CPTC Program Milestones | 2002 – Present

April 2002

Proteomics Planning Workshop

A Proteomics Planning workshop was held among the National Cancer Institute, the National Human Genome Research Institute, and the National Institute of General Medical Sciences.

- There are many challenges in measuring proteins including proteins present at low abundance, membrane bound proteins, and quantifying absolute abundance of each protein including all splice variants and modified forms.

- In the short term, examining the protein profiles of disease cells and comparing them to normal profiles can offer diagnostic and prognostic tools in medicine. In the longer term, a complete interaction map of proteins in human cells will serve as an atlas for biological and medical exploration.

- Mass spectrometry is the analytical tool presently best suited for protein profiling and related studies. However, microarray and other technologies that offer alternative paths to proteomic information must be further developed.

- The organization and distribution of proteomic data must be improved, including standardized formats and ways of expressing uncertainties.

Bethesda, Maryland

Click here for workshop summary (http://www.genome.gov/10004801)

April 2003

Proteomic Technologies for Early Cancer Detection

The National Cancer Advisory Board established an ad hoc committee on National Advanced Technology Initiative for Cancer (NATIc) co-chaired by Eric Landers and Lee Hartwell. Recommendations by this committee included:

- Most biomarkers will be proteins. There is a need to increase our knowledge of proteins that are altered or abnormally expressed in cancer and those proteins that appear in easily identifiable body fluids.

- Advances in mass spectrometry offer one of the best opportunities for current technology for biomarker discovery. However, standards must be identified to facilitate replication of results across laboratories and to permit clinical implementation with other technologies like ELISA tests.

- There has been little attempt to develop standards in the field for tissue collection, sample preparation, internal calibration of instruments, or replication across laboratories or instruments.

- Standard tissue samples, use of mouse cancer models, and standardized reagents would aid data reproduction and comparison. A universally accessible database, algorithms for data analysis and standardization of data formats are essential.

Chantilly, Virginia

June 2004

Initial draft proposal for a Clinical Proteomics/Biomarker Discovery Initiative

The draft proposal was based on the following assumptions: clinical biomarkers exist in readily available fluids; panels of biomarkers will be needed to achieve high specificity and sensitivity; current technology is capable of discovering these panels, and; current application of this technology can be improved.

- A systematic approach to discovery requires teams of investigators sharing and aggregating data is needed to advance proteomics from a research tool to a robust and reliable clinical tool.

- Achieving biomarker discovery goals will require:
  - Setting standards
  - Ensuring quality control
  - Developing an informatics platform capable of aggregating and comparing data across laboratories

- An informatics platform is central and enabling to the success of the program.

- **Technology Assessment Core-** assess technologies central to biomarker discovery in order to provide laboratories with the best possible techniques and protocols. The ability of an integrated and optimized platform to identify biomarkers is to be assessed using mouse models of human cancer.

- Experimental protocols (including sample collection and processing), MS platforms, and analysis methods will need to be highly reproducible to allow statistical power for performing class distinction across a large number of samples in high dimensional proteomic data space.

- A "team science" approach involving multiple institutions that openly share data and resources is necessary in order to adequately address these issues.

Nov 2004

Clinical Proteomics and Biomarker Discovery in Cancer Research

Workshop outcomes included:

- NCI should develop multidisciplinary centers to help train the next generation of cross-disciplinary researchers rather than establish centers based on single expertise such as informatics or technology development.

- Standards for how to measure low concentration proteins as well as tissue collection and processing methods used to assay such proteins will need to be developed for emerging proteomic technologies.

- A consortium driven environment, rather than individual investigators, is the best scenario for developing probes/targets, setting standards, and comparing technologies.

- NCI should set up a central laboratory (*now established at the National Institute of Standards and Technology*) and data repository (*currently at the NCICB*) and act as a disinterested party for data sharing and dissemination.

- The technology to ensure homogeneity of human samples does not yet exist, which is why it is important to work on mouse models in parallel with human studies. If the protocols for collecting and storing human tissue samples were robust enough, the same level of homogeneity could be reached with human samples as with mouse samples.

East Coast – Bethesda, Maryland
West Coast – Menlo Park, California

Jan 2005

Clinical Proteomics Technologies Team Initiative proposal

Feb 2005

Proteomic Technologies Informatics Workshop

This workshop focused on information management strategies that can make proteomic data the most useful for developing platforms for the early detection, monitoring, and therapy of cancer.

The goals and objectives were:

- Prioritize the development agenda of a mouse model serum and tissue proteomics data repository

- Identify the needs of a general clinical proteomics data repository that are not accommodated within the mouse proteomic technology consortia

- Outline a roadmap for developing a general clinical proteomics data repository

- Discuss proteomic data management approaches and develop strategies to frame this information to accelerate discovery and educate the public, and

- Discuss ways to establish standards in proteomics to minimize experimental variability, share data and information, and facilitate partnerships

Seattle, Washington

Click here for meeting summary
(http://www.capconcorp.com/nci05/summary.html)

March 2005

Considerations for study design and technology evaluation presented to the NCI Board of Scientific Advisors

BSA recommended that the NCI must a leadership position within the proteomics program and offer robust support for standardization, integration, and focus. Addressing issues in experimental/study design, and the development of high-quality reagents and reference materials was determined to be essential. Additionally, informatics standards need to be developed and approaches that work across platforms.

