

An Overview on Procedure Involved in the DNA Microarray

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DESCRIPTION

DNA microarray technology has become a useful approach in gene expression analysis for the development of new identifying tools and for the identification of disorder genes and therapeutic targets for human cancers. Appropriate control for DNA microarray test and dependable analysis of the array data are crucial to performing the assay and employing the data properly. The most tough challenge has been the lack of a potent technique to examine the data for all genes at the same time and to use the microarray data in a decision-making process [1]. It's believed that this new way of interpreting and examining microarray data will bring near to success in decision-making using the information attained through the DNA microarray technology.

The elementary principle behind the DNA microarray is "nucleic acid hybridization". In this process, two complementary filaments of a DNA are joined together by hydrogen bonds to form a double-stranded molecule. This helps investigators to compare and examine the DNA or RNA molecules of identical sequences [2].

DNA microarray procedure

Collection of the samples: This can be done from a variety of organisms. The two main samples collected are cancerous and healthy human skin tissues.

Isolation of the mRNA: RNA from the samples is extracted by either using a column, or a solvent like phenol-chloroform. After isolating the RNA, the segregation of the mRNA from the rRNA and tRNA is done. As mRNA has a poly-A tail we can use a column containing globules with poly-T tails to bind the mRNA. Further it's washed with buffer to release the mRNA from the globules [3]. The buffer disrupts the pH by disrupting the hybrid bonds.

Creation of the labelled cDNA: A labelling mixture to the RNA was added which contains poly-T primers, contrary transcriptase, and fluorescently dyed nucleotides. Cyanine 3 to the healthy

cells and cyanine 5 to the cancerous cells were added. The primer binds to the mRNA first, further fluorescently dyed nucleotides were added creating a complementary strand of DNA.

Hybridization: The cDNA which was created was applied to a microarray plate. For comparing the two samples, the both samples were applied to the same plate. The ssDNA will bind to the cDNA previously present on the plate.

Recognition of the relative intensities of fluorescence under microarray scanner: The scanner has a laser, a computer, and a camera where the laser causes the hybrid bonds to fluoresce, the camera records the images produced when the beam scans the plate and the computer allows to instantly view our results and it also stores the data [4].

Assaying the data: The collection of data is done by using a microarray scanner. The laser excites luminescence of the cDNA by generating the signals. When the laser scans the array, the camera records the images produced. Further the computer stores the data and provides the results instantly. The data therefore produced are further assayed. The difference in the intensity of the colors for each spot determines the character of the gene in that particular spot.

CONCLUSION

The development of DNA microarray, biochip, and lab-on-a-chip technologies continues at a very quick pace. These new technologies represent a extensively interdisciplinary and synergist effort, with contributes to a range of scientific and engineering fields that have preliminarily not worked together as nearly. The miniaturization of this technology has been achieved by using numerous of the microfabrication processes that have revolutionized the microelectronics and computer industry. Microarray technologies are quickly advancing with multiple employments in gene expression, genotyping, and pharmacogenomics [5]. The technology is now also making an impact in the area of medical diagnostics, in particular, for cancer, inherited, and infectious disease conditions.

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REFERENCES

1. Cheng CH, Leung AY, Chen CF. The effects of two different ganoderma species (Lingzhi) on gene expression in human monocytic THP-1 cells. *Nutr Cancer*. 2010;62(5):648-658.
2. Sato M, Tokuji Y, Yoneyama S, Fujii Akiyama K, Kinoshita M, Chiji H, et al. Effect of dietary maitake mushrooms on plasma cholesterol and hepatic gene expression in cholesterol-fed mice. *J Oleo Sci*. 2013;62(12):1049-1058.
3. Sato M, Tokuji Y, Yoneyama S, FujiiAkiyama K, Kinoshita M, Ohnishi M. Profiling of hepatic gene expression of mice fed with edible Japanese mushrooms by DNA microarray analysis: Comparison among *Pleurotus ostreatus*, *Grifola frondosa*, and *Hypsizigus marmoreus*. *J Agric Food Chem*. 2011;59(19):10723-10731.
4. Kawano M, Thet MM, Makino T, Kushida T, Sakagami H. DNA microarray analysis of signaling pathway in macrophages stimulated by lignin-carbohydrate complex from *Lentinus Edodes Mycelia* (LEM) extract. *Anticancer Res*. 2010;30(7):2567-2576.
5. Jiang J, Sliva D. Novel medicinal mushroom blend suppresses growth and invasiveness of human breast cancer cells. *Int J Oncol*. 2010;37(6):1529-1536.