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Studies of Single Nucleotide Polymorphism of Proteosomal Gene Complex and Their Association with HBV Infection Risk in India

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Abstract : Single Nucleotide polymorphism (SNP) of proteosomal gene complex is involved in the pathogenesis of hepatitis B Virus (HBV) infection. Some of such proteosomal gene complex are large multifunctional proteins (LMP) and antigen associated transporters that help in antigen presentation. Both are involved in intracellular processing and presentation of viral antigens in association with Major Histocompatability Complex (MHC) Class I molecules. A total of hundred each of hepatitis B virus infected and control samples from northern India were studied. Genomic DNA was extracted from all studied samples and PCR-RFLP method was used for genotyping at different positions of LMP genes. Genotypes at a given position were inferred from the pattern of bands and genotype frequencies and haplotype frequencies were also calculated. Homozygous SNP {A>C} was observed at codon 145 of LMP7 gene and having a protective role against HBV as there was statistically significant high distribution of this SNP among controls than cases. Heterozygous SNP {A>C} was observed at codon 145 of LMP7 gene and made individuals more susceptible to HBV infection as there was statistically significant high distribution of this SNP among cases than control. SNP {T>C} was observed at codon 60 of LMP2 gene but statistically significant differences were not observed among controls and cases. For codon 145 of LMP7 and codon 60 of LMP2 genes, four haplotypes were constructed. Haplotype I (LMP2 'C' and LMP7 'A') made individuals carrying it more susceptible to HBV infection as there was statistically significant high distribution of this haplotype among cases than control. Haplotype II (LMP2 'C' and LMP7 'C') made individuals carrying it more immune to HBV infection as there was statistically significant high distribution of this haplotype among control than cases. Thus it can be concluded that homozygous SNP {A>C} at codon 145 of LMP7 and Haplotype II (LMP2 'C' and LMP7 'C') has a protective role against HBV infection whereas heterozygous SNP {A>C} at codon 145 of LMP7 and Haplotype I (LMP2 'C' and LMP7 'A') made individuals more susceptible to HBV infection.

Keywords : Hepatitis B Virus, single nucleotide polymorphism, low molecular weight proteins, transporters associated with antigen presentation
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