© Kamla-Raj 2005 PRINT: ISSN 0972-3757 ONLINE: 2456-6360 Int J Hum Genet, 5(1): 33-36 (2005) DOI: 10.31901/24566330.2005/05.01.05

Host Genetic Factors in Hepatitis B Virus Infection

Runu Chakravarty

ICMR Virus Unit, Kolkata GB-4, 1st Floor ID & BG Hospital Campus, 57 Dr S C Banerjee Road, Kolkata 700 010, West Bengal, India

KEYWORDS HBV infection; chronic liver disease; genetic factors; polymorphism

ABSTRACT Worldwide about 350 million people are chronic carriers of the hepatitis B virus (HBV). The infection can cause acute and chronic liver disease including cirrhosis and hepatocellular carcinoma (HCC). Hepatocellular injuries of HBV infection are predominantly immune-mediated and a complex ill understood interplay of virological factors, host immunological factors and genetic factors as well as the environmental factors. There is strong evidence in HBV infection that host genetic factors play a major role in determining the outcome of infection. Among different approaches that may be used to determine the specific genetic factors involved, the principal method which has been used to date, is the disease association study. The association of the MHC class II alleles and interleukin-10 promoter polymorphism has been demonstrated to influence the outcome of these infections. The MBP polymorphism has also been found to be involved in chronic infection in some population groups but not in others. Since genetic interactions are complex, it is unlikely that a single allelic variant is related to HBV resistance or susceptibility. The collective influence of several single nucleotide polymorphisms (SNPs) or haplotype(s) might determine the natural combinational against HBV. The future study including the multi-cohort collaboration will be needed to clarify these preliminary associations and identify other potential candidate genes.

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