

Abstract of Presentation

Presentation Title:

From cancer genomics to cancer treatment; from hope to reality

Abstract :

cDNA microarray technologies have enabled us to obtain comprehensive data for gene expression profiles of human cancers. To isolate novel targets for diagnosis (predictive marker for the efficacy of treatment as well as tumor marker) and for treatment of cancer (molecular-targeting drug, cancer vaccine, antibody), we have been comparing expression profiles of cancer cells originated from various organs with their corresponding non-cancerous tissues using a cDNA microarray that consists of more than 30,000 genes. These experiments disclosed a number of genes that appeared to be involved in development and/or progression of cancers in those tissues. So far, we have analyzed more than 1,000 clinical cancer samples of the liver, pancreas, stomach, colon, esophagus, bile duct, uterus, lung, ovary, kidney, urinary bladder, testis, prostate, breast, and soft tissues as well as acute and chronic myeloid leukemias. We have selected hundreds of candidate genes by the criteria as follows; (1) gene expressions were transactivated in a large proportion of cancer tissues in comparison with their corresponding normal tissues and (2) expression was not observed or hardly detectable in any important vital organs. The further functional analysis identified dozens of genes that are likely to function as oncogenes in various cancers. The suppression of expression of such genes with siRNA induced cell cycle arrest, apoptosis, or suppression of anchoring-dependent cell growth. We also developed antibodies that showed growth-suppressive effect in vivo and/or in vitro. These results indicated that systematic expression analysis should be a very effective approach for identification of molecules that are potential targets for development of novel therapeutic drugs and diagnostic tools. In addition, I would like to introduce our approach to apply expression profiles of cancer cells for prediction of efficacy of the certain anti-cancer treatments. The information should be applied to establishment of personalized medicine.