

The role of micro-array gene analysis in the biology of renal cell cancer

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Renal cell carcinoma is an important cause of morbidity and mortality. Malignant transformation is associated with changes in the expression of a number of genes, and this alteration in gene expression is felt to be critical to the development of the malignant phenotype. In this study, gene expression in clear cell carcinoma of the kidney (RCC), normal kidney, and a set of diseased non-malignant kidneys, was examined. RNA was prepared and gene expression was determined using Affymetrix U95 arrays containing approximately 12,000 known genes and 48,000 ESTs. Gene expression analysis was performed with Gene Logic Gene Express® software. A large number of genes were found to be differentially expressed in these three sample sets. The genes that were expressed at 4-fold or more in RCC, those expressed only in RCC, and those expressed at 2-fold or more in RCC and also expressed in a limited number of other tissues, were analyzed for their expression in a variety of other normal and diseased tissues. Some of the genes identified were over-expressed only in RCC among the tissues examined, and some were over-expressed in several other malignant tissues as well as RCC. Other genes were over-expressed in RCC compared with normal kidney, but were also over-expressed in diseased non-malignant kidney and/or a variety of other normal tissues. The Eisen clustering technique was used to examine the gene expression in the sample sets,

and gene sets were identified that allowed good clustering of the RCC samples separate from the normal and diseased kidney samples. The observed changes in gene expression in RCC may help further the understanding of the biology of RCC, and could be useful for the diagnosis, treatment and imaging.

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