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Gene Technology

Commentary

Note on Gene Chip Technology

Mark Gerstein*

Department of Biotechnology, University of Sydney, Sydney, Australia

DESCRIPTION

A gene microarray or gene chip consists of thousands of individual DNA sequences densely arranged in a single matrix (usually a glass slide or quartz wafer, but can also be on a nylon substrate). Known identity probes are used to determine complementary binding, allowing analysis in parallel form at the gene expression, DNA sequence mutations, or protein levels.

The main principle behind microarrays is hybridization between two strands of DNA, complementary nucleic acids that specifically pair with each other by forming hydrogen bonds between complementary nucleotide base pairs. It is a characteristic of the array. The large number of complementary base pairs within a nucleotide sequence means a tighter, non-covalent bond between the two strands. After flushing the non-specific binding sequences, only the strongly paired chains remain hybridized. The fluorescently labelled target sequence that binds to the probe sequence produces a signal that depends on hybridization conditions (eg, temperature) and washing after hybridization. The overall strength of the signal from a spot (function) depends on the amount of binding of the target sample to the probe present at that spot [1]. Microarrays use relative quantification. In this case, the intensity of one feature is compared to the intensity of the same feature under different conditions, and the identity of the feature is indicated by its location.

DNA microarrays were only used as research tools when they were first introduced. Scientists continue to do extensive census today, for example, to find out how often people with certain mutations actually develop breast cancer, or to sequence genes that are most commonly associated with a particular disease. This is possible because, like computer chips, microarray chips that represent a very large part of the human genome can have so many "features".

The Microarray can also be used to study the extent to which a particular gene is turned on or off in a cell or tissue. In this case, instead of separating the DNA from the sample, RNA (a transcript of the DNA) is separated and measured [2].

Today, gene microarrays are used in clinical diagnostic tests for several diseases. Genes determine how our body handles the chemistry associated with those drugs, so they are sometimes used to help determine which drug is best prescribed to a particular person. With the advent of new DNA sequencing technologies, some of the tests that used microarrays in the past used DNA sequencing instead. However, microarray tests are usually cheaper than sequencing and can be used for very large studies and some clinical tests.

To determine if people have a mutation in a particular disease, first take a sample of DNA from the patient's blood and a control sample that does not contain the mutation in the gene of interest.

Next, the researcher denatures the DNA in the sample. This is the process of separating the two complementary strands of DNA into single-stranded molecules. The next step is to label each fragment by cutting long strands of DNA into smaller, more manageable fragments, and then attaching a fluorochrome (although there are other ways to do this but it is a common method). Individual DNA is labelled with a green pigment and control or normal DNA is labelled with a red pigment [3-4]. Both sets of labelled DNA are then inserted into the chip and hybridize or bind to the synthetic DNA on the chip. If the individual has no genetic mutation, both the red and green probes bind to the sequence on the chip that represents the mutation-free sequence (the "normal" sequence).

If an individual has a mutation, the individual's DNA does not bind properly to the DNA sequence on the chip that represents the "normal" sequence, but instead to the sequence on the chip that represents the mutant DNA.

Tumour formation involves simultaneous changes in hundreds of cells and genetic changes. Microarrays can benefit researchers by providing a platform for testing large numbers of gene samples simultaneously. In particular, it is useful for identifying Single Nucleotide Polymorphisms (SNPs) and mutations, classifying tumours, identifying target genes for tumour

Correspondence to: Mark Gerstein, Department of Biotechnology, University of Sydney, Sydney, Australia, E-mail: markg@ucsf.edu

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suppressors, identifying cancer biomarkers, identifying genes related to chemotherapy resistance, and discovering drugs. For example, different patterns of gene expression levels can be compared between a group of cancer patients and a group of normal patients to identify genes associated with that particular cancer [5].

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