Microarray technology

Microarray technology has been widely used in biological and medical research for gene expression profiling, biomarker discovery, and understanding the molecular mechanisms underlying various biological processes and diseases. However, it has largely been superseded by newer technologies such as RNA sequencing (RNA-seq), which offer higher sensitivity, broader dynamic range, and the ability to detect novel transcripts. Nonetheless, microarray data remains valuable for many research questions and is still used in certain contexts.

Microarray technology is a powerful tool for studying gene expression on a genome-wide scale. It allows researchers to measure the expression levels of thousands of genes simultaneously, providing a snapshot of the molecular state of a cell or tissue sample.

In a typical microarray experiment, DNA or RNA samples are labeled with fluorescent dyes and hybridized to a microarray chip containing thousands of DNA probes. The fluorescence signal from each probe is detected and quantified using a specialized scanner, generating a signal intensity value for each gene on the array.

The resulting data can be analyzed to identify genes that are differentially expressed between two or more conditions, such as disease vs. normal, treated vs. untreated, or different stages of development. This can provide insights into the molecular mechanisms underlying disease or other biological processes.

Microarray technology has been widely used in basic and clinical research, including cancer research, drug discovery, and personalized medicine. However, with the advent of next-generation sequencing technologies, RNA-seq has largely replaced microarrays for gene expression profiling due to its higher sensitivity and dynamic range. Nonetheless, microarrays are still used in some applications, such as quality control of RNA-seq experiments, and for the analysis of non-coding RNA species which may be missed by RNA-seq.

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see Microarray analysis.

see Microarray data.