
***HLA-B* potential associations with the of COVID-19 disease in Iraqi population**

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Abstract

Background: Host genetic factors, particularly polymorphisms in the human leukocyte antigen (*HLA*) region, have been implicated in influencing individual susceptibility to infectious diseases, including COVID-19. This study aim to investigated the distribution of *HLA-B* alleles in an Iraqi cohort to determine their association with COVID-19 susceptibility.

Methods: Using a sequence specific oligonucleotide (SSO-PCR) assay, we genotyped *HLA-B* alleles in COVID-19 patients and control individuals. Allelic frequencies were compared between groups, and odds ratios (ORs) with 95% confidence intervals (CIs) and corresponding p-values were calculated to assess the strength of associations.

Results: The analysis revealed no broad, statistically significant associations between specific *HLA-B* alleles and COVID-19 susceptibility. However, *HLA-B*52:01* was found to be more prevalent in COVID-19 patients compared to healthy controls, suggesting a potential link between this allele and increased susceptibility to the virus.

Conclusion: This study highlights the potential role of *HLA-B* alleles in COVID-19 susceptibility within the Iraqi population. Although no widespread associations were found, the findings indicate a need for continued research—particularly to explore the immunogenetics mechanisms involved and their relevance to personalized treatment strategies.

Keywords: *HLA-B*, COVID-19, COVID, SARS-CoV-2.



Introduction

Coronavirus disease 2019 (COVID-19) pandemic, caused by the SARS-CoV-2 virus, has triggered a global public health crisis(Mallah, *et al.* 2021), with COVID-19, declared a pandemic in March 2020, has resulted in over 700 million confirmed cases and 6 million deaths globally(Liu, *et al.* 2025). While many individuals experience mild or asymptomatic infections, a significant portion of patients progress to severe disease(Ballow and Haga 2021), including pneumonia, acute respiratory distress syndrome (ARDS), and multi-organ failure(Thakur, *et al.* 2021). The wide variation in disease outcomes has underscored the importance of host factors, particularly genetic variations, in shaping an individual's susceptibility to and the severity of COVID-19(Niemi, *et al.* 2022). Among these genetic determinants, the human leukocyte antigen (*HLA*) system, which plays a crucial role in the immune system's response to pathogens, has garnered attention for its potential impact on COVID-19 outcomes(Migliorini, *et al.* 2021). The *HLA-B* gene, located within the Major Histocompatibility Complex (*MHC*) on chromosome 6 (Tumer, *et al.* 2019), encodes proteins that are essential for presenting viral peptides to cytotoxic T lymphocytes, thus influencing the immune response to viral infections(Adegboro, *et al.* 2022). Multiple scientific investigations have established particular *HLA-B* alleles show favorable immune response patterns in viral infections from HIV to influenza (Barquera, *et al.* 2020). The research, (Wolday, *et al.* 2023) on SARS-CoV-2 disease severity examined specific *HLA* alleles to determine their impact on immune response outcomes which could protect against severe COVID-19 manifestations The connection between *HLA-B* alleles and COVID-19 clinical results is still not fully understood for populations beyond Western cohorts (Naidoo, *et al.* 2024). Studies about genetic background within the Iraqi population are limited despite its distinct heritage that developed through various historic migrations and environmental influences and times of conflict (Alden 2017; Jabbar and Al-Rashedi 2021). Iraq encountered extensive obstacles from the pandemic resulting in high infection numbers together with high mortality rates (Mawlood and Lafta 2022). Research aims to establish the occurrence of *HLA-B* alleles among Iraqi COVID-19 patients while studying if particular *HLA-B* alleles are associated to disease development.

Methodology

Study Design and Participants

The present case-control study examined HLA-B allele frequencies in Iraqi individuals with COVID-19. The study enrolled 80 participants which included 40 confirmed COVID-19 patients and 40 healthy controls, and the participants belonged to the Iraqi ethnic group throughout the recruitment period from November 2020 to May 2022. The study involved patients who tested positively in RT-PCR for SARS-CoV-2 at least once during the period. All participants in the control group showed negative results from RT-PCR tests to verify they were free of COVID-19 infection and its symptoms throughout the same period.

DNA extraction and HLA Typing

Peripheral blood genomic DNA extraction proceeded through procedure of Promega Wizard® Genomic DNA Purification Kit. Sequence-specific oligonucleotide PCR (SSO-PCR) served as the method to perform HLA-B genotyping because this high-throughput technology hybridizes probes with specific alleles to achieve precise identification.

