Genetics in hepatitis B

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Hepatitis itself is not a genetic disease. Hepatitis B virus got genetic diversity. HBV is DNA virus which replicates by RNA intermediate as its DNA polymerase has reverse-transcriptase RT. The mutation rate for HBV is high. HVB classified on base of genomic sequencing, antigenic subtypes of glycoprotein surface antigen HBsAg. Genotype-subtype has geographical distribution related to population movement and significant events. Mutation and mutant selection occurred among all HBV variants. They have relevant medical and public health implications. Pre-core (pre-C) defective variant has less susceptibility to Interferon with high failure rate to other antiviral drugs related to selection of resistant variants mutation in genome encoding viral RT activity. As RT overlaps HBsAg molecule code, selection of drug resistant variants indirectly leads to selection of HBsAg variants commonly encountered in chronic HBV carriers. The significance of this emerges under the pressure of neutralizing antibody response leading to resistance to both vaccination and immunotherapy noted often among liver transplant recipients and babies born to HBV-carrier. HBsAg variants also associated with false negative results in diagnosis of new infections, detection of chronic carriers, screening for blood donation and manufacture of therapeutic blood products.

Biography
Osama Hasan Othman has completed his MBChB in Mosul Medical College in 1980, gained DM, CABM Baghdad in 1992, MRCP1 in 1988 and FRCP London in 2012. He is currently a Chief of Department of Medicine, previously Sub-Dean of Scientific Affairs in Medical College. He shares in most of scientific activities in the college and Azadi Teaching Hospital and has published many papers and editorials.

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