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Evaluation of the relationship between IL-6 and IL-10 genes single nucleotide polymorphisms as an indicator of COVID-19 severity in Babylonian population

A Graduate Research Project

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بسم الله الرحمن الرحيم

﴿نَرْفَعُ دَرَجَاتٍ مَّن نَّشَاءُ وَفَوْقَ كُلِّ ذِي عِلْمٍ عَلِيمٌ﴾

صدق الله العلي العظيم

سورة يوسف الآية: ٧٦

Dedication

To Our Lord, Our Supporter... "Allah"

To the candle of my Life ... "Our Parents"

To the dearest of my heart...

"Our sisters and my brothers"

And to all who suffer ... To raise the name of our country... To Our motherland ...

IRAQ... We dedicate this work

Students

ACKNOWLEGMENTS

In the Name of Allah, the Most Merciful, the Most Compassionate all praise be to Allah, the Lord of the worlds; and prayers and peace be upon Mohamed His servant and messenger.

First and foremost, we must acknowledge my limitless thanks to Allah, the Ever-Magnificent; the Ever-Thankful, for His help and bless. We are very sure that this work would have never become truth, without His guidance.

We owe a deep debt of gratitude to our university and college for giving us an opportunity to complete this work.

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We would like to take this opportunity to say warm thanks to all my beloved friends, who have been so supportive along the way of doing our project.

We also would like to express my wholehearted thanks to my family, for their generous support they provided me throughout my entire life and particularly through the process of pursuing the Bachelor's degree. Because of their unconditional love and prayers, we have the chance to complete this work.

Students

Evaluation of the relationship between IL-6 and IL-10 genes single nucleotide polymorphisms as an indicator of COVID-19 severity in Babylonian population

تقييم العلاقة بين تعدد أشكال النوكليوتيدات الأحادية لجينات IL-6 وIL-10 كمؤشر على شدة COVID-19 لدى سكان بابل

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Abstract

The new coronavirus, which is now many respiratory illnesses in Wuhan, China, under the name SARS-CoV-2, from December 2019. The illness COVID-19 was brought on by this virus. A worldwide pandemic has been caused by the virus spreading from person to person. The investigation tries assess polymorphism effect with some genes like Interleukin-6 and Interleukin- 10 on susceptibility to covid-19 in Babylon province. A total of (113) cases in this study (63) cases have clinical symptoms of covid -19 patient, (50) blood samples were collected from healthy people as a control group in this study during (November 2021 to February 2022) at Al-Morgan Hospital. There were many demographic data included in the present study such as age distribution, sex distribution, and geographic distribution of covid patients. Among (63) samples from suspected covid -19 patients from different age groups (20 to 80 years old). The three genotypes (CC, CG &GG), respectively (5.31, 38.94, 11.50), and the allele frequency of (C, G) were (44.44, 55.56) for patients and genotypes (CC, CG &GG), respectively (15.04, 23.01, 6.19) and the allele frequency of (C, G) was (60.00, 40.00) for controls. three genotypes (GG, GA &AA), (3.54, 51.33, 0.88) respectively, and allele frequency of (G, A) was (52.38, 47.62) respectively for the patients and genotypes (GG, GA &AA), (7.96, 20.35, 15.93) respectively, and allele frequency (G, A) was (41.00, 59.00) respectively for control people.

فيروس كورونا الجديد، الذي أصبح الآن العديد من أمراض الجهاز التنفسي في ووهان، الصين، تحت اسمSARS-CoV-2 ، اعتبارًا من ديسمبر ٢٠١٩. وقد تسبب هذا الفيروس في ظهور مرض COVID-19. تسبب انتشار الفيروس من شخص لآخر في حدوث جائحة عالمي .يحاول تحقيقنا تقييم تأثير تعدد الأشكال مع بعض الجينات مثل Interleukin-6 و Interleukin- 10على القابلية للإصابة بـ covid-19في محافظة بابل. إجمالي (١١٣) حالة في هذه الدراسة (٦٣) حالة ظهرت عليها أعراض سريرية لفيروس كوفيد -١٩ مريض، (٥٠) عينة دم تم جمعها من أشخاص أصحاء كمجموعة ضابطة في هذه الدراسة خلال (نوفمبر ٢٠٢١ إلى فبراير ٢٠٢٢) في- Al مستشفى

