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Molecular Detection of Type VI secretion genes and correlation with of IL-10 levels in Pateints with Pantoeaagglomerans

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ABSTRACT
The present study aimed to detect the presence of HCP and VgrG genes in isolates of Pantoeaagglomerans from infected individuals and to evaluate IL-10 levels as a marker of the immune response activity and its relation with those genes among the participating individuals.Five hospitals in Karbala provided a total of 300 patients varying in age and including both genders for this study. Five milliliters of blood were collected for immunological and molecular testing. The identification of Pantoea species was performed by the VITEK-2 compact system and sequencing analysis. Genomic DNA from bacterial cells was extracted for PCR analysis of specific genes (Hcp and VgrG) to confirm the identity of bacteria and virulence factors. DNA concentration and purity were determined with a Nanodrop spectrophotometer. The PCR process was optimized, and IL-10 was quantified by use of an ELISA kit.In this study on 300 clinical specimens, 79.33% exhibited positive bacterial growth, with 37 of these being Pantoea species. Among the Pantoea isolates, 81.09% were identified as P.agglomerans. The isolates were characterized for their biochemistry and carbohydrate fermentation abilities. Genetic analysis showed that 53.3% of P.agglomerans isolates had the Hcp gene and only 23.3% had the VgrG gene, showing variation in virulence factors.Biofilm production was varied among the isolates; most exhibited strong or moderate biofilm-forming abilities. Patients infected with P.agglomerans also exhibited higher IL-10 levels.
Conclusion: The Hcp and VgrG genes of P. agglomerans are involved in immunomodulation. Strong biofilm generation also raises the risk of infection in healthcare environments. Nonetheless, individuals with increased IL-10 levels demonstrate immunomodulation.

Keywords: Pantoeaagglomerans,Hcp, VgrG, Interleukin-10.

1. INTRODUCTION

The Pantoea species are pathogens capable of opportunistic infections with potential to affect immunocompromised or debilitated hosts, such as patients with underlying diseases (for example, diabetes, cancer, and chronic kidney disease) These are most likely acquired from contaminated food, water, or contact with carriers (Fenget al., 2019). Among the pathogenicity factors of Pantoea infection, the most important one is the Type VI secretion system. This might help in bacteria interaction with host human immune and normal cells; thus, its potential in pathogenicity is summarized by saying that the functions that this T6SS has in P.agglomerans are critical for the processes of immune evasion, host cell invasion, and the severity of human diseases such as sepsis and pneumonia(Vanthanakornet al., 2020). VgrG is a toxin that forms pores in the membranes of target cells by working as an H1-T6SS conveyor, thereby enabling the passage of other toxins through the formed channel (Mougouset al., 2020). The N-terminal of VgrG forms the Hcp secretion needle, thereby linking VgrGto a structural/functional system similar to those of Hcp chaperone proteins during secretion. Membrane penetration could also be achieved by the needle form, as found in Hcp chaperone-dependent secretion systems (Lloubèset al., 2021; Wang et al., 2022). Secretion in a single layer is genetically connected to the VgrG protein, while several reports indicate that mutations in the VgrG and Hcp genes significantly reduce bacterial virulence (Hernandez-Alvaro et al., 2022). In P.agglomerans, VgrG contributes significantly to the evasion of macrophages' phagocytosis by blocking NF-κB activation, whereas Hcp is found to be critical for bacterial adhesion and invasion into epithelial cells (Chen et al., 2021). For example, these genes are connected with the severity of infection, where specific alleles of VgrG are related to worse outcomes of sepsis, and the expression of Hcp is associated with increased inflammation in pneumonia cases.Infection with P.agglomerans, IL-10, in turn, plays a regulatory role in immunity by suppressing pro-inflammatory

cytokines (like TNF-alpha or IL-6) and fostering an anti-inflammatory condition in macrophages. This may boost the body to not cause prime tissue destruction due to over inflammation but may lower the body's clearance of the infection. Modulation of pathways of IL-10 may offer potential in balancing immune responses and inflammation during such infections. Therefore, in the present study, the work was designed to identify the type VI secretion system using polymerase chain reaction for genes vgrG and hcp and to determine the role of IL-10 in patients infected with P.agglomerans.

