There are many techniques available today to measure the expression of certain genes in a particular genome. One of the most notable ones is the DNA microarray, which provides scientists a way to not only measure, but also to compare relative genetic expression of thousands of genes at the same time(1). With this technique, the possibility to visualize expression patterns and understand more about the differences between the investigated transcripts is greatly enlarged(2). Today, DNA microarrays are one of the most important means in studying pathologies, such as many types of cancer. They have also been used to recognize genetic variation among populations to construct evolutionary relationships(3).

DNA microarray analysis involves a glass microscope slide, on to which many DNA fragments are bound. These fragments contain nucleotide sequences that serve as probes for particular genes of interest (1). Thousands of hybridizations are possible on just one slide, using robots to place the probes on the slides. The sequence and position of every fragment of DNA or oligonucleotide on the slide is known, and this information is later used to identify the nucleotides bound to it. The samples being studied must be converted to cDNA, and then colored with different fluorescent dyes(4). After an incubation period, it is possible to verify which samples are bound to what probe. This will be used to determine the relative amount of the genes of interest in the samples being investigated, by comparing the position of the different colors used in the dye(1).

DNA microarray technology has been a very useful tool for scientists in many different biological disciplines. The method has been particularly useful in the field of evolutionary biology for studying evolutionary relationships. Using DNA microarrays, it is possible to assess the variation in the expression of certain genes among individuals of

a population. It is also possible to investigate the differences in gene expression between two populations of the same species that comprise of different characteristics. Data obtained from these studies, have even been used to suggest that there is a substantial natural variation in gene expression among populations(3). This variation is now an important aspect of research in evolutionary biology, which could not be done without DNA microarray(3).

An example of DNA microarrays being used for cancer research can be seen in the experiments done by Sorlie and colleagues(5). It is possible to investigate the transcription abundances of particular genes in carcinomas, and compare this to healthy cells. This is a powerful tool, in relating these genes to their respective clinical outcomes. With this information, gene expression patterns can be drawn and specific measures can be taken in terms of medical treatment for breast cancer patients(5). The possibility to group these expression patterns gave origin to different sub classifications of breast carcinomas. Sorlie and her team used a vast sample of tissues in order to take this analysis and grouping further. This kind of work has been done before, however using a larger number of samples, may provide a more refined result and a better understanding of the clinical value of these different subtypes.

Using microarrays and hierarchical clustering data analysis, they were able to separate ER-positive (estrogen receptor) tumors into two, and possibly three, groups with particular expression profiles and diagnosis(5). The subtypes were categorized as Luminal Subtype A, and Luminal Subtype B and C. Other subtypes found were the Basal-Like, ERBB2+, Normal Breast-like, which had been previously recognized. In order to verify the validity of these new results, a second hierarchical clustering had to be

done, using the samples from the previous work that originated the first set of subtypes. Using comparisons with the clinical outcomes in patients, the scientists found a significant variation in the survival rate of the different subtypes. ERBB2+ were linked with the shortest survival times(5), and a considerable difference in relapse was observed in the new subtypes. From this study, DNA microarray was able to provide the genetic expression patterns in tumors that allowed the team to classify them and provide better clinical assistance to the patients, since old methods were unable to recognize differences between some of the neoplasm subtypes.

There are several advantages to using DNA microarray technology. The procedure is relatively inexpensive compared to other methods(2). It is also a safe and easy process, since there are no toxic or radioactive chemicals involved. One of the main advantages, is the fact that this method allows a simultaneous analysis of thousands of genes, which is not possible in the northern blotting technique(1). This particular feature of DNA microarray was seen to be the main advantage for the scientists researching the breast tumor study mentioned above. However, during an analysis using this technique, there is a possibility for cross-reactivity of the cDNA samples, which would affect the clarity of the results(6).

Even though DNA microarray technology is fairly new, it has been used in a great number of biological fields. The advantages of this method has certainly influenced many researches, and helped scientists to make elegant conclusions from these analysis. It is a prominent method that should direct future studies to many more exciting discoveries.

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