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ABSTRACTS

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PO-C-01

Post-treatment wisteria floribunda agglutinin-positive Mac-2-binding protein combined with platelet predict hepatocellular carcinoma development in chronic hepatitis C patients

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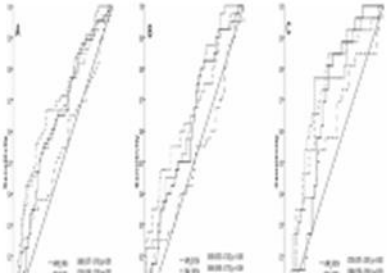
Background: Wisteria floribunda agglutinin-positive Mac-2-binding protein (WFA+-M2BP) is a novel marker for liver fibrosis assessment. We aimed to predict the hepatocellular carcinoma (HCC) occurrence after antiviral therapy in Taiwanese patients with chronic hepatitis C (CHC) using WFA+-M2BP.
Method: Seventy patients with HCC and another 140 age, gender,

Conclusion: Post-treatment WFA+-M2BP, especially combined with platelet, predict HCC development in Taiwanese CHC patients after antiviral therapy.



virological breakthrough and compound mutations to HBV polymerase gene, and genotypic resistance confirmed in 18 patients. 1 patient achieved HBsAg loss at week 84 and HBsAg seroconversion at week 96. For early responders, 92.9% achieved undetectable HBV DNA at week 96, compared with 58.6% in suboptimal responders (P=0.0001),while HBeAg loss/seroconversion rate were comparable(24.3% vs. 10.3%, P>0.05; 12.9% vs. 6.9%, P>0.05). LdT was well tolerated in most patients, no myopathy, myositis or rhabdomyolysis occurred. At week 96, eGFR level increased by 3.3 ml/min/1.73 m^2 versus baseline (from 99.6 to 102.9). For patients with normal eGFR level at baseline (eGFR≥90 ml/min/1.73 m^2), no obvious change occured at Week 96 (P=0.2684). For patients with low baseline eGFR level (eGFR<90 ml/min/1.73 m^2), eGFR increased by 9.6 ml/min/1.73 m^2, (from 82.6±5.9 to 92.2±10.8, P=0.0007). 50.0% (11/22) patients with low baseline eGFR had normal eGFR at Week 96.

Conclusion: In HBeAg-positive cirrhosis patients, LdT optimization strategy was effective and well tolerated. Comparing to suboptimal responders, early responder can achieve better virological response. Patients with low baseline eGFR level got obvious eGFR improvement after LdT optimization treatment.

HBV-C17

Fibrosis-4 index predicts cirrhosis risk and liver-related mortality in patients with chronic HBV infection

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HBV-C18

Association between IFN-gamma+874 polymorphisms and hepatitis C virus infection

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Background: Genetic polymorphisms in cytokines have been shown to affect HCV infection. The aim of the study was to evaluate the association between the gene polymorphisms in interferon gamma (IFN-γ) gene and chronic hepatitis C virus (HCV) infection among our patients.

Method: IFN-γ +874 T/A genotypes were determined in 79 chronic HCV patients and 48 healthy controls using Real-Time Polymerase Chain Reaction (RT-PCR) from the DNAs. Genomic DNA was isolated using DNA isolation kit (Roche, Switzerland).

Result: In patients and control groups IFN-γ +874 TT, TA, AA genotypes were detected 27 (31,4%), 34 (%39,5), 25 (%29,1) and 11 (22,9%), 18 (%37,5), 19 (%39,6) respectively. Although there is no statistical significant was observed, in patient group TT and TA genotype's ratio were higher than control group (p=0.396). When the distribution of allele frequencies of IFN-γ +874 T/A polymorphism was evaluated in the patients and control groups, the ratio of T alleles

in patient population was higher than control group (51,8% 41,7% respectively), but it was not statistically significant (p=0.136).

Conclusion: As a result IFN-γ +874 T/A polymorphisms had not a strong association with susceptibility to HCV infection. But studies with larger patient populations can help to demonstration of relationship with polymorphisms in interferon gamma (IFN-γ) gene and chronic hepatitis C.

HBV-C19

HBV-C20

Prognostic value as to 3-month mortality of neutrophil-to-lymphocyte ratio, lymphocyte-to-monocyte ratio and NLR and LMR ratio among patients with decompensated liver cirrhosis secondary to hepatitis B

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