mal control group and HCV-related chronic hepatitis regarding the HGFA H-score and TGF-β1 H-score.
Conclusions: Parallel expression of HGFA and TGF-β1 with the grade of activity and stage of fibrosis in HCV-related chronic hepatitis could make HGFA as an activity and regenerative marker.

PP-138 Screening and cloning of gene of hepatocyte protein interacting with HCV NS5ATP4A protein

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Objective: We screen proteins of hepatocyte protein interacting with hepatitis C virus NS5ATP4A protein to clarify the signal transduction pathway of HCV.
Methods: "Bait" plasmids of hepatitis C virus NS5ATP4A were constructed. After verifying that hepatitis C virus NS5ATP4A protein could be steadily expressed in AH109 yeast strain, yeast-two hybrid assay was performed by mating AH109 with Y187 that pre-transformed with liver cDNA library plasmids pACT2, and the diploidy yeast cells were plated on quadruple dropout (QDO) medium and assayed for X-α-gal activity. Nineteen yeast colonies that could grow on QDO and hadα-gal activity were obtained, then the library plasmids were extracted and sequenced.
Results: 7 genes were screened out and one of them was unknown gene. These genes were associated RNA synthesis, protein translation, cell cycle and tumor immune.
Conclusion: NS5ATP4 binding proteins were successfully screened,which offer new clues to the signal transduction pathway of NS5ATP4A and the pathogenic mechanism of HCV.

PP-139 The evaluation of the hepatic fibrosis and its progression rate in chronic hepatitis C

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Aim: The evaluation of fibrosis through Ishak and Metavir scoring systems and it's progression rate.
Methods: We studied 242 naïve patients with chronic hepatitis C, admitted between 2003 and 2006, who performed liver biopsy for diagnosis, being evaluated according two scoring systems.
The evaluation of the fibrosis progression rate was performed only in 55 patients with a previous history of transfusions, using the ratio between the fibrosis stage and the estimated infection duration (years).
Results: The mild and moderate fibrosis lesions predominated, with a concordance between the scoring systems.
The mean fibrosis index was significantly larger in patients with moderate/severe necroinflamatory lesions, irrespective of the normal or increased AST or ALT levels.
The mean fibrosis progression rate of 0.23±0.34 units/year according to the Metavir system, and 0.32±0.51 units/year - Ishak system.
The age at the time of infection and it's estimated duration correlate with the Metavir fibrosis progression rate (p =0.000, respectively p =0.001). The patients who have been infected before the age of 40 and those with a duration of infection of less than 20 years have a significantly lower mean fibrosis progression rate.
Conclusions: 1. The mild and moderate fibrosis predominated, with equivalent results between the two scoring systems.
2. The severity of fibrosis correlated with the age and the increased AST or ALT levels.
3. The mean fibrosis progression rate was 0.23±0.34 units/year in the Metavir system, respectively 0.31±0.51 units/year in Ishak, being correlated with the age at the moment of infection and it's estimated duration of evolution.

PP-140 The occult HCV infection

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Aim: evaluating the presence and localisation of the HCV antigens (NS3, NS5, NS5A) in patients with chronic hepatitis C and undetectable versus detectable serum HCV-RNA.
Methods: 93 patients with chronic hepatitis C were included in the study, 55 with detectable viremia. Using immunohistochemical techniques involving monoclonal and policlonal antibodies, we analysed the presence, localisation and semiquantitative grading of coloured cells.
Results: All untreated patients with detectable viremia presented hepatocyte expression of viral proteins, especially in the hepatocyte cytoplasm and less in the nucleus. The untreated subjects with undetectable viremia had similar detection rate as the untreated patients with detectable viremia, 92.3% respectively 92.4% and 84.61% for NS3, NS5, NS5A.
In treated patients with undetectable viremia, the proportion of positive results were comparable for NS3 (92%) but lower for NS5 and NS5A (80% and 60%). The positive immunohistochemical reaction was observed in fewer hepatocytes (< 30%), with focal lobular distribution and mild/moderate intensity in treated subjects with undetectable viremia, respectively moderate/important in the rest of patients.
The patients with undetectable viremia were found to have correlationships between the presence of NS3 and NS5 antigens and the fibrosis level. The presence of steatosis correlated with NS3 and NS5 only in untreated patients with undetectable viremia.
The portal space involvement was observed especially at macrophages.
Conclusions: Identifying the presence of viral antigens in the liver tissue in patients with undetectable viremia, who have either received antiviral therapy or not, can bring into discussion the occult HCV infection.

PP-141 Predicting treatment response in hepatitis C virus infected patients: from gene to protein expression

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Objectives: Chronic hepatitis C virus (CHC) infection is treated with interferon/ribavirin, but only a subset of patients respond. We previously reported that treatment nonresponders have marked pre-treatment upregulation of a subset of interferon stimulated genes (ISGs) in their livers, including ISG15 (*Chen, et al*. Gastroenterology 2005). Here, we study the source of the ISG expression signature and uncover the cellular basis of the phenotype through ISG15 and MxA protein expression.
Methods: ISG15 and MxA immunohistochemistry was performed on a subset of 31 liver biopsies and the expression pattern was correlated with response status.
Results: Using a simple histology scale scored from 0 to 3 (0: no staining in any cell, 3: staining in every cell), we found significantly more hepatocyte ISG15 expression in treatment non-responders versus responders (2.4±0.6 *vs* 1.1±0.6, p<0.0001), but less macrophage ISG15 staining (0.2±0.4 *vs* 0.8±0.6, p<0.005). MxA protein expression had a similar cell-specific pattern of expression. Treatment response was linked to cell-specific activation patterns: ISG15 and MxA protein upregulation was more pronounced in hepatocytes in treatment nonresponders, but in Kuppfer cells in responders.
Conclusions: Our previously defined differential gene expression pattern in the livers of HCV responders and nonresponders is driven by activation of different cell types: hepatocytes in treatment nonresponders, and macrophages in treatment responders.