مورغان. كان هناك العديد من البيانات الديموغرافية المدرجة في هذه الدراسة مثل التوزيع العمري، وتوزيع الجنس، والتوزيع الجغرافي لمرضى كوفيد. من بين (٦٣) عينة من مرضى كوفيد -١٩ مشتبه بهم من مختلف الفئات العمرية (٢٠ إلى ٨٠ سنة) .الأنماط الجينية الثلاثة CC) ، CG، (GG، على التوالي (٥,٣١ ، ٣٨,٩٤ ، ١١,٥٠) ، وتكرار أليل C) ، (Gكانت (٤٤,٤٤ ، ٥٥,٥٦) للمرضى والأنماط الجينية CC) ، CG، (GG، على التوالي (١٥,٠٤ ، ٢٣,٠١ ، ٦,١٩) وكان تردد أليل C) ، 60.00) (G ، ٤٠,٠٠ (لعناصر التحكم. ثلاثة طرز وراثيةGG) ، GA، (AA، 3.54) ، ٥١,٣٣ ، ٠,٨٨ (على التوالي ، وتواتر الأليل G) ، (Aكان (٥٢,٣٨ ، ٤٧,٦٢) على التوالي للمرضى والأنماط الجينية GG) ، GA، (AA، 7.96) ، ٢٠,٣٥ ، ١٥,٩٣ (على التوالي ، وتردد الأليل G) ، (Aكان (٤١,٠٠ ، ٥٩,٠٠) على التوالي لأفراد المجموعة الضابطة.

Keywords:

IL-6, IL-10, genes, single nucleotide polymorphisms, COVID-19 Babylonian, PCR

Introduction

Millions of people have been impacted by 2019, Coronavirus disease Covid-19, which is brought on by the SARS-CoV-1 (SARS-CoV-2) coronavirus that causes the severe acute respiratory syndrome (MERS-CoV) and four seasonal coronaviruses that cause moderate infections are all members of the Coronaviridae family (Wang *et.al*.,2020, Corman *et.al*.,2018).

Immune responses in the host and immune-related signs and symptoms highly varied. Patients with SARS-CoV-2 under effective control, i.e., asymptomatic, and those without effective management, i.e., impacted via COVID-19 severe infection, host immune responses and immunological-related symptoms are tremendously diverse. This shows that in some circumstances, host immunological dysregulation plays a role in pathogenesis. However, it is unclear whether the emergence of a severe variation of the illness governed by immunological either excessive activity or an inability to stop the inflammatory reaction as a result of continued virus reproduction and immunologic mis regulation. In mild cases, the relationship between cytokine levels, viral load in the nasopharynx, and falling viral burden implies that immunological reaction is linked to viral burden (Yang *et.al*.,2021, Fajgenbaum and June,2020).

Inflammatory cytokines are crucial in the pathogenesis of disease, as the COVID-19 cytokine storm illustrated (Pedersen and Ho.,2020,Wu and Yang.,2020). which could linked to the progression of COVID-19. The number of nations having information the range of cytokine

polymorphisms was 16 to 54. The cytokine polymorphisms utilized, as well as the quantity of nations involved. The allele frequency associate with CFR , DDR (de Meira Leite *et.al*.,2021).

MATERIALS AND METHODS

Study subjects

The practical side of the present study was done during the period from November 2021 to March 2022.Fifty healthy and sixty-three patients were selected for the study**.** Patients hospitalized at the medical center in Mergan Medical City, Iraq, diagnosed with Covid -19 were compared to 50 healthy controls and 63 patients with the disease. The current study comprised 19 males and 44 females, ranging in age from 20 to 80, who were diagnosed with covid-19 using serological and molecular assays. Patients' blood and serum samples were properly analyzed.

Healthy control group

Fifty healthy individuals (Aged 20-80 years) from Babylon Iraqi communities who have been proven laboratory, clinically, and genetically that they do not have covid-19 were included.

