R585
Publication Only
Virology: Hepatitis

Clinical and paraclinical considerations on class II HLA associations in chronic C hepatitis

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Obejctive: The objective of this preliminary study was to determine the distribution of HLA(human leukocyte antigen) class II alleles, their association with chronic HCV(hepatits C virus) infection and their response to interferon therapy in our population.

Methods: The selected group comprised 54 patients diagnosed with chronic C hepatitis with different clinical outcomes. We assessed HCV-RNA in serum with RT-PC using MasterAmp RT-PCR Kit, we genotyped for HLA-DRB*1 using PCR SSO HLA typing systems, any ambiguities being solved with HLA SSP, the genotypes were assigned by the Pattern Matching Program. The independent variable was considered the DR genotype and the dependent variables were onset viral load, response to PegIFN(Pegylated interferon)/R(Ribavirin) and the extent of liver fibrosis.

Results: Based on treatment results(TR- therapeutic response) patients were retrospectively divided in four groups: sustained responders(SR)-64.9%, relapsers(R)-33.3%, non responders(NR)-22.2% and partial responders(PR)-12.9%. Allele DRB*1 0701 was most frequent among the NR group and was associated with high viremia, whilst allele DRB*1 11 was frequent in the SR group and associated low viremias.

Conclusion: Genetic predisposition may play a role in hepatitis C virus infection, the outcome of the infection varying with ethnic background of the study population. Our data suggest that among our population, certain HLA alleles influence the therapeutic response in HCV infection as a host genetic factor, such as the DRB*1 07 allele associated with viral persistence, chronicity and hepatic injury, data that is similar with speciality literature(Alric et al.1999).