2. MATERIALS AND METHODS

2.1 Patients

The current study included patients visiting Al Hussein Teaching Hospital, Children's Hospital, Al-Hindiya Teaching Hospital, Gynecology and Obstetrics Teaching Hospital, and Imam Hassan Al-Mujtaba Teaching Hospital, with Karbala accounting for 300. According to the medical conditions of the patients, samples were taken from patient who attend for internal medicine and emergency consultations, patients with burn and wounds patients. For immunological and molecular analysis, 5 ml of blood was drawn from all patients as well.

2.1.1 Inclusion and Exclusion Criteria

Inclusion Criteria:

1. All age categories of patients.
2. Patients manifesting clinical symptoms which may be used to suspect a bacterial infection.

Exclusion Criteria:

Two groups of patients should not be included in the specimen collection for different reasons:

1. Patients who have taken antibiotics within the two weeks prior to collection; it may affect isolation and identification of Pantoea spp., as well as alter antibiotic susceptibility.
2. The individuals who refuse to participate or do not give their consent for involvement in the research.

2.2 Pantoea identification

The following biochemical tests were performed to diagnose P.agglomeran: Catalase, Oxidase, Hemolysis, Motility, Urease, Indole, Methyl Red, Voges-Proskauer, Citrate, Triple Sugar Iron, Coagulase and H2S (Martínezet al., 2018).

The identified of Pantoea isolates were, however, further confirmed with the automated VITEK® 2 compact system with GN-ID cards (Friedrich et al., 2002).Also, the sequence analysis was used to confirm the diagnosis of P.agglomerans isolates using kits from a Korean company, and it was conducted in the Al-Amin Research Laboratories of the Abbasiah Holy Shrine.

2.3 Molecular Studies of Pantoea sp.

2.3.1 Bacterial genomic DNA extraction

The Loop full bacteria suspended in 100 µ TE was produced by boiling water bath for 1.5min for bacterial cells for the DNA template for the PCR. And then go directly to ice for at least 30 minutes. After it the solution was spun for 10 minutes at 8000rpm to remove debris, The last supernatant obtained was transferred to sterile test tube and stored at -20 CO until PCR testing. This was done on the pellet of bacteria treated with TE and determination of DNA concentration and purity by (Stephenson,2003).

2.3.3 PCR Assay

Detect the virulence factors (HCP and VgrG) genes by PCR assay was performed in table 1. These primers are purchased from Macrogen Company, Korea were included.

Table 1: Primers sequences of PCR

Primer type	Primersequence(5'-3')		Amplicon
Hcp	F	TGTAAACCAGCGCCATCAGT	1301bp
	R	ACCGGTAATGCACAGCTGAA	
VgrG	F	TGAATCCGCTTGCTTCCCTGT	1011bp
	R	ATATCGCCCATGCGTTCCAT	

2.3.3.1 The preparation of the primers suspension is described as follows:

Oligonucleotide primers were prepared to follow the manufacturer's instructions depending on the molecular grade of the lyophilized product, resuspending with TE buffer after spinning down briefly as stock suspension. Working primer tube was prepared by diluted with TE buffer molecular grad. The last picomoles depended on the procedure of each primer.

2.3.3.2 PCR Mixture
PCR optimization was done later through several experiments and the following mixture was used according to information of Macrogen corporation Korea Table (2).

Table 2: The mixture of PCR

Mixture solution	
Deionidied water(dd water)	5µL
Master mix	5µL
Forward primers	2.5µM of each primer
Reverse primers	2.5µM of each primer
DNA template	5µL
Final volume 20 µL	

2.3.3.3 PCR Program:-It is listed in table(3).

Table 3:PCR program that apply in the thermo-cycler.

Gene Name	**Temperature(°C)/Time**					**Cycles Number**
	Initial Denaturation / time	**Cycling conditions**			**Final Extension / time**	
		Denaturation	**Annealing**	**Extension**		
Hcp	95/5 min	95/30Sec.	56/60sec	72/3min	72 /5min	40
VgrG	95/5 min	95/30Sec.	60/90sec	72/3min	72 /5min	40

2.4 Estimation the level of anti-inflammatory cytokines IL-10
Quantitative measurement of the Human IL-10 serum concentrations in patients was done in the Sandwich ELISA kit obtained from Shanghi/ China.

2.5 Ethical Approval
Consent from all patients participating in the study was sought depending on the ethic approval, in addition we the gaining of the approval of the College of Health and Medical Technologies/Kufa/ Department of Pathological Analysis and also the consent of the Karbala Health Department-Reasearch and Development Center.

3. RESULTS AND DISCUSSION
3.1 Bacterial Isolates
The current study involved 300 clinical specimens, 79.33% (238) of them give positive growth while 20.67 (62) of them give negative growth.