Blood samples collection

The blood samples totaling around five milliliters of patients in this trial were collected. EDTA-containing tubes were used to collect around two milliliters of blood for genetic testing. Two samples of blood were taken from each subject and the first was put in gel tubes for 30 minutes; the second was centrifuged for 15 minutes and the serum was recovered and stored in the freezer (-20 ^{o}C).

Control Samples collection

Fifty healthy individuals with a similar age distribution as the patients were selected to take their venous blood samples for the study.

Isolation of genomic DNA

EDTA tubes were used to collect human genomic DNA for molecular analysis, and proteinase K is advised for the purification of DNA from frozen blood samples. The Geneaid and Promega kits Geneaid- Ltd were used.

Estimation of DNA concentration and purity:

Patients' and controls' whole blood samples were used to extract genomic DNA using the protocol for DNA separation from patient and control subjects' whole blood samples. Blood

samples were analyzed using the gSYNCTm gDNA Extraction kit from fresh blood to extract DNA and RNA (Geneaid-Ltd).

With the Nano drop, 2.5 l of DNA extracted from the samples was put into the machine to measure the concentration (ng/L) and purity (OD: 260/280nm), which was used to determine the presence of protein in the samples. According to the standard 260/280 ratio for purifying DNA, this ranged from one to two. Following genomic DNA extraction, agarose gel electrophoresis was used to confirm the closeness and uprightness of the separated DNA. Acrylate dissolved in 1x TBE buffer and Safe stain were used to expose the DNA bands (75 min/100 Volt).

Primer's preparation:

IL-6 (174 Promoter) primer given in the accompanying was used to identify diagnostic and virulence genes (Table 1). Ligo /USA provided the primer. Before removing the cap from the primer's tubes, all primer pairs were spun down. A specified volume of nuclease-free water was added to each primer per the manufacturer's instructions, resulting in a primer stock solution with a 100 Pico-mole/microliter concentration. Transferring 10 l of the primer stock solution into an Eppendorf tube containing 90 l of free nuclease water yielded 10 Pico-mole/microliter of free nuclease water that was utilized in PCR amplification.

Table 1. Sequence of primers for IL-6 and IL-10 gene

Gene	Primer		bp.	Reference
IL-6 (174 Promoter)	**F**	**5´-CCC CTA GTT GTG TCT TGC C-3´**	**288**	**(Marzieh etal,.2016)**
	R	**5´-GCC TCA GAG ACA TCA CCA GTC C-3´**		
IL-10 1082	**F**	**5-CTACTA AGG CTT CTT TGG GAG-3 5-ACT ACT AAG GCT TCT TTG GGA A-3**	**258 bp**	**(Samaneh et.al,.2014)**
	R	**5-CAG TGC CAACTG AGA ATT TGG-3**		

Detection of IL-6 (174 Promoter)

Genotype determination for three selected SNPs was performed by (SSP-PCR) method (Gao et al,. 2009). PC*R mixture 5-µl (DNA), 5-µl master mix, 5µl forward, reverse primer. Conditions of *PCR conditions for *IL-6* performed of following table **(**2).

Table 2. PCR condition for *IL-6 (174* Promoter)

Step	Temperature C°	Tim/min.	Cycles
Initial denaturation	*95	4	1
Denaturation	*95	20s	15
Annealing	58	40s	
Extension	72	40s	
Denaturation	95	20s	25
Annealing	54	50s	
Extension	72	50s	
Final extension	72	7	1
Storage	4	∞	

Detection of IL-10 1082

Using polymerase chain reaction, two IL-10 SNPs (IL-10-592 and IL-10-1082) were identified and genotyped (SSP-PCR) (Lu, Y.L et al., 2010). The initial stage was utilizing a gradient temperature to optimize the PCR. This is crucial in figuring out the ideal annealing temperature. 5 l of template DNA, 5 l of master mix, 5 l of each forward and reverse primer, and 20 l of total reaction volume made up the PCR reaction mixture for the gradient. The following table displays the gradient's PCR condition (table 3).

