Cooperative Human Tissue Network (CHTN)
Lymphoma survey TMA 1 (CHTN Lymphoma TMA 1)

Purpose:
To provide researchers with a survey tissue microarray of formalin-fixed paraffin-embedded samples of human lymphomas. Since surgical resection of lymphomas is not a standard clinical practice, not all possible lymphoma types are present in this array, which reflects the clinical experience of one institution. This TMA may detect strong trends in differential gene expression among cancer types; it is intended for pilot surveys and generation of hypotheses. This TMA is not designed to prove the utility of a marker for clinical prognosis.

Tissue samples:
The cases represent various subtypes of B and T cell non-Hodgkin lymphomas as well as Hodgkin lymphoma. Please see the separate document that contains the TMA grid, diagnostic classification and demographic data for the cases present in the TMA.

TMA design:
Each cancer case was sampled one time with a 2.0 mm needle cores in the original array design. There are four Lymphoma TMA-1 blocks slated for dispersal. Each array block is serially sectioned at 4 micron thickness. The histologic sections are placed on charged glass slides (Superfrost Plus, Fisher Scientific). At intervals, sections are stained and examined by a pathologist for quality assurance (QA) purposes.

The TMA also contains normal human tonsil as control tissue.

Notes:
These arrays are annotated with clinical data including the available results of immunohistochemical stains, flow cytometry and genetic analysis performed for clinical diagnosis.

Quality assurance procedures:
Due to the variability inherent to tissue samples and histologic methodology, some *of the tissue microarray sections will not contain all of the tissue spots in the original design.* The number of tissue spots in which the desired tissue types resides will vary from section to section.

The following guidelines are used during histologic quality assessment:
A tissue spot is defined as being present if tissue occupied at least 25% of the possible surface area OR if at least 10 cells of target tissue are present. Target tissue is defined as being present if at least 10 cells were present in a tissue spot. TMA slides are being released up to the histologic level in which there at least 35 cases remaining.

Copies of the QA scoring sheets are also available upon request. THE TISSUE SAMPLES HAVE BEEN ANONYMIZED, NO FURTHER DATA ON THE DONORS IS AVAILABLE OTHER THAN THAT FOUND IN THE ACCOMPANYING GUIDE SHEETS.

Guide sheets in Microsoft Excel format and H&E stained whole-slide images representative of the array are available on the CHTN TMA website: http://chtn.sites.virginia.edu/.

If despite our efforts there are fewer than the minimum number of target tissue samples on your array sections, please contact the CHTN Mid-Atlantic Division at (434) 924-9879.

Frequently asked questions:
Why aren't all there as many tissue spots on my section of the array as are listed on the TMA key? The key represents the original TMA design. Tissue cores are of various lengths, hence at deeper sections, some cores have been exhausted while others remain. In addition, some tissue spots may be lost during the process of transferring the TMA section to the glass slide.

Why isn't the target tissue type present in the tissue spot?
Although TMA manufacture is guided by a histologic section that represents the surface of the donor tissue, this target tissue may not be uniformly represented in the deeper sections of the tissue. This problem is greatest with small structures (e.g. breast ducts and lobules). Why doesn't the representative microscopic image of the target tissue exactly match the tissue spot on my TMA?
The representative images have been taken from a single spot from a single QA section from a single array. Four different replicate TMA blocks were made for this series, each of which has different tissue cores. Even the same tissue core at a deeper section would not exactly match a more superficial section due to the variability inherent in tissue architecture.

Can I use antigen retrieval methods (boiling, microwave, pressure cooker, etc) on these sections?
Yes.

Can I perform in situ hybridization on these sections?
Yes.

Definitions and abbreviations:
Donor block: a tissue paraffin block (see below) that contains tissue of the desired type to be placed into the tissue microarray.

Histologic section: a flat sheet of paraffin and embedded tissue cut from a paraffin block on a microtome. The thickness of the section can vary, but a typical thickness is 4 microns (micrometers).

QA: quality assurance

Recipient block: The blank paraffin block into which tissue cores are inserted to form the tissue microarray.

Tissue core: the cylindrical tissue sample removed from the donor block, which is placed in the recipient block.

TMA: tissue microarray. A recipient paraffin block into which tissue cores have been inserted in a gridded array.

Tissue paraffin block: a sample of tissue that has been fixed in formalin, processed to remove water, then infused with molten paraffin, which is allowed to harden within and around the tissue in a square mold. This is the standard method of preparing tissue for clinical histologic analysis. The paraffin block is subsequently cut on a microtome to produce thin histologic sections which are placed on glass slides. In the manufacture of TMAs, these become the donor blocks.

Tissue spot: the tissue sample present on a histologic section of a tissue microarray that corresponds with a tissue core.