**Republic of Iraq**
**Ministry of Higher Education**
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**College of Science**
**Department of Biology**

# Genetics Variation in *HLA_DP* Gene Associated with increase risk of Hepatitis B infection in Al Muthanna province –IRAQ

A Thesis Submitted to the Council of College of Science / Al Muthanna University in Partial Fulfillment of the Requirements for the Degree of Master of Science in Biology

**BY**

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Abstract:

Given that cirrhosis and hepatocellular cancer can develop as a result of viral hepatitis B infection, it is one of the most prevalent human diseases and a significant global public health issue. In order to prevent negative outcomes from such an infection, a state of immunological homeostasis must be achieved. Therefore, the purpose of this work was to develop an assay for liver function by evaluating various parameters and utilizing a restriction fragment length polymorphism assay to find variants of the HLA-DP gene (rs3128917, rs9380343). Additionally, to gene expression analysis utilizing SYBRTM Green PCR Master qPCR. Blood samples from 40 Hepatitis B virus patients and 40 controls (seemingly healthy people) from AL-Muthanna Province were used in this study, which was conducted from January to April 2022. The current findings showed that males had a greater incidence of the Hepatitis Bvirus than females, Male patients had the highest concentration of the liver function test parameters compared to the other categories.

The age range of 41 to 50 was shown to have the highest liver function concentration. as opposed to other groupings. The resident reported that the seroprevalence of HBV infection using ELISA method indicated that the prevalence rates of infection in Al- Samawa, Rumathya, AL-Khather, and Warkaa were, 40%, 25%, 15%, and 20% respectively, relating to genotype polymorphism distribution using REFLP method the results revealed significant differences for the HLA-DP rs3128917 and rs9380343 genes ($P > 0.05$). *HLA-DP* rs3128917 genotyping in 40 pateints revealed increased levels of dominant type homozygous TT (OR 0.7959), heterozygous TG (OR 0.7959), and mutant type homozygous GG (OR 0.7959) In compared to other types also in control group. Appeared significant differences of genotype (for each *HLA-DP* rs3128917), allele(GG), ($P<0.05$). When compared to the control group, genotyping for *HLA-DP* rs9380343 in 40 patients revealed wild-type

homozygotes TT (OR 0.492), heterozygotes TC (OR 0.539), and mutant-type homozygotes CC (OR 0.539)

In addition to a significant differences of genotype (*HLA-DP* rs9380343), allele (TC), allele (CC) (P<0.05 (.The results showed that the TT genotype was most frequent in both patients and healthy controls, and that the frequency of the CC genotype was higher in patients than in controls. The dominant model showed that the TC+CC genotypes were more frequent in patients than in controls, while the recessive model showed that the TT genotype was more frequent in controls. The over-dominant model showed that the TT and CC genotypes were more frequent in controls and patients, respectively.

The wild type homozygate of rs3128917 polymorphism of HLADP gene was more than rs9380343 polymorphism of HLADP gene in HBV patients. While, the heterozygate and mutant type homozygote of rs3128917 polymorphism of HLADP gene was less than of rs9380343 polymorphism of HLA-DP gene in HBV patients. In conclusion, the SNP has represented as a risk factor in HBV B disease although it appeared significant differences for the concentration of rs3128917 and rs9380343 in the genotypes. While the genotype and allele of SNP might be a protective factor in cirrhosis and hepatocellular cancer whereas allele G was observed increasing levels of which associated with genotypes GG and CC in HBV B disease while its level declined in the genotype TT which proves that this genotype has a protective role.