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Relationship of HLA-B alleles on susceptibility to and protection from HIV infection in Turkish population

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ABSTRACT

OBJECTIVE: Many human leukocyte antigen (HLA)-B alleles are associated with an increased risk of Acquired Immune Deficiency Syndrome (AIDS) and Human Immunodeficiency Virus (HIV) progression; however, their distribution varies among different racial/ethnic groups. Abacavir used in the treatment of AIDS significantly increases the risk of hypersensitivity reactions in patients with HLA-B*57:01. The aim of this study was to determine the distribution of HIV-associated HLA-B subgroups (high and low resolution) and HLA-B*57:01 associated with Abacavir sensitivity in Turkiye.

METHODS: This retrospective case-control study consisted of 416 (F/M:111/305) HIV positive patients and 416 (F/M:111/305) healthy controls. HLA-B alleles were identified using Luminex based low-resolution method and further subgrouped by sequence-based high-resolution typing.

RESULTS: Our data showed that in patients with HIV-1 infection, HLA-B*15, *35, and *51 allele frequencies were higher, while the HLA-B*07, *14 and *55 allele frequencies were lower as compared to the controls. It was determined that HLA-B*15:01, *35:01, *35:08, and *51:01 alleles frequencies were higher in the patients with HIV-1 infection compared to the controls as HLA-B*07:02, *14:01, *44:01, and *55:01 allele frequencies were detected low. HLA-B*57:01 allele positivity, which is important in Abacavir hypersensitivity, was lower than controls, and this difference was not statistically significant.

CONCLUSION: Our results suggest that, HLA-B*07, *14, and *55 alleles and HLA-B*07:02, *14:01, *44:01, and *55:01 subgroups might have a protective effect, while HLA-B*15, *35, and *51 alleles and HLA-B*15:01, *35:01, *35:08, and *51:01 subgroups might play a role in susceptibility to HIV-1 infection.

Keywords: Antiretroviral therapy; HIV; HLA-B alleles distribution; hypersensitivity reaction.

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Human Immunodeficiency Virus ([HIV] MIM 609423) is a retrovirus that causes Acquired Immune Deficiency Syndrome (AIDS), a chronic infectious disease destroying the human immune system [1, 2]. The disease does not occur immediately after the HIV enters the organism. Once the HIV enters the body, it first targets T lymphocytes, one of the most important immune system cells. In the meantime, HIV-infected patients become disease carrier. Over the years, decline in CD4+ T cells results in the loss

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of cell mediated immune responses, leading to AIDS. Human leukocyte antigen (HLA), which presents antigens to T cells, plays a major role in the adaptive immune responses against HIV-1. Polygenic and polymorphic properties of HLA are known to affect susceptibility or resistance to many viral infections including HIV-1, and certain autoimmune diseases, and malignancies. For example, studies demonstrated that the overexpression of HLA Class I alleles plays a critical role in HIV-1 suppression of cytotoxic T lymphocytes (CTLs) as it limits viral spread [3–8].

The biogeographic, socioeconomic, behavioral factors, and demographic distribution of the disease were not homogeneous all over the world. Therefore, HIV prevalence is variable [9, 10]. Class I major histocompatibility complex (MHC) genes have been reported to be related to fast, slow, or non-progression to AIDS [11]. HLA-B molecules have been reported to have stronger effects in AIDS disease, compared to HLA-A and HLA-C molecules [6, 11, 12]. To the best of our knowledge, few studies showing the relationship between HIV positivity and HLA-B allele distribution were undertaken and different results were reported depending on the populations. Some studies showed that many HLA-B alleles were associated with protection from or susceptibility to AIDS or disease progression, but these findings remained limited and controversial [13–17].

Abacavir is an important retroviral treatment option in HIV infection and has been included in both national and international treatment guidelines. However, the presence of the HLA-B*57:01 allele may cause a possible hypersensitivity reaction to abacavir. Therefore, it was suggested that detecting the HLA-B*57:01 allele can help to identify patients at risk of developing a hypersensitivity reaction to abacavir [3, 5, 6, 9]. The frequency of HLA-B*57:01 allele in Turkish HIV-1 infected population was found to be 1.1–4.8%, and this rate varied according to geographical regions in Turkiye [18–20].

