

Association between Genotypic and Phenotypic Formation of Biofilm in *Pseudomonas aeruginosa* Isolated from Diabetic Foot Patients

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Abstract

The purpose of this research is to determine the relationship between genotypic and phenotypic characteristics associated with biofilm formation in *Pseudomonas aeruginosa* isolated from diabetic foot patients. Methods: The identification of *Pseudomonas aeruginosa* isolates was performed using morphology, microscopic examination, biochemical assays, and the vitek-2 system. In addition, the phenotypic detection of biofilm by CRA and TCP. Finally, biofilm genes (quorum-sensing) identification by PCR (Las I and Las R genes). Results: In accordance with the results obtained from 100 samples based on morphological and cultural characteristics as well as biochemical characteristics and the vitek-2 system only 47 (47%) isolates were identify as *Pseudomonas aeruginosa*. Biofilm formation found 41 (87.23%) isolates from *Ps. aeruginosa* able to produce biofilm by CRA and TCP are the number of isolates showing high biofilm formation was 33 (70.2%), moderate biofilm formation was 7 (14.9%) and non-biofilm formation was 7 (14.9%). Finally, the PCR data showed that LasI gene high prevalence 43/47 (91.4%), also LasR gene was positive in 33/47(70.2%) which encode for Biofilm formation in this study.

Keywords: *Pseudomonas aeruginosa*, biofilm, Congo red agar and tissue culture plate.

1. Introduction

Insufficient insulin production by the pancreas or inadequate insulin production induces diabetes mellitus (DM). Increased blood glucose levels cause damage to many biological systems, including blood vessels and nerves, and are the most common cause of diabetes-related hospitalization [1]. Resistance mechanisms developed by bacteria in mature biofilms make them difficult to eliminate from the host. *Pseudomonas aeruginosa* is a frequent infection in chronic wounds that can build resistant biofilms. *Ps. aeruginosa* is an opportunistic pathogen commonly associated with respiratory and urinary infections, burn wounds, and chronic wounds [2].

Scientists have been studying *Pseudomonas aeruginosa* because it can chronically invade and infect cystic fibrosis sufferers [3]. Adaptability of this bacteria to its environment is a result of extensive and intricate transcriptional control of virulence genes in the host environment. In the *Ps. aeruginosa* community, the quorum-sensing (QS) cell-to-cell communication mechanism serves to coordinate activity. In fact, two AHL-dependent QS systems, LasI/R and RhII/R, govern the transcription of numerous virulence genes [4].

As part of the LasI/R system, lasI synthesizes 3-OXODODECANOL, which interacts with and activates the cognate response regulator LasR, therefore controlling the expression of target genes. RhII initiates the production of N-(butanoyl)-homoserine lactone (C4-HSL) in the RhII/R system, which then interacts with RhIR, influencing target gene transcription. *Pseudomonas aeruginosa*'s pathogenicity is dependent on these two QS systems, which are among the most extensively studied in bacteria [3].

2. Materials and Methods

2.1. Patients and clinical specimens

There was a total of 100 samples isolated from AL-Sader hospital in Najaf City, Iraq, from 1/11/2020 to 1/4/2020, patients with diabetic foot ulcer. Physical and clinical examinations were conducted for each patient, and data were entered in a data sheet. This study coincided with the ethics of the Health Ministry and the AL-Sader hospital.

All respondents were notified verbally. Specimens were carried by sterile transport swabs and inoculated with a direct inoculation method on the cultivation of selective media such as MacConkey, blood and nutrient agar, and inoculated for 18-24 hours at 37°C [5].

2.2. Identification of bacteria

From each primary positive culture on the MacConkey, blood and nutrient agar, a single colony was taken to reinforce pure culture and was identified according to morphological and cultural characteristics (blood hemolysis, lactose fermentation, colonial form, size, color, frontiers and texture) and examined under microscopic therapies and then further identified by biochemical tests [6]. Finally, identified by vitek-2 system.

2.3. Biofilm formation

1- **Congo Red Agar method (CRA):-** According to Freeman et al. [7].

2- Tissue culture plate method (TCP):- According to Nibras et al. [8].

2.4. Total DNA Extract

By using the Genomic DNA Extraction kit (Intronbio/USA), DNA may be extracted from bacteria.

2.5. PCR Amplification and Gel Electrophoresis

All isolates' DNA was subjected to polymerase chain

reaction (PCR) to detect quorum-sensing (QS) genes such as (*LasI* and *LasR* genes). Tables 1 and 2 detail the primers and reaction conditions used in this study.

Table (1): The Primer was utilized in this research.

