Genetic signatures provide new direction in liver cancer

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Results of an international clinical study conducted in Europe and the US presented today at the International Liver Congress 2010, the Annual Meeting of the European Association for the Study of Liver in Vienna, Austria, have identified a genomic portrait able to predict recurrence in hepatocellular carcinoma (HCC), the fifth most common cancer in men .

HCC is a primary cancer of the liver. Worldwide, it accounts for approximately 5.4% of all cancers1 and it is the third cause of cancer-related death with more than 660,000 deaths per year1. Only around 20-30% of patients are treated with curative treatments, including resection and local ablation, but recurrence complicated the outcome in more than two thirds of these cases .

Results of this study identified two gene signatures- one coming from the tumor and the other from the cirrhotic liver - able to identify patients with poor disease outcome. The study concluded that these genetic tools can ultimately be used to select patients for preventive therapies. In addition, specific genes included in these signatures should be evaluated as potential targets for adjuvant treatment, following surgical intervention in HCC patients.

Dr Josep Llovet, Professor from the Hospital Clinic of Barcelona-IDIBAPS and Mount Sinai School of Medicine in New York, who led the study and highlighted this topic at EASL's official press conference said, "The results of our study demonstrate the potential that molecular classification offers to future clinical management of diseases such as

HCC. By successfully identifying certain genomic signatures that clearly predict both overall and early recurrence of HCC post-surgery, we now have a clearer focus for future research into therapeutic options that may in time improve patients' chances of survival".

The study was presented at EASL by Augusto Villanueva, MD member of the International HCC Genomic Consortium. The genomic profiles of 287 HCC patients using whole-genome gene expression platforms were analysed. The study focussed on patients with early HCC (n=257, principally male 189/257, with a mean age of 64) with tumoral tissue (n=257) and adjacent non-tumoural cirrhotic tissue (n=209). Patients were on average followed up after 46 months - there were 167 recurrences (64%) and 89 deaths (34%). In total, 20 gene signatures were evaluated with reported ability to predict survival and or recurrence of HCC. Genomic signatures from the tumour (Proliferation-G3) and adjacent tissue (with poor prognosis) of patients with HCC were identified as important in predicting both overall and early recurrence in HCC. The multinodularity gene signature was also identified as a predictor for HCC recurrence while tumor size was identified as predictor for early recurrence.

More information: References:

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