In southwest region of Turkiye, the HLA-B allele distribution in HIV-infected patients is still unknown. The purpose of this retrospective case–control study was to determine the distribution of the various alleles of HLA-B loci in HIV-1 infected patients in the region. Furthermore, we could identify whether presence of specific alleles could be a factor in determining susceptibility to or protection against HIV-1 infection.

Highlight key points

- HLA-B allele frequencies in patients infected with HIV-1 in Turkiye.
- The presence of certain HLA-B alleles is a factor in determining susceptibility or protection against HIV-1 infection.
- There is a relationship between HLA-B alleles and HIV-1 infection in the Turkish population.

MATERIALS AND METHODS

Subjects

HIV-1 infected patients who applied to Infectious Diseases Clinic at Akdeniz University Hospital were included in the study regardless of whether they received treatment or not. The case–control retrospective study included 305 male and 111 female (F/M:111/305) patients who were infected with HIV-1. The case group consisted of four hundred and sixteen (F/M:111/305) patients with HIV-1 infection between November 2017 and January 2020. Ages of the patients were between 32 and 56 (median range: 44.34±12.39). The control group was consisted of 416 healthy bone marrow and kidney donors with no history of HIV-1 and matched by sex and age as the case group. This study was approved by Akdeniz University, the Clinical Research Ethics Committee of the Faculty of Medicine (862/11.11.2020). Our study was conducted in HLA Tissue Typing Laboratory of Akdeniz University Hospital, which is accredited by the Ministry of Health. External quality control tests are routinely performed in our laboratory by the UK National External Quality Assessment Service.

HLA-B Genotyping

Genomic DNAs of patients and healthy controls were isolated from 200 µl aliquots of peripheral blood samples using the Bio-robot EZ1 advanced XL magnetic bead-based workstation (Qiagen, Hilden, Germany). The HLA-B genotyping was performed in all subjects by low resolution polymerase chain reaction with sequence-specific oligonucleotide probe (PCR-eRES SSO) hybridization method using Luminex technology (IMMUCOR-Lifecodes, Georgia), as previously described [21, 22] and subgroups of HLA-B were typed by high resolution Sequence-based typing (ABI PRISM 3130xl Genetic Analyzer, California) according to manufacturer's instructions.

Table 1. The distribution of HLA-B* frequencies in HIV- infected patients and controls

Genotype	HIV (2n=832)	Control (2n=832)	Statistical analysis	p
HLA-B*	n-AF (%)	n-AF (%)	OR-(95% CI)	
07	18 (2.16)	48 (5.77)	**0.36 (0.21–0.63)**	**0.0003**
08	34 (4.09)	19 (2.28)	1.82 (1.03–3.22)	0.051
12	0 (0.00)	3 (0.36)	–	–
13	21 (2.52)	32 (3.85)	0.65 (0.37–1.13)	0.163
14	12 (1.44)	47 (5.65)	**0.24 (0.13–0.46)**	**<0.0001**
15	45 (5.41)	28 (3.37)	**1.64 (1.01–2.66)**	**0.042**
18	54 (6.49)	68 (8.17)	0.78 (0.54–1.13)	0.188
19	3 (0.36)	2(0.24)	1.50 (0.25–9.01)	0.687
27	9 (1.08)	18 (2.16)	0.49 (0.22–1.11)	0.121
35	147 (17.67)	74 (8.89)	**2.20 (1.63–2.96)**	**<0.0001**
37	13 (1.56)	5 (0.60)	2.63 (0.93–7.40)	0.097
38	32 (3.85)	42 (5.05)	0.75 (0.47–1.20)	0.234
39	13 (1.56)	4 (0.48)	3.29 (1.07–10.12)	0.051
40	23 (2.76)	32 (3.85)	0.71 (0.41–1.23)	0.273
41	14 (1.68)	16 (1.92)	0.87 (0.42–1.80)	0.854
42	1 (0.12)	0 (0.00)	–	–
44	64 (7.69)	67 (8.05)	0.95 (0.67–1.36)	0.785
45	4 (0.48)	0 (0.00)	–	–
46	3 (0.36)	5 (0.60)	0.60 (0.14–2.51)	0.726
47	2 (0.24)	4 (0.48)	0.50 (0.10–2.73)	0.452
48	9 (1.08)	3 (0.36)	3.02 (0.82–11.20)	0.147
49	44 (5.29)	30 (3.61)	1.49 (0.93–2.40)	0.096
50	41 (4.93)	34 (4.09)	1.22 (0.76–1.94)	0.408
51	128 (15.38)	72 (8.65)	**1.92 (1.41–2.61)**	**<0.0001**
52	36 (4.33)	36 (4.33)	1.00 (0.62–1.60)	1.000
53	3 (0.36)	6 (0.72)	0.50 (0.12–2.00)	0.507
54	0 (0.00)	5 (0.60)	–	–
55	15 (1.80)	84 (10.10)	**0.16 (0.09–0.29)**	**<0.0001**
56	5 (0.60)	0 (0.00)	–	–
57	10 (1.20)	17 (2.04)	0.58 (0.27–1.28)	0.244
58	29 (3.49)	28 (3.73)	0.93 (0.56–1.56)	0.793

