

Original Study Article

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Association of *TRIM22* gene polymorphisms (*N155D* and *T242R*) with HIV infection in the Northwestern Federal District of Russia

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Abstract

Introduction. The human immunodeficiency virus (HIV) remains a global health challenge. The *TRIM22* gene, which encodes a protein with antiviral activity, is a promising candidate for research, but its role in the pathogenesis of HIV infection in population of the Russian Federation has not been previously studied.

The aim of the study was to analyze the polymorphic variants rs7935564 (*N155D*) and rs1063303 (*T242R*) of the *TRIM22* gene in HIV-infected individuals in the Northwestern Federal District.

Materials and methods. Polymorphic variants rs7935564 (*N155D*) and rs1063303 (*T242R*) of the *TRIM22* gene were analyzed in groups of HIV-infected individuals with virological failure of antiretroviral therapy ($n = 378$) and practically healthy individuals ($n = 319$). Genotyping was performed using the polymerase chain reaction method followed by sequencing. Statistical analysis included testing for Hardy-Weinberg equilibrium of genotype distributions, assessing associations under 3 inheritance models (dominant, recessive, additive) with odds ratio (OR) and 95% confidence interval (CI) calculation, linkage disequilibrium analysis, and haplotype frequency analysis.

Results. The distribution of genotypes for the analyzed polymorphic variants was conformed to Hardy-Weinberg equilibrium expectations ($p > 0.05$). A significant association was found between the G allele of the rs7935564 polymorphism and the presence of HIV infection in both recessive (OR = 1.76) and additive (OR = 1.37) inheritance models. For polymorphism rs1063303, a significant association was observed only in the dominant model (OR = 1.40). Moderate linkage disequilibrium was found between the loci ($D' = 0.4478$; $r^2 = 0.1572$; $p < 0.001$). The G-G haplotype (rs7935564_G — rs1063303_G) was associated with the presence of infection (OR = 1.57).

Conclusion. In the Russian population, the polymorphic variant rs7935564 (*N155D*) of the *TRIM22* gene is a significant genetic factor associated with HIV infection, while the results for rs1063303 (*T242R*) were statistically ambiguous. The association of the G-G haplotype with the presence of infection suggests a potential synergistic effect of these alleles. The data obtained highlight the importance of considering a population genetic background when evaluating the genetic determinants of the interaction between HIV and the host organism.

Keywords: HIV infection, virus-host interaction, *TRIM22*, polymorphism, prognostic markers, laboratory diagnostics

Ethics approval. The study was conducted with the informed consent of the patients. The research protocol was approved by the Ethics Committee of the Saint-Petersburg Pasteur Institute (protocol No. 110/a, November 27, 2020).

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Ассоциация полиморфных вариантов гена *TRIM22* (*N155D* и *T242R*) с ВИЧ-инфекцией в Северо-Западном федеральном округе России

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Аннотация

Введение. Вирус иммунодефицита человека (ВИЧ) остается глобальной проблемой здравоохранения. Ген *TRIM22*, кодирующий белок с противовирусной активностью, является перспективным кандидатом для исследований, однако его роль в патогенезе ВИЧ-инфекции в популяциях Российской Федерации ранее не изучалась.

Целью работы был анализ полиморфных вариантов rs7935564 (*N155D*) и rs1063303 (*T242R*) гена *TRIM22* у ВИЧ-инфицированных лиц в Северо-Западном федеральном округе.

Материалы и методы. Проведён анализ полиморфных вариантов rs7935564 (*N155D*) и rs1063303 (*T242R*) гена *TRIM22* в группах ВИЧ-инфицированных лиц с вирусологической неэффективностью антиретровирусной терапии ($n = 378$) и практически здоровых лиц ($n = 319$). Генотипирование выполнено методом полимеразной цепной реакции с последующим секвенированием. Статистический анализ включал проверку соответствия распределения генотипов равновесию Харди–Вайнберга, оценку ассоциаций по 3 моделям наследования (доминантной, рецессивной, аддитивной) с расчётом отношения шансов (ОШ) и 95% доверительного интервала (ДИ), анализ неравновесия сцепления и частот гаплотипов.

