Journal of Cell Science & Therapy
ISSN: 2157-7013
OPEN ACCESS Freely available online
Short Communication

Genetic Characteristics of the Course of Chronic Hepatitis

Sevara B. Azimova*, **Bakhtiyar U. Iriskulov**
Department of Pathological Physiology, Tashkent Medical Academy, Tashkent, Uzbekistan

ABOUT THE STUDY

Comparative analysis of genotypic variants of TNF-α and CTLA-4 genes in patients with chronic hepatitis C and liver cirrhosis and their effect on the course of the disease. The analysis of the effect of TNF-α gene genotypes on the course of the disease indicates an increased risk of CVHC development with both moderate and highly active course of the disease in carriers of the G/A+A/A genotype combination. The data obtained allow us to conclude that the carriage of the "G" allele and the combination of genotypes A/G+G/G of the -A49G polymorphism of the CTLA-4 gene are associated not only with a decrease in the risk of CVHC development, but also with a lower intensity of inflammation and fibro-formation in the liver and a high probability of favorable course of the disease.

The problem of the spread and treatment of chronic viral hepatitis C continues to be one of the significant problems of internal medicine. The urgency of the problem of hepatitis C is determined by the high epidemiological and socio economic significance of this disease, as well as the widespread occurrence, severity of the course and the frequency of development of chronic forms [1-3]. It is HCV infection that is the main reason for the formation of the entire group of chronic liver diseases-chronic hepatitis, cirrhosis, hepatocarcinoma [4-6]. At the same time, the study of this issue is not only medical, but also socio-economic in nature. It is believed that chronic hepatitis C is always potentially dangerous, but the pathogenesis of this disease is not fully understood. This will require a search for new approaches and new fundamental research [7,8].

The main group of the study included 107 patients with Chronic Viral Hepatitis C (CVHC). To assess the association of polymorphic markers of TNF-4 and CTLA-4 genes, patients with CVHC were divided into three subgroups. The first subgroup includes patients with moderate activity, chronic hepatitis C (CHC) (n=33). The second subgroup consisted of patients with a high degree of CHC activity (n=37). The third subgroup included patients with liver cirrhosis (n=37). The criteria for inclusion in the study were clinical, biochemical and instrumental verification of the diagnosis with the definition and stage and severity of the disease, as well as the detection of hepatitis C virus RNA by the AmpliSens HCV-FRT test system detected by Polymerase Chain Reaction (PCR) on a Rotor Gene 6000 device. As a comparison group, a population control was used, which was represented by DNA samples (n=81) of apparently healthy donors without chronic liver infection. The material for the molecular genetic study was the peripheral blood of the examined persons. DNA isolation was carried out according to the standard procedure with some modifications and using the reagents of the "Interlabservice" company (Russia). Identification of alleles of gene polymorphism was carried out using polymerase chain reaction.

CONCLUSION

The carriage of the "G" allele and the combination of genotypes A/G+G/G of the -A49G polymorphism of the CTLA-4 gene are associated not only with a decrease in the risk of CVHC development, but also with a lower intensity of inflammation and fibro-formation in the liver and a high probability of favorable course of the disease.

REFERENCES

1. Pavlov CS, Bakulin IG. Hepatitis B virus is the main etiological factor of chronic hepatitis, liver cirrhosis and hepatocellular carcinoma. RMZh. 2000;5:-32.
2. Ivashkin VT, Pavlov CS. Fibrosis of the liver. GEOTAR. 2011;6:168.
3. Luchshev VI, Sanin BI, Zharov SM. Viral hepatitis C is a global problem of our time. J Med Sci. 2004;3:40-45.
4. Sun D, Dai M, Shen S, Li C, Yan X. Analysis of naturally occurring resistance-associated variants to NS3/4A protein inhibitors, NS5A protein inhibitors and NS5B polymerase inhibitors in patients with chronic hepatitis C. Gene Expr. 2017.
5. Razavi H, Waked I, Sarrazin C,Myers RP,Idilman R,Calinas F, et al. The present and future disease burden of hepatitis C virus (HCV) infection with today's treatment paradigm. J Viral Hepat. 2014;21:34-59.
6. Kanwal F, Hoang T, Kramer JR, Asch SM, Goetz MB, Zeringue A, et al. Increasing prevalence of HCC and cirrhosis in patients with chronic hepatitis C virus infection. Gastroenterology. 2011;140:1182-1188.
7. Grassi G, Di Caprio G, Fimia GM, Ippolito G, Tripodi M, Alonzi T. Hepatitis C virus relies on lipoproteins for its life cycle. World J Gastroenterol. 2016;22:1953-1965.
8. Vladimir AM, Sylvie L. Hepatitis C virus: Morphogenesis, infection and therapy. World J Hepatology. 2018;10:186-212.

Correspondence to: Sevara B. Azimova, Department of Pathological Physiology, Tashkent medical academy, Forobiy-3 street, Tashkent, Uzbekistan
E-mail: sevara.azimova@yahoo.com

Received: November 05, 2021; **Accepted**: November 19, 2021; **Published**: November 26, 2021

Citation: Azimova SB, Iriskulov BU (2021) Genetic Characteristics of the Course of Chronic Hepatitis. J Cell Sci Therapy.S8:326.