

Reconstruction and analysis of the gene network of the external pathway of apoptosis in viral hepatitis C

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Viral hepatitis C is one of the most common and dangerous infectious diseases in the world, caused by the hepatitis C virus (HCV) and affecting primarily liver cells. The infection can develop in the body for years, becoming chronic, and almost never manifest itself. Chronic hepatitis C is one of the main causes of liver cirrhosis and hepatocellular carcinoma. Existing drugs are expensive and not enough effective due to the frequent occurrence of drug resistance of the hepatitis C virus due to mutations in its genome. Penetrating into the body, HCV seeks to exercise control over the biological processes occurring in the host cells in order to increase its survival and replication efficiency. Several studies have shown that HCV has a regulatory effect on apoptosis, which plays an important role in the regulation of physiological and pathological processes.

The study of molecular-genetics mechanisms of regulation of biological processes by viral proteins can help in the search for new targets for drug exposure. The creation of antiviral drugs aimed at cellular targets can solve the problem of drug resistance in pathogens. Understanding the mechanisms of regulation of apoptosis by HCV proteins can help in the search for targets and the development of pharmacological drugs for the treatment of diseases such as hepatocellular carcinoma, neurodegenerative disorders, etc., in which the process of programmed cell death is disrupted.

The aim of the work is to reconstruct and analyze the molecular-genetics mechanisms of regulation of the external pathway of apoptosis in viral hepatitis C.

In this work, using the ANDSystem [1], the gene network for regulating the external pathway of apoptosis in viral hepatitis C and frame models were reconstructed. We described the potential regulation of the apoptosis process by viral proteins through the FADD, CASP8, and CFLAR proteins. Further, a comprehensive analysis of the associative gene network was performed.

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References

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