Diagnostic use of microarray technology.

Veinam Kim*

Department of Pulmonary Medicine, Fudan University, Shanghai, China

Received: *02-Jan-2023, Manuscript No. RNAI-23-89731;* **Editor assigned:** *04-Jan-2023, PreQC No. RNAI-23-89731(PQ);* **Reviewed:** *19-Jan-2023, QC No. RNAI-23-897;* **Revised:** *27-Jan-2023, Manuscript No RNAI-23-89731(R);* **Published:** *03-Feb-2023, DOI: 10.35841/2591-7781.19.1000130*

Description

Microarray analysis is a powerful tool used to study the expression of thousands of genes at once. It allows us to study the expression of genes in a particular sample, such as a cell or tissue, and compare it to the expression of genes in another sample. This method involves immobilizing DNA fragments on a solid surface, which then hybridize with labelled nucleic acids from the samples being studied. Microarray assays were developed to allow profiling of the expression of thousands of genes. Microarray analysis of entire transcriptomes of clinical samples is extremely useful for understanding the molecular biology of disease, providing opportunities for molecular classification of disease, the identification of novel molecular targets for intervention in disease, and the prediction of therapeutic response. Microarray analysis can be used to study gene expression in a wide range of organisms, from bacteria to humans. It has a wide range of applications, from basic research to clinical diagnostics. For example, microarray analysis can be used to study the genetic basis of diseases, identify biomarkers for cancer, and track the progression of infectious diseases.

Use of DNA Microarray in Diagnostics

Early diagnosis of an infectious disease is always desirable to prevent its spread among livestock species, and thus to prevent its spread among livestock species, and thus reduce the economic losses. Microarray technology has been utilized in the identification of various infectious disease pathogens, such as Avian influenza (H5N1), FMD, Viral Fever (Marburg virus), SARS virus, etc. University of Florida and Centre of Disease Control in the United States has collaborated to develop an improved version of the flu chip that requires only matching sequences from a single gene of the influenza virus (matrix), which mutates at a slower rate than the other two genes in the previous version (hemagglutinin and neuraminidase genes). This chip only needs 15 sequences from a single gene to reliably identify avian influenza. Greene chip microarray analysis has been utilized for the investigation of samples from patients with viral hemorrhagic fever-like syndrome for its differential diagnosis from malarial cases.

A microarray-based resequencing test was first used for detecting p53 mutations in cancer. The tumor suppressor gene p53 plays a key role in multiple cellular pathways and functions as a transcription factor by regulating genes that control cell proliferation, cell survival, and genomic integrity. Disrupting its function promotes checkpoint defects, genomic instability, and inappropriate survival, leading to the uncontrolled proliferation of damaged cells. In fact, p53 mutations are the most common genetic alterations found in cancer. Between 30 and 70% of human cancers in almost every organ contain a point mutation in one of the two p53 gene copies. Mutations of the p53 gene have been associated with poor prognosis in numerous human cancers and are a major determinant of patient outcome in response to adjuvant chemotherapy or radiotherapy.

Conclusion

Overall, microarray analysis is a powerful tool that has revolutionized our understanding of gene expression and its role in various biological processes and diseases. Its applications in research, diagnostics, and personalized medicine are vast and have the potential to greatly improve human health and well-being. One of the main advantages of microarray analysis is its ability to analyze large amounts of data simultaneously, making it a valuable tool for high-throughput analysis. However, the interpretation of the data can be complex and requires specialized knowledge and software. Additionally, there can be limitations in the accuracy and sensitivity of the results.

*Correspondence to

Dr. Veinam Kim

Department of Pulmonary Medicine,

Fudan University

Shanghai, China

E-mail: venikim@gmail.com

Citation: *Kim V. Diagnostic use of microarray technology. 2023;19(1):1.*