

Gene-expression signatures that identify cirrhosis patients “at risk” for liver cancer and predict the probability of HCC recurrence following early-stage diagnosis and resection.

Context

The ability to personalize cancer treatment could both maximize the survival rate and alleviate undue suffering due to ineffective treatment. More effective and personalized treatment regimes would also allow health care systems to allocate resources appropriately. Knowing an individual’s susceptibility to cancer recurrence in advance could lead to significant health gains as well as lower health costs. There is an urgent need to (1) identify “at risk” patients, and (2) sort out those patients with the greatest risk of experiencing cancer recurrence after “standard of care” chemotherapy so that appropriate treatment decisions can be made. Gene-expression profiling of cancer is an effective method to do such “sorting.”

Liver cancer is the sixth most common cancer in the world and recurrence occurs in more than 70% of patients. More than 600,000 new cases of liver cancer are diagnosed worldwide each year (NCI SEER Study 2008).

Invention

Scientists in the Golub lab discovered and validated two different gene expression signatures that predict either a poor survival outcome (73 gene signature) or good survival outcome (113 gene signature) in early stage hepatocellular cancer (“HCC”) (liver cancer) patients.

Potential

The gene signature described here “bring[s] the possibility of individualized therapy for hepatocellular carcinoma one step closer.”
New England Journal of Medicine editorial, Nov. 6, 2008

→ Identify “At Risk” Cirrhosis Patients

The two signatures could be used to identify those cirrhosis patients most at risk of developing liver cancer. Individual treatment plans could then be developed for such patients to maximize survival.

→ Predict Recurrence

With the appropriate treatment, five-year survival rates of as high as ninety percent (90%) have been reported. This gene signature will allow physicians to identify those liver cancer patients who are at the greatest risk of recurrence and screen these patients more regularly or more intensively for new tumors.

→ More Effective Treatment Plan Upon Diagnosis

Physicians could be empowered to determine which patients would benefit from adjuvant chemotherapy and which patients would derive no value from additional treatment. Individualized HCC treatment plans could then be developed based on the signatures.

→ More Focused & Less Expensive Clinical Trials

Incorporating the two gene expression signatures into clinical trials for new liver cancer treatments could make the clinical trial process more precise, more efficient and less costly. The signatures could also be used as a baseline to monitor and predict the success of experimental treatments.

→ Diagnostic Kit

The signatures can be easily assayed using current technologies, hence their development into a standard diagnostic tool could become an important element of standard medical care.

Published reference



The NEW ENGLAND
JOURNAL of MEDICINE

Hoshida, Y., *et al.*, Gene Expression in Fixed Tissues and Outcome in Hepatocellular Carcinoma, *N Engl J Med* 2008; 359:1995-2004.

<http://content.nejm.org/cgi/content/full/NEJMoa0804525>