Target Gene	Sequence	bp	Reference
<i>Las I</i>	5'-CGTGCTCAAGTGTCAAGG-3'	295	MacFaddin [6]
	5'-TACAGTCGGAAAAGCCAG-3'		
<i>Las R</i>	5'-AAGTGGAAAATTGGAGTGGAG-3'	130	
	5'-GTAGTTGCCGACGACGATGAAG-3'		

Table (2): Thermocycling conditions for PCR

Gene Name	Temperature (°C) / Time					Cycles Number
	Initial Denaturation	Cycling Conditions			Final Extension	
		Denaturation	Annealing	Extension		
<i>Las I</i> and <i>Las R</i>	94 C° for 2 min.	95 C° for 40 Sec	50C°/60 for 1 min	72 C° for 2min.	72C° for 10min.	30

3. Results

3.1 Description of study samples

This research was conducted with a total of (100) samples,

sourced from individuals who had diabetes foot ulcers (DFU). Patients who attended to AL-Sader Hospital in AL-Najaf City, Iraq, between 1/ 11/ 2020, and 1/ 4/ 2021, during the time. The 47 (47%) *Pseudomonas aeruginosa*-positive samples, another 53 (53%) samples were also considered positive (causes by other causative agent).

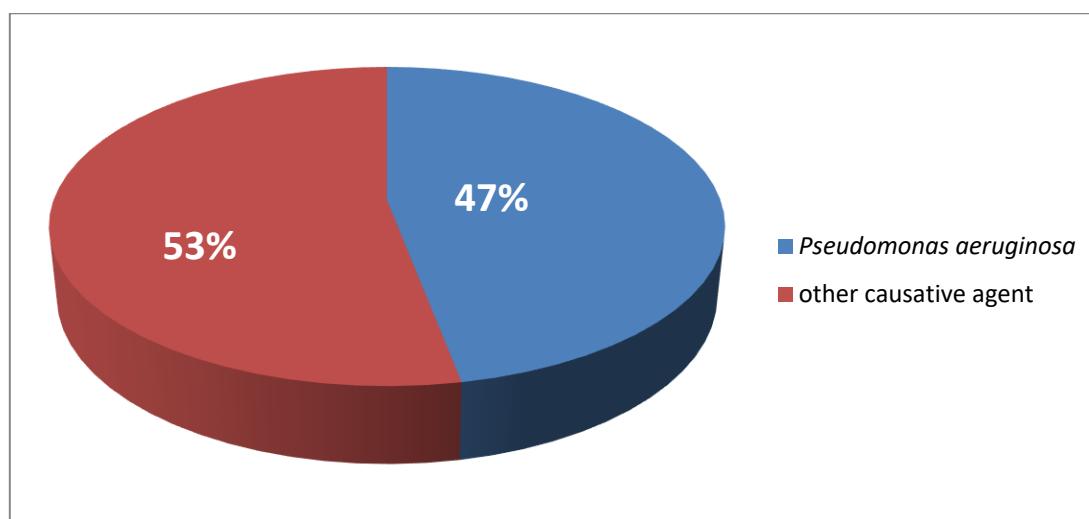


Fig. (1): The occurrence of *Pseudomonas aeruginosa* in 100 clinical samples.

Negative growth may be due to the presence of other infectious agents, such as anaerobic bacteria, fungi, and viruses [7], or it may be because the wounds were not infected at the time of the study or the medicines administered were successful [8].

3.2. Identification of bacteria specimens.

Initially, bacterial specimens were recognized using a variety of criteria, including Gram stain, cultural, morphological, and biochemical tests, before being identified using the vitek-2 method. Only 47 (47%) of the 100 clinical specimens contained isolates of *Pseudomonas aeruginosa*.

This study in same line with some other studies have shown *Ps. aeruginosa* predominant in DFIs such as Iyanar et al. [9], who demonstrated that *Ps. aeruginosa* was most common in DFI Also in line with Al-Shabaki [10]. Those who suffer from foot ulcers are more susceptible to bacterial infections that spread quickly, causing permanent tissue damage [11].

Because the colonies of *Ps. aeruginosa* look diffuse-

haemolytic when grown on blood agar, but not when grown on MacConkey agar, this indicates that *Ps. aeruginosa* is unable to ferment lactose sugar, as light colored tiny colonies are formed [12].

3.3. Biofilm production

3.3.1- Congo Red agar (CRA) detection of Biofilm

It was found 41 (87.23 %) of the isolates from *Ps. aeruginosa* were capable of producing biofilm when tested on CRA, as shown in figure (2).

