Abstract No.111

Identification of New Candidate Lung Cancer Genes by Network of Overexpressed Genes Obtained from EST Analysis

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Genes involved in related biological pathways and diseases are usually expressed cooperatively for their functions, and thus information on their coexpression is a key to understand the biological systems at the molecular level. Publicly available databases of coexpressed gene sets are a valuable resource for a wide variety of experimental studies, including gene targeting for functional identification, and for investigations of regulatory mechanisms or protein–protein interaction networks. Recent improvements in DNA EST techniques have made a large variety of gene expression data available in public databases. This data can be used to evaluate the strength of gene coexpression by calculating the correlation of expression patterns among different genes between many experiments. The original COXPRESdb (coexpressed gene database) (http://coxpresdb.jp) represented the coexpression relationship for human and mouse.In this study, we investigated new genes that may involve in lung cancer but hitherto haven't reported, by drawing coexpressed genes network. EST libraries analyzed by Digital Differential Display (DDD) to identify overexpressed genes turmeric comparing to normal lung tissues. IDS of sixteen overexpressed genes imported to COXPRESdb and gene networks drew. Forty eight genes linked and showed coexpression to our overexpressed genes and all coexpressed genes carefully examined. The results showed nine genes (EIF1B, PPP2R2B, BTK, ATXN1, GABARAPL2, MAP1LC3A, RANBP9, SNCA and LOC344887) have not so far reported as genes involved in lung cancer and could be considered as new candidate genes for being investigated their participation in lung cancer.

Keywords: Lung Cancer, EST Analysis, Gene Network, Coexpressed Genes.

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Micellar SDS –TsIm – Hemin Complex as a Peroxidase-Like Nano Artificial Enzyme

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Biomimetic chemistery tries to design novel system by using chemical strategies considering the chemistry of living systems and attempts to imitate enzymatic processes and improve the performance of chemical reactions and enzymes. Artificial enzymes are constructed from synthetic materials by functional simulation . In many hemoproteins such as peroxidasese heme group has the functional role. The catalytic activity of hemoproteins depends on the microenvironment surrounding the heme and also the heme ligands . Heme itself has catalytic property but it has tendency to dimerization in aqueous solutions, so its catalytic activity is decreased in aqueous solutions . It is known that porphyrins may be solubilized by detergents like sodium dodecyl sulfate (SDS). There are strong hydrophobic interactions between detergents and porphyrin which overcome the porphyrin – porphyrin forces and porphyrin is solubilized at detergent concentrations corresponding to critical micelle concentration (CMC) . Micelles mimic the polypeptide envelope in proteins as the heme environment. Hemoproteins containing heterocylic nitrogen like histidine as proximal ligands can catalyze the oxidation of variety of substrates through reacting with hydrogen peroxide as oxidatative enzymes . In biomimetic chemistery the coordination chemistery of histidine is stimulated by imidazole containing ligands . A surfactant – Imidazole – heme ternary complex is known as nano artificial enzyme which shows peroxidase activity in aqueous solutions . In this study the SDS – TsIm – heme ternary complex has been designed as a peroxidase like nano artificial enzyme. 1-tosyl-1H-Imidazole (TsIm) was employed as an imidazole moiety to mimics histidine ligand in the native horseradish peroxidase(HRP). Enzymatic activation parameters, using spectrophotometeric measurements showed that the catalytic efficiency of SDS – TsIm – heme enhancement up to 26.38% relative