



Gene expression profiles in liver cancer and normal liver tissues

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Abstract

AIM: To describe a liver cancer = specific gene expression profile and to identify genes that showed altered expression between liver cancer tissues and their adjacent nearly normal tissues.

METHODS: The cDNA probes which were labeled with α -³²P dATP were synthesized from total RNA of liver cancer and adjacent normal tissues and hybridized separately to two identical Atlas human cancer cDNA expression array membranes containing 588 known genes.

RESULTS: Autoradiographic results were analyzed by specific Atlas Image TM (version 1.0) software. Among the 588 genes analyzed, 18 genes were found up-regulated in cancer, including *TFDP2*, *Akt1*, *E2F-3* etc, and 25 genes were down-regulated in cancer, including *TDGF1*, *BAK*, *LAR*, etc. Expression levels of genes that associated with the regulation of cell proliferation, apoptosis, differentiation, cell-cell interaction, invasion regulators and cytokines altered mostly.

CONCLUSION: The result obtained from Atlas microarray provides a comprehensive liver cancer specific expression profile. The results can lead to the identification of liver cancer-specific biomarkers and may be helpful in early diagnosis and identification of target genes for designing rational therapeutic strategies.

Key words: Liver neoplasms/diagnosis; Gene expression; Differential hybridization; Microarray

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