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<p><b>Title</b></p>	<p><b>miR-155 T/A (rs767649) and miR-146a A/G (rs57095329) single nucleotide polymorphisms as risk factors for chronic hepatitis B virus infection among Egyptian patients.</b></p>
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### ABSTRACT

Genetic variants in microRNAs (miRNAs) can alter the miRNAs expression and/or function, accordingly, affecting the related biological pathways and disease risk. Dysregulation of miR-155 and miR-146a expression levels has been well-described in viral hepatitis B (HBV). In the current study, we aimed to assess rs767649 T/A and rs57095329 A/G polymorphisms in miR-155, and miR-146a genes, respectively, as risk factors for Chronic HBV (CHBV) in the Egyptian population. Also, we aimed to do in silico analysis to investigate the molecules that primarily target these miRNAs. One hundred patients diagnosed

as CHBV and one hundred age and sex-matched controls with evidence of past HBV infection were genotyped for miR-155 (rs767649) and miR-146a (rs57095329) using real-time polymerase chain reaction. The rs767649 AT and AA genotypes in CHBV patients confer four folds and ten folds risk respectively, as compared to control subjects [(AOR = 4.245 (95%CI 2.009–8.970,  $p < 0.0001$ ) and AOR = 10.583 (95%CI 4.012–27.919),  $p < 0.0001$ , respectively)]. The rs767649 A allele was associated with an increased risk of developing CHBV (AOR = 2.777 (95%CI 1.847–4.175),  $p < 0.0001$ ). There was a significant difference in the frequency of rs57095329 AG and GG genotypes in CHBV patients compared to controls. AG and GG genotypes showed an increase in the risk of developing CHBV by about three and six folds respectively [AOR = 2.610 (95%CI 1.362–5.000),  $p = 0.004$ ] and [AOR = 5.604 (95%CI 1.4563–2.157,  $p < 0.0001$ ). We concluded that rs57095329 and rs767649 SNPs can act as potential risk factors for the development of CHBV in the Egyptian population.