy that participate to foot ulceration [8]. in this study P.aerginosae connected with diabetic foot ulcers, this consequence correspond with previously studies shown S. aureus, PROTEUS MIRABILIS and P.aeruginosa as common bacterial species frequently connected with wound fluids in diabetic foot ulcers [9, 10].

In this study according to diagnosis by bacteriological culture and VITEK method, P.aerginosae was found to be the most common isolate 30 (30%), this result agrees with a previous study P.aerginosae was isolated in 16%, other authors reported P.aerginosae in 17.5% of cultures from diabetic ulcers [5].

Pappu K et al. [11] also found correlate good with results they reported about 76% gram negative bacilli of the organisms which were isolated, Pseudomonas being the predominant pathogen (23%), then S.aureus (21%). Zubair et al [12] reported E.coli the predominant gram negative isolates, about (26.6%) and (10.6%) in the center while the rest acquired the infection and from large than half of the patients already had pseudomonas infection. P.aeuroginosa this opportunistic bacteria show the mist resistance to Cefepim, Amoxiclave, Ceftazidime, Cefotaxime, Cephalexine, and Gentamicin (00 %), followed by Timethoprime (91.6 %), Ciprofloxacin (25 %) and very low resistance to Imipenime, Amikacin and Pipracillin – Tazobactam (8.3 %).

This results agree with [13] who found P. aeruginosa were showed highest resistance against Amoxicillin/clavulanic acid, Cefotaxime and Trimethoprim. The lower result resistance to Ciprofloxacin was (33.3%).

Antibiotic predisposition, manner P. aeruginosa appears of isolates about 53% were renitent to further than five antibiotics. In Thailand, Poonsuk et al. appaers resistance of P. aeruginosa isolates increase in Ceftazidime (96%), Gentamicin (99%), Ciprofloxacin and (95%) Amikacin (92.1%). Fazeli et al. reported the P. aeruginosa isolates were renitent to Gentamicin (32.2%) and Ciprofloxacin (29%) [14].

The results showed that the integron Class1 IntI, IntII and IntIII were detected in 12 out 30, 16 out 30 and 6 out 30 respectively from P.aerginosae isolates as shown in figure (1, 2 and 3 respectively).

In this study the results appear that the spread of Class 1, Class 2 and Class 3 integron genes in some P. aeruginosa isolates, class II integron was large spread than other integrons. P. aeruginosa is an opportunistic pathogen that contain a large ambit of human contagion, especially resistant to numerous antibiotics that makes it hard to cure. The transfer of resistance genes is appeared recent studies through integrons has significant role in acquiring resistant in bacteria. These genes can be originated by plasmids and transposons [15]. In a study conducted in 2010 by Yosefi [16], the prevalence of Integron gene I was reported 56.3%. Moreover, Fonseca [17] reported 41.5%, in China in 2009, it was reported 38% [18], and in the Gu study, it was reported 40.8% [15]. In a study by Shibata [19] in Japan, integron I was reported to be more prevalent, whereas integron III was observed to be sporadic [19].

The prevalence of Integron II in the study of Keramati was reported 9% in 2014 in Zanjan [20]. Khosravi also reported, 5.3% in 2011 [21]. Coding genes of antibiotic impedance are often imparted via mobile genetic elements called integrons [20] that can be placed in, transposons, chromosomes, and plasmids. These elements are very important in the evolution of several drug resistance, such as plasmids and transposons. The overall structure of integrons, resistance genes are on determined gene cassettes. The transfer of resistance genes occurs due to the connection ability of cassette in the integron set during a particular recombination process [22]. At the end of 3' and 5' integrons, two nucleotide sequences are protected. Essential components of area 5 in all integrons consist of: 1. integrase gene that is site-specific for recombinase enzymes, 2. attI sequence is a particular recombination place situated in the vicinity of intI, used as a receiver for the gene cassette, 3. The promoter is required for expression of available gene cassette, integrated between sector 3' and 5' integrons [23].



Figure 1. Yields of PCR amplification to P.aerginosae isolates that amplified from IntI gene primer by way of produce 160 bp.Lane (L), DNA molecular size marker (100-bp ladder), Lanes (1 to10) appear positive results with intI gene.



Figure 2. Yields of PCR amplification to *P.aerginosae* isolates that amplified from IntII gene primer for produce 787 bp.Lane (L), Lanes (1 to 10), DNA molecular size marker (100-bp ladder), appear the int II gene positive results.



Figure 3. Yields of PCR amplification to *P. aeruginosa* isolates that amplified from *IntIII* gene primer by way of produce 980 bp. Lane (L), Lanes (1 to10), DNA molecular size marker (100-bp ladder), appear positive results with *int III* gene.

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