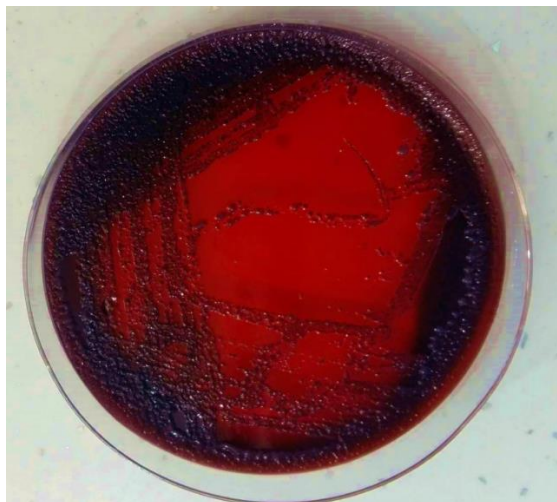


Fig. (2): The biofilm production by Congo Red assay. Microcolony development, biofilm maturation, and detachment (also known as dispersion) are all phases of biofilm formation. Sessile bacteria are in a stationary or latent development phase and have different

characteristics from planktonic bacteria [13]. Lima et al. [14] obtained similar results, demonstrating that 75% of *Ps. aeruginosa* clinical isolates were biofilm makers.

3.3.2- Tissue Culture Plate (TCP) Detection of Biofilm Formation:

A semi-quantitative microtiter plate test to measure biofilm growth on polymeric surfaces was tested (biofilm assay). To boost the accuracy of the assay, three distinct runs were completed for each of the strains to be assayed. The results as determined by the mean of OD value (630nm) had a mean OD value of >0.240, 0.120, and <0.120.

According to table (4-6), only 33/47 (70.2 percent) *Ps. aurogenosa* formed strong biofilms, whereas 7/47 (14.9 %) and 7/47 (14.9 %) of *Ps. aurogenosa* formed moderate biofilms and non-formation, respectively (figure 3). This study dissimilar with Perez et al. [15] biofilm production was being distributed in the following categories: 60% (51/85) poorly adherent, 25.9% (22/85) moderately adherent, and 14.1% (12/85) strongly adherent.

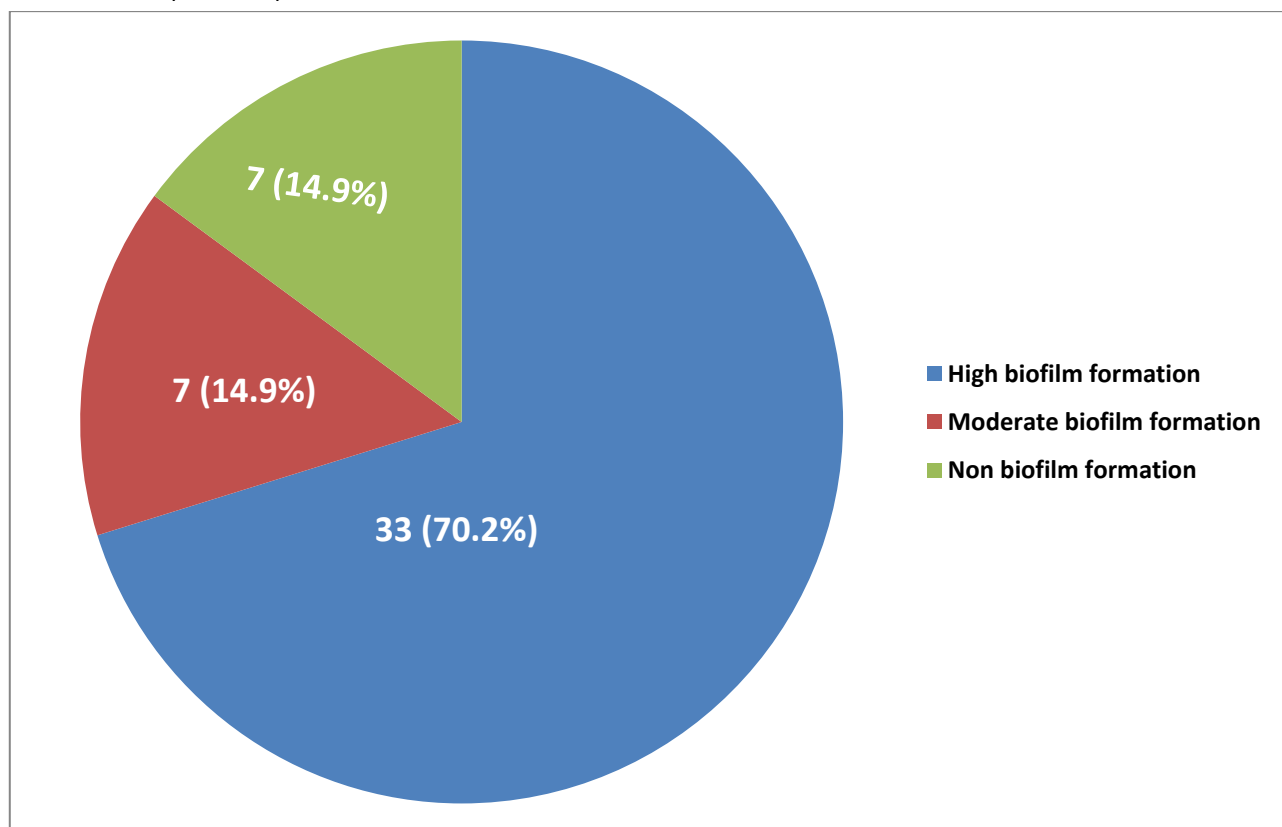


Fig. (3): Frequency of the biofilm formation in *Ps. aurogenosa*.

