GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Aberrant gene expression profiles in hepatocellular carcinoma detected by microdissection

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Genet. Mol. Res. 12 (4): 5527-5536 (2013)
Received August 30, 2012
Accepted January 22, 2013
Published November 18, 2013
DOI http://dx.doi.org/10.4238/2013.November.18.3

ABSTRACT. The aim of this study was to identify genomic aberrations in hepatocellular carcinoma (HCC) by using laser capture microdissection (LCM) combined with microarray analysis. Samples were procured by LCM from HCC and patient-matched normal liver tissue surgically resected from 4 patients. RNA was isolated from the samples and reverse transcribed into cDNA. After 2-cycle linear amplification and 2-color fluorescent labeling, the cRNA was hybridized onto a whole genome microarray. All genes expressed in the normal and HCC samples were counted and analyzed. Differentially expressed genes were identified and the top 10 up and downregulated genes (totally 20 genes) were further evaluated. LCM was able to accurately capture 50-200 cells from HCC and control tissues. The microarray spectrum showed satisfactory detection of HCC-enriched genes. A total of 1361 differentially expressed genes were identified, among which, 607 were upregulated and 754 were downregulated. Among the top 20 up and downregulated genes, 4 genes had not been documented in the literature as being differentially expressed in any tumors. Thus, LCM

is an effective approach for identifying aberrantly expressed genes in HCC, and may lead to the discovery of biomarkers for diagnostic and therapeutic applications.

Key words: Laser capture microdissection; Hepatocellular carcinoma; Microarray; Gene expression