Результаты. Распределение генотипов для анализируемых полиморфных вариантов соответствовало равновесию Харди–Вайнберга ($p > 0,05$). Выявлена достоверная ассоциация аллеля G полиморфизма rs7935564 с наличием ВИЧ-инфекции в рецессивной (ОШ = 1,76) и аддитивной (ОШ = 1,37) моделях наследования. Для полиморфизма rs1063303 значимая ассоциация наблюдалась только в доминантной модели (ОШ = 1,40). Обнаружено умеренное неравновесие сцепления между локусами ($D' = 0,4478$; $r^2 = 0,1572$; $p < 0,001$). Гаплотип G-G (rs7935564_G — rs1063303_G) был ассоциирован с наличием инфекции (ОШ = 1,57).

Заключение. В российской популяции полиморфный вариант rs7935564 (*N155D*) гена *TRIM22* является значимым генетическим фактором ассоциации с ВИЧ-инфекцией, в то время как для rs1063303 (*T242R*) получены статистически неоднозначные результаты. Ассоциация гаплотипа G-G с наличием инфекции свидетельствует о потенциальном синергетическом эффекте данных аллелей. Полученные данные подчёркивают важность учёта популяционной специфики при оценке генетических детерминант взаимодействия ВИЧ и организма-хозяина.

Ключевые слова: ВИЧ-инфекция, взаимодействие вирус–хозяин, *TRIM22*, полиморфизм, прогностические маркеры, лабораторная диагностика

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Introduction

The human immunodeficiency virus (HIV) continues to be one of the most significant global public health challenges. According to the latest epidemiological data¹, over 40 million people are living with this infection in 2024. Despite significant advancements in the development of antiretroviral therapy (ART), which has transformed the infection from a death sentence into a manageable chronic disease, complete eradication of the virus from the body remains an unattainable goal [1]. One of the key obstacles along this path is the virus's high genetic variability and the complex nature of its interaction with the host's immune system [2]. The most important component of innate immunity against viral infections is interferon-stimulated genes, whose products form a multi-component antiviral system [3]. In recent years, increasing attention has been given to the role of cellular restriction factors among these components, which represent an evolutionarily ancient first line of defense against pathogens [4]. These constitutively expressed proteins are capable of recognizing and directly inhibiting viral replication in the early stages of its life cycle, before the adaptive immune response is triggered.

Among the numerous factors of innate immunity, the TRIM (Tripartite Motif) family is of particular interest. It encompasses proteins with E3 ubiquitin ligase activity that are involved in various cellular processes, including proliferation, apoptosis, autophagy, and antiviral defense [5, 6]. The key mechanism of their action is the ubiquitin-mediated degradation of viral components or the activation of signaling pathways leading to the synthesis of type I interferons and pro-inflammatory cytokines [7, 8]. Members of this family, such as TRIM5 α , are well-known for their ability to suppress retroviruses, including HIV, by specifically binding to the viral capsid and prematurely destabilizing it [9]. However, another member of this family, TRIM22, located on chromosome 11 in a cluster with other TRIM family genes, is attracting increasing attention as a potent regulator of the antiviral response, although its role in HIV infection has been much less studied and remains controversial [10]. It has been shown that TRIM22 is capable of suppressing the replication of a wide range of viruses, but data on the function of this protein in relation to HIV are complex and often contradictory. Several studies demonstrate its direct antiviral activity. Thus, it has been established that TRIM22 can inhibit HIV-1 transcription by suppressing the activity of its long terminal repeats (LTR), as well as disrupt virion processing and assembly through interaction with the Gag precursor protein [12]. Furthermore, TRIM22 expression is negatively correlated with viral load in patients, and its overexpression *in vitro* leads to effective sup-

pression of HIV-1 replication [11, 12]. These data suggest that TRIM22 is an important component of cellular defense against HIV. On the other hand, there is evidence of a potentially proviral role for TRIM22 in certain contexts. Some studies suggest that TRIM22 may enhance the pro-inflammatory response through NF- κ B activation, which could theoretically contribute to chronic immune activation and disease progression [13]. Furthermore, there are suggestions that depending on the cell type and phase of infection, TRIM22 can have opposing effects, acting either as a restriction factor or as a modulator of the immune response, indirectly influencing viral persistence [14]. This ambiguity highlights the complexity of the host immune system's functioning and the necessity for further research to elucidate the precise role of TRIM22 in HIV infection.