Table 3. Gradient condition of *IL-10 1082*

Step	Temperature C°	Tim/min.	Cycles
Initial denaturation	*95	*5	1
Denaturation	*95	*0.5	35
Annealing	55.4-56.2-59.3-61.6-63.4-63.3	0.5	
Extension	72	40s	
Final Extension	*72	7	1
Storge	*4	-∞	

Following identification of the clearest band, which was 61.6 C°, as the ideal annealing temperature of IL-101082 genes, a PCR combination of 5 l DNA, 5 l master mix, and 1.5 forward & reverse primers was created. According to the following table, PCR conditions were used (3-21).

Table 4. PCR prerequisite to *IL-10 1082*

Step	Temperature C°	Tim/min.	Cycles
Initial denaturation	*94	1	-1
Denaturation	*94	1	40
Annealing	*61.6	1	
Extension	*72	-1	
Final **Extension**	*72	10	-1
Storge	4		

Result and discussion

IL-6 gene polymorphism

The three genotypes (CC, CG & GG), respectively (5.31, 38.94, 11.50), and the allele frequency of (C, G) were (44.44, 55.56) for patients and genotypes (CC, CG &GG), respectively (15.04, 23.01, 6.19) and the allele frequency of (C, G) was (60.00, 40.00) for controls. Tables (4-5) and

Figure 5. exhibit the genotyping results for patients with Covid-19 and controls.

Table 5. Genotype frequency of polymorphisms of (*IL-6*) gene associated with Covid-19 patients and control

Genotype	**patients** (63)		Healthy (50)		Total (113)	
	No	%	No	%	No	%
CC	6	5.31	17	15.04	23	**20.35**
CG	44	38.94	26	23.01	70	**61.95**
GG	13	11.50	7	6.19	20	**17.70**
TOTAL	**63**	**55.75**	**50**	**44.25**	**113**	**100.00**
Allele Frequency						
C	56	44.44	60	60.00	116	**51.33**
G	70	55.56	40	40.00	110	**48.67**
TOTAL	**126**	**100.00**	**100**	**100.00**	**226**	**100.00**

Table 6. Genetic association of Genotype *IL-6* gene with disease.

Polymorphisms of (*IL-6*) gene			
ALLELE	OOD RATIO	Significance level	**CI 95%**
CC*CG	0.2086	0.0034	**0.0730 to 0.5956**
CC*GG	0.1900	0.0128	**0.0514 to 0.7028**
GG*CG	1.0974	0.8608	**0.3883 to 3.1015**

As showed in the above table, there is significant between CC*CG (0.0034), CC*GG (0.0128), GG*CG (0.8608).These results agreed with the findings of the WHO, which indicated Population

diversity of the IL-6 gen polymorphisms at the rs1800796/rs1800795 loci revealed that populations of Chin, Spain, Sweden, Poland, Germany, the UK frequently have the GC genotype while populations from India, Mexico, Turkey, Brazil, Russa, Italy, South Africa, & Greece frequently have the GG genotype. For the rss1800796 polymorphism, only the Japanese population typically had the CC genotype (WHO, 2020). And these results agreed with the findings of (Falahi *et al*., 2022) indicated no appreciable variations when it comes to the genotype or allele distribution off a few There are some differences between patients with severe COVID-19 and those with mild COVID-19 in the promoter region of the IIL-6 gene. Another local Study by Iman S.H. (2022) explained that G allele from the Iraqi population and there is an association between *IL-6*-174 G/C polymorphism and COVID-19 patients.

