MELANOMA PROGRESSION TISSUE MICROARRAY (TMA)

Purpose:

To provide researchers with a tissue microarray that includes specimens from different stages of melanoma progression. The TMA is designed to investigate differences in prevalence of markers in various stages of melanoma progression from nevi to malignant melanoma.

Tissue samples:

The NCI has assembled a collection of 273 tissue specimens including nevi, primary melanomas and metastatic melanoma, including dermal, lymph node and visceral organ metastasis. The TMAs are constructed from archival, i.e. formalin fixed, paraffin embedded tissue specimens, obtained from patients who were naïve to prior chemotherapeutic/biologic therapy prior to resection of a lesion.

TMA design and construction:

There are four separate arrays-nevi, primary melanoma, melanoma that metastasized to distant sites, and melanoma that metastasized to lymph nodes. Each array is constructed with 1.00 mm cores of tissue, with no core replicates. Normal tissue control cores and several melanoma cell lines established from primary and metastatic melanomas are included in each array. The schematic maps of the arrays are attached. All lesions included in the array were reviewed by three pathologists and met stringent inclusion criteria. A test TMA consisting of a small number of primary and metastatic melanoma lesions for testing a technical approach is also available.

TMA beta test analysis:

The TMAs were serially sectioned at 6 micron thickness using a “water bath” method and placed on positively charged glass slides. Every 25^{th} section was stained with H&E for histopathology review. The number of tissue spots in which the desired tissue resides varies from section to section due to the heterogeneity of the specimens. Immunohistological staining with antibodies to several different antigens, known to be expressed in nevi and/or melanomas, was performed by two independent laboratories for beta testing of the TMAs. The results of the analyses showed general concordance with respect to pattern and level of staining, or lack thereof (beta test results are available upon request).

Clinical and pathological information:

All tissues included in the TMAs were derived from de-identified specimens, and demographic and clinical outcome data are not available. The TMA should be considered a screening array, with interpretation limited to the expression pattern of a selected biomarker in the different stages of melanoma progression.

The TMAs perform adequately for well validated immunohistochemical assays on formalin fixed, paraffin embedded tissue. Although *in situ* applications are possible, RNA integrity of the tissue cores is not known. The tissue specimens were obtained from multiple institutions, collected over many years. The tissue lacks the uniformity in specimen handling and processing that would be seen in a single institution collection.

Assays that have not been previously performed on formalin fixed, paraffin embedded tissue are not appropriate on these TMAs. The majority of the tissue cores are pigmented and the use of chromogens other than 3, 3’ Diaminobenzidine (DAB) should be considered.