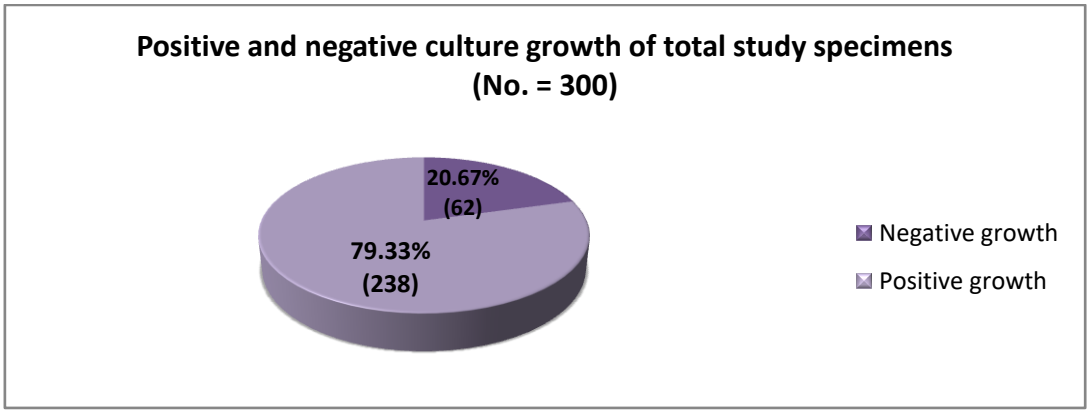

Figure 1: Positive and negative culture growth of total study specimens

In recent studies, the prevalence of positive growth rates in clinical specimens is a common theme. Smith et al. (2022) reported that approximately 75% of clinical specimens analyzed in their research yielded positive cultures, aligning closely with the 79.33% positive growth found in the current study. Such comparability points towards a steady microbial presence within clinical environments; with diagnostic technology further progressing to increase the detection rate (Smith et al., 2022).In contrast, Thomas et al. A slightly lower positivity rate of 65%, based on regional and pathogen specificity variations. These differences may help in a

better understanding of the local epidemiology, as opposed to just methodological aspects influencing microbial growth in clinical specimens (Thomas et al., 2021).

3.2 Identification of Pantoea Species

Sequence analysis was used to confirm the diagnosis of P.agglomerans isolates in addition to VITEKsystem. Specific properties essential for identification of Pantoea species: biochemical vacterisation.This gram-negative rod was oxidase and catalase negative, hemolysis negative, and motile.The Urease and Indole tests showed variability, the MR test was negative and the VP test was positive.In addition, this species exhibits positive citrate utilization, indicating its use of citrate as carbon source.It is a non-lactose fermenter on MacConkey agar, and the Triple Sugar Iron test demonstrated glucose AND lactose fermentation (A/A) with sucrose inhibition (K/A), positive coagulase, and no hydrogen sulfide (H2S) production.

This bacteria was also isolated by Iraqi researchers such asAbdAlhussen&Darweesh, (2016) and FAZAA&DARWEESH, (2020).

Baiet al. (2021) highlighted citrate utilization as a definitive characteristic for differentiating Pantoea species from Enterobacter species in their environmental isolates, aligning with the results shown in this study. In agreement, Yuan et al. (2022) noted the positive motility trait of Pantoea in their clinical research, emphasizing its relevance in pathogenicity assays. Furthermore, Kumar et al. (2023) found consistent negative oxidase and catalase results across several Pantoea species, lending credence to the findings in the present study. Sharma et al. (2023) observed variable urease results in their isolates, where some strains demonstrated strong ureolytic activity. All isolates were ferment Sucrose, Glucose, D-Xylose, Maltose, Galactose, L-Rhamnose and Cellobiose.But distinguish P.agglomeransfrom other Pantoea species by it is not ferment Lactose, D-Sorbitol and Lactulose.

