Review Article

DNA microarray, types and its application in medicine

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Abstract: The rapid growth in the field of biochemistry and organic semiconductors to produce microchips, which began a new movement in the production of DNA and gene chips were chips. There are many types of biological microchip technology are ongoing. The generation of DNA, RNA, proteins and living cells are used in biological microchip. So far for the study of the properties, activities and the role of genes and proteins and molecular processes within cells and tissues mostly of a gene discovery and gene or protein is the maximum number of individual studies that include a variety of methods use in PCR and markers, blotting (Western blotting, Northern blotting and Southern blotting) and other techniques. Microarray technology allows the expression of thousands of genes simultaneously is little monitoring. From its origins to the present, a number of databases, software and technology that has been developed in the update. This article discusses the basics of each of the technologies and applications and how to analyze it pays Microarray explains.
Keywords: Microarray, gene expression, cDNA array, an oligonucleotide array.

INTRODUCTION

After completion of the human genome that contain 3 billion nucleotides encoding the 30,000 genes. It was found that a gene and a protein study and explore a separate process does not help to solve the problem. Because the process is so complex that sometimes involved tens of hundreds of gene involved in the development of an activities. In the same way, proteomic and genomic technologies could help to investigate the activities and Changes of genes and proteins. DNA microarray technologies is a public utility in molecular biology .The main advantage is that unlike traditional methods, it is not limited to studying one gene at a time.

Microarray Technology

Microarray technology is that allows monitoring thousands of gene expression [1]. The basic principle on microarray is based supplement. For example, the A supplementary T and G is C supplements .In a microarray is a thousand points in a rectangular or square shape. Anywhere contains a large number of DNA fragments on a particular gene is placed. The array of molecular probes that are complementary to specific sequences of cDNA and On a solid phase, for example, glass slides have been fixed .Stabilization is done by robot. Is detected by fluorescent markers.DNA microarray based is hybridized DNA strand. The more

base pairs are complementary hydrogen bond becomes stronger. Such a connection is not lost in the wash. Final signals dependent on the sequence of levels that have established a strong connection.

All methods microarray includes five distinct experimental stage that are Search biological, sample preparation, biochemical reaction, revealing, Modeling, data visualization. According Yuk faileung et al 2003[2] ordinary microarray experiments involving the extraction of the sample, the fluorescent labeling, hybridization, scanning and finally is analyzed. Microarray technology may be classified to DNA microarray and protein microarray.

DNA microarray

DNA microarray is a simple and natural tool to assess the genome. DNA microarray is the types of CDNA and oligonucleotide arrays [3].

Oligonucleotide arrays

Oligonucleotide arrays for robotics punctuation of (printed) on a solid support (glass, coated glass, silicon or plastic). oligonucleotide arrays containing short pieces of DNA (25 bp). Gene chips have been developed by companies like Affymetrix. Tens to hundreds of thousands of different oligonucleotide probes have been produced, in each

array. Gen chips Affymetrix is a pioneer in making cDNA microarray [4]. The benefit of oligonucleotide arrays in quality and the proliferation as well as arrays printed on a unit is a cheap. In addition, long oligonucleotide probes can be produced directly in the surface array. Oligonucleotide array is limited to gene expression and analysis. That firstly requires a large amount of biological material. GE Health care, Ocimun Biosolutions, Agilent some commercial providers are available for oligonucleotide microarray.

CDNA arrays

CDNA arrays containing long segments of DNA from 100 to thousand bp. CDNA arrays is spotting by robot.Net cDNA clone is created on a solid backup. Some basics of CDNA: 1) delivery targets directly from databases such as Gen Bank, dbEST and Uni Gene.2) CDNA array selected target on the known location of the glass cover using a high-speed robot with a computer can be placed. 3) with fluorescence labeling of total RNA instances of reference and samples using a single color occurs with a round of reverse transcription (reverse transcription).

