GAS5 rs2067079 and miR- 137 rs1625579 functional SNPs and risk of chronic hepatitis B virus infection among Egyptian patients.

مكان النشر : Scientific Reports11, 20014 (2021)

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Published date: October 2021

Abstract

Hepatitis B virus (HBV) infection is a significant health issue worldwide.

We attempted to fulfill the molecular mechanisms of epigenetic and genetic factors

associated with chronic HBV (CHBV). Expression levels of the lncRNA growth arrest- specific 5 (GAS5) and miR- 137 and their corresponding SNPs, rs2067079 (C/T) and rs1625579 (G/T) were analyzed in 117 CHBV patients and 120 controls to investigate the probable association between these biomarkers and CHBV pathogenesis in the Egyptian population. Serum expression levels of GAS5 and miR- 137 were significantly down- regulated in cases vs controls. Regarding GAS5 (rs2067079), the mutant TT genotype showed an increased risk of CHBV ($p < 0.001$), while the dominant CC was a protective factor ($p = 0.004$). Regarding miR- 137 rs1625579, the mutant genotype TT was reported as a risk factor for CHBV ($p < 0.001$) and the normal GG genotype was a protective factor, $p < 0.001$. The serum GAS5 was significantly higher in the mutant TT genotype of GAS5 SNP as compared to the other genotypes ($p = 0.007$). Concerning miR- 137 rs1625579, the mutant TT genotype was significantly associated with a lower serum expression level of miR- 137 ($p = 0.018$). We revealed the dysregulated expression

levels of GAS5 and miR- 137 linked to their functioning SNPs were associated with CHBV risk and might act as potential therapeutic targets.