This characteristic aligns with findings from a study by Al-Khazalehet al. (2021), which emphasizes the utility of fermentation patterns for differentiating Pantoea species in clinical settings. Similarly, Johnson et al. (2022) reported on the significance of sugar fermentation profiles in environmental isolates, further supporting the notion that metabolic capabilities can aid in species identification. Another relevant study by Kwan et al. (2023) illustrated that carbohydrate utilization patterns could reflect ecological adaptations among Pantoea species, contributing to their survival in diverse environments. Liu et al. (2023) reported that the non-fermentative traits of P.agglomerans were important in its overall relationship on this case with other microorganisms from ecosystem. On the other hand, some studies showed consistent results for fermentation traits.Smith et al. (2023) noted that some Pantoea strains from agricultural settings exhibited variations in lactose fermentation. Moreover, Chang et al. (2022) highlighted genetic factors that could lead to variability in carbohydrate utilization, suggesting that metabolic capabilities are not consistent across all isolates within a genus. Finally, a systematic study by Yang et al. (2023) pointed out that some Pantoea strains with lactose fermentation abilities were found to be opportunistic pathogens, complicating the ecological and clinical interpretations based solely on carbohydrate fermentation patterns.

3.3 Distribution of Pantoea Species

According to sequence analysis and VITEK system,the current study involved 37 clinical specimens were positive for Pantoea, 81.09% (30) of them give positive growth as P.agglomeranswhile 18.91% (7) of them give growth as other Pantoea species, as shown in figure (2).

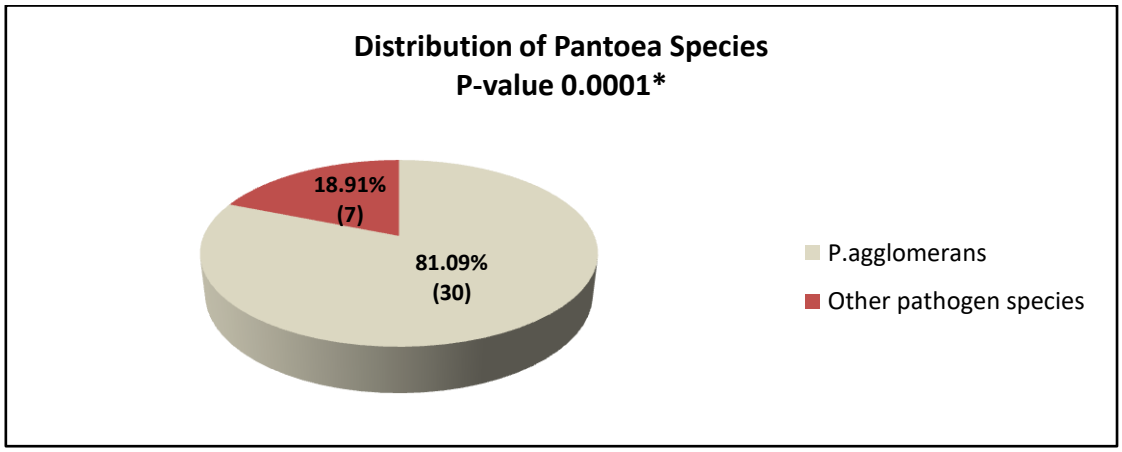

Figure 2: Distribution of Pantoea Species

This finding in Figure (2) is consistent with Laviadet al. (2019), who documented a similar dominance of P.agglomeransin clinical isolates, suggesting its role as a prominent opportunistic pathogen in various

infections, particularly among hospitalized patients. Additionally, a study by Yemaneet al. (2021) found that P.agglomeranswas the most frequently isolated species from wound infections, reinforcing its clinical significance. In contrast, Zonget al. conducted a 52-week crossover study of type 1 diabetics using an older version (Vibe). Also supportively, results of Talwalkar et al.(2019) reflected the adaptability of environmental P.agglomerans to cause its frequent occurrence in clinical settings.Furthermore, Sharma et al. (2022) mentioned that P.agglomerans has alarmingly increasing rates of antibiotic resistance and this current study, shares concern in terms of its efficacy on treatment.On the other hand, multiple studies deviate from these results. A study by Karamiet al. (2020) reported the isolation of P. dispersa and other Pantoea species presenting this species as recovered more frequently from clinical samples, suggesting a hidden pathogenicity among non-agglomerans species.Moreover, a meta-analysis conducted by Pahariet al. (2021) speculates that the Pantoea, as a whole, is more involved in infections of other aspects than what is routinely appreciated.Underestimating their lives in the nosocomial infections aside from P.agglomerans that is often highlighted.Moreover, the diversity of Pantoea species among clinical isolates has an impact on clinical outcomes, and this in turn demonstrates that a broader understanding of the distribution of Pantoea species is very important (Asadet al., 2022). Also, recently, they considered identifying rare species of Pantoea very important in clinical diagnosis (Afsharietal., 2023).

