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Novel Classification of Genomic Technology to Study Human Cancer

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Perspective

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INTRODUCTION

High-density complementary DNA (cDNA) microarrays for "profiling" gene expression allows for the simulation analysis of thousands of known human genes from a biological specimen in a single experiment. In fact, with the present technology, the gene expression levels of the entire human genome can be represented in a single experiment. This technology gas been utilizing by nearly all files of cancer research, as it has provided a more comprehensive analysis of the genetic changes that occur in cancer cells and identified novel disease genes for many cancer types and cancer mechanisms.

In addition, this technology has been used to classify several common cancer types at the molecular level. Current studies in many laboratories around the world are using these novel classification models to predict clinical outcomes and to proper new molecular targets for therapy. The first randomized clinical trials using the gene expression data to make treatment decision for patients with breast cancer are underway in the United States, Canada, and Europe.

Gene expression profiling using cDNA microarray technology is one method to obtain a more comprehensive view of the consequences of genetic changes in the cancer cells. Currently, many other microarray platforms have been developed, including oligonucleotide microarrays, microarrays of bacterial artificial chromosome clones, comprehensive genomic hybridization to examine high resolution DNA copy number and oligonucleotide single nucleotide polymorphism arrays that report both copy number and genotype in the same hybridization but the principle for all these types of microarrays is essentially the same.

DESCRIPTION

A brief description of gene expression profiling is the most utilized of the genomic technologies. Gene expression profiling uses RNA form a sample of interest and a common reference source of RNA. The RNA is differentially labelled using a single round of reverse transcription and incorporating fluorescently labelled nucleotides. The fluorescently labelled reference cDNA and tumor cDNA is polled and hybridized to the clones or probes in the microarray. Each clone is derived from a specific sequence of an individual human gene and located at a unique position on the array surface. The glass slide is scanned with a confocal laser microscope measure the fluorescence ratio of each gene. The data from as single hybridization experiment represents the abundance of each specific gene transcript, and is viewed as a normalized ratio of each gene in each sample enumerated as either a ration to a reference sample or as an absolute intensity value. Normalization is required for proper data analysis because differences exist in labelling and detection exist in the quantity of RNA form the various samples. Once the ratios have been normalized, the experiment can be examined for differential gene expression. The data is then imported into statistical software programs, and the information that comes from the array is exhibited as a pseudocolor image.

CONCLUSION

Typically, gene overexpressed in the tumor is shown in red and gene with decreased expression in the tumor is shown in green. Visualization tools are common methods used to represent the data generated form microarray experiments. Because many genes with many different expression patterns are being assayed in each experiment, these visualization tools are helpful for representing the data in a format that can produce biologic input. Two-dimensional hierarchical clustering dendograms are a frequently used method for viewing gene expression data. In general, the dendograms is s two-dimensional matrix where the tumor samples constitute the columns and the gene constitutes the rows. The matrix makes it possible to quickly recognize the areas where highly correlated expression sets of genes differentiate the sample types.