HLA: Human leukocyte antigen; HIV: Human immunodeficiency virus; AF: Allele frequency; OR: Odds ratio; CI: Confidence interval; 2n: Each individual was represented by two codominant allelic data.

Statistical Analysis

Statistical analysis was performed using Base v23 version of SPSS software (SPSS Inc., Chicago IL, USA). The student's t-test was used for continuous variables and Pearson Chi-square for categorical variables to compare case and control groups. Odds ratios (ORs) and 95% confidence intervals (CIs) were calculated to measure relationships between patients with HIV-1 infection and healthy controls for HLA-B genotyping. A two-sided $p<0.05$ was considered significant.

RESULTS

HLA-B allele frequencies of 416 patients with HIV-1 infection and 416 healthy controls are given in Table 1. HLA-B allele frequencies are given as the "2n" level for both patients and controls in Tables 1 and 2, as MHC-HLA alleles show codominant inheritance pattern. In our study, HLA-B alleles; HLA-B*15, *18, *35, *44, and *51 were found over 5% in the patient group, (5.41%, 6.49%, 17.67%, 7.69%, and 15.38%, respectively). In

the control group, alleles over 5% were HLA-B*07, *18, *35, *38, *44, *51, and *55 (5.77%, 8.17%, 8.89%, 5.05%, 8.05%, 8.65%, and 10.10%, respectively) (Table 1). In this study, 65 subgroups of the HLA-B allele were examined, among different alleles of the 53 subgroups of the HLA-B allele, HLA-B*15:01, *18:01, *35:01, *44:02, *49:01, and *51:01 were found to be over 5% (5.17%, 6.37%, 10.10%, 6.25%, 5.29%, and 13.94%, respectively). Similarly, in the control group, HLA-B alleles represented over 5% were HLA-B*18:01, *38:01, *44:02, *51:01, and *55:01 (7.93%, 5.05%, 5.29%, 8.17%, and 10.10%, respectively) (Table 2).

In the patients with HIV-1 infection, frequencies of HLA-B*15, *35, and *51 alleles were higher (OR; 1.64 [95% CI; 1.01–2.66], [p=0.042]), (OR; 2.20 [95% CI; 1.63–2.96], [p=0.0001]), (OR; 1.92 [95% CI; 1.41–2.61], [p=0.0001], respectively), while the HLA-B*07, *14, and *55 alleles frequencies were lower than the controls (OR; 0.36 [95% CI; 0.21–0.63], [p=0.0003]), (OR; 0.24 [95% CI; 0.13–0.46], [p=0.0001]), (OR; 0.16 [95% CI; 0.09–0.29], [p=0.0001], respectively). Although frequencies of HLA-B*08 and *39 alleles were higher in patients with HIV-1 infection compared with the controls, these differences were not statistically significant (OR; 1.82 [95% CI; 1.03–3.22], [p=0.051]), (OR; 3.29 [95% CI; 1.07–10.12], [p=0.051] respectively) (Table 1).