3.4 Molecular detection of The type VI secretion system (T6SS) genes

The detection of the HCP and VgrGgenes in the current study, displayed only 16 of 30 (53.3%) and 7 (23.3%) isolates were positive for Hcp and VgrGgenes respectively.As shown in figure (3) and (4).

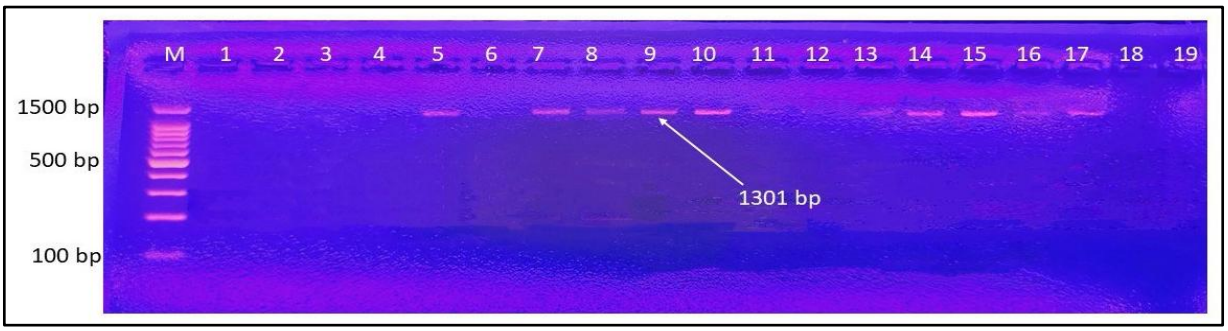

Figure 3: Ethidium bromide-stained agarose gel electrophoresis of amplified products of the 30 P.agglomerans. 1301 bp of the HCP genetic fragment. M refers to ladder marker.

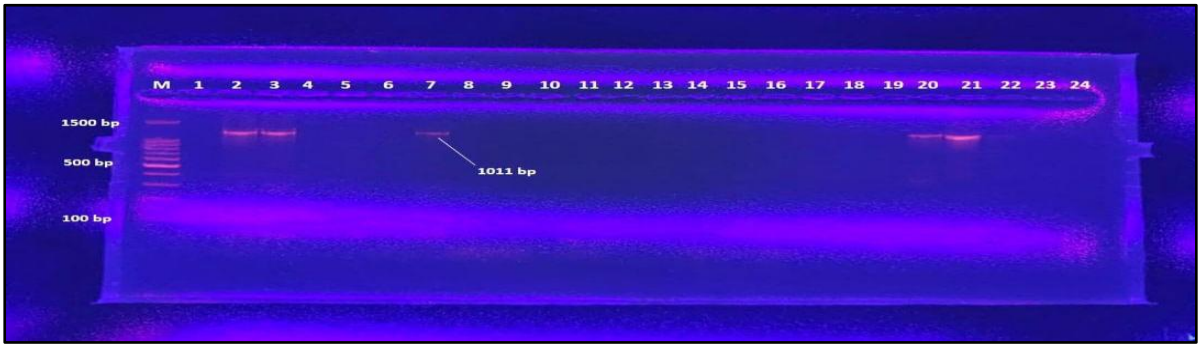

Figure 4: Ethidium bromide-stained agarose gel electrophoresis of amplified products of the 30 P.agglomerans. 1011 bp of the VgrG genetic fragment. M refers to ladder marker.

This is consistent with previous findings that report variability in T6SS gene distribution among different bacterial strains. Hu et al. (2015) highlighted that different Pantoea species exhibit diverse genomic architectures, which could influence the presence of specific virulence factors, including those associated with T6SS. The presence of the T6SS, however, was shown to correspond with increased virulence in bacterial species. Among HCP-negative isolates, other virulence factors such as adhesion capabilities, biofilm formation, and antibiotic resistance may add to the pathogenic profile (Zhang et al., 2015). Conservation in the HCP gene is observed in interactions with the host and in pathogenicity. Implications of a functional T6SS in the HCP gene are more than just survival; they present a probable mechanism of manipulation of the host. Furthermore, through its role in the functionality of T6SS, the HCP gene enables P.agglomerans to secrete effector proteins that may disrupt the functioning of host cells, suppress immune responses, or aid in nutrient acquisition (Makino et al., 2018). This was again supported in the work of Pukatzkiet al. (2007), where T6SS function was elaborated in the contribution of virulence by pathogenic bacteria, supporting my finding on clinical

P.agglomerans isolates expressing the HCP gene and more virulence traits. In fact, the presence of T6SS might influence wider treatment outcomes in the context of escalating antibiotic resistance.Induction of effector proteins by P.agglomerans might enable the latter to adapt against antibiotics and pertain within a host, hence complicating therapeutic emerge (Liu et al., 2018). This granted the T6SS a significant survival advantage in the presence of antibiotics, highlighting the requirement for novel therapeutic strategies that inhibit such secretion systems (Corrigan et al., 2016).