4)Participation fluorescent target for hybridization,5) measuring the laser excited incorporated targets using a scanning confocal lasermicroscope.6) analysis images from scanners to import software with Invitrogen, Genome systems, Biodiscovery, Xeno, Affymetrix, Genetix, Siliconetc, are some ofthe companies which produce commercial arrayers. Apart from cDNA array applications in comparative Genetic analysis and applications genome analysis, Recent applications include gene expression in lung cancer cells [5], drug-resistant, the identification of genes under osmotic stress in cells and veterinary diagnosis [6].

DNA array applications

Important applications of DNA arrays include: 1) investigate gene expression changes as a result of factors such as pathogens and damages cells [7] 2) Comparative genomic hybridization determine the content of the genome of living organisms and comparing them with each other[8,9] 3) Identification of single nucleotide polymorphism SNP. With this technology, a single nucleotide polymorphism can be studied in different populations. These studies can be effective in various fields such as genotyping to measure the risk of certain diseases, estimate mutations in germ cells and somatic, genetic linkage analysis [10]. The gene expression cDNA or cRNA incorporation of biotin labeled nucleotide which is subsequently stained (Browse labeling in Richter et al)that Frequently used for the incorporation of fluorescently labeled nucleotides in the DNA or cRNA or biotin labeled nucleotide incorporation to provide washed hybrid microarray.

The size of the fluorescence signal is detected anywhere. Provide the biotin tag array, after hybridization with streptavidin fluorescence they are stained. Laser-induced fluorescence is typically measured with a Confocal scanning. Signal strength anywhere as a measure of the level of gene expression is concerned. Microarray also in combination with chromatin iminophrispitiation[11](Solomon et al., 1988) were used to determine the binding sites of transcription factors.This technique is known as ChIP-chip. To bacteria or yeast, the gene areas is relatively small .the same arrays used for gene expression work can be applied to ChIP-chip. But for the human genome and the genomes of mammals have large gene areas and Transcription factor (TF) often bind many kbp away from the gene of interest. In the mammalian genome oligo arrays with oligo's spaced evenly across the entire genome are typically used for ChIP-chip experiments. Micro-arrays widely as SNP (single nucleotide polymorphism) used in genotyping. Several alternative approaches have been used to detect SNP's but the most commonly used are allele discrimination by hybridization as used by Affymetrix[12].

The Arrayed Primer Extension assay of Kurg et.al. [13] or the Infinium Assay of Illumina [14]are diagnostic methods.

In addition, the array can be used to detect many types Copy number. Illumina SNP Affymetrix genotyping method has been very successful and is used for many types.

Analysis of micro-array data

Micro-array data that is a lot of into meaningful biological information includes: First of all, check quality control that the company's data such as Affymetrix and Teca for data quality control have software Including: Multicheck, Laser check and QcPace1.The first phase of normalization includes ofchanging raw data into normal data. Which is an important step for the analysis data to minimize the biological and technical changes. GEPAS (Gene Expression Pattern Anadys Suites) and Ginko, software that are used for it. The next step is to summarize patterns of gene expression using gene interpretation tools. Finally defining the summarized concept of biological gene can be report by ontology .Software that is used for cluster analysis are CAGED and DNA -chip analyzer. Software is used in statistical analysis microarray is given below.
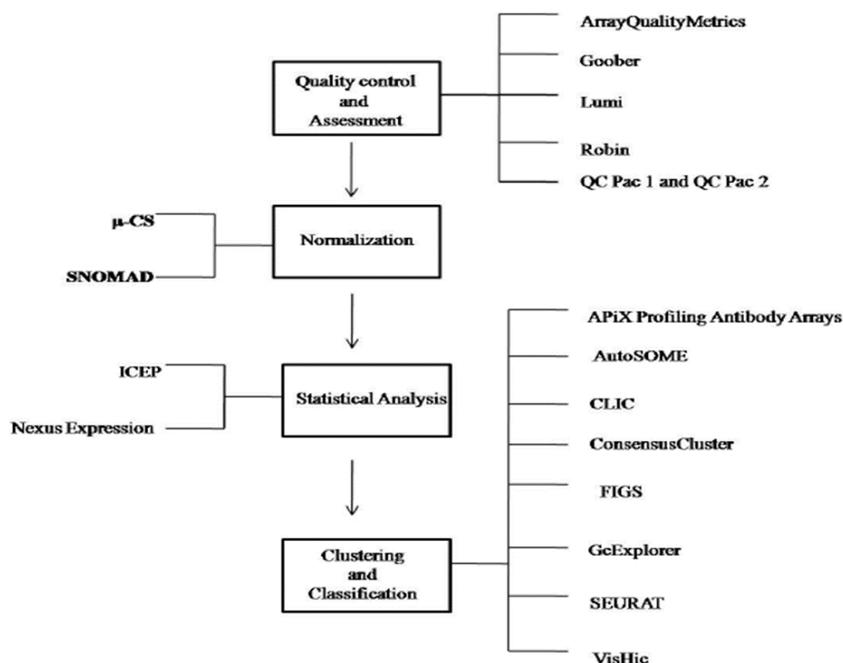
Fig-1: Schematic of used for cluster analysis are CAGED and DNA -chip analyzer