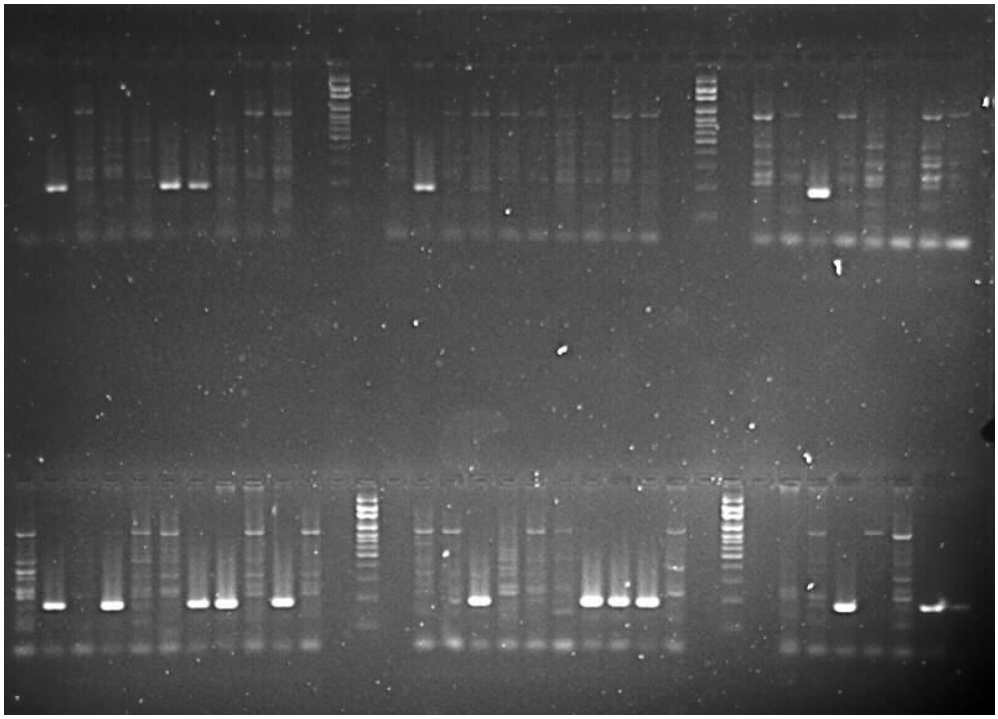

Figure (1): The Electrophoresis Pattern of *IL6* gene Polymorphisms. At 100 V. The 100 bp DNA Ladder is in the L lane along with a 1X TBE buffer with 5% NuSieve® 3:1 agarose gel with 5 l of Safe red dye for an hour.

A reliable predictive test that can reasonably anticipate a patient's progression to a severe stage of disease is urgently needed for effective diagnosis and care given the continued prevalence of COVID-19 in most societies. Early studies on COVID-19 suggested that the respiratory tract submucosa of activated mast cells has a role in escalating the inflammatory state and pathogenesis by releasing pro-inflammatory cytokines like IL-6 and TNF- (Conti *et.al.,*2020, Kritas *et.al.*,2020, Ross and Conti 2020). When SARS-CoV2 activates the innate and adaptive immune systems, a high number of cytokines, including IL-6, are released. Many individuals with severe COVID-19 experience a systemic inflammatory reaction known as cytokine release syndrome (CRS), which is a significant cause of death. (Zhang and Li 2020.) Increased levels of IL-6, a pro-inflammatory molecule, are known to suppress NK cell activity and have also been linked to decreased levels of granzyme and perforin, which degrade lytic activities (Cifaldi *et.al*.,2015). Exacerbation symptoms in COVID-19 patients included elevated body temperature, elevated inflammatory markers such CRP and serum ferritin, and advanced chest computed tomography imaging. These symptoms were linked to elevated IL-6 levels, which decreased as the condition improved (Liu *et.al*.,2020). IL-6 has been linked to pulmonary diseases before, namely in individuals with pneumonia potentially severe pneumonitis brought on by radiation treatment (Chen *et-.al*.,2001). Since the coronavirus disease of 2019 (COVID-19) epidemic in Wuhan, China, it has spread quickly to numerous other nations. While the majority of individuals were thought to be mildly unwell, deaths from critically ill patients who suffer from respiratory failure and multiple organ dysfunction syndrome are not unusual. It has been hypothesized that cytokine storm is connected to negative results (Han *et.al*.,2020). looked at 113 people; 50 healthy controls, 63 people with Covid, and a total of 113 people. Results for the *IL-6* polymorphism were obtained. Logistic regression use evaluates a distribution frequency of variables across the study groups. The *IL-6* GG*GA genotype (p ,= 0.049) & male gender (p 0.001) relate with severe COVID-19.COVID-19 severity was found to be associated with the *IL-6* genotype through In the context of the co-dominant inheritance paradigm, multiple logistic regression GG*CG, CC*GG, and CC*GG alleles all have 95% confidence intervals of 0.0730 to 0.5956, 0.0034 for significance and 0.2086 for odds ratio, respectively (1.0974). assuming that severity off Covid-19 associated with a *IL6*-CC*CG genotype. this study agreed with (Han *et.al*.,2020) 102 -COVID-19 patients who had

