Search of potential molecular markers for early diagnostic of epithelial tumors using microarray data

Olga Bogatyrova[1,*], Vladimir Kashuba[1,2]

1. Institute of Molecular Biology and Genetics, National Academy of Sciences of Ukraine, Kiev 03680, Ukraine
2. Microbiology and Tumor Biology Center, Department of Clinical Science and Education, Sodersjukhuset, Karolinska Institute, Stockholm 17177, Sweden

*Contact author: o.o.bogatyrova@gmail.com

Keywords: Microarray, Expression Profile, Molecular Marker

Today microarray technologies are some of the most efficient methods used in gene expression studies. Through one microarray experiment we can simultaneously determine the expression of thousands of genes, thus facilitating research of examined biological models. It is very promising to use the potential of microarrays to distinguish tumor tissue from normal, to classify different types of carcinomas according and their histological subtypes, to identify expression profiles predicting metastasizing in primary tumors, and to determine the prognosis of particular carcinoma patients.

To identify markers of epithelial tumors as targets for novel therapeutic drugs, we investigated genome-wide expression profiles using bioinformatics analysis of all publicly available cDNA microarray experiments. We attempted to select a set of differentially expressed genes (gene expression signature) and use it for molecular biology-based characterization of certain cancer cases such renal, colon and prostate. We used R Bioconductor to process initial microarray data, for additional normalization of processed data we applied a method used for quantitative PCR [ref1] and analyzed differentially expressed genes with limma package.

We have screened microarray databases for searching genes with expression level changes and for selection of potential epithelial renal tumor markers and studying expression level of most significant differentially expressed genes using real-time qPCR, investigation genetic/epigenetic changes of potential candidates. We were searching for genes with expression level changes and have selected potential epithelial tumor markers. For each group we obtained 20 differentially expressed genes, which can be used for creation of gene expression signature for renal, colon and prostate tumors. Our results were confirmed by wet-lab investigation expression level of choosing genes in all different localizations. Our data suggest that one of chosen gene GPX1 is a candidate of renal tumor suppressor genes (TSG) for the centromeric 3p21.3 region.

Our algorithm permits to select a set of differentially expressed genes and use it for molecular biology-based characterization of certain cancer cases. The identification of differentially expressed genes in renal cell carcinoma could lead to the identification of potential marker set for biological phenomena such as invasiveness or metastasis, which would be of significant value for diagnosis, prognosis, and treatment, where GPX1 and GPX3 could be included.