The use of DNA microarrayin medicine

Perhaps the most promising technologies of DNA micro-array inmedical microbiologyare to Use it to measure simultaneously a large number of microbial genetic targets [15,16]. Anoligonucleotide microarray was developed to target rRNA gene for the detection of 40 most pathogenic intestinal bacteria [17, 18]. The PCR assay using microarray helps to shown the rapid detection and identification of bacteria in blood culture[19,20].The same method for rapid diagnosis of bloodstream infections due to bacterial pathogens common in children was Publically used[21,22].PCR amplification in combination with Oligonucleotide micro-array is used to identify B. anthracis [23,24]. In another study DNA micro-arrays used for the detection and identification of emergence of fungal in clinical collected samples from patients were neutropenia [25, 26]. In addition to bacterial and myco-bacterial organisms, microarrays following broad-range PCR amplification have been used to detect and identify fungal, parasitic, and viral pathogens [27-29]. A new method based on micro-arrays for simultaneous human immunodeficiency type 1 (HIV-1), hepatitis B and c in plasma samples was described[30].A microarray technique for the detection and identification of enteropathogenic bacteria at the species and subspecies levels was developed covering pathogenic E -coli, Vibrio cholera, Vibrio Parahaemolyticus, Salmonella enterica, Campylobacter jejuni, Shigella species, Yersinia enterocolitica, Listeria monocytogenes [31]. Microarray system by a panel of pathogens that cause meningitis, viral and bacterial detection was used[32].The system detection 9 microorganisms including Neisseria meningitidis, Streptococcus pneumoniae, Staphylococcus aureus, Listeria monocytogenes, Streptococcus agalactiae, Herpes

simplex type virus 1 and 2, and Varicella Zoster Virus was detected directly from the CSF.DNA microarray of comparative genomics to study the differences between the genome of Bacillus strains of M. tuberculosis and .BOVIS M Calmett-Guerin (BCG) is used[33]. H. pylori species and tuberculosis [34] tuberculosis were used between different isolates S. Pneumoniae [35].

These data suggest that DNA micro-array can better understand the genetic differences between closely related living organisms. useful Information to identify virulence factors, molecular phylogeny, improve diagnosis and offerthe development of a vaccine. Micro-arrays can also be adapted to detect information about genetic content changes [36] .E. coli for Duplication and Deletion for the idea that Duplication the gene plays a crucial role in adaptation, examined. Identification of appropriate antibiotics, diarrheal disease intervention and management of clinical epidemiological research facilities is important. Micro-array-based methods with other genetic techniques that can replace the classical method for many common pathogens of bacterial diarrhea, it is currently presented.

Future micro-array technology

Micro-array technology is low-cost and effective technology with high efficiency. In finding solutions leading to treat many diseases such as cancer is important. This method can overcome the flaws in the old ways. Meanwhile, the expression of thousands of genes can be studied. Due to its immense benefits in proteomics and genomics are considerable prospects for this technology was made. This new method is a daily progress and development of high throughput technologies in genomics and proteomics. The scientific

community needs to increase in the near future may lead to a pattern of genetic disease.

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