# Mathematical and computer modeling of hepatocellular carcinoma caused by chronic viral hepatitis B

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The results of mathematical and computer modeling of liver activity at norm and at cancerous tumors of viral etiology are presented. We consider interconnected activity between molecular-genetic systems of liver and hepatitis B viruses based on the developed functional-differential equations with taking into account regulatory role both virus and liver microRNA's [1,2]. The results of qualitative and quantitative research of offered functional differential equations have shown that there are stable stationary, self-oscillating solutions inherent to the normal functioning of the liver; chaotic solutions and "black hole" effect that can be identified with an abnormal functioning of the genetic system of the liver with the occurrence of chromosomal aberrations with polymorphic variants of genes. Results of researches allow, at computer support of laboratory and clinical researches of infectious process at hepatitis B, to define molecular-genetic bases of pathogenesis at different level of microRNA concentration, to carry out diagnostics and forecasting of characteristic stages of disease course during hepatitis B. The results make it possible to diagnose phase of unpredictable changes in liver gene regulation and the beginning of the transition to cirrhosis and hepatocellular carcinoma using computer.

## References

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