been admitted to Renmin Hospital were enrolled (Wuhan, China). In accordance with their symptoms, all patients were divided into three groups: moderate, severe, and critical. Additionally, 45 healthy volunteer control samples were used. This study agreed with (Michot *et.al.,*2020) COVID-19 with hyperinflammatory pulmonary symptoms is associated with a cytokine storm involving interleukins and chemokine dysregulation. This study agreed with (Batur and Hekim 2020). This study agreed with (Ulhaq and Soraya 2020) Excessive cytokine production and a higher mortality rate are characteristics of these severe COVID-19 cases. shows the course of COVID-19 is closely correlated with an increased level of interleukin-6 (IL-6) and C-reactive protein (CRP). This study agreed with (Szulc-Kielbik, Kielbik, Nowak, and Klink, 2021) Patients with ovarian cancer had high IL-6 levels in their serum and ascites. In light of this, its level is addressed in the literature as a potential biomarker that may aid in differentiating between malignant and benign ovarian tumors and enable the prediction of the chemotherapy response.

IL-10 gene polymorphism

Figures 2 show the three genotypes (GG, GA &AA), (3.54, 51.33, 0.88) respectively, and allele frequency of (G,A) was (52.38, 47.62) respectively for the patients and genotypes (GG, GA &AA), (7.96, 20.35, 15.93) respectively, and allele frequency (G,A) was (41.00, 59.00) respectively for control people. Table 4-7 displays the genotyping results for patients with Covid-19 and control people.

Table 7. Genotype frequency of polymorphisms of *(IL-10)* gene associated with Covid-19 patients and control

Genotype	Control (63)		Healthy (50)		**Total (113)**	
	No	%	No	%	No	%
GG	4	3.54	9	7.96	13	**11.50**
GA	58	51.33	23	20.35	81	**71.68**
AA	1	0.88	18	15.93	19	**16.81**
TOTAL	**63**	**55.75**	**50**	**44.25**	**113**	**100.00**
Allele Frequency						
G	66	52.38	41	41.00	107	**47.35**
A	60	47.62	59	59.00	119	**52.65**
TOTAL	**126**	**100.00**	**100**	**100.00**	**226**	**100.00**

Table 8. Genetic association of Genotype *IL-10* gene with disease.

Polymorphisms of (*IL-10*) gene			
ALLELE	OOD RATIO	Significance level	**CI 95%**
GG*GA	0.1762	0.0075	**0.0493 to 0.6295**
GG*AA	8.0000	0.0806	**0.7761 to 82.4596**
GA*AA	45.3913	0.0003	**5.7231 to 360.0120**

As showed in the above table, there is significant between GG*GA (0.0075), GG*AA (0.0806), GA*AA (0.0003).These results agreed with (Neumann *et.al*.,2020) A characteristic of activated regulatory T cells, which are found in organs like the lung, is the production of IL-10. This population, which is typically uncommon in healthy people, increased to around 10% of the regulatory T-cell pool in patients with severe COVID-19. The murine counterpart of this population has a strong anti-inflammatory effect and environmental interactions. (Bedoya *et.al*.,2013) When it comes to lung viral infections, *IL-10* restrains a development of *IIL-17*-producing cells that damage the tissue, (Chaudhry *et.al*.,2011,McKinstry *et.al*.,2009) reduces the generation of cytokines including IL-6, which have been linked to COVID-19 morbidity, and suppresses the innate inflammatory response to particles.(Chang, Kunkel and Chang (2009). (Rojas, Avia, Martín, and Sevilla (2017) Potentially, A blood-based biomarker for cases that proceed to more severe lung injury could be provided by increased IL-10. A more intriguing possibility is that individuals with higher *IL-10*-Regulatory T cells with impaired adaptive immunity produce. Many persistent viral infections are characterized by the presence of IL-10+ regulatory T cells, which are also linked to long-term persistence. IL-10 effectively inhibits antiviral responses in respiratory infections. (Sun, Torres, and Metzger (2010) , reduces the immunological response superinfection with bacteria.(Chaudhry *et.al*.,2011,van der Sluijs *et.al.*,2004) Since secondary infection leading to pneumonia ,a leading reason for mortality of influenza, and perhaps for some patients with COVID-19 is well,(Cox, Loman, Bogaert and O'Grady (2020), Zhou *et.al*.,2020) excessive *IL-10* production.

