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Deep sequencing analysis of HBV in chronic HBV patients from Saudi Arabia

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Hepatitis B virus (HBV) has ten genotypes (A-J) and 34 subtypes. These genotypes differ in geographic distribution, HBeAg seroconversion rate, clinical outcome, prognosis and response to antiviral treatment. The prognosis of chronic HBV (CHB) infection includes hepatic failure, cirrhosis and hepatocellular carcinoma (HCC). The introduction of mandatory vaccination in Saudi Arabia have reduced the prevalence in young Saudis, but the prevalence in individuals more than 25 years is about 4%. Studies exploring the evolutionary aspect and molecular variations of HBV in correlation with the development of HCC in Saudi Arabia are very limited. Deep next generation sequencing is more frequently used to investigate low frequency mutations in HBV that might be associated with resistance to antiviral treatment or the development of HCC. We performed deep sequencing on samples from 20 HBV chronically infected patients from Saudi Arabia. Subjects were all of genotype D, positive for HBsAg and negative for HBeAg. A common finding in all samples was the 33 base deletions in the preS region in all cases. Low frequency mutations in the rt-region related to antiviral resistance together with mutations in the pre-core and core regions associated with the development of HCC were detected. The results of these studies as well as their clinical data will be presented.

Biography

Sherif A El-Kafrawy has completed his PhD in 1999 from Menoufiya University, Egypt. He was appointed as an Assistant Professor of Molecular Biology at the National Liver Institute and he is currently working as an Assistant Professor of Molecular Virology in King Abdulaziz University. He has published more than 25 papers in reputed journals.

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