Tissue arrays

UHN Microarray Centre

Tissue Microarray Platform

Introduction

Tissue microarrays (TMA) were first described in 1987 by Wan, Fortuna, and Furmanski and popularised following the 1998 publication by Kononen *et al*.[1,2]. TMA are a fast, cost-effective and tissue-saving method used for the high-throughput molecular profiling of tumour specimens. These arrays are comprised of hundreds of paraffin-embedded core tissue samples arranged on a slide. The protein expression of all arrayed tissue specimens can be evaluated in a single immuno-staining or in situ hybridisation reaction.

The TMA platform can increase the speed at which clinicopathological studies are performed and, at the same time, reduce the amount of damage to donor paraffin blocks. Since tens of thousands TMA sections can be obtained from a typical paraffin block (approximately 10x10x3mm), compared with 300 sections using conventional techniques, more target proteins can be analysed from one tumour sample.

One of the most significant advantages of TMA, compared with conventional methods, is automated analysis. The regular pattern of arrayed samples allows specialised software to analyze and quantify target proteins. In addition, TMA technology will help optimise and standardise the interpretation of immunostainings which is currently subjective and often not reproducible[3].

One of the disadvantages of TMA is that some information may be lost due to the small sample size. For heterogeneous samples, it is possible that not all cell types will be present in every small tissue slice. Despite this drawback, TMA technology will continue to be used in research laboratories as it provides a greater degree of consistency and standardisation than the immunoassaying of hundreds of individual slides, and the quantification and analysis of TMA is much easier than the analysis of immunostainings on hundreds of large tissue sections.

Applications

Torhorst and colleagues have used breast cancer as a model system for finding associations between molecular changes and clinical endpoints[3]. Results show that arrayed tissue samples can sufficiently represent their donor tumours to establish association between molecular alterations and clinical diagnosis. The objective of the study was to address limitations of the TMA technique, especially the sampling of potentially heterogeneous tumors, to determine to what extent TMA data can reproduce large section data, and to find out whether clinicopathological associations can be detected on TMA.

References:

1. Wan, W.H., Fortuna, M.B., Furmanski, P. A rapid and efficient method for testing immunohistochemical reactivity of monoclonal antibodies against multiple tissue samples simultaneously. J. Immunol. Methods (1987) Vol.103(1):121-129.
2. Kononen, J. et al. Tissue Microarrays for high-throughput molecular profiling of tumor specimens. Nature Medicine (1998) Vol.4(7):844-847.
3. Torhorst, J. *et al*. Tissue Microarrays for Rapid Linking of Molecular Changes to Clinical Endpoints. American Journal of Pathology (2001) Vol.159(6);2249-2256.