Aims and Objectives
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It has been noticed that in a population, different individuals have different susceptibility levels towards disease development under similar exposure levels of infectious agent. Even in the same family, different members show varying susceptibility levels. The differential susceptibility can be explained in terms of genetic factors like excessive or low level production of important host proteins involved in self-defense or pathogenesis.

The variable levels of expression of several important genes can be explained in terms of presence of different allelic forms of the same gene. Although this concept is still in its infancy, but it is fast gaining ground.

Hepatitis B is a dreaded disease worldwide and is caused by hepatitis B virus, which is a DNA virus of hepadnavirus family. Hepatitis B virus can manifest itself as acute, chronic or fulminant hepatitis depending on host age, sex, immunity levels and other factors. Persistent infection can also lead to development of Hepatocellular carcinoma. It has a paraenteral route of transmission. It is estimated that globally 2,000 million people have been infected with HBV at some time of their lives and that 350 million are chronic carriers of HBV. In India, the prevalence is estimated to be approximately 2-7%. Importance of genetic susceptibility in the study of hepatitis B can be gauged by the fact that different individuals show varying symptoms after infection by the virus. Some people remain healthy carriers of the virus, whereas, others show acute symptoms or develop chronic infection. Difference at genetic level in terms of presence of polymorphic forms of a set of relevant candidate gene can be one way of explaining this variance.

The present work was undertaken to understand the role of the polymorphisms in the candidate genes: TGF-β1, Fas ligand, Fas, IL-6 and TNF-alpha in determining the susceptibility to hepatitis B in Indian population, laying down the following objectives:

- Identify and characterize the Single Nucleotide Polymorphisms (SNPs) in selected regulatory regions of the candidate genes, Transforming growth factor beta1 (TGF-beta1), Fas Ligand (FasL), Fas, Tumour necrosis factor-alpha (TNF-alpha) and Interleukin-6 (IL-6) in a case-control study of hepatitis patients of Indian origin and to confirm the variations observed by PCR-SSCP (Single Strand Conformational Polymorphism) by automated sequencing.
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- Calculate the levels of significance by subjecting the data to various statistical analysis like chi square, Fisher’s test, odds ratio with 95% confidence interval, logistic regression, interaction analysis etc. for the associations observed between individual polymorphisms or in combinations and the presence of viral hepatitis, Hepatitis B status, disease progression, seropositive, seronegative status and other clinical parameters.

- Characterize functionally using in vitro reporter assays some of the polymorphisms observed in a regulatory region of a candidate gene.