Methods: Nested-PCR was used to amplify the HBV S gene and the PCR products were sequenced directly or sequenced after cloning, the sequences of ‘a’ epitope were then analyzed by sequence alignment.

Results: Direct sequencing of PCR products showed that there was one amino acid (AA) residue in ‘a’ epitope less conserved region emerged polymorphism in each of all 4 HBV infected patients with both positive HBSAg and HBsAb markers. Clone sequencing showed that the AA residue 126 of ‘a’ epitope in patient 1 could be Thr, Ile and Ser; the AA residue 134 could be Phe and Ser; the AA residue 126 in patient 2 could be Ala and Thr, and patient 3 could be Ile and Asn; AA polymorphism was not found in patient 4.

Conclusions: Mixture virus may exist in HBV infected patients positive for HBSAg and HBsAb; the polymorphism of HBV quasi-species ‘a’ epitope sequence should be one of the reasons caused both HBSAg and HBsAb positive in HBV infected patients.

PP-096 A retrospective study on risk factors of HBV and HCV in Esfahan, Iran

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Background: The Hepatitis viruses, a heterogenous group of viruses with a tropism for the liver, are the major cause of viral hepatitis. HBV and HCV are among the most important agents of viral hepatitis. These viruses are spread parenterally by blood or needles, by sexual contact and perinatally etc.

Methods: 254 patients included 163 HBV and 91 HCV were studied in this research. This study was carried out using recorded information in file of patients in Tropical and Infectious Research Center in Esfahan, and information was extracted from these files.

Results: The history of:
- surgery: HBV: 71 (28% of all patients) - HCV: 48 (18.9% of all patients)
- blood transmission: HBV: 15 (6.1% of all patients) - HCV: 16 (6.2% of all patients)
- contact with hepatitis patient: HBV: 36 (14.2% of all patients) - HCV: 15 (6.1% of all patients)
- accident: HBV: 23 (9% of all patients) - HCV: 20 (7.9% of all patients)
- tattooing: HBV: 30 (11.8% of all patients) - HCV: 7 (2.7% of all patients)
- cupping: HBV: 22 (8.66% of all patients) - HCV: 6 (2.4% of all patients)
- sexual contact: HBV: 21 (8.3% of all patients) - HCV: 1 (0.39% of all patients)
- renal dialysis: HBV: 48 (18.9% of all patients) - HCV: 1 (0.39% of all patients)

Conclusion: It seems that the above mentioned risk factors are very important in epidemiology of Hepatitis. Therefore efficient education to population and patients to control and prevention of disease is necessary.

PP-097 Role of hepatitis B virus genotypes, BCP, precore/core and X gene mutations and the risk of hepatocellular carcinoma

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Objectives: We aimed to characterize mutations of HBV genome involving X gene, basal core promoter (BCP), and Precore/core regions and also define HBV genotypes in patients of HCC from India.

Methods: HBV genotypes and mutations were determined in 150 HCC and 136 chronic liver disease patients without HCC. All HBV DNA positive cases were subjected to mutational analysis using SSCP and genotyping by RFLP.

Results: Amongst 150 HCC patients, 79.4% and 20.6% had genotype D and A, respectively. The prevalence of genotype D was significantly higher in HCC patients compared with controls (p=0.03). The T1484, T1504, T1653, C1705, C/G1753, T1762/A1764, A1896 and G1914 mutations were frequent in HCC cases. The prevalence of the T1504 mutation in the X gene, the V1753 and T1762/A1764 mutations in BCP region and G1914 mutation in core gene were significantly higher in the HCC group compared to controls (48% vs 7%, 44% vs 7%, 70% vs 33% and 41% vs 6.7%, respectively). Also, T1653 (58% vs 14%) mutation was significantly higher for HCC cases. Multivariate analyses showed that the TT1504, T1653, T1705, T1753, and A1762T G1764A mutations and patient age significantly increased the risk of HCC development. Also HCC had lower levels of serum albumin and platelet count, but higher values of ALP, AST, ALT, Bilirubin and AFP compared to controls (P<0.001).

Conclusion: HBV genotype D and the exclusively found prevalence of certain mutations detected in those with HBV-related carcinoma nevertheless indicate a degree of association with disease progression in Indian patients.

PP-098 Resolved hepatitis B virus infection is associated with poor prognosis in patients with primary biliary cirrhosis

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Objective: To study the prevalence of resolved hepatitis B virus (HBV) infection in patients with primary biliary cirrhosis (PBC) and whether the resolved infection is associated with much poor prognosis.

Methods: Sixty PBC patients with negative serum HBsAg were further measured for other serum HBV infection markers, including anti-HBs, HBeAg, HBeAb, HBcAb and HBV DNA. Patients with resolved HBV infection were termed as serum HcAb positive (± anti-HBs±HBeAb), HBsAg negative and HBV DNA undetectable. The severity of the disease including the occurrence of hypoalbuminemia and/or jaundice, complications of decompenated cirrhosis portal hypertension such as ascites, hepatic encephalopathy, upper gastrointestinal variceal bleeding or the occurrence of hepatocellular carcinoma was compared between patients with and without resolved HBV infection.

Results: There were 25 patients (41.7%, 58.9 ± 11.3 yr) with resolved HBV infection and 35 patients (58.3%, 57.8 ± 11.5 yr) without resolved HBV infection. Complications of decompensated cirrhosis portal hypertension or the occurrence of HCC were more frequently occurred in PBC patients with resolved HBV infection than patients without resolved HBV infection (72% vs. 37.14%, P < 0.01).

Conclusion: Resolved HBV infection was common in Chinese PBC patients and may be related with much poor prognosis.

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PP-099 Hepatitis B surface antigen mutation Thr to Met at position 118 leads to antigenicity change and causes some blood screening kits failure

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Background: We found a new point mutation A to T in the HBSAg