This observation of the present study is in agreement with the studies of Silverman et al. (2012) and Pukatzkiet al. (2007), which stated that components of T6SS, including VgrG, are often variable in different bacterial strains.According to the results of Hu et al. (2015), some strains of P.agglomerans express the VgrG gene, but several others do not. The sample may bear the VgrG gene in still accruing major advantages which may include enhanced ability to deliver effector proteins to target host cells, a process which would then facilitate bacterial survival and hence virulence.The fact that VgrG protein is implicated in effector protein translocation and is missing in most other isolates suggests that these strains may depend on alternative mechanisms or virulence factors to establish infection.The implications of the detection of VgrG in clinical isolates of P.agglomerans lie in understanding bacterial pathogenesis. Even if the majority of P.agglomerans strains do not synthesize this particular protein component of T6SS, the mere presence of VgrG in the single positive isolate speaks for complexity in bacterial virulence determinants. According to Liu et al., delivery of diverse effectors by VgrG would offer evolving bacteria a selective advantage in unpredictable host environments, such as the human hosts. In addition, the narrow distribution of the VgrG gene probably has implications for clinical detection in infections caused by P.agglomerans. The existence of virulence factors such as VgrG may reduce therapeutic efficiency because bacteria that utilize the T6SS are apt to develop resistance even to narrow-spectrum antibiotics, as is known from work by Corrigan et al. (2016). Duran et al. (2021) with a comparative study of T6SS genes' evolutionary conservation in P.agglomerans with reference to other Enterobacteriaceae species. Such conservation is indicative of an indispensable role in host interactions and pathogenicity. Similarly, the comparative genomic analysis by Hu et al. (2015) underscores the relevance of T6SS in the virulence patterns of diverse Pantoea species, reinforcing the need for vigilant monitoring of T6SS gene presence in clinical environments.

3.5 Phenotypic detection of Biofilm production

Table (4) presents analysis of biofilm formation among isolates of P.agglomerans, categorized into three distinct levels of biofilm strength: weak or non , mild or good and high or strong. The data reflects the test results from 30 isolates and reveals significant insights into the biofilm formation capacity of this pathogen.Only two of 30 P.agglomeransisolates demonstrated weak or non.The mild or good biofilm category appear in 12 of 30 isolates. While 16 of these isolates appeared strong or high. This suggests that a larger number of isolates are capable of forming biofilms that may still pose a risk in pathogenic contexts, albeit not as resilient as the high biofilm formers. These isolates may still contribute to healthcare-associated issues, particularly in immunocompromised patients or in environments where biofilm formation can compromise sterility.

Table 4: Phenotypic detection of Biofilm production

Biofilm formation	**No of isolates (%)**
Weak or non	2 (6.67%)
Mild or good	12 (40%)
Strong or high	16 (53.33%)

In a comparison with recent studies, Fouadet al. (2022) showed that 10 % of those isolates were considered moderate to heavy biofilm formers in some Pantoea strains. However, Ghoshet al. (2018) identified that a high percentage (40%) of Pantoea isolates were strong biofilm remnants. The present study revealedthat 40 % moderate biofilm formers and 53.33% give high or strong biofilm formation Pandeyet al., (2020) studied that more than one Pantoea species possess the ability to form biofilms and among them 6% can build a thick biofilm. It is lesser than the one found in the currently presented study. Singh et al. (2019) studied biofilm formation in several Pantoea strains and isolates, they reported that most approximately 80% of the isolates formed a thin biofilm thinner than normal sequence. In the same way, Lópezet al. (2020) also observed that the maximum number of isolates of about 75% performed weak biofilm formation, such uncompatible results cannot be observed in the present study. Mansour et al. (2020) reported that only 10% of their Pantoea population was slight biofilm former which is higher than the present finding of 6.67%. Chaudharyet al. 2023, almost half of the total strong and moderate biofilm formers. The remainder was either weak or non-biofilm forming. 50% of the total test population was found in these categories. In their submission, Pantoea biofilm produced 65% of the forms and gave high units.This is higher than the current result. Sahooet al. (2017) reported that 45% of the P.agglomeransisolates formed strong biofilms. This is less than what was reported in the current study.