An important aspect determining the functional activity of TRIM family proteins is their genetic polymorphism. Single nucleotide polymorphisms (SNPs) in the coding and regulatory regions of the *TRIM22* gene can affect its expression level, protein stability, or functionality, thereby modulating individual susceptibility to infection and disease progression rate. However, the results of studies on the association between *TRIM22* polymorphism and HIV infection are often contradictory in populations with different genetic backgrounds. Ethnic differences in allele frequencies, haplotype structure and the presence of specific genetic modifiers can profoundly influence the phenotypic manifestations of polymorphic variants. Therefore, data obtained from Asian, African or Western European populations cannot be automatically extrapolated to the Russian population, which is characterized by a unique and complex genetic landscape shaped by centuries of mixing of Slavic, Finno-Ugric, Turkic and other groups [15]. Specifically, populations in the Northwestern Federal District (NWFD) of Russia exhibit a distinct genetic profile within the country, making them a particularly interesting subject for population genetic research [16]. Furthermore, the HIV strains circulating in the region are predominantly genotype A6 [17, 18], which has a limited global distribution and is characterized by certain molecular biological features. The reciprocal adaptation that occurs between the genetic background of a specific human population and the viral variants circulating within it shapes a unique evolutionary dynamic, the understanding of which requires local regional studies. Despite its obvious importance and potential clinical significance, the analysis of associations between *TRIM22* gene polymorphisms and HIV infection in Russian populations, particularly in the North-Western Federal District, has been virtually non-existent until now. Filling this gap is a necessary step toward a deeper understanding of the pathogenesis of HIV infection, identifying genetic markers of individual risk, and, in the future, developing personalized approaches to the prevention and treatment of this disease. In

¹ Global HIV & AIDS statistics — Fact sheet / UNAIDS 2024 epidemiological estimates. URL: <https://www.unaids.org/en/resources/fact-sheet> (data of access: 14.08.2025).

light of the above, the polymorphic variants rs7935564 (A>G N155D) and rs1063303 (C>G T242R) of the *TRIM22* gene, previously characterized in other geographical regions, are of particular interest.

The aim of the study was to analyze the polymorphic variants rs7935564 (*N155D*) and rs1063303 (*T242R*) of the *TRIM22* gene in HIV-infected individuals in the Northwest Federal District.

Materials and methods

Whole blood samples were used as material for the study, obtained from 378 HIV-infected patients experiencing virological failure of ART and 319 practically healthy individuals without acute or chronic infectious or somatic diseases at the time of examination, permanently residing in the Northwestern Federal District. In the control group, the age ranged from 18 to 60 years, with an average of 38.9 years; there were slightly more men ($n = 166$; 52.04%) than women ($n = 153$; 47.96%). In the group of HIV-infected individuals, the age ranged from 18 to 73 years, with an average of 38.3 years; the proportion of men ($n = 240$; 63.49%) was significantly higher than that of women ($n = 138$; 36.51%).

An important aspect of sample formation was the control of HIV infection risk factors. All participants in the study (both the target and control groups) are natives and residents of the Northwestern Federal District, deny involvement in any high-risk groups for HIV infection (injection drug users, commercial sex workers, men who have sex with men, individuals who have sexual contact with representatives of key risk groups), and also practice risky sexual behavior (inconsistent use of barrier contraception, multiple sexual partners), which suggests a common social and epidemiological environment. This approach was aimed at minimizing potential bias associated with unequal probability of encountering the virus in the compared groups, and allows for a more confident interpretation of the identified associations as being related specifically to genetic characteristics rather than behavioral factors.

The choice of patients with virological failure of ART as the target group was due to the necessity to ensure the inclusion of individuals with a confirmed diagnosis of HIV infection in the analysis, excluding possible errors or undetected seroreversion. This cohort of patients is under constant observation, which ensured the reliability of diagnosis verification and the availability of necessary biological samples.

All participants were informed about the purpose and methodology of the study and signed informed consent. A positive decision for conducting this study was obtained from the local Ethics Committee of the Pasteur St. Petersburg Research Institute of Epidemiology and Microbiology (protocol No. 110/a dated November 27, 2020).

Total DNA/RNA extraction was performed using the RIBO-prep reagent kit (Central Research Insti-

tute of Epidemiology) with the use of the Hemolytic reagent. Primers described previously [19, 20] were used to amplify gene fragments containing the target loci of *TRIM22* (rs7935564 A>G *N155D*; rs1063303 C>G *T242R*). The amplification mixture consisted of a buffer solution containing Tris-HCl pH 8.8 (at 25°C), KCl, 6–7 mM MgCl₂, deoxynucleoside triphosphates, glycerol, Tween-20 and Taq+Phusion polymerases. PCR was performed under the following conditions: after denaturation at 95°C for 15 minutes, 45 amplification cycles were set up in the following mode: 95°C for 30 seconds, 52–64°C for 30 seconds, 72°C for 1 minute 30 seconds — 3 minutes 30 seconds; then final elongation at 72°C for 10 minutes. The quality of amplification was determined visually in a 2% agarose gel (120 V, 40 min; 1xTBE) stained with ethidium bromide, using a gel documentation system and subsequent analysis for the presence of target fragments and their length.