The distribution of HLA-B subgroups both in HIV-1 positive patients and healthy controls are given in Table 2. In the patients with HIV-1 infection, it was determined that HLA-B*15:01, *35:01, *35:08, and *51:01 alleles frequencies were higher (OR; 1.76 [95% CI; 1.06–2.91], [p=0.026]), (OR; 3.35 [95% CI; 2.15–5.22], [p=0.0001]), (OR; 4.07 [95% CI; 1.52–10.91], [p=0.005]) (OR; 1.82 [95% CI; 1.33–2.50], [p=0.0002], respectively), while the HLA-B*07:02, *14:01, *44:01, and *55:01 alleles frequencies were lower than the controls (OR; 0.43 [95% CI; 0.23–0.81], [p=0.011]), (OR; 0.19 [95% CI; 0.09–0.40], [p=0.0001]), (OR; 0.36 [95% CI; 0.15–0.87], [p=0.030]) (OR; 0.16 [95% CI; 0.09–0.29], [p=0.00019], respectively). HLA-B *08:01 allele frequency was higher in patients with HIV-1 infection compared with the controls; however, this difference was not statistically significant (OR; 1.77 [95% CI; 1.00–3.13], [p=0.06]) (Table 2). HLA-B*57:01 allele positivity, which is important in abacavir hypersensitivity, was determined in 10 patients (1.2%). However, this difference was not statistically significant (OR; 0.58 [95% CI; 0.27–1.28], [p=0.244]) (Table 2). As a result of our findings, two digits HLA-B*15, *35, and *51 alleles were found to be positively associated with HIV positivity, suggesting these alleles could be important for disease susceptibility. On the other side, HLA-B*07, *14, and *55 alleles were determined to be negatively associated with HIV, suggesting these alleles could be protective against the infection. Furthermore, in this study, HLA-B*15:01, *35:01, *35:08, and *51:01 subgroup alleles were found to be positively associated with HIV, suggesting susceptibility to infection, while HLA-B*07:02, *14:01, *44:01, and *55:01 subgroup alleles were determined to be negatively associated with HIV infection. Thus, it might be speculated that these alleles could be protective for the infection.

DISCUSSION

HIV is a retrovirus that causes AIDS by destroying the human immune system [1, 2]. HIV/AIDS is a prevalent concern for people around the world. In 2019, an estimated 38 million people had HIV, and 1.7 million people were newly infected with HIV. There were, furthermore, 690,000 people who died of HIV-related causes in the same year [23]. The spread of HIV disease can vary significantly between countries and different populations in a country. These differences may be particularly relevant to family life, upbringing, occupational preferences, and lifestyles and can often be attributed to a range of socioeconomic, biological, demographic, and behavioral factors [24]. Host genetic factors, including HLA alleles were shown to involve in HIV infection and progression to AIDS [25]. Over the past decade, there have been many associations between AIDS symptoms and MHC's Class I and II HLA alleles. These studies have enriched and guided our knowledge of the immunopathogenesis of the disease. In HLA Class I, each allele is responsible for presenting a different peptide to CTLs [13]. The HLA-B allele from the HLA Class I gene family plays a role in identifying pathogens, protection from them, and immune response. In addition, it mediates hypersensitivity reactions [11, 12, 26]. Moreover, in HIV infection, various HLA-B alleles have been associated with the progression to AIDS [14, 15].

The first large population study of HLA-B alleles in HIV infection indicated a relation between the HLA-B *27 and HLA-B *57 alleles and the time of onset of AIDS. It also showed that these alleles had the greatest effect in slowing the course of the disease [17]. Win-

TABLE 2. The distribution of HLA-B* subgroup frequencies in HIV infected patients and controls

