

**Methods:** 78 chronic hepatitis B patients who were given telbivudine 600mg daily were divided in different groups according to the sex, age, HBeAg seroconversion, biochemical response and virological response. The rate and average of CK elevation were analyzed in these groups.

**Results:** CK elevation was observed in 61.54% patients (48/78), 69.12% in male (47/68), 10% in female (1/10), 46.15% in seroconversion group (6/13), 60.98% in SVR group (25/41). High CK elevation (3 times higher than average) was observed in 4 patients with kinetic intensity during the treatment.

**Conclusion:** Sex and seroconversion are the factors related to CK elevation during telbivudine treatment and the kinetic intensity is related to high CK elevation level.

**PP-099** Evaluating the immunogenicity of TGF- $\beta$ 1 antigen peptide coupled-KLH as anti-hepatic fibrosis vaccine

S.S. Dang<sup>1\*</sup>, Y.P. Li<sup>1</sup>, X.F. Wang<sup>1</sup>, W.J. Wang<sup>1</sup>, M. Li<sup>1</sup>, Y. Wang<sup>1</sup>. <sup>1</sup>The Department of Infectious Diseases, Second Affiliated Hospital of Medical School of Xi'an Jiaotong University, Xi'an, 710004, China

**Objective:** To lay a foundation for the further development of a novel vaccine based on TGF- $\beta$ 1, a pivotal cytokine, leading to hepatic fibrosis, we detected the neutralization activity and evaluated anti-liver fibrosis activity by keyhole limpet hemocyanin (KLH) coupled TGF- $\beta$ 1 domain antigen peptide vaccine.

**Methods:** Possible TGF- $\beta$ 1 domain B-cell epitope was predicted by bioinformatics, then KLH-coupled peptide was synthesized by the Fmoc method. Hepatic injury model rats were induced by CCl<sub>4</sub> for 10 weeks. 40 male SD rats were randomly divided into four groups: normal group (olive oil), adjuvant group (Freund's adjuvant), vaccine group (50  $\mu$ g TGF- $\beta$ 1 peptide vaccine+CCL<sub>4</sub>), model group (CCL<sub>4</sub>). Serum TGF- $\beta$ 1 antibody, HA, IV-C, ALT, AST, TBIL, ALB and GLB were detected; Levels of Hydroxyproline in hepatic tissue were measured and liver tissues were obtained for pathological observation.

**Results:** A certain amount of serum antibody was induced by TGF- $\beta$ 1 peptide vaccine in vaccine group, but no significantly different statistics were observed compared to other groups ( $P > 0.05$ ). The data showed high levels of ALT, TBIL, HA, IV-C and Hyp in both of model and vaccine groups compared with normal group respectively ( $P < 0.05$ ). The ALT, AST and TBIL levels in vaccine group were lower than model group ( $P < 0.05$ ), but HA, IV-C and Hyp content were no statistical significances ( $P > 0.05$ ). HE and VG staining showed different degree hepatic fibrosis in model and vaccine groups.

**Conclusions:** TGF- $\beta$ 1 peptide vaccine cannot remarkably stimulate antibody production, but the liver function of vaccine group can be mitigated to some extent.

**PP-100** Simulation of clinical data under the therapy of adefovir by mathematical model

L. Meng<sup>1</sup>, Y.M. Su<sup>1\*</sup>, L.Q. Min<sup>1</sup>. <sup>1</sup>University of Science and Technology Beijing, China

**Background:** Based on the existing model of virus infection, we bring up a new model which has logistic growth term and loss of free virus term caused by virus's entering uninfected cells. In this presentation, we do an individual simulation with the new model to test the consistency of clinical and simulation data.

**Methods:** The patient has received a 96 weeks therapy of Adefovir. The model was described with three variables:  $x, y, v$  and 7 parameters:  $\lambda, d, b, a, u, p, M, k$  where  $p, M$  represent uninfected cells' growth rate and environmental carrying capacity respectively and the other symbols have

the same meaning as those in the basic Nowak model. We chose  $\{\lambda, d, b, a, u, p, M, k\} = \{1.2067e+6, 0.0181, 0.1158, 0.0217, 0.1600, 0.0163, 6.6667e+012, 0.0140\}$ .

**Results:** The clinical data and simulation result are presented in Table 1.

**Conclusion:** The simulation data is relatively consistent with clinical data which means our model can capture the dynamic character of HBV virus to some extent.

**Acknowledgment:** This paper is jointly supported by the Fundamental Research Funds for the Central Universities (No 06108040) and the Key Special Project of China (No.2008ZX10502), the National 11-5 Scientific Technology Research Program of China.

Table 1: HBV DNA (log copies/ml)

Virus load/weeks	0	12	24	36	48	60	72	84	96
Clinical data	1.27e8	7.78e4	2.28e4	2.28e4	1.84e4	1.22e4	7.73e2	250	250
Simulation data	1.27e8	6.74e5	1.83e5	4.97e4	1.35e4	3.68e3	1.00e3	273.03	74.32

**PP-101** A dynamic model of entecavir therapy and after therapy for HBV Infection

X.J. Zhuo<sup>1\*</sup>. <sup>1</sup>School of Science, Beijing University of Posts and Telecommunications, China

**Background:** Entecavir (ETV) is believed to reduce covalently closed circular DNA. Leonieke et. al gave some patients' clinical data of 28 days' therapy of ETV and the data after withdraw of therapy. Leonieke et. al also simulated the data by bi-phasic model, but the bi-phasic model was only simplification of Nowak's basic model under some conditions. Based on Leonieke et. al's data and Nowak's model, we formulate a new dynamic model to simulate one patient's data during and after the ETV therapy.

**Methods:** A model of HBV is described by four variables:  $x, y, v, e$ , representing uninfected cells, infected cells, free virus, and immune cells. The model includes 10 parameters:  $l, d, b, a, p, k, u, k_2, k_3, k_4$  where the meanings of  $l, d, b, a, p, k, u$  are the same as those given in Nowak's model,  $k_2$  represents the curative effect,  $k_3, k_4$  are relevant to the immune.

We chose the following parameters during treatment:  $\{l, d, b, a, p, u, k, k_2, k_3, k_4, k_5\} = \{4.621e5, 6.9e-3, 2.19e-11, 7.3e-3, 1.5e-4, 0.45, 2.37, 2.18, 3e-8, 3.65e-10, 0.1154\}$ . When the therapy was stopped, we chose  $\{a, u, k_2\} = \{6.9e-3, 0.25, 0\}$  in which  $k_2=0$  implies no therapy effect,  $a, u$  becoming smaller means the die rate of infected cells and free virus decrease after treatment.

**Results:** Our dynamic model can simulate the patient's clinical data during the course of treatment and the rebound of HBV DNA after withdraw of therapy well.

**Conclusion:** The difference between the therapy and withdraw of therapy can be embodied by our model, which shows our model may possibly capture the dynamics of anti-HBV infection treatment with ETV.

**PP-102** A time-delay HBV therapy mathematical model for entecavir and adefovir

Y.M. Su<sup>1\*</sup>, L.Q. Min<sup>1</sup>. <sup>1</sup>School of Mathematics and Physics, University of Science and Technology Beijing, China

**Background:** Entecavir (ETV) and Adefovir dipivoxil (AD) are often used for HBV infection therapy. The use of Mathematical models to interpret the experimental and clinical data has made a significant contribution to anti-HBV infections. Based on Jurrien et al's experimental data with AD and ETV, considering the time delay of therapy effect and antiviral drug resistance, we set up a mathematical model with time delay to simulate the viral dynamics under the therapy of ETV and AD.