Amplification products, as well as the subsequent sequencing reaction products, were purified by ethanol precipitation. The purified fragment with a concentration of 50–100 ng, depending on the nucleotide composition of the analyzed region, was used to set up sequencing reactions with forward and reverse amplification primers. The sequencing reaction was performed using the ABI PRISM BigDye Terminator v. 3.1 reagent kit (Applied Biosystems). The obtained fragments of the analyzed samples were sequenced using the ABI PRISM 3500 genetic analyzer (Applied Biosystems).

Statistical data processing was performed using licensed software: MS Excel (Microsoft) and Prism 9.5.1 (GraphPad Software Inc.). We checked the genotype distribution for compliance with the Hardy–Weinberg principle. To assess the significance of the differences, depending on the characteristics of the samples, Fisher's exact test or the χ^2 test with Yates' correction were used, and the odds ratio (OR) with a 95% confidence interval (CI) was calculated. Additionally, the values of the non-equilibrium linkage coefficient were assessed, and haplotype frequencies were calculated. The significance level for differences was set at a probability value of $p < 0.05$.

Results

The distribution of genotypes and allele frequencies for the studied polymorphic variants rs7935564 (A>G *N155D*) and rs1063303 (C>G *T242R*) of the *TRIM22* gene, with an assessment of Hardy–Weinberg equilibrium compliance, is presented in **Table 1**.

In the analyzed groups, the distribution of genotypes for all polymorphic variants conformed to Hardy–Weinberg equilibrium expectations ($p > 0.05$), indicating the absence of significant deviations caused by selection, migration, or inbreeding, confirming the representativeness of the formed samples and the reliability of the obtained genetic data.

Based on the data obtained, the odds ratio (OR) was calculated within the framework of 3 alternative inheritance models: recessive, dominant and additive, to comprehensively assess the association between the studied polymorphic variants and the presence of HIV infection. The results are presented in **Table 2**. We assessed the equilibrium/disequilibrium of the analyzed loci: $D = 0.0969$; $D' = 0.4478$; $r^2 = 0.1572$; $p < 0.001$. Thus, moderate linkage disequilibrium is shown for the two analyzed SNPs in the study groups.

The frequency of haplotypes in the groups was estimated and their association with HIV infection was analyzed (**Table 3**).

Discussion

The TRIM22 protein exhibits a complex and multi-level mechanism of antiviral activity, particularly against HIV. Its expression in peripheral blood lymphocytes and its constitutive presence in a number of human tissues are induced by both type I and type II inter-

Table 1. Distribution of genotype and allele frequencies, and assessment of conformity to Hardy–Weinberg equilibrium

Polymorphism	Genotypes, alleles	Control group ($n = 319$)			HIV-infected individuals ($n = 378$)		
		Distribution of genotypes, alleles		p_{HWE}	Distribution of genotypes, alleles		p_{HWE}
		n	%		n	%	
rs7935564 (A>G <i>N155D</i>)	A/A	103	32.29	0.3	98	25.93	0.68
	A/G	165	51.72		195	51.59	
	G/G	51	15.99		95	25.13	
	A	0.58			0.5		
	G	0.42			0.5		
rs1063303 (C>G <i>T242R</i>)	C/C	127	39.81	0.24	121	32.01	0.2
	C/G	140	43.89		197	52.12	
	G/G	52	16.3		60	15.87	
	C	0.62			0.58		
	G	0.38			0.42		

Note. p_{HWE} — significance level under Hardy–Weinberg equilibrium.