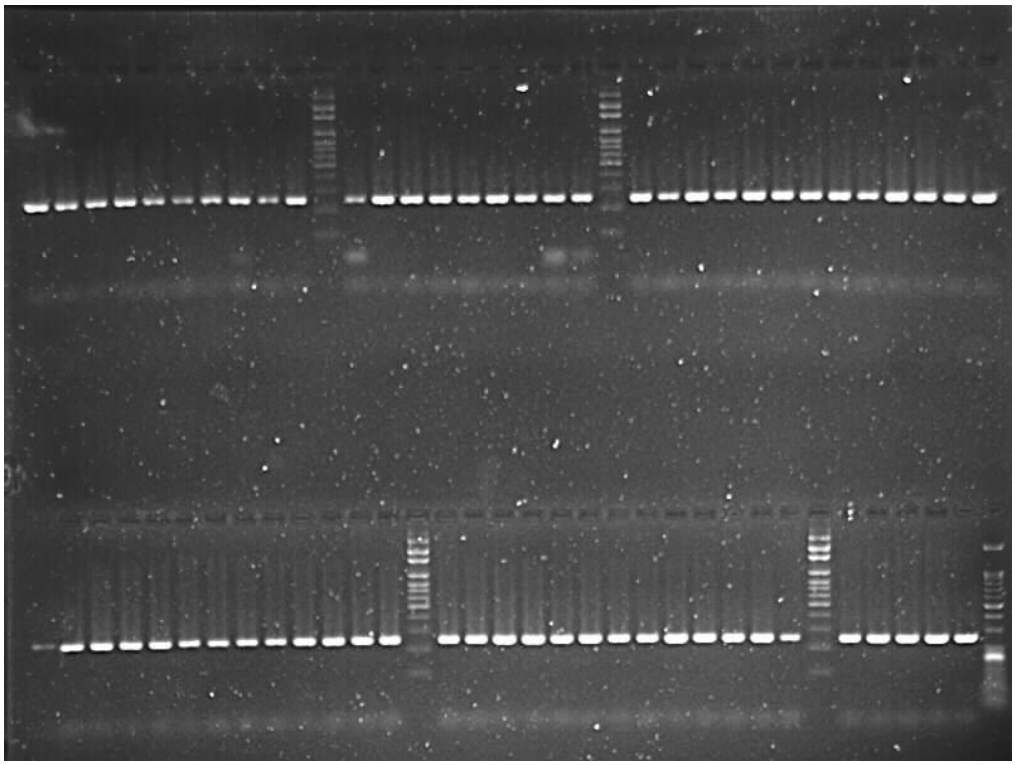

Figure 2. The Electrophoresis Pattern of *IL10* gene Polymorphisms. At 100 V. The 100 bp DNA ladder is in the L lane along with a 1X TBE buffer with 5% NuSieve® 3:1 agarose gel and 5 l of Safe red dye for an hour.

IL-10 is an anti-inflammatory cytokine that was discovered to be increased with COVID-19 (Huang *et.al*.,2020, Chen *et.al*.,2019). The main purpose of the multipurpose cytokine *IL-10* is to suppress the inflammatory response. *IL-10* is also known to cause T-cells to become anergic or unresponsive during the anti-tumor cell response (Moore, *et al* , 2001) as well as in viral infection (Maris, Chappell, and Jacob, 2007). One of the several mediators involved in the pathophysiology of COVID-19 is *IL-10. IL-10* is present in high concentrations during influenza infection, particularly during the adaptive immune response. 58 Critical COVID-19 patients had considerably greater serum *IL-10* and *IL-6* levels than moderate. Viral infection was eradicated by blocking *IL-10* with an antibody against *IL-10* or its receptor or by genetically removing *IL-10*. (Brooks et.al.,2006, Ejrnaes *et.al*.,2006) or bacterial pathogen (Biswas *et.al*.,2007). our looked at 113 people; 50 healthy controls, 63 people with Covid, and a total of 113 people. Results for the *IL-10* polymorphism were obtained. Regression using logit was used to assess distribution frequencies of variables across the study groups. COVID-19 severity was found to be associated with the

