

Sample Collection, Processing, and Storage for Large-Scale Studies: Biorepositories to Support Cancer Research

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The use of biomarkers in cancer research is rapidly advancing, with applications of biomarkers to studies of cancer etiology, detection, treatment, and prognosis. Due to the use of biomarkers for cancer research, there is growing recognition of the value of biospecimen banks. Specimen banks may exist in the context of ongoing studies based on specific hypotheses or be collected from cohorts of healthy individuals or from cancer patients for further, as yet undetermined, assessments and scientific aims.

The validity of results from biomarker studies using archived specimens, however, will likely be dependent on the integrity of the specimens and the manner in which they were collected, processed, and stored. For samples collected specifically to assess defined biomarkers, collection techniques can be tailored to the requirements for the specific biomarker, but for banks to be used later for as yet undetermined hypotheses, issues surrounding sample collection, processing, and storage require extensive forethought and planning. The effects of methods of collection, time from blood draw to processing and freezing, and storage conditions may all affect the integrity of biomarkers.

With the growing use of biospecimen banks and use of DNA and RNA in large studies, there is a need for consistent approaches to high-throughput extraction and handling methods. Whole-genome amplification is often used to increase quantities of DNA available; however, these approaches also require validation studies. Approaches to high-throughput handling merit studious attention, particularly because of the trend toward consortia and pooling of data and samples from numerous large studies.

In addition to consideration of maintenance of samples likely to yield valid results, specimen banks must also be structured so that all elements of patient rights, privacy, and

confidentiality are maintained, with an informed consent that is thorough and addresses potential use of samples. Furthermore, detailed tracking, specimen storage, and retrieval software are of the utmost importance for proper sample handling and management.

To address these issues, a methods workshop was held in 2006 at the 97th Annual Meeting of the AACR, with the goal of providing information on approaches to sample collection, processing, and storage, particularly in light of potential markers to be evaluated and requirements for maintaining high-quality analytes. Approaches to extraction and preservation of RNA and DNA and whole-genome amplification were also addressed as well as maintenance of sample inventories and bioinformatics. Christine Ambrosone (Roswell Park Cancer Institute, Buffalo, NY) chaired the session and began with an overview of approaches to establishing a biorepository at a cancer center. Susan Hankinson (Channing Laboratory, Boston, MA) then discussed collection, processing, and storage of biologic samples in epidemiologic studies using sex hormones, carotenoids, inflammatory markers, and proteomics as examples. Jimmie B. Vaught (National Cancer Institute, Bethesda, MD) discussed blood collection, shipment, processing, and storage. A presentation by Regina M. Santella (Columbia University, New York, NY) and Douglas Bell (National Institute of Environmental Health Sciences, Research Triangle Park, NC) covered approaches to DNA/RNA extractions and whole-genome amplification. The final talk was given by Michael Becich (University of Pittsburgh, Pittsburgh, PA) on cancer Biomedical Informatics Grid initiatives and specimen tracking and bioinformatics. Articles based on the first four presentations are included in this special *Cancer Epidemiology, Biomarkers & Prevention* Focus section.

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Note: This article is one of a series of articles that were presented at a methods workshop, "Sample Collection, Processing and Storage for Large Scale Studies: Biorepositories to Support Cancer Research," held during the AACR 97th Annual Meeting in 2006.

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