Genotype	HIV (2n=832)	Control (2n=832)	Statistical analysis		Genotype	HIV (2n=832)	Control (2n=832)	Statistical analysis	
HLA-B*	n–AF (%)	n–AF (%)	OR-(95% CI)	p	HLA-B*	n–AF (%)	n–AF (%)	OR-(95% CI)	p
07:01	2 (0.24)	6 (0.72)	0.33 (0.07–1.65)	0.179	39:01	10 (1.20)	4 (0.48)	2.52 (0.79–8.06)	0.180
07:02	14 (1.68)	32 (3.85)	**0.43 (0.23–0.81)**	**0.011**	39:04	1 (0.12)	0 (0.00)	–	–
07:05	2 (0.24)	7 (0.84)	0.28 (0.06–1.37)	0.179	39:06	2 (0.24)	0 (0.00)	–	–
07:07	0 (0.00)	2 (0.24)	–	–	40:01	20 (2.40)	23 (2.76)	0.87 (0.47–1.59)	0.757
07:09	0 (0.00)	1 (0.12)	–	–	40:02	2 (0.24)	4 (0.48)	0.50 (0.09–2.73)	0.452
08:01	33 (3.97)	19 (2.28)	1.77 (1.00–3.13)	0.067	40:06	1 (0.12)	5 (0.60)	0.20 (0.02–1.71)	0.218
08:26	1 (0.12)	0 (0.00)	–	–	41:01	14 (1.68)	9 (1.08)	1.57 (0.67–3.64)	0.401
12:01	0 (0.00)	3 (0.36)	–	–	41:02	0 (0.00)	7 (0.84)	–	–
13:01	6 (0.72)	4 (0.48)	1.50 (0.42–5.35)	0.751	42:01	1 (0.12)	0 (0.00)	–	–
13:02	15 (1.80)	28 (3.37)	0.53 (0.28–0.99)	0.640	44:01	7 (0.84)	19 (2.28)	0.36 (0.15–0.87)	0.030
14:01	8 (0.96)	41 (4.93)	**0.19 (0.09–0.40)**	**<0.0001**	44:02	52 (6.25)	44 (5.29)	1.19 (0.79–1.81)	0.400
14:02	4 (0.48)	6 (0.72)	0.67 (0.19–2.37)	0.751	44:03	5 (0.60)	4 (0.48)	1.25 (0.33–4.68)	1.000
15:01	43 (5.17)	25 (3.00)	**1.76 (1.06–2.91)**	**0.026**	45:01	4 (0.48)	0 (0.00)	–	–
15:08	1 (0.12)	2 (0.24)	0.50 (0.05–5.52)	0.625	46:01	3 (0.36)	5 (0.60)	0.60 (0.14–2.51)	0.726
15:09	1 (0.12)	0 (0.00)	–	–	47:01	2 (0.24)	3 (0.36)	0.67 (0.11–4.00)	0.687
15:17	0 (0.00)	1 (0.12)	–	–	47:03	0 (0.00)	1 (0.12)	–	–
18:01	53 (6.37)	66 (7.93)	0.79 (0.54–1.15)	0.216	48:01	9 (1.08)	3 (0.36)	3.02 (0.82–11.20)	0.147
18:08	0 (0.00)	1 (0.12)	–	–	49:01	44 (5.29)	30 (3.61)	1.49 (0.93–2.40)	0.096
18:09	1 (0.12)	1 (0.12)	1.00 (0.06–16.02)	1.000	50:01	41 (4.93)	34 (4.09)	1.22 (0.76–1.94)	0.408
19:01	3 (0.36)	2 (0.24)	1.50 (0.25–9.01)	0.687	51:01	116 (13.94)	68 (8.17)	**1.82 (1.33–2.50)**	**0.0002**
27:02	6 (0.72)	10 (1.20)	0.60 (0.22–1.65)	0.451	51:05	1 (0.12)	0 (0.00)	–	–
27:03	2 (0.24)	7 (0.84)	0.28 (0.06–1.37)	0.179	51:07	5 (0.60)	4 (0.48)	1.25 (0.33–4.68)	1.000
27:05	1 (0.12)	0 (0.00)	–	–	51:08	6 (0.72)	0 (0.00)	–	–
27:07	0 (0.00)	1 (0.12)	–	–	52:01	36 (4.33)	34 (4.09)	1.06 (0.66–1.71)	0.807
35:01	84 (10.10)	27 (3.25)	**3.35 (2.15–5.22)**	**<0.0001**	52:05	0 (0.00)	2 (0.24)	–	–
35:02	11 (1.32)	11 (1.32)	1.00 (0.43–2.32)	1.000	53:01	3 (0.36)	6 (0.72)	0.50 (0.12–2.00)	0.507
35:03	30 (3.61)	28 (3.37)	1.07 (0.64–1.81)	0.789	54:01	0 (0.00)	5 (0.60)	–	–
35:04	0 (0.00)	3 (0.36)	–	–	55:01	15 (1.80)	84 (10.10)	**0.16 (0.09–0.29)**	**<0.0001**
35:05	2 (0.24)	0 (0.00)	–	–	56:01	5 (0.60)	0 (0.00)	–	–
35:08	20 (2.40)	5 (0.60)	**4.07 (1.52–10.91)**	**0.005**	57:01	10 (1.20)	17 (2.04)	0.58 (0.27–1.28)	0.244
37:01	12 (1.44)	5 (0.60)	2.42 (0.85–6.90)	0.144	58:01	29 (3.49)	28 (3.37)	1.04 (0.61–1.76)	0.893
37:03	1 (0.12)	0 (0.00)	–	–	58:02	0 (0.00)	3 (0.36)	–	–
38:01	32 (3.85)	42 (5.05)	0.75 (0.47–1.20)	0.234					

