Conclusions: HLA-DP might be the causative gene that contributes to the prevalence discrepancy of HBV all over the world.

THU-174

ASSESSMENT OF HEALTH-RELATED QUALITY OF LIFE IN CHRONIC HEPATITIS B INFECTION PATIENTS IN TURKEY: A MULTICENTER STUDY

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Background and Aims: The study aims to assess Health-Related Quality Of Life (HRQOL) among patients with hepatitis B and to determine the factors related to HRQOL in Turkey.
Methods: This multicenter study was conducted in 30 cities in Turkey from January 1 to April 15, 2015. A total of 57 researchers from 74 centers participated in the study. The patients were allocated into three groups. Group 1; inactive HBsAg carriers, group 2; patients which were undergoing antiviral treatment, group 3; other chronic hepatitis B (CHB) patients. The data were collected by a face to face sociodemographic form, Short Form-36 (SF-36) and Hepatitis B

Quality of Life (HBQOL) questionnaire form. Because five-factor structure for the HBQOL fitted well into Turkish data in publised study, Transmissibility subscale was not analyzed. The data analyzed via SPSS v.22.0 (SPSS Inc., Chicago, IL, USA). The factors related to HRQOL were determined. $p < 0.05$ was considered significant.

Results: A total of 4257 patients (1529 patients in group 1, 1721 patients in group 2, 1007 patients in group 3) were studied. The study group included 2559 (60.1%) male and 1698 (%39.9) female with a median age of 40 years (min-max: 18–84 years). The median ALT levels was 25 U/L (min-max: 0–961 U/L), and the median HBV DNA levels was 76 IU/mL (0–19 × 10^9 IU/mL). 3657 (85.9%) cases were HbeAg negative. There were statistically significant differences among the study groups according to SF-36 physical component scores, mental component scores and HBQOL total scores (respectively p = <0.001, p = <0.001, p = <0.001). The statistically significant differences were found between SF-36 physical component scores and education level (p = 0.028), undergoing antiviral treatment (p = <0.001), ALT levels (p = 0.004); also SF-36 mental component scores and undergoing antiviral treatment (p = 0.012), ALT levels (p = 0.038). Statistically significant differences were noted regarding HBQOL total scores and gender (p = 0.001), marriage status (p = 0.002), undergoing antiviral treatment (p = 0.011), other chronic disease status (p = <0.001), hospital type (p = <0.001), HBeAg status (p = <0.001), ALT levels (p = 0.001). When all these factors were controlled simultaneously, the scores were higher significantly in inactive CHB patients.

Conclusions: HRQOL is worse in patients with active CHB. In addition, antiviral treatment does not increase the quality of life in these patients.

THU-175

VIROLOGICAL CHARACTERIZATION OF CHRONIC HEPATITIS B IN AUSTRALIA: HIGH PREVALENCE OF VARIANTS ASSOCIATED WITH DISEASE PROGRESSION

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Background and Aims: Chronic hepatitis B infection (CHB) is a major health problem in Australia and worldwide. Recent data suggests that the hepatitis B virus (HBV) genotype and HBV variants including the basal core promoter (BCP) and precore (PC) variants influence the natural history of patients with CHB including risk of fibrosis progression and hepatocellular carcinoma. Aim: To determine the association between HBV genotype, common HBV variants and clinical features and virological profile in a large cohort of Australian patients with CHB.

Methods: A retrospective cross-sectional analysis of all treatment-naïve patients with available data for HBV genotype, A1762T/G1764A BCP variant and G1896A PC variant was performed. HBV genotype / BCP/PC variant were correlated with age, gender, ethnicity, hepatitis B e antigen status (HBeAg), HBV replication status (ALT and HBV DNA), and liver fibrosis stage Advanced liver fibrosis was defined as either METAVIR F3-4 on biopsy.

