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MINI REVIEW

Microarrays: Rise of Novel Technology

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ABSTRACT

Microarrays are used for solitary analysis to research the manifestation of thousands of attributes. It is one of the most recent advances which is used for biological research. It provides assistance in treatment of antibodies, detection of chronic diseases, pharmacological approach, mechanism detection etc. Microarray analyses large amount of samples at a time by saving the time, resources and providing best efficacy. The samples used during the analysis can be previously recorded or newly identified or unidentified. The output of a microarray attempt is termed as a "quality joint profile." In recent times the microarray's usage has increased in multiple biological sectors and providing best records. Its presence in dentistry is limited, but may be increased in near future. As innovation becomes increasingly affordable, a microarray test reveals uses in several scientific domains. The study discusses about the various techniques, hypothesis and applications of microarray.

Keywords: mRNA, cDNA, cancer, genes, microarray

1. INTRODUCTION

Microarray is a laboratory technique which provides genotypic information of thousands different loci at a given time. It is a multiplex two dimensional lab-on-chip technique on a solid substrate. The technique is basically high throughput designed to detect multiple diseases [1].

Prevention, diagnosis, and treatment in dental practice are based on an understanding of the biology of underlying oral health and disease. Few aspects of patient care will remain untouched by today's rapid advances in biological research. In the future, dentists may use cheap diagnostic tests to diagnose infection, oral lesions, and various symptoms. The small variations in the DNA sequence that lead to different characteristics (such as skin color, facial features, or height) are known as polymorphisms, which also can cause or contribute to the development of many syndromes and diseases [2]. These genetic variations can be easily identified by the microarray technique which is useful for association and linkage studies to isolate chromosomal regions related to a particular disease. This array also can be used to locate

chromosomal aberrations related to cancer, such as segments of allelic imbalance, which can be identified by loss of heterozygosity [3].

2. PRINCIPLE

The basic principle behind microarrays is that complementary sequences will bind to each other and hence leading to rapid result. The mRNA carries the genetic information from the cell for protein synthesis regularly [4]. It is important to assess the various mRNAs, for studying the gene expression. But it is not that easy due to unstability of mRNA and rapid degradation leading to no information. Therefore the mRNA is converted into a more stable cDNA [5].

Every microarray tests is based on the main rule that recording wealth may be generated by calculating a reciprocal RNA hybridization measure [6]. A microarray is possible to build up a field of several thousands of tests in a territory of maybe 5 sq cm, in which each test tackles an addition of a piece. Usually these are fluorescent in colour so that the laser can discriminate between the hybridization at the test location [7]. The force of the sign made by atoms of a certain record should be twice as spectacular as the sign supplied by 500 particles. It should be equally dazzling as the sign supplied by 10,000 particles or 20,000 particles. However, it does not assure that the protein is available to see a record. If despite the fact that record wealth is distinguished between at least two situations it is normal to induce a differentiation.

3. TECHNIQUE

The unknown DNA molecules are cut by restriction endonucleases into fragments. The labelling of cDNA is done by fluorochrome dyes like Cy3 and Cy5 which are green and red in colour respectively [8]. The fluorescent markers are attached to these fragments and reacted with DNA probes. The target DNA fragments along with complementary sequences bind to the DNA probes. The extra DNA fragments which are not bind gets washed off. The targeted DNA fragments are identified by the fluorescence emission. The pattern of fluorescence emission and DNA identification is recorded on a computer. This technique is very rapid and specific for the identification of several DNA fragments simultaneously.

4. HYPOTHESIS

The ability to investigate record numbers over an increasing scope of situations allows geneticists to get a fresh perspective on their cell frameworks. It often offers a broader view about science and yet take care of the classic hypothetic-deductive logical structure. The innovation has evolved swiftly; using competitor qualities easily and now the applications are distinct than clinical forecasts, biological observation systems, quantitative planning and the analysis of transformational instruments.

There are two best-known cases about the exchange among theory testing and microarray profiling. The last creators analysed the variation in articulation among fly strains which were discretely picked for positive or negative geotaxis, an unanticipated way of distinguishing whether flies preferred to

ascend or remain close to the ground [9]. They identified two dozen attributes that were conveyed differently, some of which were treated with freak or transgenic stocks, enabling the effect of the quality measurement on the behaviour.

In any case, four of the next traits certainly impact geotaxis statistically. This technique was utilized above and beyond to argue for an iterative four-venture input between profiling, recognition of the candidate attributes, removal and subsequent profiling. They demonstrated how intelligent experiments may comprehensively improve our understanding of legacy administrative routes, such as the yeast galactose reaction.

A quality education to this field was provided which shows that huge B-cell lymphomas disseminate had two substantial subgroups with atomic profiles [10]. While it is difficult to forecast histologically based clinical results, these profiles identify a set of features that constitute a very reliable indicator of endurance. Essentially, a "helpless prediction" signal has been depicted in bosom malignant development biopsies from young women before the advent of metastases in the lymph jets.

5. APPLICATION

Cancer

Cancer is one most chronic auto-immune disease. Its identification during the onset is essential to stop the aftereffect. During formation, there are several changes in the genes of the cells. These variations are useful for easy detection to the researchers and provide simultaneous testing platform across different genes present in the cells. A comparative study between a healthy and cancerous cell reveals many affected genes. Such results are extremely useful in identification of single-nucleotide polymorphisms (SNPs) and mutations, classification of tumors, identification of target genes of tumor suppressors, identification of cancer biomarkers, and identification of genes associated with chemoresistance, and drug discovery [11].

Detection of Leukoplakia

Leukoplakia also called as white lesions which results by a series of reversible conditions. The microscopic examination fails to identify the cancerous subset of cells leading to contiguous disease. The genomic profiling helps to classify the cancerous lesions at a very early stage. Biopsy samples can be directly sent for gene expression analysis through microarray. Thus early diagnosis will allow for better management of these cancerous cells [12].

Antibiotic treatment

With passing decades the rising numbers of resistant bacteria has led to failure of antibiotics. DNA microarray analysis helps to analyse bacterial genomic DNA using very small amount of DNA. In case of oral anaerobic bacteria which are not easily culturable; microarray comes handy technique for easy detection [13].

Drug development

Microarray is a powerful tool for the investigation of drug action. Several studies targeted to study about the drug target and

seems to be successful. The human cells and tissues are targeted directly for the identification and validation of novel therapeutics. In the long term, microarrays will contribute to the analysis of metabolic pathways for which new signalling pathways are being identified [14]. Monitoring expression of genes with toxicity potential has elicited the interest of large pharmaceutical companies as well as specialized biotech companies.

Others

Microarray technologies can also be coupled with different studies such as classification of diseases, or molecular phenotyping, the study of gene function in relation to gene regulatory networks, or functional genomics; pharmacogenomics and developmental biology [15].

6. CONCLUSION

A microarray is therefore an investigation of hundreds of attributes from different cell populations. In consequence, if the fluorescence is not observed for any one population, the quality might be interpreted independently. However, with correct replication, standardization and measurements, quantifiable disparities are recognized as quickly as feasible. Eventually, the return of all microarray hybridizations is a succession of numbers, which extends from one record per cell to two or three thousand recordings for each cell. Before these instruments reach clinical use a great deal of quantifiable and experimental work is still necessary, but the promise of excellent articulation coordinating information from the environment and genotype offers significant incentive to study micro-array infection.

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8. CONFLICT OF INTEREST

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