24. Standard curves for blood Interferon concentration were generated for given doses. Interferon levels were measured daily for 7 days in all patients using ELISA assay specific to used Interferon molecule.
Results: All samples were reactive with ELISA assay. Concentration and assay results correlated in a linearly manner. Standard curve was generated for each run of samples for all patients. Interferon level has been traced from 1st to 7th day.
There was significant inter-patient variation in levels of detectable interferon for both responders and non-responders. In all 7 cases with sustained viral response, interferon levels were low or undetectable in days 6 and 7. Even one patient whose interferon level was traced in the 4th day was also a responder. There is no significant difference between responders and non-responders either in daily median concentration through-out the 7 days, nor in the association of viral load or genotype to interferon concentration with viral clearance.
Conclusion: Tracing of single dose Reiferon Retard® demonstrated detectable interferon levels up to 7 days. Although interferon levels were low or undetectable in 7 out of 14 cases at days 6 and 7, sustained viral response was achieved in all cases. Suggested explanation: interferon attaches to cell receptors by PEG molecule and acts on cellular level till next dose is received. There might be other host factors predicting interferon response other than pharmacokinetics of PEG interferon.

PP-142 Prevalence and risk factors for hepatitis C virus infection in the rural area of Jilin China: A cross-sectional population-based survey

J. Jiang[1]*, Y. Pan[2], Z.F. Jia[1], X.M. Chi[2], M.L. Wang[2], P. Zhang[2]. *[1]1. Department of Clinical Epidemiology, First Hospital of Jilin University, Changchun, China, [2]Department of Hepatology, First Hospital of Jilin University, Changchun, China*

Background: Despite the fact that hepatitis C virus (HCV) is a common infection in China, there is little information on prevalence rates, particularly in the rural area of Jilin province. Blood transfusions and more intravenous drug used are risk factors of spreading the virus. In order to investigate HCV infection status and related factors associated with HCV infections among rural people in Jilin province, a cross-sectional population-based survey was conducted.
Methods: Blood samples from 2,849 subjects were analyzed for Anti-HCV, hematological, blood chemistry and HCV-RNA tests. A standardized questionnaire concerning the socio-demographic characteristics and potential risk factors was carried out.
Results: The HCV infection was detected in 33.2% (947/2849) of subjects at this survey. HCV RNA were detected in 873 HCV-infected individuals, 18.8% (164) of HCV-infected individuals has a spontaneous clearance of virus infection. 57.7% (409/709) of HCV-infected individuals were detected to have high-levels of the viral load (>400000 IU/μl). HCV genotypes of 252 samples were examined, 142 (56.3%) individuals had the infection of subtype 1b; 101 (40.1%) had subtype 2a; 9 (3.6%) had a co-infection of subtype 1b/2a. Multivariate analyses revealed that risk factors related to HCV infection were unsafe injections (OR: 11.7; 95%CI: 5.6–24.2), caffeine-sodium benzoate injections (OR: 7.1; 95%CI: 4.4–11.3), age (⩾40years, OR: 5.8; 95%CI: 3.9–8.1) and sex (in male, OR: 1.8; 95%CI: 1.5–2.2).
Conclusion: The most common source of HCV spreading was a caffeine-sodium benzoate injection. Subtype 1b and 2a are predominant HCV genotypes in the area of Jilin province. Public health measures should be taken to reduce the abuse of intravenous injections and exposure of unsafe injections.

PP-143 Hepatitis C virus genotype and subtype distribution in China

W. Ju[1]*, S. Yang[1], Q. Wang[1], H.C. Xing[1], W. Xie[1], Y. Xie[1], J. Cheng[1]. *[1]Beijing Ditan Hospital, Capital Medical University, China*

Background: Hepatitis C virus (HCV) heterogeneity accounts for the lack of successful anti-viral therapy in some patients. The object of this study is to determine HCV genotype and subtype distribution in China mainland.
Methods: A total of 788 HCV RNA positive serum samples were collected from chronic HCV infected patients from 14 geographic areas in China during 2009.10–2011.4. Nucleotide sequence analysis of the NS5B and/or CORE-E1 regions of the HCV genome was performed on samples. Phylogenetic analysis was used for analysis of HCV genotype and subtype.
Result: HCV genotype was determined in 747 samples [94.80% (747/788)]. Genotype 1, 2, 3 and 6 were detected, at frequencies of 73.49%, 18.88%, 4.95% and 2.68%, respectively. No genotype 4 and 5 strains were found. We detected subtypes 1b, 2a, 3a, 6a, 3b, 6n, and 1a at frequencies of 73.09%, 18.88%, 3.21%, 2.14%, 1.74%, 0.54%, and 0.40%, respectively. Subtype 1b was the most predominant [73.09% (546/747)] followed by 2a [18.88% (141/747)].
Conclusion: This study demonstrated a genetic heterogeneity of HCV infection in China, with at least four HCV genotypes and seven subtypes. Clinical trials of direct anti-HCV agents should consider this genetic heterogeneity.

PP-144 NS5ATP9 contributes to inhibition of cell proliferation by NS5A

Q. Wang[1]*, X.S. Gao[1], Y. Li[2], W. Li[1], Q. Yang[1], J. Cheng[1]. *[1]Department of Infection Disease, Beijing Ditan Hospital, Capital Medical University, [2]Beijing Center for Physical and Chemical Analysis, China*

HCV NS5A is a remarkable protein as it clearly plays multiple roles in mediating viral replication, host-cell interactions, and viral pathogenesis. But on the impact of cell growth, there were different study results. NS5ATP9, also known as $p15^{PAF}$, L5, OEACT-1, and KIAA0101, was first identified as a proliferating cell nuclear antigen-binding protein. Earlier studies have shown that it might play an important role in HCV infection. In the present study, we showed that overexpression of NS5ATP9 inhibited the proliferation of HCC cells, whereas knockdown of NS5ATP9 by interfering RNA (RNAi) promoted the growth of HCC cells. Under conditions of NS5A overexpression, RNAi targeting of NS5ATP9 could reverse the inhibition of HCC cell proliferation by NS5A, suggesting that NS5ATP9 could be an anti-oncogene that plays an important role in the suppression of cell growth mediated by HCV NS5A via MEK/ERK signal pathway. These findings may provide new insight into the NS5A and NS5ATP9.

PP-145 BST2/Tetherin inhibits hepatitis C virus release from human hepatoma cells

X.B. Pan[1], J.H. Chang[2], T.M. Block[2], J.-T. Guo[2]. *[1]Peking University People's Hospital, Peking University Hepatology Institute, [2]Drexel Institute for Biotechnology and Virology Research, China*

Background: Hepatitis C virus (HCV) infection is a common cause of chronic hepatitis and is currently treated with