A biofilm can protect bacteria from immunological reactions and antibiotics. Microbes can live alone or form micro-communities inside a biofilm matrix of extracellular polymeric molecules. The ability to form biofilm is an important virulence trait because it protects against medicines. Multidrug-resistant bacteria thrive in these biofilms, causing persistent infections like diabetic foot ulcers and treatment failure [9]. Due to the difficulty of eliminating biofilms with traditional antibiotics, finding biofilm producers among clinical isolates may help control wound infections in diabetics who have failed antibiotic

therapies [10]. Biofilms form more easily in diabetic wounds, says Ashok [16].

3.4. Molecular detection of bacterial isolates

3.4.1. Detection of the *LasI* and *LasR* genes

Using particular forward and reverse primers, *LasI* and *LasR* genes express acyl-homoserine lactone (acyl-HSL) enzymes. In the current investigation, 43/47 (91.4%) of the bacterial isolates had the *LasI* gene, while 33/47 (70.2%) had the *LasR* gene.

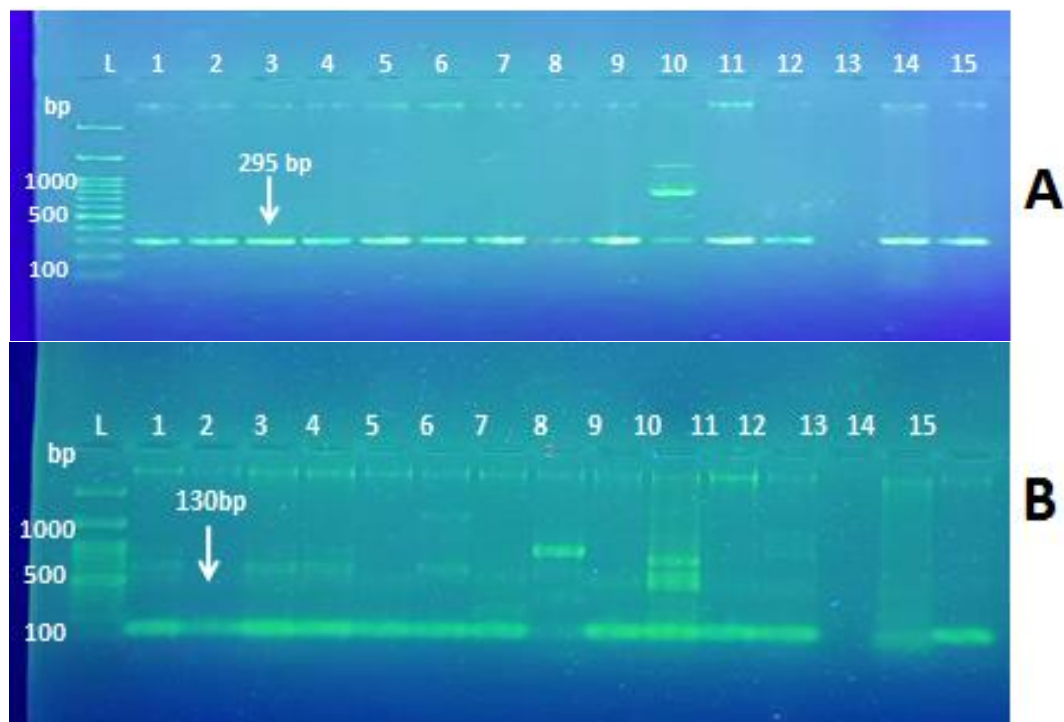


Fig. (4) Product from bacterial isolates that amplified with A) *LasI* gene and B) *LasR* gene primer were dyed with red safe dye, a blue gel stained with various dyes, and agarose gel electrophoresis with a PCR amplification product as an analytical tool.

When quorum sensing is activated, the expression of different virulence factors in *Ps. aeruginosa* is regulated. Quorum sensing is thought to be mediated mostly by N-acyl-L-homoserine lactones (AHLs) as the signaling molecules in cell-to-cell communication through quorum sensing [17].

In terms of the presence of QS genes, our findings are consistent with those of MacFaddin [6] who observed that 90.1% (82/91) of the examined isolates possessed *lasI* genes. In comparison, the results provided by Hasan [18] indicated that the identification of QS genes was not as high as those obtained in our work (81.25% for the *lasI* and *lasR* genes, 68.75% for the *rhlI* gene).

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