Statistical Analysis

The allelic frequencies of HLA-B in COVID-19 patients and controls were determined and compared using either the chi-square test or Fisher's exact test, depending on the data type. To quantify the association between specific HLA-B alleles and COVID-19 susceptibility, odds ratios (ORs) with 95% confidence intervals (CIs) were calculated. A two-tailed p-value of <0.05 was considered statistically significant. All statistical analyses were performed using IBM SPSS Statistics version 20. The statistical results, including ORs, 95% CIs, and p-values derived from either the chi-square or Fisher's exact test, are presented in Table 2.

Ethical approval

Ethical approval was obtained from the ethics board committee from the Baghdad Medical City, Ministry of Health of Iraq with approval number 1157, 8/11/2020 and Dr. Saad Al Watri Hospital with approval number 81595, 25/11/2020.

Results and Discussion

Table 1; comparative gender among study groups

			Groups		
			Control (n=40)	Patients (n=40)	Total
Gender	Males	n	28	26	54
		%	70	65	67.5%
	Females	n	12	14	26
		%	30	35	32.5%

Table (1) presents a comparative analysis of gender distribution among the study groups, showing that males constituted 70% of the control group and 65% of the patient group, while females represented 30% and 35%, respectively. The study suggests male participants predominance females in this population while also backing up worldwide COVID-19 epidemiological patterns showing men experience severe complications more often. Various biological and immunological factors as well as behavioral components produce this difference (Ortolan, *et al.* 2020).

Latest studies indicate male patients experience greater risks of severe COVID-19 because their immune responses differ from those of female patients. The increased innate and adaptive immune response exhibited by females results mainly from estrogen effects combined with immune-related genetic factors located on the X chromosome (Takahashi, *et al.* 2020). The improved immune response might explain why more males are enrolled in the patient group rather than the female group since they better protect against serious disease. The expression of angiotensin-converting enzyme 2 (ACE2) receptors represents a vital determinant of gender-related COVID-19 outcomes through its role in viral cell entry. several studies indicate men display elevated ACE2 expression levels which could explain why they face a higher risk of developing serious Infection (Bwire 2020). The combination of behavioral and lifestyle factors at higher levels among males leads to worse COVID-19 outcomes (Kim, *et al.* 2021) and lower healthcare-seeking behavior among men results in a higher number of male participants in both control and patient groups. The gender distribution presented during this study leads to significant clinical implications in addition to affecting public health outcomes. The higher proportion of males in patients indicates their susceptibility to severe illness which underscores the importance of specific defensive strategies including vaccination programs and early medical care.

Research into women-specific risk factors for COVID-19 infection requires immediate attention because data shows the significant involvement of female patients (Bambra, *et al*, 2021). The results of the current study are consistent with the findings of (Barek, *et al*. 2020) regarding males being more infected with COVID-19 than females. The identification of sex-based differences among individuals requires attention because it serves as a foundation for both treatment and prevention strategy development (Witt, *et al*, 2024).

Table 2: The association between *HLA-B* alleles and the risk of Covid-19 among Iraqi population

<i>HLA-B</i> alleles	Patients		Control		P value	OR	95% CI
	2n	F%	2n	F%			
<i>B*07:01</i>	7	0.0875 (8.75)	1	0.0125 (1.25%)	0.05	8.27	0.96-70.73
<i>B*07:02</i>	2	0.025 (2.5%)	0	0	0.49	1.05	0.98-1.13
<i>B*08:01</i>	2	0.025 ((2.5%)	6	0.075 (7.5%)	0.26	0.29	0.05-1.57
<i>B*08:02</i>	1	0.0125 (1.25%)	4	0.05 (5%)	0.35	0.23	0.02-2.16
<i>B*08:27</i>	1	0.0125 (1.25%)	0	0	1.00	1.02	0.97-1.07
<i>B*13:01</i>	1	0.0125 (1.25%)	4	0.05 (5%)	0.35	0.23	0.02-2.16
<i>B*14:01</i>	1	0.0125 (1.25%)	0	0	1.00	1.02	0.97-1.07
<i>B*15:01</i>	2	0.025 ((2.5%)	2	0.025 (2.5%)	1.00	1.00	0.13-7.47
<i>B*15:02</i>	2	0.025 ((2.5%)	6	0.075 (7.5%)	0.26	0.29	0.05-1.57
<i>B*15:03</i>	0	0	1	0.0125 (1.25%)	1.00	0.97	0.92-1.02
<i>B*18:01</i>	1	0.0125 (1.25%)	1	0.0125 (1.25%)	1.00	1.00	0.06-16.56
<i>B*18:02</i>	1	0.0125 (1.25%)	3	0.0375 (3.75%)	0.61	0.31	0.03-3.17



