Mini Review
Volume 7:5, 2022

Journal of Molecular Histology and Medical Physiology

ISSN: 2684-494X

Open Access

New Technique to Diagnose Tissue Microarray

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Abstract

A recent development in pathology is tissue microarray. A microarray enables high throughput analysis of multiple specimens at once because it contains numerous small representative tissue samples from hundreds of distinct instances combined on a single histologic slide. Tissue microarrays are paraffin blocks created by re-embedding cylindrical tissue cores at predetermined array coordinates into a single recipient (microarray) block from various paraffin donor blocks. This method enables the arraying of up to 1000 tissue samples or more into a single paraffin block. On a single glass slide, it can allow simultaneous study of molecular targets at the DNA, mRNA, and protein levels under the same, uniform circumstances, as well as maximise the preservation and utilisation of finite and priceless archival tissue samples. This adaptable method, which automates data processing, makes it easier to conduct both retrospective and prospective human tissue investigations. It has a variety of potential uses in fundamental research, prognostic oncology, and drug discovery. It is a useful and efficient technique for high-throughput molecular analysis of tissues that is assisting in the identification of new diagnostic and prognostic markers and targets in human cancers. The pros, uses, and restrictions of tissue microarray fabrication and sectioning are outlined in this article.

Keywords: Microarray • Pathology • Prognostic

Introduction

The development of the novel technology known as the tissue microarray (TMA) has increased the efficiency of molecular profiling in cancer research by enabling researchers to quickly carry out extensive research projects while reducing experimental variables and saving priceless tissue samples. On a single glass slide, the method enables the simultaneous evaluation of proteins or genes in a variety of hundreds of paraffin-embedded cored tissue specimens. TMAs can be evaluated using immunohistochemistry, fluorescent-dye assays, and in situ hybridization (ISH). TMAs make it possible to quickly analyse both healthy and cancerous tissues, and they are very useful for research into the validation of cancer biomarkers. The development of prognostic and predictive biomarkers derived from genomes research in oncology is made possible by the ability to link TMA results to clinical variables [1]. Particularly in the context of breast and ovarian cancers, TMA analysis methods are used. We will highlight crucial points to think about in order to prevent the technology's biggest issues, with a focus on TMA quality control and analysis. A new age of molecular morphology translational study has begun with the identification of the human genome and its expression. New technologies, such as array technology in its different forms, have been developed to help in the identification of genetic material gains and losses as well as the expression of encoded genes as a result of the explosion of genomic data. Expression arrays based on on-chip synthesis or hybridization to cDNA or other targets initially dominated array technology applications. Recently, one of the most important new methods for directly analysing the aberrant genome has emerged: arrays that detect changes in DNA targets rather than multiplexed RNA targets [2]. Both array-based comparative genomic hybridization and expression array results can be very helpful in creating RNA and DNA-based signatures, but both methods need to go through some sort of validation process. Validation can be performed using an RT-PCR-based multiplexed test, fluorescence and/or bright field DNA in situ hybridization, RNA in situ hybridization, or immunohistochemistry. It has not always been clear that the material extracted from a pathologic process has been representative due to insufficient quality control, despite the DNA array's excellent quality control and recent demonstrations of reproducibility between arrays analysed on different instruments and in different locations [3].

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Received: 05 September, 2022; Manuscript No: jmhmp-23-86950; **Editor assigned:** 07 September, 2022, PreQC No: P-86950; **Reviewed:** 19 September, 2022, QC No: Q-86950; **Revised:** 26 September, 2022, Manuscript No: R-86950; **Published:** 01 October, 2022, DOI: 10.37421/2684-494X.2022.7.49

Description

The study of a large number of validating examples would involve whole paraffin sections from a separate cohort of patients. However, the cost of labour and materials, such as fluorescent and bright field in situ hybridization probes, mouse or rabbit monoclonal antibodies, are sometimes too high, making extensive study involving whole sections impossible and ineffective. International cooperation is urgently required to further this research and lower the incidence of significant adverse drug events in paediatric oncology [4].

One of the most frequent complaints about tissue microarrays is that, especially in cases of heterogeneous tumours like Hodgkin lymphoma and prostate adenocarcinoma, the small cores sampled may not be representative of the entire tumour. However, in immunohistochemical studies of various tumour types, many groups have demonstrated remarkable agreement between tissue microarray spots and entire sections. Parker et al. discovered that, in 96% of cases, the results of the microarray core for oestrogen receptors were the same as the results of the whole sections of the tumours when comparing the results of whole tissue sections with those of tissue microarray in quality assessment of oestrogen receptor status in breast cancer. In a different study that looked at the validation of tissue microarray technology for immunohistochemical tests, it was discovered that in more than 95% of cases, the analysis of two core sections from a single case was comparable to the analysis of complete tissue sections. In a third research of more than 2000 bladder tumours, information from four 0.6-mm cores per case was very consistent with information from entire sections for the assessment of histologic grade and proliferative index [5].

Conclusion

A useful and efficient method for high-throughput molecular analysis of tissues, tissue microarray is assisting in the discovery of novel diagnostic and prognostic indicators and targets in human cancers. It offers a variety of possible uses in basic research, prognostic oncology, and drug discovery, with

varied degrees of research utilisation. The usage of tissue microarray as a tool for all kinds of tissue-based research is predicted to increase quickly. The translation of discoveries from basic research into clinical applications will be significantly accelerated by the use of tissue microarray technology.

Acknowledgement

None.

Conflict of Interest

None.

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How to cite this article: Arpi, Darshini. "New Technique to Diagnose Tissue Microarray." J Mol Hist Med Phys 7 (2022): 49.