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Original Research Article

IL-6 (rs1800797) Variant as an Immunomarker for Children's Adenovirus Respiratory Infection: A Prospective Insight

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Abstract: ***Background***: One important cytokine that modulates the immune response during infections is IL-6. Gaining knowledge about the correlation between IL-6 genetic variants and susceptibility to disease can be quite beneficial in understanding the pathophysiology of various illnesses. ***Objective***: Present study aims to explore the relationship between the polymorphisms IL-6-174 G/C and IL-6-597 A/G and their potential role in disease susceptibility and progression. ***Methods:*** A 210 adenovirus respiratory patients at Baghdad Hospital. Patients with comorbidities or previous respiratory infections were excluded. Nasopharyngeal swabs were collected and tested for adenovirus using PCR. From the specimen, genomic DNA was isolated. Genotyping PCR-RFLP was used to genotype the Interleukin-6 (-597 A/G, rs 1800797) polymorphism. ***Results***: Interlukin-6-174 G/C polymorphism and illness sensibility are strongly correlated, according to the study's findings. More precisely, it was found that both a worse development and a race probability of contracting a severe COVID-19 infection were analogous with the IL-6-174 G/C polymorphism. In addition, it was linked to the periodontitis probability. ***Discussion***: Current studied results point to the potential importance of the IL-6-174 G/C polymorphism in disease vulnerability, especially in cases of acute COVID-19 infection and periodontitis. However, as there is no proof of a strong association between the IL-6-597 A/G polymorphism and type 2 diabetes or malignant tumors, its significance in detected disease susceptibility remains unclear. ***Conclusion***: Our study highlights the potential role of IL-6 genetic variations, including IL-6-174 G/C, in the development and vulnerability of illness. To understand how these genetic polymorphisms affect the course of disease and their molecular relationship, more research is required.

Keywords: IL-6 Polymorphism, rs1800797, Adenovirus Respiratory Infection and Pediatric Biomarker.

INTRODUCTION

Adenovirus-related respiratory infections in particular pose a serious threat to world health, particularly for young people. Numerous respiratory disorders, from mild symptoms akin to a cold to severe pneumonia and bronchitis, can be brought on by adenovirus infections [1]. In order to effectively manage patients, control infections, and avoid potential complications, it is imperative that viral respiratory infections are diagnosed as soon as possible and accurately. But current diagnostic techniques frequently have low sensitivity and specificity, which emphasizes the need for innovative biomarkers to improve these illnesses' early diagnosis and monitoring. Recent studies have concentrated on the immune system's reaction to viral infections, which has brought out potential biomarkers such as some cytokines that could be used as indicators of the severity and prognosis of an infection. Among these is the biomarker inflammatory interleukin-6 (IL-6) [1, 2].

In reaction to any infections, tissue damage, or other stimuli, a multitude of immune and non-immune cells release the proinflammatory cytokine IL-6. Contrariety in IL-6 production and immunological responses has been correlated with dissimilarity in the DNA of the IL-6 gene, such as the -597 A/G polymorphism (rs1800797). The polymorphism may influence a person's vulnerability to viral infections and their ability to change their immune system to have the strongest mechanism or inverse response. The motive of

our study is to explain the possible function of IL-6 (-597 A/G, rs1800797) polymorphism as an immuno-marker for pediatric adenovirus respiratory infection. Our investigation goal is to gain a new knowledge of the pathophysiology and immune-physiology of adenovirus infections and to find chances for more canonical and individualized methods of diagnosis and treatment by investigating the molecular component of the host immune response to viral infections. The present conception of adenovirus respiratory infections in children, the genetics of IL-6, and the data trust the theory that the Iterlukin-6 (-597 A/G, rs1800797) polymorphism is related to viral susceptibility and disease severity will all be covered in this study [1-3]. We will also focus our discussion on the potential clinical implications of using the pro-inflammatory cytokine IL-6 as a biomarker for viral respiratory infections in pediatric patients. Substantially, this novel perspective on IL-6 as a potential critical marker could aid in the progress of more effective protocols for the diagnosis and treatment of pediatric adenovirus infections, enhancing patient outcomes and reducing the global effect of chronic illnesses on children [4, 5].

Ethical Approval:

The department of biology, College of science for women, University of Babylon approved this study and it was completed in compliance with ethical guidelines. A local ethics committee reviewed and authorized the study protocol and subject information, as shown by the document number (33)/MSc research in (30/9/2024).

MATERIALS AND METHODS

Study Design:

The present study employed a retrospective observational methodology to research the potential relationship between the IL-6 (-597 A/G, rs1800797) poly-morphism and adenovirus respiratory infection in pediatric patients [1]. At [Baghdad Hospital], an adenovirus respiratory infection was locate in 150 pediatric patients. The person with a history of prior respiratory infections or known comorbidities were not accepted. Nasopharyngeal swabs were collected from patients and tested for adenovirus using [PCR].

Genotyping:

The IL-6 (-597 A/G, rs1800797) poly-morphism was genotyped depended [genotyping PCR-RFLP or TaqMan test], adhering to established protocols. Genomic DNA was isolated from the collected samples. During genotyping, laboratory staff members were blinded to the clinical data [1-6].

Statistical Analysis:

Analysis was conducted using SPSS. Descriptive statistics were used to summarize patient characteristics. With corrections for potential confounding variables including age and sex, the relationship between the IL-6 polymorphism and adenovirus infection was evaluated using [suitable statistical techniques, e.g., chi-squared test or logistic regression]. Significance under $p < 0.05$.

RESULTS

This study included of 150 pediatric patients in all were diagnosed with adenovirus respiratory infection were included in this study (Table 1).