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<i>B*35:01</i>	2	0.025 ((2.5%))	3	0.0375 (3.75%)	1.00	0.64	0.10- 4.11
<i>B*35:02</i>	5	0.0625 (6.25%)	1	0.0125 (1.25%)	0.20	5.57	0.62- 50.03
<i>B*35:03</i>	2	0.025 ((2.5%))	0	0	0.49	1.05	0.98- 1.13
<i>B*37:01</i>	2	0.025 ((2.5%))	3	0.0375 (3.75%)	1.00	0.64	0.10- 4.11
<i>B*38:01</i>	4	0.05 (5%)	4	0.05 (5%)	1.00	1.00	0.23- 4.31
<i>B*38:02</i>	1	0.0125 (1.25%)	0	0	1.00	1.02	0.97- 1.07
<i>B*39:01</i>	0	0	1	0.0125 (1.25%)	1.00	0.97	0.92- 1.02
<i>B*39:02</i>	0	0	1	0.0125 (1.25%)	1.00	0.97	0.92- 1.02
<i>B*40:01</i>	2	0.025 ((2.5%))	7	0.0875 (8.75%)	0.15	0.24	0.04- 1.27
<i>B*40:02</i>	2	0.025 ((2.5%))	1	0.0125 (1.25%)	1.00	2.05	0.17- 23.58
<i>B*41:01</i>	2	0.025 ((2.5%))	2	0.025 (2.5%)	1.00	1.00	0.13- 7.47
<i>B*41:02</i>	2	0.025 ((2.5%))	1	0.0125 (1.25%)	1.00	2.05	0.17- 23.58
<i>B*44:01</i>	0	0	3	0.0375 (3.75%)	0.24	0.92	0.84- 1.01
<i>B*44:02</i>	0	0	1	0.0125 (1.25%)	1.00	0.97	0.92- 1.02
<i>B*49:01</i>	4	0.05 (5%)	1	0.0125 (1.25%)	0.35	4.33	0.46- 40.60
<i>B*49:02</i>	2	0.025 ((2.5%))	3	0.0375 (3.75%)	1.00	0.64	0.10- 4.11
<i>B*50:01</i>	5	0.0625 (6.25%)	2	0.025 (2.5%)	0.43	2.71	0.49- 14.90
<i>B*50:02</i>	1	0.0125 (1.25%)	3	0.0375 (3.75%)	0.61	0.31	0.03- 3.17
<i>B*51:01</i>	6	0.075 (7.5%)	5	0.0625 (6.25%)	0.74	1.23	0.34- 4.43

<i>B*51:02</i>	4	0.05 (5%)	2	0.025 (2.5%)	0.67	2.11	0.36- 12.24
<i>B*51:04</i>	0	0	1	0.0125 (1.25%)	1.00	0.97	0.92- 1.02
<i>B*52:01</i>	7	0.0875 (8.75%)	0	0	0.01*	1.21	1.05- 1.39
<i>B*52:02</i>	0	0	3	0.0375 (3.75%)	0.24	0.92	0.84- 1.01
<i>B*55:01</i>	2	0.025 (2.5%)	2	0.025 (2.5%)	1.00	1.00	0.13- 7.47
<i>B*55:02</i>	2	0.025 (2.5%)	1	0.0125 (1.25%)	1.00	2.05	0.17- 23.58
<i>B*57:01</i>	2	0.025 (2.5%)	1	0.0125 (1.25%)	1.00	2.05	0.17- 23.58

2n = number of alleles observed (each individual contributes two alleles)

F% = allelic frequency percentage.

P-value < 0.05: Statistically significant

P-value ≥ 0.05: Not statistically significant.

As shown in Table 2, One of the most notable findings of our study is the *HLA-B*07:01* allele, which was associated with a significantly increased odds ratio of 8.27 and a p-value of 0.05. Genetic evidence shows that *B*07:01* represents a possible vulnerability factor for contracting COVID-19 among Iraqi individuals. Studies involving different populations have documented comparable research results. For instance, a study by (Saadati, *et al.* 2020) observed that *HLA-B*07:01* was more prevalent in COVID-19 patients, suggesting a potential link between this allele and heightened susceptibility to the disease. Some studies have identified *HLA-B*07:01* as a protective genetic factor which aids T-cells during HIV and other infections by presenting viral target proteins to them for analysis (Darbas, *et al.* 2023). The contradictory findings regarding the role of *B*07:01* in different infectious diseases may stem from variations in immune responses depending on the pathogen involved, highlighting the need for further investigation into its exact role in COVID-19 (Zivna, *et al.* 2002).

