Journal of Molecular Histology & Medical Physiology

Mol Histol Med Physiol 2021, 6:1

Editorial Note Open Access

Tissue Microarrays: Powerful Tools for Molecular Morphology

Vikrant Singh*

Department of Pharmacy, GD Goenka University, India

***Corresponding authors:** Vikrant Singh, Department of Pharmacy, GD Goenka University, India, E-mail: Vikrant9671@outlook.com

Received: 9 Jan, 2021**; Accepted:** 13 Jan, 2021**; Published:** 19 Jan, 2021

Tissue microarray (TMA) is a new technology that has been created to improve the effectiveness of molecular profiling in cancer research by allowing researchers to quickly conduct large-scale investigations while lowering experimental variables and preserving valuable tissue samples. The approach enables for the simultaneous examination of protein or genes in an array of hundreds of paraffin-embedded cored tissue specimens on a single glass slide. Immunohistochemistry, fluorescent-dye tests, and in situ hybridization can all be used to assess TMAs (ISH). TMAs enable the quick analysis of normal and cancer tissues, and are particularly valuable for cancer biomarker validation investigations. The ability to link TMA results to clinical factors is particularly useful in oncology for the development of therapeutically useful prognostic and predictive biomarkers obtained from genomics research. TMA analysis approaches, especially in the context of breast and ovarian malignancies. Important topics to consider in order avoiding the technology's major problems will be highlighted, with a special emphasis on TMA quality control and analysis.

The discovery of the human genome and its expression has ushered in a new era in molecular morphology translational research. With the explosion of genomic data has come the creation of new technologies to aid in the detection of genetic material gains and losses, as well as the expression of encoded genes, such as array technology in its various forms. Array technology applications were initially dominated by expression arrays based on on-chip synthesis or hybridization to cDNA or other targets. Arrays that detect alterations in DNA targets rather than multiplexed RNA targets have lately emerged as key new techniques for directly investigating the aberrant genome.

Although the results of both expression array and array-based comparative genomic hybridization are quite useful in the production of RNA and DNA-based signatures, both approaches require some type of validation. An RT-PCR-based multiplexed test, fluorescence and/or bright field DNA in situ hybridization, RNA in situ hybridization, or immunohistochemistry can all be used for validation. Though the DNA array's quality control has been excellent, and reproducibility between arrays analyzed on different instruments and in different locations has recently been demonstrated to be reproducible in the generation of meaningful signatures, it has not always been clear that the extracted material from a pathologic process has been representative due to insufficient quality control.

Whole paraffin sections from an independent cohort of cases would be used in the analysis of a large number of validating instances. However, the expense of labour and reagents—whether mouse or rabbit monoclonal antibodies or fluorescent and bright field in situ hybridization probes—are frequently prohibitively expensive, making large-scale research with entire sections unfeasible and ineffectual. To improve this research and reduce the prevalence of serious adverse medication events in paediatric oncology, there is an urgent need for international collaboration.