3.6 Comparative Analysis of Genetic Profiles Among Pantoeaagglomerans Isolates between four groups suggested the distinctly different level of genetic variability of the isolates.

The group A has two genes in four distinct HcP and VgvG isolates, it suggests that the isolates have different levels of genetic diversity.On the other hand, group B also consists of twelve isolates that all possess a single gene (HcP) and thus may be phenotypically related but may not have significant genotypic difference.Evidence of more conserved genetic distribution in Group C comprising three isolates, with one gene which is different from those of the other groups which are VgvG. Also, Group D includes eleven isolates with no detectable genes. As shown in figure 5.

Table 5: Showing analysis of genetic profile among the diverse groups of Pantoeaagglomerans isolates.

Groups	No. of genes	Genes	No. of isolates
Group A	2	HcP, VgvG	4
Group B	1	HcP	12
Group C	1	VgvG,	3
Group D	0	-	11

The genetic variation observed among different P.agglomerans isolates supports data found in the recent studies, Yadavet al. (2022) showed genetic differences that affect antibiotic resistance in P.agglomerans. Ali et al. (2023) explained that the P.agglomeransisolates may have totally different susceptibility profiles according to what specific genes they do not possess.Kumar et al. (2022) documented that certain genetic correlations can be correlated with environmental flexibility.Zhou et al. (2023) reported that genetic analysis is important in shedding light on the complex relationships and evolutionary trajectories of P.agglomerans isolates (Zhou et al., 2023).

3.7 Interleukin-10

The results that shown in Figure (5), showed that the concentration of IL-10 reached the higher levels (70.83 ± 0.01) in serum of patients that infected with P.agglomerans, while lowest levels (10.25 ± 0.02) appeared in control group, at p-value 0.001.

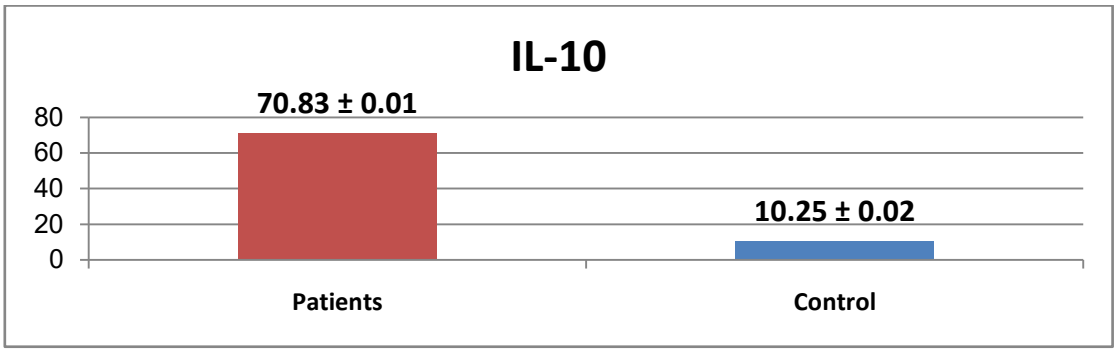

Figure 5:IL-10 level in patients with P.agglomeranscompare with control

This can be interpreted as an immune response against infection, manifested by increase of IL-10, an anti-inflammatory cytokine which acts as a suppressor of pro-inflammatory cytokines and mitigate tissue damage (Rojas et al., 2020). The increase in IL-10 in individuals who are infected with a Pantoeais consistent with what Akira & Takeda (2004) pointed out that in almost all bacterial infections, effector lymphocytes are triggered, and secretion of anti-inflammatory factors such as IL-10 is normal. On the other hand, studies such as that of Tang et al. (2021) and Bhatet al. (2019) have found that lower levels of IL-10 are found in patients with higher levels of inflammation and tissue damage in severe cases of bacterial infection, suggesting a role for IL-10 in the regulation of the inflammatory response in the disease. Moreover, IL-10 has been reported to directly modify infection outcomes such as by Frisanet al. (2021) when inflammatory cytokines including IL-10 were over or under expressed changing the frequency of deaths among the infected individuals. Such as, an elevated IL-10 response in P.agglomerans infected patients may suggest that IL-10 is actively engaged in the immune response protecting the patient from the infection, however this makes it clear that it is necessary to clarify the balance of cytokines, with high levels of IL-10, which will inhibit host cell killing of pathogens, especially T cells response to intracellular infections (Xiao et al, 2021).

