

POSTER PRESENTATION

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Association of IFN- γ gene polymorphism and levels in HBV related disease chronicity in India

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Background

Hepatitis B Virus (HBV) infection is a primary causative factor for hepatocellular carcinoma (HCC), the fifth most frequent cancer, worldwide. The present study evaluated the association of IFN- γ +874T>A polymorphism and its levels with HBV related HCC risk in Indian population.

Methods

Five groups of subjects were enrolled viz. control (n=146), HBV-carriers (n=68), chronic active HBV (n=64), HBV-cirrhotics (n=60) and HBV-related HCC (n=59). Allele-specific-PCR was performed to study various polymorphic forms of IFN- γ (+874) and blood levels were estimated by ELISA. Genotype distribution was compared using chi square analysis and the odds ratios (ORs) and 95% CI were calculated to express the relative risk.

Results

In IFN- γ (+874), the (TA) heterozygous genotype was found to be a significant risk factor for chronic-active hepatitis (OR=2.94, $p<0.01$) and HCC (OR=2.7, $p<0.01$) development, among controls and carrier groups, respectively. Similarly, the variant (AA) genotype, was also found to be significantly in positive association with HCC risk ($p<0.01$), among controls. Further, the spontaneous median IFN- γ levels were 151.09pg/mL in control population. While, the levels were significantly elevated ($p<0.01$) in HCC group (252.34pg/mL) in comparison to controls as well as other categories studied. However, no significant association was found between the genotype and the cytokine levels.

Conclusions

IFN- γ polymorphic forms and its levels share a strong association with HBV-HCC risk in Indian population and thus, should be further evaluated as a candidate gene to determine individual susceptibility for the same.

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