In contrast, we found no significant association between *HLA-B*07:02*, *B*08:01*, *B*08:02*, and other alleles with COVID-19 susceptibility, as evidenced by odds ratios close to 1 and high p-values. These findings are consistent with some studies, which have reported a lack of significant association between certain *HLA-B* alleles and COVID-19 susceptibility

(Marchal, *et al.* 2024). However, it is important to note that these results are not universal. For example, a study by (Correale, *et al.* 2025) found a significant association between *HLA-B*08* and the severity of COVID-19 in certain European populations, suggesting that the role of *HLA-B* alleles may vary across different ethnic and geographical groups. This discrepancy underscores funderpinnings of COVID-19 susceptibility (Tymoniuk, *et al.*, 2024).

Interestingly, our study also identified *HLA-B*52:01* as having a potential protective role against COVID-19, with an odds ratio of 1.21 and a significant p-value of 0.01. Although the finding is significant, further validation in larger cohorts is necessary to confirm this protective effect. In previous studies, *HLA-B*52:01* has been associated with associated with the severity of COVID-19(Khor, *et al.* 2021).

Furthermore, the study found that several alleles, such as B*35:02, B*39:02, and B*49:02, did not show any significant association with COVID-19 susceptibility. These results are in line with other research that failed to identify strong links between these alleles and COVID-19 risk (Dobrijević, *et al.* 2023). Immunological responses to COVID-19 maintain complexity because multiple genetic and environmental elements interact with each other during the immune process. A combination of risk and protective alleles present together in an individual produces a susceptibility effect for COVID-19 that cannot be seen by analyzing individual alleles (Ovsyannikova, *et al.*, 2020). While our findings provide valuable insights into the genetic factors contributing to COVID-19 susceptibility, the study does have limitations. One limitation is the relatively small sample size, which may reduce the statistical power to detect subtle associations. Larger cohort studies are needed to validate our results and explore the interplay of *HLA-B* alleles with other genetic markers, environmental factors, and clinical variables, such as the severity of the disease and comorbidities. Additionally, future research should aim to elucidate the functional mechanisms behind these associations, particularly how specific *HLA-B* alleles may influence viral recognition and immune response in COVID-19.

Conclusion

This study explored the potential association between *HLA-B* alleles and COVID-19 susceptibility within the Iraqi population. While no broad, statistically significant correlations were found between specific *HLA-B* alleles and COVID-19 outcomes, certain alleles, such as B*52:01, showed a notable association, suggesting a potential link. These findings emphasize the complexity of genetic influences on COVID-19 susceptibility and highlight



the need for further investigation into the role of *HLA-B* alleles in modulating immune responses. Understanding these genetic factors could pave the way for more personalized treatment approaches, improved risk assessment, and better predictive models, contributing to more targeted strategies in managing COVID-19 across diverse populations.

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الإرتباطات المحتملة لجين HLA-B مع مرض كوفيد-19 في السكان العراقيين

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مستخلص البحث:

تم ربط العوامل الجينية للمضيف، لا سيما التغيرات الوراثية في منطقة المستضدات البيضاء البشرية (*HLA*)، بتأثيرها على قابلية الأفراد للأمراض المعدية، بما في ذلك كوفيد-19. تهدف هذه الدراسة إلى التحقيق في توزيع أليلات *HLA-B* في مجموعة عراقية لتحديد ارتباطها بالقابلية للإصابة بفيروس كوفيد-19.

الطرق:

باستخدام اختبار البوليميراز المتسلسل (SSO-PCR)، قمنا بالتحري عن أليلات *HLA-B* في مرضى كوفيد-19 والأفراد الأصحاء. تمت مقارنة التكرارات الأليلية بين المجموعات، وتم حساب نسب الأرجحية (OR) مع فترات الثقة 95% (CIs) وقيم ال-p المرتبطة لتقييم قوة الارتباطات.

النتائج:

أظهرت التحليلات عدم وجود ارتباطات واسعة ذات دلالة إحصائية بين أليلات *HLA-B* المحددة و القابلية للإصابة بكوفيد-19. ومع ذلك، تم العثور على أن *HLA-B*52:01* كان أكثر انتشاراً في مرضى كوفيد-19 مقارنةً بالأفراد الأصحاء، مما يشير إلى وجود رابط محتمل بين هذه الأليل وزيادة القابلية للإصابة بالفيروس.

الخاتمة:

تسلط هذه الدراسة الضوء على الدور المحتمل لأليلات *HLA-B* في قابلية الإصابة بكوفيد-19 داخل السكان العراقيين. على الرغم من عدم العثور على ارتباطات واسعة، تشير النتائج إلى الحاجة إلى استمرار البحث، وبالأخص لاستكشاف الآليات المناعية الجينية المتورطة وأهميتها في استراتيجيات العلاج الشخصي.

الكلمات المفتاحية: *HLA-B*، كوفيد-19، كوفيد، SARS-CoV-2.