Korean UniGene Collection for Cancer Genome Study of Human Stomach and Liver Tumors

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To explore the expression profile of the human cancer genomes and to provide a resource for DNA microarray studies, Korean UniGene Collection Project (KUCP) has been performed on cDNA libraries constructed from tissues and cell lines of human stomach and liver. In total, we have constructed 70 cDNA libraries including full-length enriched cDNA libraries using the capping method. To date, About 153,785 sequences were obtained through large-scale single-pass sequencing from randomly picked cDNA clones and sequence analysis was performed using bioinformatics tools. Results concerning about systematic analysis and functional classification of genes expressed in the stomach and liver cancer will be presented. For the functional study of cDNA, we have constructed the high-throughput expression system of collected full-length cDNAs using GATEWAYTM cloning system, which provides universal protein expression from E. coli to mammalian cell. These results obtained from this project will be useful to elucidate the genetic events associated with stomach and liver tumorigenesis. The pools of rearray-clone of UniGene and full-length cDNA are now available as common resources for functional study. This work was fully supported as one of Functional Study of Human Genome of 21C Frontier R&D programs funded by Ministry of Science and Technology, Korea.

Molecular dissection of multistep hepatocellular carcinogenesis model using spotted oligonucleotide microarray

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Because 90% or more of hepatocellular carcinoma (HCC) occur in cirrhotic livers, it is possible that certain cirrhotic nodules could become preneoplastic. The mere fact that some cirrhotic nodules may outgrow others in the same liver has been recognized for decades. The lesion referred to as the dysplastic nodule (DN) or adenomatous hyperplasia which has further defined "low-grade" and "high grade" DN in 1995 by an international working party. From this point of view, formation of DN in cirrhotic liver might be first step of hepatocarcinogenesis, with subsequent development into overt HCC nodule through low-grade DN, high-grade DN and early HCC in a multistep fashion. However, the molecular mechanisms implicated in this progression remain unknown. On the other hands, DNA microarray technology enables investigators to obtain comprehensive data with respect to gene-expression profiles and have already demonstrated the usefulness of this technique for identifying novel cancer-related genes and for classifying human cancer at the molecular level in several studies. We have performed gene expression analysis on 51 cases of hepatic tumor with 6 different histological grades including LGDN (10), HGDN (10), early HCC (1), HCC Edmondson grade I (10), grade II (10), and grade III (10) through the use of a genome-wide oligonucleotide microarray containing 18,912 genes.