HLA: Human leukocyte antigen; HIV: Human immunodeficiency virus; AF: Allele frequency; OR: Odds ratio; CI: Confidence interval; 2n: Each individual was represented by two codominant allelic data.

chester et al. [27] detected a higher HLA-B*14 allele frequency in HIV-1 infected children than uninfected ones. Fabio et al. [15], reported a decrease in the frequency of HLA-Bw 52 in HIV-1 positive patients compared to HIV-1 negative people in Italy. In addition, several studies reported that alleles B*22, B*29, B*35, and B*51 were associated with a fast progression to AIDS, while alleles B*14, B*27, B*55, and B*57 were associated with protection against the infection and with slow progression to AIDS [13–18]. The findings from our case-control retrospective study showed similarities with the literature. HLA-B*15, *35, and *51 alleles were positively associated (susceptibility to infection) with HIV, while HLA-B*07, *14, and *55 alleles were negatively associated (protection against infection) with HIV. Similar to a study conducted in the Caucasian population; B*14 was found to be protective and B*35 showed susceptibility to the disease in our study [26, 28]. In contrast to this study, B*51 which was found to be a protective allele against disease in the same population was found as a susceptibility allele in our study [29].

In the literature, some studies also investigated the relationship between HIV-1 positivity and HLA-B subgroups. In one of these studies, HLA-B*35:05 were determined to be more frequent in Southeast Asian people (2–5% in population frequency) than in Africans and Caucasians [30]. Furthermore, another study found that HLA-B*58:01 could be a protective allele in African populations while HLA-B*58:02 allele could be a disease-sensitive allele [31]. International HIV Controllers study showed that B*07:02, B*08:01, B*18:01, B*35:01, B*35:02, B*35:03, B*45:01, B*51:01, B*53:01, and B*58:02 were associated with susceptibility to HIV disease, while B*13:02, B*14:02, B*27:05, B*42:01 B*44:03, B*52:01, B*57:01, B*52:02 B*57:03, B*58:01, and B*81:01 alleles were protective. HLA-B*35:01 and B*51:01 were found as protective alleles against the disease in the North American European/South Africa/Botswana/Zimbabwe population [26, 29]. Similar to this study, HLA-B *35:01 and *51:01 alleles were protective in our study. While HLA-B*14:01, B*44:01 were found to be protective in our study, B*14:02, B*44:03 were also found to be protective in the American/South African population [26, 29, 31]. In our study, HLA-B *07:02 was defined as the disease-sensitive allele; in contrast to the study of Pereyra et al. [26], in which this allele was shown to be a protective allele against the disease. As mentioned above, these differences are expected in population studies in general.

Recently, an HLA-B subtype, *57:01 has become an effective phenomenon in HIV viral load suppression, and the risk of developing a hypersensitivity reaction to abacavir has been reported in different ethnicities, including Caucasians, Hispanics, and individuals of African descent [2, 3]. It has been reported that the frequency of B57 is low in HIV-infected patients in the Thai population [30]. However, there are limited reports in the literature regarding the HLA-B*57:01 prevalence of patients infected with HIV in Turkiye. In a study by Inan et al., the frequency of the HLA-B*57:01 allele in HIV-1 infected Turkish patients was 1.1%, while in another study the frequency of this allele was 4.8% [19, 20, 32]. These frequencies are lower than those in North America but higher than those in Chinese populations [32–34]. Our results for HLA-B*57:01 allele frequency was higher in healthy controls than in HIV-1 patients. But it was not statistically significant. To the best of our knowledge, our study is considered as the first report determining the frequency of HLA-B*57:01 allele in healthy individuals in Turkiye.

In conclusion, HLA-B *15, *35, *51, *15:01, *35:01, *35:08, and *51:01 alleles were found to be associated with HIV-1 infection in patients, while HLA-B*07, *14, *55, *07:02, *14:01, *44:01, and *55:01 alleles were determined as protective against disease in our study. Besides, knowledge of the HLA-B allele distributions of AIDS patients (especially HLA-B*57:01) could help clinicians to choose pharmacogenetically personalized treatment for patients against drug allergies. The limitation of this study is that we could not investigate other HLA alleles (HLA-A, -C, -DRB1, and -DQB1) in HIV-infected patients. However, to our knowledge, this is the first study in Turkiye that determined the frequency of HLA-B alleles by high-resolution HLA typing in HIV positive patients.

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