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Commentary

Applications of Genomic DNA Arrays in Research, Drug Discovery, and Diagnostics

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DESCRIPTION

The most frequently applied instrument for study, drug discovery, and diagnostics has been acclaimed as microarrays or DNA chips. They have the ability to run a slew of molecular assays at the same time, yielding a wealth of data from a single clinical sample. Genotyping, expression analysis, and sequencing are some of the applications. The most typical application of DNA microarrays is to monitor transcript expression levels in cells, viruses, and bacteria. Polymerase Chain Reaction (PCR) amplicons created from genomic regions defining expected open reading frames; cDNA generated from mRNA by Reverse Transcriptase (RT)-PCR; and oligonucleotides are three types of probes that can be spotted onto slides. The mRNA target can be used directly from culture or amplified and labelled by RTPCR. The requirement to extract mRNA fast due to its short half-life in many organisms is one obstacle in undertaking microarray analysis in bacteria. Random hexamers or short oligonucleotides can be used to prime cDNA synthesis. According to a recent study, using random hexamer priming resulted in the best accurate quantification of expression levels. Profiling gene expression levels in an isolate can help forecast the function of unidentified genes or analyse the expression of virulence-associated genes. Measuring the levels of expression of specific genes in pathogens may be useful for detecting particularly aggressive strains or comparing medication responses. This type of antibody may be helpful when identifying an effective pharmacological treatment for organisms that are initially unresponsive to therapy. Whole genome microarrays are not just for bacteria. The expression of the human cytomegalovirus and herpes simplex virus used microarray analysis.

Pathogens employ a number of mechanisms. With the availability of human gene arrays, researchers may now explore the relationship between host and pathogen in greater depth. Results from this type of study may provide indicators to identify those persons most susceptible to infection as well as prognostic markers for the course of the illness, in addition to providing clues into the mechanisms of microbial pathogenicity. This type of data could be used to forecast the most successful course of therapy during an infection or even to screen susceptible people in order to take preventative actions. In human cancer studies, comparing gene expression patterns has already been established as a method of classifying tumour types. Host expression patterns could also be employed as a diagnostic tool and an indicator of illness progression in infectious diseases. The finding that the patterns of gene expression elicited in primary human monocytes infected by two closely similar strains of Ebola viruses, Zaire and Reston, differ significantly supports this type of application.

Microarray technique was used in this investigation to identify between host gene expressions profiles formed during infection with the two Ebola strains. One of the most essential parts of this approach, which involves the simultaneous examination of thousands of genes, is the creation of algorithms for analyzing the massive volumes of data collected. For many years, comparative genomic hybridization has been employed. Scanning for changes in DNA sequence copy number in tumour cells to classify certain tumour types or phases of tumour growth is an important application. This kind of study is directly adaptable to an array format to generate data on the quantity of DNA copies and the persistence of certain genes between infections. Amplicons encoding some or all of a species' genes are spotted onto arrays and interrogated with labelled genomic target sequences originating from different strains or disease states. A study on bacilli Calmette-Guérin vaccination strains resulted in a reconstruction of the vaccine's phylogeny across time, demonstrating the efficacy of this technology. One disadvantage of this method is that only known sequences may be displayed on the array, therefore insertions in the target sequence are not detected. The more sequence information obtained from genomic sequencing projects and functional genomic investigations, the higher the potential for reference array creation as diagnostic and monitoring tools.

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