P23

Identification of genes related to Parkinson's disease using expressed sequence tags

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In a search for novel target genes related to Parkinson's disease (PD), two full length cDNA libraries were constructed from a human normal substantia nigra (SN) and a PD patient's SN. An analysis of the gene expression profiles between them was done using the ESTs frequency. Data for the differently expressed genes were verified by semi-quantitative RT-PCR, immunohistochemical analysis and cell death assay. Among seventy six genes identified with a significant difference ($P > 0.9$), 21 upregulated genes and 13 down-regulated genes were confirmed to be differentially expressed in human PD and/or in an MPTP-treated mice model by semi-quantitative RT-PCR. Among those genes, an immunohistochemical analysis using an MPTP mice model for alpha-tubulin including *TUBA3* and *TUBA6* showed that the protein levels are down-regulated, as well as the RNA levels. In addition, *MBP, PBP* and *GNAS* were confirmed to accelerate cell death activity, whereas *SPP1* and *TUBA3* to retard this process. Using an analysis of ESTs frequency, it was possible to identify a large numbers of genes related to human PD. These new genes, *MBP, PBP, GNAS, SPP1* and *TUBA3* in particular, represent potential biomarkers for PD and could serve as useful targets for elucidating the molecular mechanisms associated with PD.

Key words : Parkinson's disease; expressed sequence tags; gene expression profiling; immunohistochemistry; cell death.

P24

Identification of Intrahepatic Cholangiocarcinoma Related Genes by Comparison with Normal Liver Tissues Using Expressed Sequence Tags

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Intrahepatic Cholangiocarcinoma (ICC), a malignant tumor derived from the bile duct epithelium, is one of the leading causes of death from cancer, worldwide. However, the mechanisms related to it remain largely unknown. In this study, an analysis of the gene expression profiles for ICC was done using the frequency of the ESTs obtained from nine cDNA libraries that constructed from 4 ICC cell lines and 4 normal liver tissues. 137 genes were identified as being either up- or down-regulated in human ICC cells. 30 genes were randomly selected to confirm their differential expression in 4 human ICC cell lines and 5 ICC tissues compared to normal liver tissues by semi-quantitative RT-PCR. Among these genes, ANXA1, ANXA2, AMBP and SERPINC1 were further verified by immunohistochemical analyses. In conclusion, these identified genes represent potential biomarkers for ICC and represent potential targets for elucidating the molecular mechanisms that are associated with ICC.

Keyword : expression profiling, ESTs frequency, intrahepatic cholangiocarcinoma, liver