Genomics of liver cells and liver cancer cells

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2001 Fiscal Year Final Research Report Summary

Genomics of liver cells anォ liver cancer cells

Research Project

Project/Area Number	11307010
Research Category	Grant-in-Aid for Scientific Research (A)
Allocation Type	Single-year Grants
Section	一般
Research Field	Gastroenterology
Research Institution	Kanazawa University
Principal Investigator	**KOBAYASHI Kenichi** Medical school, Kanazawa University Professor, 大学院・医学系研究科, 教授 (70019933)
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Project Period (FY)	**1999 – 2001**
Keywords	hepatocellularcarcinoma / Genomics / SAGE / DNAmicroarray / geneexpressionprofile / clusteranalysis
Research Abstract	Gene expression profile of normal liver, liver tissue from chronic hepatitis C (CH-C) and liver cancer (HCC) were analyzed by SAGE (serial analysis of gene expression) method. Total of 30,982 sequence tags were separated from normal tissue, in which 8,596 tags were derived from unique genes. The genes highly expressed in the normal liver were those encoding plasma proteins (>21.8% of total transcripts), cytoplasmic proteins (>8.6%), enzymes (>4.8%), protease inhibitors (>1.7%), complements (>1.1!%), and coagulation factors (>0.75%). About 13.9% of all transcripts encoded genes not reported in GenBank thus far. Tags from the HCC library exhibited the existence of many differentially expressed genes compared with those from the CH-C and NL libraries. Up-regulation of IFN-gamma inducible genes and oxidative stress-inducible genes were identified in both the CH-C and HCC libraries, and some unpublished new genes were specifically up- or down-regulated in the HCC library. DNA micro array containing 1,080 genes covering various categories of genes including oncogenes, tumor suppressor genes, apoptosis related genes, cell cycle related genes were originally developed. Hierarchical clustering analysis of the gene expression profiles showed that Hepatitis B and C virus infection, but not age, sex, or histology of hepatitis, were significant factors determining clustering (P 0.05). In hepatitis B tissue lesions, genes involved in inflammation were predominant, whereas in hepatitis C, expression of anti-inflammatory response genes was relatively dominant. In addition, clustering analysis of DNA micro array data showed that tumor marker alpha-fetoprotein producing hepatoma cell lines shares common expression profile of genes in various categories. Analysis of gene expression profile of HCC tissues showed that some genes had characteristic gene expression pattern according to tumor differentiation.

Research Products (10 results)

All | Other

All | Publications

[Publications] Yamashita T et al.: "Serial analysis of gene expression in chronic hepatitis C and hepatocellular carcinoma"BBRC. 282. 647-654 (2001) ⌄

[Publications] Yamashita T et al.: "Comprehensive gene expression profile of a normal human liver"BBRC. 269. 110-116 (2000) ⌄

[Publications] Honda M et al.: "Differential gene expression between chronic hepatitis B and C hepatic lesion"Gastroenterology. 120. 955-966 (2001) ⌄

[Publications] Kawai H et al.: "α-fetoprotein-producing hepatoma cell lines share common expression profile of genes in various categories demonstrated by cDNA microarray analysis"Hepatology. 33・3. 676-691 (2001) ⌄

[Publications] Shirota Y et al.: "Identification of differential expressed genes in hepatocellular carcinoma with cDNA microarrays"Hepatology. 33・4. 832-840 (2001) ⌄

[Publications] Yamashita T, Hashimoto S, Kaneko S, Nagai S, Toyoda N, Suzuki f, Kobayashi K, et al: "Comprehensive gene expression profile of a normal human liver"Biochem Biophys Res Commun. 269. 110-6 (2000) ⌄

[Publications] Yamashita T, Kaneko S, Hashimoto S, Sato T, Nagai S, Toyoda N, Suzuki T, et al: "Serial analysis of gene expression in chronic hepatitis C and hepatocellular carcinoma"Biochem Biophys Res Commun. 282. 647-54 (2001) ⌄

[Publications] Honda M, Kaneko S, Kawai H, Shirota Y, Kobayashi K: "Differential gene expression between chronic hepatitis B and C hepatic lesion"Gastroenterology. 120. 955-66 (2001) ⌄

[Publications] Kawai HF, Kaneko S, Honda M, Shirota Y, Kobayashi K: "alpha-fetoprotein-producing hepatoma cell lines share common expression profiles of genes in various categories demonstrated by cDNA micro array analysis"Hepatology. 33. 676-91 (2001) ⌄

[Publications] Shirota Y, Kaneko S, Honda M, Kawai HF, Kobayashi K.: "Identification of differentially expressed genes in hepatocellular carcinoma with cDNA micro arrays"Hepatology. 33. 832-40 (2001) ⌄