J Cancer Sci Ther 2013, 5:10
http://dx.doi.org/10.4172/1948-5956.S1.030

OMICS Group Conferences
Accelerating Scientific Discovery

3rd World Congress on
Cancer Science & Therapy

October 21-23, 2013 DoubleTree by Hilton Hotel San Francisco Airport, CA, USA

Insufficiency of peripheral blood as a substitute tissue for detecting EGFR mutations in lung cancer: A meta-analysis

Yongjun Zhang, Zhijun Li, Wenlong Bao, Hua Shi and Chuming Jiang
Zhejiang Cancer Hospital, China

Aim: Detection of epidermal growth factor receptor (EGFR) mutations in non-small cell lung cancer tissues is necessary for effective treatment with EGFR tyrosine kinase inhibitors. However, tumor tissue may not be available in all situations. Studies have evaluated the potential use of serum or plasma for detecting the EGFR mutation status, but the results have been inconclusive. Here, a meta-analysis was performed to determine whether blood samples could serve as substitutes for tissue specimens in detecting the EGFR mutation status.

Methods: Databases, including PubMed and Embase, were searched for relevant studies published from 2005 to 2013 that included true-positive, false-positive, true-negative, and false-negative values of the EGFR mutation status of the blood compared with tissue specimens. Summary receiver operating characteristic curves were developed to explore the threshold effect. Spearman's correlation coefficient was calculated to analyze the heterogeneity between studies. Pooled sensitivity and specificity were evaluated using Meta-Disc version 1.4.

Results: Thirteen articles involving 1591 cases were enrolled, with a pooled sensitivity and specificity of 64.5% (95% CI: 0.605-0.683) and 88.5% (95% CI: 0.863-0.904), respectively. Heterogeneity among the studies was caused by factors other than threshold effect. The findings were influenced by test method (p = 0.0354).

Conclusion: Blood samples had a high specificity and relatively low sensitivity for detecting EGFR mutations compared to tumor tissues. The results of this meta-analysis suggest that peripheral blood is insufficient as a substitute for tumor tissue in detecting EGFR mutations in clinical practice.

zhangyongjun770323@163.com

MAGE-4 gene m-RNA and TGF in blood as potential biochemical markers for HCC in HCV-infected patients

Yousri M. Hussein, Fouad E. Morad, Magda A. Gameel, Wafaa A. Emam, Wael H. El Sawy, Shereen A. El Tarhouny Eman S. Bayomy and Nermin Raafat
Anhui Provincial Hospital, Anhui Medical University, P. R. China

Progression from chronic hepatitis C virus infection to cirrhosis then to hepatocellular carcinoma usually results in some protein changes in peripheral blood. We evaluated MAGE-4 mRNA, TGFb1 and AFP in peripheral blood as potential biochemical markers for diagnosis and prognosis of some complications of HCV infection. MAGE-4 mRNA in blood by reverse transcription polymerase chain reaction, serum TGF-B1 and AFP by ELISA was assayed in seventy-five individuals who were classified into five groups: group I (control) comprised fifteen apparently healthy volunteers, group II involved fifteen HCV-infected patients without cirrhosis, group III involved fifteen HCV fifteen HCV-infected patients with cirrhosis, group IV included fifteen HCV-infected patients with cirrhosis and early stage HCC, and group V included fifteen HCV cirrhotic patients and late-stage HCC. We found that the frequency of positivity of MAGE-4 among the late hepatoma group was 40 %, while in the early hepatoma group, the positivity was 6.7 %. The results for TGF-B1 revealed a significant increase in serum TGF-B1 in groups IV and V as compared to control, II, and III groups. The obtained results of AFP showed a significant positive increase in serum AFP in groups IV and V when compared to groups II and III. Detection of MAGE-4 transcripts in blood, especially with follow-up survey, may help to predict the prognosis and monitoring of the response to the therapy, and serum TGFB1 level in HCC patients is directly correlated with metastasis and recurrence of tumors and increases gradually with the progression of HCC.