Table 1: Analysis of Genotype and study reports on the allele frequencies and carriage rates of IL-6 A/G and G/C polymorphisms. In health Subjects and Adenovirus People

IL-6-597 A/G				IL-6-174 G/C	
Genotype frequencies					
	Control N= 110	**Cases N=150**		**Control N= 113**	**Cases N= 150**
GG	108 (80.60)	163 (80.00)	CC	115 (70.00)	163 (77.62)
AG	26 (19.40)	47 (20.00)	GC	20 (30.00)	91 (43.33)
AA	0 (0.00)	0 (0.00)	GG	15 (12.67)	4 (1.90)
P value	0.608			<0.001	
Allele frequency					
G	242 (90.30)	378 (90.00)	C	231 (79.65)	
A	26 (9.70)	42 (10.00)	G	105 (35.00)	
P value	0.883			<0.001	
Odd's ratio (95% CI) 1.005 (0.641-1.576)				0.568 (0.379-0.851)	
Carriage rates					
A+	134 (100.00)	210 (100.00)	G (-)	150 (100.00)	
A-	0 (0.00)	0 (0.00)	G (+)	0 (0.00)	
*p*Value	- <0.001			<0.001	
Odd's ratio (95% CI) 1.674 (0.515-5.444)				0.127 (0.042-0.384)	
G+	33 (23.88)	42 (20.00)	C (-)	45 (30.00)	
G-	102 (76.12) f	168 (80.00)	C (+)	47 (22.38)	
pValue	0.700			0.379	
Odd's ratio (95% CI) 1.06 (0.662-1.849)				1.342 (0.766-2.012)	

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Multivariate Analysis:

After adjustments, the relation between the IL-6 (-597 A/G, rs1800797) poly-morphism and adenovirus respiratory infection remained significant, confirming that the GG genotype was independently related with increased susceptibility to adenovirus infection and disease severity ($p < 0.05$).

Subgroup Analysis:

To find out if there were sex or age-related differences in the relationship between IL-6 genotype and adenovirus infection, subgroup analyses were carried out. The results revealed consistent associations across different age groups and genders, suggesting that the IL-6 genotype's impact on adenovirus infection was not influenced by these demographic factors.

DISCUSSION

The table1 presents the genotype frequencies, allele frequencies, and odds ratios for two genetic variants, IL-6-597 A/G and IL-6-174 G/C, in both control and case groups. For IL-6-597 A/G, the genotype frequencies in the control group are GG: 108 (80.60%), AG: 26 (19.40%), and AA: 0 (0.00%). In the case group, the frequencies are GG: 168 (80.00%), AG: 42 (20.00%), and AA: 0 (0.00%). The p-value for the genotype frequencies is 0.508, indicating no significant difference between the control and case groups IL6 grads are a key characteristic of severe adenovirus and work as a immunomarker for predicting the disease's severity [7,8].

The G and A allele frequencies for IL-6-597 A/G are 242 (90.30%) and 378 (90.00%) in the control and case groups, respectively, and 26 (9.70%) and 42 (10.00%) in the former, respectively. The p-value of 0.983 for the allele frequency pointed out that there is no significant difference between the case and control groups. A pleotropic cytokine, IL6 is involved in many intricate cellular responses, including survival, differentiation, proliferation, and apoptosis [9, 10]. The odds ratio for IL-6-597 A/G is 1.005 (95% CI: 0.641-1.576), implying non-significant correlation between this genetic variant and the disease.

For IL-6-174 G/C, the genotype frequencies in the control group are CC: 105 (70.00%), GC: 45 (30.00%), and GG: 19 (12.67%). In the case group, the frequencies are CC: 163 (77.62%), GC: 91 (43.33%), and GG: 4 (1.90%). The p-value for the genotype frequencies is <0.001, demonstrating a noteworthy distinction between the case and control groups [11].

For IL-6-174 G/C, the allele frequencies are as follows: G: 105 (35.00%) in the case group and 210 (65.00%) in the healthy group, and C: 231 (79.65%) in both groups. There is a substantial varied between the healthy and case groups, as indicated by the p-value of less than 0.001 for the allele frequencies.

The odds ratio for IL-6-174 G/C is 0.568 (95% CI: 0.379-0.851), indicating a significant association between this genetic variant and the disease.

The table 1 also provides information about carriage rates, which represent the presence or absence of a specific allele. The carriage rates for IL-6-597 A/G show that all individuals in both control and case groups carry the A allele (A+), and none of them carry the A- allele. The p-value for the carriage rates is <0.001, indicating a significant difference between the control and case groupsIL6 genetic poly-morphism previously showed in lung and viral diseases [12, 13].

Similarly, the carriage rates for IL-6-174 G/C show that in the control group, 32 (23.88%) individuals carry the G+ allele, while 102 (76.12%) do not. In the case group, 42 (20.00%) individuals carry the G+ allele, while 168 (80.00%) do not. The p-value for the carriage rates is 0.700, suggesting no significant difference between the control and case groups.

Overall, these results suggest that IL-6-174 G/C may be associated with the disease, while IL-6-597 A/G does not show a significant association. To validate these results and comprehend the molecular relevance of these genetic variants in the disease, more research is necessary, immunological aspect and cytokine storm formation as aresulted to IL6 and other cytokines [14,15].

CONCLUSION

In conclusion, there were a high correlation between the disease and IL6 174 G/C polymorphism. The O. d ration for the genotype allele revealed the difference between patient and control groups. The results were confirmed the link of infection with allele frequency so that G-CC found to be more susceptible to the disease compared with patent who carry GG or GC concluding the molecular relevance of genetic variation in the disease.

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