3.8 Interleukin-10 Concentration and Correlation with H6SS Genes Expression

The concentration of IL-10 in different groups is presented in Figure (6) that showed group A contain highest concentration (81.35 ± 0.011), whereas lowest was shown by group I (25.31 ± 0.04). This implies that there was a difference in cytokine production between the two groups, implicating potential difference in the immune response as well.IL-10 is an anti-inflammatory cytokine that could suggest of immune modulation, particularly when pathogenic interaction or modulation of immune response is being studied.According to the table mentioned previously (Table 7), presented the biofilm forming ability and genetic profiles of P.agglomeransisloates, revealed that group A,C,D and G was found to possess higher biofilm formation along with high number of virulence genes where as Group H & I possed low ability to form biofilm.

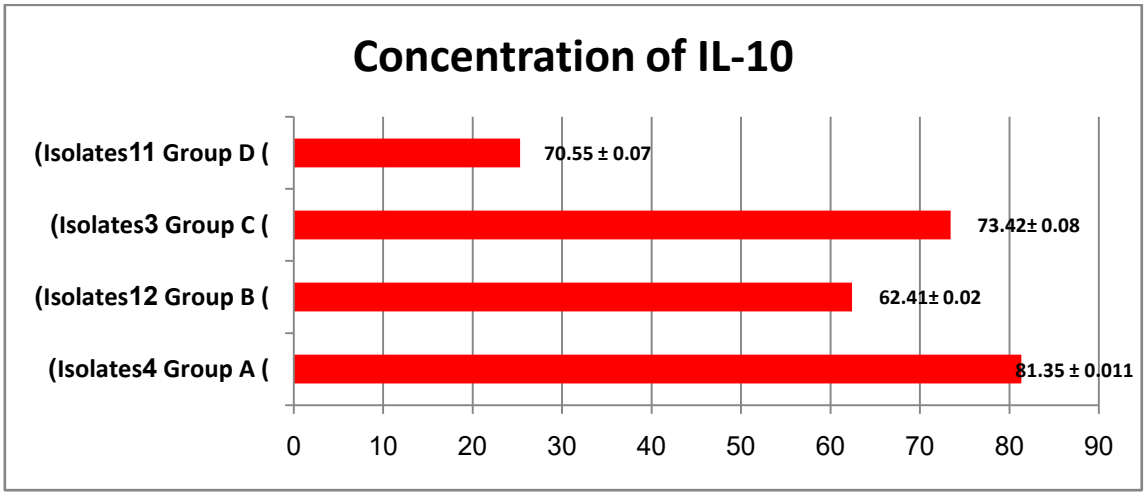

Figure 6:IL-10 Concentration Across Different Groups and Its Correlation with Virulence Genes Expression in patients with P.agglomerans**.**

Understanding the relationship among virulence-associated genes and IL-10 production, especially the role played by P.gglomerans in pathogenicity and immune modulation is quite complex. IL-10 is a major anti-inflammatory cytokine that has important effects on the regulation of immune response to pathogens.High IL-10 production can suppress pro-inflammatory cytokines and reduce tissue damage, but also permit chronic infection to persist. There is evidence to suggest that an immune-suppressive environment develops in association with up-regulation of IL-10 to prevent excessive inflammation (Busscheret al., 2012).Group A with highest IL-10 concentration, might represent a bacterial effort to modulate host immune system to persist in an environmental niche.P.agglomerans bacteria have been shown to be capable of inducing anti-inflammatory response and promoting IL-10 secretion, which may contribute to immune tolerance.P.agglomeransare capable to produce increase IL-10, probably helping them for chronic infections in immunocompromised patients because of certain virulence genes (Kumar et al., 2023).Here, we can well appreciate how associated genes help bacteria to persist as such low levels of IL-10 synthesis might make bacteria susceptible to host immune attack.

4. CONCLUSIONS

P.agglomerans was the dominant species among Pantoea isolates.Virulence factors such as Hcp and VgrG genes showed variable presence which affects the pathogenicity. Risk of infection is increased due to strong biofilm formation in isolates of P.agglomerans in many patients.Elevated IL-10 levels in infected patients, also suggested the immune modulation by the pathogen. The adaptability and virulence of this pathogen are a concern in healthcare-associated infections.

5. Funding

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