Table 2. Assessment of the association of polymorphic variants with HIV infection

Polymorphism	Model	Genotype	OR	95% CI	p
rs7935564 (A>G <i>N155D</i>)	Dominant	A/A	1		0.065
		A/G-G/G	1.36	0.98–1.89	
	Recessive	A/A-A/G	1		0.0029
		G/G	1.76	1.21–2.58	
	Additive		1.37	1.11–1.71	0.0035
rs1063303 (C>G <i>T242R</i>)	Dominant	C/C	1		0.032
		C/G-G/G	1.4	1.03–1.92	
	Recessive	C/C-C/G	1		0.88
		G/G	0.97	0.65–1.45	
	Additive		1.17	0.94–1.45	0.16

Table 3. Association of haplotypes rs7935564/rs1063303 with HIV infection

rs7935564	rs1063303	Control group	HIV-infected individuals	OR, 95% CI	p
A	C	0.454	0.3912	1	–
G	G	0.2518	0.3065	1.57 (1.16–2.12)	0.0033
G	C	0.1667	0.1895	1.21 (0.91–1.60)	0.2
A	G	0.1275	0.1128	0.89 (0.61–1.30)	0.55

ferons, and it is also modulated in response to various viral pathogens and their antigens [21]. One of the key mechanisms of TRIM22 antiviral action is the suppression of HIV replication, which has been demonstrated in models of promonocytic cell lines and primary macrophages differentiated from human monocytes. The molecular mechanisms of this suppression are multifaceted: TRIM22 is capable of inhibiting the basal activity of the HIV promoter without affecting Tat-dependent or NF- κ B-mediated transactivation, but effectively blocking LTR-mediated and phorbol ester and ionomycin-induced viral gene expression.

Although TRIM22, like other members of the TRIM family, does not have the ability to directly bind to DNA, it mediates its effect by interfering with cellular transcription factors. Specifically, it has been shown that TRIM22 disrupts the binding of the transcription factor Sp1 to its consensus sites in the HIV LTR, which is explained by the coiled-coil (CC) ability of the domain of these proteins to engage in heterotypic protein-protein interactions [22]. The two-domain organization of TRIM22 defines the duality of its functions: the N-terminal RING domain exhibits E3 ubiquitin ligase activity, leading to the polyubiquitination of viral target proteins and their subsequent degradation via the proteasomal pathway [23]. At the same time, the C-terminal CC domain is involved in the formation of high-molecular-weight protein complexes, mediating more complex and less studied restriction mechanisms that may include: disruption of virion assembly, interference with intracellular transport of viral components, or modulation of innate immunity signaling pathways [24]. It is important to note that this process is not limited to the direct degradation of targets, but also mediates the activation of key components of the innate immune system. Specifically, it has been shown that oligomerized TRIM22 is able to specifically activate NOD2 (nucleotide-binding oligomerization domain-containing protein 2), an intracellular pattern recognition receptor that plays a central role in initiating the pro-inflammatory response upon pathogen detection [25]. Activation of NOD2 triggers a signaling cascade leading to the activation of NF- κ B and the production of pro-inflammatory cytokines, which enhances the cell's antimicrobial defense. Thus, amino acid substitutions in the coiled-coil domain caused by the polymorphic variants studied in this work could potentially disrupt the TRIM22 multimerization process, which in turn could alter its polyubiquitination ability and weaken the activation of the NOD2-mediated immune response, reducing the effectiveness of antiviral defense [26]. *In vitro* data indicate that these amino acid substitutions are associated with reduced protein suppressor activity against HIV transcription and correlate with a more severe disease course in infected individuals [10], suggesting their critical role in the protein's functional integrity and its ability to coordinate a multi-component antiviral response.

The conducted study represents the first analysis of the association between non-synonymous polymorphic variants of the *TRIM22* gene, rs7935564 (*N155D*) and rs1063303 (*T242R*), and HIV infection in the population of the Northwest Federal District. The data obtained revealed a complex and multifaceted nature of the association between the studied genetic variants and the presence of HIV infection.

The key finding of this study is the identification of a significant association between rs7935564 and the presence of HIV infection. Compelling evidence has been obtained for the association of the *G* allele with the presence of HIV infection. This is indicated by the significance in the most powerful additive model (OR = 1.37; 95% CI 1.11–1.71; p = 0.0035), as well as in the recessive model (OR = 1.76; 95% CI 1.21–2.58; p = 0.0029). This suggests that the effect of this variant is most pronounced in the homozygous state (*G/G*), which may be related to a more significant change in the charge and structure of the protein at position 155, which is critical for its function. Our results are consistent with the findings of a study in an Italian cohort, where the *G* allele of the *TRIM22* gene rs7935564 was linked to HIV infection [10]. It is interesting to note that in the cited study, the most significant association with rapid HIV infection progression was identified within a dominant inheritance model.