ACE2–CT genotype through. The co-dominant inheritance model and multivariate logistic regression GG*GA Allele, 95% CI (0.0493 to 0.6295), Significance level, 0.0075, Odd Ratio, 0.1762, GG*AA Allele, 95% CI (0.7761 to 82.4596), Significance level, 0.0806, Odd Ratio, 8.0000, and GA*AA Allele (45.3913). assuming that the severity of covid-19 was related to the genotype *IL10*-GG*GA. This study agreed with (Chen *et.al*., 2020) increased cytokine levels of *IL-10* to correlate with COVID-19 disease severity. This study differed with (Zhu *et.al*.,2021) the levels of *IL-10* of male were noticeably higher than those of female.

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الخلاصة

فيروس كورونا الجديد، الذي أصبح الآن العديد من أمراض الجهاز التنفسي في ووهان، الصين، تحت اسمSARS-CoV-2 ، اعتبارًا من ديسمبر ٢٠١٩. وقد تسبب هذا الفيروس في ظهور مرض COVID-19.تسبب انتشار الفيروس من شخص لآخر في حدوث جائحة عالمي .يحاول تحقيقنا تقييم تأثير تعدد الأشكال مع بعض الجينات مثل Interleukin-6 و Interleukin- 10على القابلية للإصابة بـ covid-19 في محافظة بابل. إجمالي (١١٣) حالة في هذه الدراسة (٦٣) حالة ظهرت عليها أعراض سريرية لفيروس كوفيد -١٩ مريض، (٥٠) عينة دم تم جمعها من أشخاص أصحاء كمجموعة ضابطة في هذه الدراسة خلال (نوفمبر ٢٠٢١ إلى فبراير ٢٠٢٢) في مستشفى مرجان.

كان هناك العديد من البيانات الديموغرافية المدرجة في هذه الدراسة مثل التوزيع العمري، وتوزيع الجنس، والتوزيع الجغرافي لمرضى كوفيد. من بين (٦٣) عينة من مرضى كوفيد -١٩ مشتبه بهم من مختلف الفئات العمرية (٢٠ إلى ٨٠ سنة) .الأنماط الجينية الثلاثة CC) ، CG، (GG، على التوالي (٥,٣١ ، ٣٨,٩٤ ، ١١,٥٠) ، وتكرار أليل C) ، (Gكانت (٤٤,٤٤ ، ٥٥,٥٦) للمرضى والأنماط الجينية CC) ، CG، (GG، على التوالي (١٥,٠٤ ، ٢٣,٠١ ، ٦,١٩) وكان تردد أليل C) ، 60.00) (G ، ٤٠,٠٠ (لعناصر التحكم. ثلاثة طرز وراثيةGG) ، GA، (AA، 3.54) ، ٥١,٣٣ ، ٠,٨٨ (على التوالي ، وتواتر الأليل G) ، (Aكان (٥٢,٣٨ ، ٤٧,٦٢) على التوالي للمرضى والأنماط الجينية GG) ، GA، (AA، 7.96) ، ٢٠,٣٥ (، ١٥,٩٣ (على التوالي ، وتردد الأليل G) ، (Aكان (٤١,٠٠ ، ٥٩,٠٠) على التوالي لأفراد المجموعة الضابطة.

وزارة التعليم العالي والبحث العلمي
جامعة بابل
كلية العلوم للبنات
قسم علوم الحياة

تقييم العلاقة بين تعدد أشكال النوكليوتيدات الأحادية لجينات IL-6 وIL-10 كمؤشر على شدة COVID-19 لدى سكان بابل

بحث تخرج مرحلة رابعة

مقدم الى مجلس قسم علوم الحياة/كلية العلوم للبنات كجزء من متطلبات نيل شهادة البكالوريوس في علوم الحياة/الاحياء المجهرية

من قبل

حوراء محمد كوم **حنين طالب جاسم**

اشراف
الأستاذ الدكتور

علي حسين المرزوكي

٢٠٢٣م **١٤٤٤هـ**