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# Molecular association of lncRNA-uc003wbd and lncRNA-AF085935 expression with a genetic variant profile in Egyptian patients with hepatocellular carcinoma and HBV

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Hepatocellular carcinoma (HCC) was among the most common solid tumors, rated third in cancer-related mortality worldwide. The burden of HCC has been increasing in Egypt with a doubling in the incidence rate in the past 10 years. This has been attributed to several biological (e.g. hepatitis B (HBV) and C (HCV) virus infection) and environmental factors. HBV infection is of particular interest, for its coherent distribution with the HCC prevalence. Thus, new diagnosis measures and targeted treatments for HCC and HBV are in need. Long non coding RNAs (lncRNAs) are dysregulated in different cancers and have critical roles in various biological processes such as HULC and MALAT1 may participate in HCC development and progression. Besides, considerable studies have investigated the effects of lncRNAs genetic variations on cancer susceptibility. Through this study, we aimed at exploring the expression profile and the potential clinical value of two lncRNAs (lncRNAuc003wbd and lncRNA-AF085935) in differentiating HCC from both HBV patients and the healthy specimens and their associations with single nucleotide polymorphisms (SNPs) in HULC and MALAT-1 and the susceptibility to HBV chronic infection and HCC. Serum samples were extracted from 70 HBV patients, 70 HCC patients, and 70 healthy controls. The level of serum lncRNA-uc003wbd and lncRNA-AF085935 of all the subjects were assayed by quantitative real-time reverse transcriptase polymerase chain reaction (qRT-PCR). Moreover, we have genotyped two SNPs, rs7763881 in HULC and rs619586 in MALAT1, in all subjects to test the association between the two SNPs and susceptibility to HCC and HBV chronic infection. The level of serum lncRNA-uc003wbd and lncRNA AF085935 was significantly upregulated in HCC patients and HBV patients compared with that in normal controls. The variant genotypes of rs7763881 were significantly associated with decreased HCC risk. Similarly, variant genotypes of rs6682925 were associated with non-significant decreased HCC risk compared with the wild-type AA genotype. However, no significant association was found between the two SNPs and HBV clearance. In conclusion, our results showed that both lncRNAuc003wbd and lncRNA-AF085935 are able to be potential biomarkers for HCC and HBV screening as well that SNP rs7763881 in lncRNA HULC was significantly associated with the decreased susceptibility to HCC in HBV persistent carriers.

## Biography

Tarek Mohamed Kamal Mohamed Metawie is a Professor of Biochemistry in the Faculty of Pharmacy, Cairo University. He has completed his PhD in Pharmaceutical Sciences in 1984; MSc in Pharmaceutical Sciences in 1979; BSc in Pharmaceutical Sciences in the Faculty of Pharmacy at Cairo University in 1976. Professional experience: Instructor; 1976, Lecturer Assistant; 1980, Lecturer, 1984; Assistant Professor, 1989; Professor, 1994; Head of the Department of Biochemistry, Faculty of Pharmacy, and Cairo: - 2008-2014.

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