The observed discrepancy with our data, in which the maximum association was found for the recessive model, may have several explanations. Firstly, fundamental differences in the genetic background between the Italian and Northwest Russian populations can significantly influence patterns of genetic associations, including the inheritance model, which is consistent with the well-known phenomenon of population specificity in the genomic architecture of complex traits. Secondly, the study design appears to be a critical factor: unlike our work, which analyzed the overall group of HIV-infected individuals with virological failure of ART, the study by S. Ghezzi et al. stratified patients into subgroups with different rates of disease progression. This approach allows for the identification of genetic determinants that specifically influence the rate of disease progression, which may remain unnoticed when analyzing an unstratified cohort. Additionally, it cannot be ruled out that different inheritance patterns reflect the pleiotropic effect of the studied polymorphism, which manifests differently at various stages of the infectious process — from initial infection to the late stages of immunopathology.

For the rs1063303 (*T242R*) polymorphism, our results are less conclusive. Despite the identification of a weak association in the dominant model (OR = 1.40; 95% CI 1.03–1.92; p = 0.032), the lack of significance in the additive and recessive models, as well as the wide confidence interval crossing unity, do not allow for a definitive conclusion about its independent

role in the studied sample. Similar studies in other geographical regions have yielded conflicting results. Thus, in the aforementioned study of HIV progressors in Italy, no association was found between rs1063303 and the disease [10]. At the same time, in the aforementioned study, the haplotype rs7935564 G + rs1063303 G showed a significantly higher prevalence among HIV-infected individuals with rapid disease progression compared to those with slow progression. Additionally, it is known that the rs1063303 polymorphism has the opposite functional effect, increasing TRIM22 expression and decreasing its antiviral activity [27], and increased TRIM22 expression in peripheral blood mononuclear cells of HIV-infected patients is associated with a lower viral load [28].

An important aspect of our analysis was the assessment of linkage disequilibrium between the loci studied. The observed values ($D' = 0.4478$; $r^2 = 0.1572$) indicate the presence of moderate but statistically significant historical linkage, which, however, is not sufficient to consider these polymorphisms markers for each other. The low r^2 value, in particular, indicates that only about 15% of the variation in one locus can be explained by variations in another. This confirms that the identified association for rs1063303 is likely independent and not mediated thru linkage with rs7935564. It should be noted that according to open genetic databases, such as the 1000 Genomes Project [29], the analyzed SNP show linkage disequilibrium ranging from weak to moderate. Strong linkage disequilibrium (D' values can be high, ~ 0.8 – 1.0) can be expected in East Asian populations, but even here the r^2 value (which is most important for prediction) often remains low (< 0.3), meaning that despite a historical tendency for co-inheritance, one SNP cannot be reliably predicted from another. In European populations, linkage is weaker (r^2 values are often low, < 0.2) or absent [10]. Despite weak or moderate linkage, the "preferred" (co-occurring alleles) haplotype rs7935564 - rs1063303 is *A-C*, while the haplotype associated with the presence of HIV infection is *G-G*. In the current study, haplotype *A-C* was the most common in both the control and target groups. How-

ever, we did not find a logical protective effect of this haplotype against HIV infection; only a trend toward a protective effect was shown, which did not reach statistical significance. Conversely, for the "risk haplotype" *G-G*, an association with HIV infection was confirmed ($OR = 1.57$; 95% CI 1.16–2.12; $p = 0.0033$), indicating a possible synergistic effect of the two amino acid substitutions. This haplotype may determine a protein conformation that is less effective at suppressing HIV replication or modulates the immune response in a way that indirectly contributes to viral persistence.

A limitation of this study is its case-control design, which does not allow us to establish causality, as well as the relatively small sample size, which may have limited the power to detect weak associations, particularly for rs1063303. The results illustrate the phenomenon of population-specific genetic associations, which is widely recognized in modern complex disease genetics [30, 31]. This highlights the necessity for further longitudinal studies with increased sample sizes and thorough clinical-genetic comparisons to fully elucidate the role of *TRIM22* gene polymorphisms in the pathogenesis of HIV infection.

Conclusion

The study conducted demonstrates a significant association between the non-synonymous polymorphic variant rs7935564 (*N155D*) of the *TRIM22* gene and the presence of HIV infection in the population of the North-Western Federal District, while statistically ambiguous results were obtained for the variant rs1063303 (T242R). The identified association of haplotype *G-G* (rs7935564_G — rs1063303_G) with the presence of infection suggests a potential synergistic effect of these alleles. The obtained data contribute to understanding the molecular mechanisms of innate antiviral immunity, highlighting the role of the TRIM22 protein in modulating the virus-host interaction during HIV infection, and reflect the importance of considering population specificity of genetic factors when studying the interaction between HIV and the host organism.

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