The Influence of the Genetic Diversity of the Virus and the Host in Patients with Chronic Hepatitis C.

Leão, F.B.¹; Ramos, J.A.¹,²; Hoffmann, L.²; De Souza, E.V.²; Ramos, A. L.³; Villela-Nogueira, C.A.³; Úrményi, T.P.²; Silva, R.²; Rondinelli, E.

¹ Dep. de Biotecnologia, IFRJ-Campus Rio de Janeiro, RJ, Brazil; ² IBCCF, UFRJ-Rio de Janeiro; ³ Dep. de Clínica Médica da Faculdade de Medicina, UFRJ-Rio de Janeiro.

Hepatitis C is a health problem in Brazil with 3 million people infected. The evolution of the infection and the response to treatment varies according to HCV quasispecies and/or host genetic factors. The aim of this work is to assess the viral quasispecies in patients with HCV, besides to investigate the role of the polymorphisms in the cytokines genes. We evaluated the influence of viral genetic diversity and the host genetic diversity in the response to treatment in patients with chronic hepatitis C. The viral genetic diversity was studied in three regions of the virus (E2, NS5A and NS5B), associated with treatment response in patients with chronic hepatitis C. The diversity of the host was studied by analysis of SNPs in cytokine genes related to TH1 (IFN-g, TNF-a), TH2 (IL-4, IL-10) response and the activation of the antiviral state (IL-28B) in patients with chronic hepatitis C. For the study of viral genetic diversity, we found a relationship between the numbers of substitutions with treatment response. Patients with SVR had a larger number of substitutions in the E2 and NS5B region. We also find some specific sites in the three regions associated with no response or response to treatment. In the study of genetic diversity of the host, we found that the polymorphisms rs8099917 and rs12979860 of the gene for IL-28B were associated with treatment response in patients with HCV. Thus, we can see that both the viral and the host sides can influence the response to treatment.

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