S1-01

Gene expression profile analysis of squamous cell carcinoma

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Lung cancer is the leading cause of cancer death world-widely. Histological subtypes of lung cancer are distinguished by tumor morphology under the light microscope. Lung cancers are classified into small cell lung cancer and non-small cell lung cancer, and the latter is sub-divided into squamous cell carcinoma, adenocarcinoma, and large call carcinoma. Squamous cell carcinoma (SCC) accounts for roughly 30% of all lung cancers. SCC is thought to derive mainly from epithelial cells lining the larger airways and closely associated with tobacco smoking. We have examined the gene expression profiles of some sixty SCC samples and their normal counterparts with cDNA microarray. Gene expression patterns of SCC samples were distinct from that of normal samples. SCC-specific signature genes were isolated by class comparison analysis. Using the information from Gene Ontology Consortium, biological processes associated with the signature genes were identified. Interesting functional categories were found to be significantly associated with the signature genes. The functions of the genes in relation to the carcinogenesis are under investigation.

S1-02

Multi-Purpose Expression System for High-Throughput Cancer Genome Study of Human Stomach and Liver Tumors

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To validate the cellular function of candidate genes that are related to gastric and liver cancers, the material resources such as multi-purpose expression clones, purified proteins as well as monoclonal antibodies for candidate genes are necessary. The first step for production of these materials is construction of the multi-purpose expression clones of candidate genes based on high-throughput system (HTS). To date, about 2,500 candidate genes were isolated by the frequency analysis of cDNA or analysis of proteom expressed in gastric and liver cancers, and the analysis of the expression profiling of the genes using high-density cDNA chip. Among them, 3,000 expression clones for about 500 candidate genes, which are already obtained as full-length cDNA by EST collection project, were constructed by using GATEWAY™ cloning system. Our expression clones can be expressed as fusion protein with His, GST or GFP in E. coli, insect cell or mammalian cell, respectively. These clones can be directly used in mass-scale cell based assay for the functional study of candidate genes as well as in mass-scale preparation of protein for the antibody production. We will report about our whole system for constructing multi-purpose expression clones. This work was supported as one of Functional Study of Human Genome of 21C Frontier R&D programs funded by Ministry of Science and Technology, Korea.