Research Data Archive,Center for Disease Control, Department of Health, Taiwan, R.O.C.
Readme file
Project Title: Studies on chronic type B, C, D and novel viral hepatitis : molecular epidemiology, pathogenesis, natural history and treatment
Project Number: DOH93-DC-1028
Executing Institute: Hepatitis Research Center, National Taiwan University College of Medicine and National Taiwan University Hospital
Principal Investigator(P.I.): Ding-Shinn Chen
P.I. Position Title: Professor
P.I. Institute: National Taiwan University College of Medicine

Abstract:

I. Hepatitis B:

1. 13 patients with HBeAg-positive chronic hepatitis who had received short-term lamivudine therapy were enrolled. HBeAg loss or seroconversion occurred in 11, but 8 relapsed after stopping therapy and 5 had reversion of HBeAg. Before treatment, basal core promoter mutation was found in 1. In the first 3 months of therapy, a rapid decline of serum HBV DNA level accompanied with basal core promoter mutation appeared in 11 of 13 patients (vs. before therapy; P=0.003). However, this mutant was replaced by wild-type virus in 4 of 8 patients who relapsed after treatment. There was no significant change of precore sequences before and during therapy. Lamivudine therapy may result in the rapid development of basal core promoter mutation of HBV [Liver Int. 2004 Feb;24(1):9-15].
2. HBV genotype was determined in 40 HBsAg, anti-HCV, and anti-HDV co-positive intravenous drug users, and mixed HBV genotype B and HBV genotype C was found in 7. By direct sequencing of the pre-S region, we found that HBV/B is the dominant strain in HBV genotypes B and C co-infected intravenous drug users in Taiwan, and recombinations between different HBV genotype are not unusual. The impact of recombination on the evolution of HBV and their clinical significance remains to be studied [J Med Virol. 2004 May;73(1):13-22].
3. 62 patients with HBV-related HCC were tested for HBV genotype Concomitant cirrhosis was encountered more frequently in patients with genotype C. During a mean follow-up period of 26.3 months, patients with genotype B had a lower overall tumor recurrence rate than those with genotype C. Stepwise multiple Cox proportional hazards regression analysis showed that multiplicity of tumor was associated with tumor recurrence, whereas genotype C and age were associated with borderline significance. Our data suggest that patients with HCC with genotype C have a greater tumor recurrence rate after curative resection of HCC compared with those with genotype B [Clin Gastroenterol Hepatol. 2004 Jan;2(1):64-71].
4. HBV genotypes as well as mutations in the precore and basic core promoter regions were determined in 18 hepatitis B carriers with fulminant or subfulminant hepatitis. Eighteen age- and sex-matched patients with chronic active hepatitis B served as controls. The distribution of HBV

genotype and the prevalence of precore A1896 mutation in the fulminant and subfulminant hepatitis patients were similar to those in 18 control patients. Thus, the genomic variability of HBV does not seem to contribute to the fulminant and subfulminant exacerbation of chronic hepatitis B in Taiwanese HBV carriers [J Med Virol. 2004 Apr;72(4):545-50].

5. Hepatitis B virus genotypes and core promoter variant [Gastroenterology. 2004 Feb;126(2):633].
6. 146 Taiwanese adult HBeAg-positive hepatitis B carriers followed-up for a mean of 52 months were tested for HBV genotype. During the follow-up period, genotype C patients had a significantly lower rate of spontaneous HBeAg seroconversion than genotype B patients Spontaneous HBeAg seroconversion occurred one decade later in genotype C patients compared with genotype B patients. Multivariate analyses identified age < or =35 years, baseline serum alanine aminotransferase level and HBV genotype B as independent factors associated with spontaneous HBeAg seroconversion [Med Virol. 2004 Mar;72(3):363-9].
7. Clinical relevance of hepatitis B virus genotypes Ba and Bj in Taiwan [Gastroenterology. 2003 Dec;125(6):1916-7].
8. 5 HBeAg-positive HBV carriers who experienced transient seroconversion followed by seroreversion of HBeAg and 3 HBeAg-negative HBV carriers with documented reversion of HBeAg in a prospective cohort of 272 patients with chronic hepatitis B were identified. Our data suggested that HBeAg seroreversion might be due to the lack of sustained precore and BCP mutations after HBeAg seroconversion [J Med Virol. 2004 Oct;74(2):237-45].
9. The full-length viral genome and extent of quasispecies were obtained from serum and liver biopsy specimens at the same time from 9 subjects with hepatitis B exacerbation. Dominant viral strains for serial AEs in a single patient did not show a sequential evolution, but presented as a horizontal selection of a minor population from the original viral pool. Thus random reactivation of the original HBV pool, rather than a sequential evolution of one strain, also contributes to the onset of repeated AE [Hepatology. 2004 Aug;40(2):310-17].
10. Quantification and genotyping of hepatitis B virus in a single reaction by real-time PCR and melting curve analysis [J Hepatol. 2004 Oct;41(4):659-66].
11. HBV genotypes were determined in 325 HBV-infected intravenous drug users (IVDU) by using a newly developed line probe assay. The distribution of HBV genotype was as follows: genotype A alone in 2 (0.6%); genotype B alone in 256 (78.8%); genotype C alone in 10 (3.1%); mixed genotype A and B in 18 (5.5%); genotype B and C in 30 (9.2%); genotype B and D in 1 (0.3%); genotype A and C in 1 (0.3%); and mixed infections of genotype A, B, and C in 3 (0.9%). Clonal analysis confirmed further the existence of mixed genotype infection and recombination between different genotypes [Med Virol. 2004 Dec;74(4):536-42].
12. We prospectively analyzed 26 patients with chronic hepatitis B, who received at least 9 mo of lamivudine treatment. Our results suggest that end-of-treatment virologic response cannot predict post-treatment relapse in patients with HBeAg-negative or -positive chronic hepatitis B [World J

Gastroenterol. 2004 Dec 15;10(24):3574-8].

II. Hepatitis C:

1. Nucleotide sequences of the PKR-eIF2alpha phosphorylation homology domain (E2-PePHD) and PKR-binding domain (NS5A-PKR bd) of the HCV genome were analyzed in 30 HCV genotype 1b patients who had been treated with IFN and ribavirin. Our data showed that genetic heterogeneity in NS5A and E2-PePHD regions of the HCV genome may not serve as a predictor for treatment outcome with combination therapy in Taiwanese patients with chronic HCV genotype 1b infection.

Key words: Hepatitis B, hepatitis C, hepatitis D, SEN virus, molecular epidemiology, pathogenesis, natural history, treatment