Results: 279 treatment naïve patients were identified. The patients were predominantly male (66%) with an average age of 41 years. The majority of patients were Asian (78% vs. Caucasian 13% vs. African 4%). The majority of patients were HBeAg-negative (60% vs. 40%). HBV disease phase included: immune-tolerant 8%, immune clearance 32%, immune control 7% and immune escape 53%. Genotype B HBV was most common (43% vs 6% A, 33% C and 17% D). Genotype was strongly correlated with ethnicity; patients infected with genotypes B and C were Asian, genotypes A and D Caucasian. BCP/PC sequence was performed in 162 patients. A significant proportion of patients (73%) had either a BCP or PC mutation. A1762T/G1764A BCP double variant was detected in 44% (n = 71);18% (n = 30) only had the G1896A PC variant and 27% (n = 43) had both BCP and PC mutations. BCP variants were strongly associated with genotype C. BCP/PC variants were associated with immune escape and HBeAg negative disease. The presence of a mutation was independently associated with a high rate of fibrosis (attached Table).

Univariable analysis				Multivariable analysis			
Effect	OR	95% Confidence Limits	P-value	Effect	OR	95% Wald Confidence Limits	P-value
Age > 40yrs	1.040	1.006 - 1.076	0.0211	Age > 40yrs	1.226	0.378 - 3.977	0.7438
Male	4.792	1.062 - 21.612	0.0415	Male	3.518	0.734 - 16.851	0.1155
HBeAg-pos vs. neg	0.620	0.246 - 1.568	0.3130	-	-	-	-
Genotype AD vs. BC	2.278	0.879 - 5.903	0.0901	Genotype AD vs. BC	1.721	0.607 - 4.878	0.3075
PC/BCP vs. WT	6.273	1.32- 28.137	0.0165	PC/BCP vs. WT	5.178	1.065 - 25.181	0.0416

Conclusions: The Australian CHB epidemic is notable for the presence of 4 common genotypes of HBV, reflecting the multi-ethnic population. BCP / PC variants that have been associated with aggressive disease course are common, and are associated with immune escape and HBeAg-negative disease. BCP and PC mutations are also independently associated with higher rates of fibrosis. This is a unique population for the study of natural history and prospective studies are warranted.

Viral hepatitis: Hepatitis B & D – experimental

THU-176

NK CELLS FROM CHRONIC HBV PATIENTS IN DIFFERENT CLINICAL PHASE EXHIBIT ALTERED GENE EXPRESSION PROFILES BY RNA-SEQ

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Background and Aims: We previously studied the transcriptomes of the peripheral blood of chronic hepatitis B virus (HBV) infected patients, and identified the NK cell module as one of the most actively transcribed immune components in the clinical phases with high ALT. To attain more insight into the activity of NK cells, we now studied the transcriptomes of purified NK cells during the natural course of chronic HBV by performing RNA-seq.

Methods: Enrolled chronic HBV patients (n = 32) were treatment-naïve, with well-defined HBV clinical phases according to international guidelines. Healthy individuals (n = 8) were enrolled as controls. NK cells were isolated from peripheral blood using flow cytometric sorting based on $CD3^-/CD56^+$ expression (>95% purity). RNA was extracted from isolated NK cells and subjected to RNA-seq.

Results: By studying the NK cell-specific transcriptomes, we identified 110 genes with significantly different expression (DE) in NK cells from HBV cases and healthy controls (Fold change > 1.5, q-value < 0.2). Out of these, 54 were protein-coding genes, including IRF4, IL7R, and CD83. To better understand the altered transcriptome of NK cells during HBV progression, we studied the NK cell transcriptomes of each individual clinical phase by comparing them with that of healthy controls. The immune active phase showed the most DE genes (n = 83) (Fold change > 1.5,q-value < 0.2), followed by the IC (n = 81), IT (n = 73) and ENEG (n = 72) phases. interferon-stimulated genes (ISG), that showed comparable expression throughout the HBV clinical phases, a specific set of genes