June 2005

Clinical Proteomic Technology Initiative Presented to and Approved by the NCI Board of Scientific Advisors

Dec 2005

Proteomic Technologies Reagents Resource Workshop

This workshop was held to identify the cancer research community's expressed needs for validated and well characterized affinity capture reagents (e.g. antibodies, aptamers, and affibodies) to advance proteomics research platforms for the prevention, early detection, treatment, and monitoring of cancer. The workshop brought together leading scientists in proteomics research to discuss model systems for evaluating and delivering resources for reagents to support MS and affinity capture platforms.

Chicago, IL

Click here for white paper (http://www.mcponline.org/cgi/reprint/T600020-MCP200v1.pdf)

April 2006

Argonne National Laboratory begins protein production

Polanski and Anderson, Biomarker Insights 2:1-48; 2006
(http://www.ncbi.nlm.nih.gov/sites/entrez)

Oct 2006

CPTC Program is launched

CPTAC Lead Centers:
- The Broad Institute of MIT and Harvard
- Memorial Sloan-Kettering Cancer Center
- Vanderbilt University School of Medicine
- Purdue University
- University of California, San Francisco

Advanced Proteomic Platforms:
- University of Houston
- Northeastern University

University of California, Los Angeles
Institute for Systems Biology
Emory University
Battelle Pacific Northwest Laboratories
Michigan State University

Computational Sciences:

University of Maryland, College Park
College of William and Mary
Massachusetts Institute of Technology
University of Michigan
Fred Hutchinson Cancer Research Center
University of Colorado at Boulder
Vanderbilt University
University of Virginia

Oct 2006

Governing body developed

Program Coordinating Committee (PCC) members:

Steve Carr, Ph.D., Broad Institute
Susan Fisher, Ph.D., University of California, San Francisco
Dan Liebler, Ph.D., Vanderbilt University
Paul Tempst, Ph.D., Memorial Sloan-Kettering Cancer Center
Fred Regnier, Ph.D., Purdue University
Henry Rodriguez, Ph.D., M.B.A., National Cancer Institute

Ad-Hoc PCC members:

Lee Hartwell, Ph.D., Fred Hutchinson Cancer Research Center
Gordon Mills, M.D., Ph.D., M.D. Anderson Cancer Center
Joe Gray, Ph.D., Lawrence Berkeley National Laboratory
David Ransohoff, M.D., University of North Carolina Lineberger Comprehensive Cancer Center

Oct 2006

First inter-laboratory study

Benchmarking platforms

Nov 2006

Inter-lab Working Groups are established

Working Groups:

Discovery
Verification
Digestion
Protein Standards
Post-Translational Modifications
Data Analysis, Storage, and Dissemination
Biospecimens
Analyte Selection
Cell Lysate

Feb 2007

Second inter-lab study

Assessing discovery platform variability

April 2007

Memorandum of Understanding Between the National Cancer Institute and the Food and Drug Administration

MOU published in the Federal Register

June 2007

CPTAC biospecimen collection protocol is established and implemented

Click here to view the poster pdf.

http://brnsymposium.com/meeting/brnsymposium/docs/2008pres/Poster16_CPTAC_annual_mtg.pdf

July 2007

Third inter-lab study

Assessing variability in a complex material

Sept 2007

Fourth inter-lab study

Benchmarking verification platforms

Oct 2007

CPTC 2007 First Annual Meeting

This inaugural event drew over 170 researchers from private and public organizations from around the country, along with international leaders, to discuss progress and address the hurdles proteomics faces. The meeting highlighted significant progress to date from investigator-initiated work along with multi-institutional, cross disciplinary team-based efforts to optimize and benchmark current proteomic technologies. In addition, unique attributes to the program included the unparalleled open data sharing and collaboration between all members - not just parallel play, but substantive cooperation.

Washington, D.C.

Click here for further information

http://www.capconcorp.com/meeting/proteomic2007/

Nov 2007

Fifth inter-lab study

Assessing limits of detection in a complex material

July 2008

Sixth inter-lab study

Assessing detection efficiency for discovery platforms

Aug 2008

Proteomic Data Release and Sharing Policy International Summit

On August 14, 2008, the NCI sponsored a summit in the Netherlands that included members from the international proteomics community with one goal: To define what it would take to have proteomics data released into the public

domain as soon as they are produced. This international one-day summit was a major step forward for the proteomics community. It is anticipated that after this process and the release of a white paper that the principles developed at this meeting can be readily adopted by the field as guidelines for releasing and sharing proteomics data.

J Proteome Res. 2008 Nov;7(11):4609. Epub 2008 Oct 7
(http://www.ncbi.nlm.nih.gov/pubmed/18837532)

Sept 2008

Seventh inter-lab study

Assessing variability in verification platforms

Oct 2008

CPTC 2008 Second Annual Meeting

CPTC held its second annual meeting in Cambridge, Mass. on October 28–29, 2008, bringing together more than 200 participants representing the full gamut of scientific fields that contribute to the initiative's mission to review the technological progress made over the previous year. Giving a sense of the links between CPTC and other technology focused initiatives supported by NCI, the first day of the meeting was held jointly with members of NCI's Innovative Molecular Analysis Technologies (IMAT) program.

Both days featured keynote addresses by researchers speaking on their experiences in integrated research. David Altshuler, M.D., Ph.D., a founding member of the Eli M. and Edythe L. Broad Institute of MIT and Harvard and director of the institute's Program in Medical and Population Genetics, spoke of the lessons learned from conducting large-scale genomics research and how those lessons could apply to large-scale proteomics. The second day's keynote, by Vamsi Mootha, M.D., of the Broad Institute and Massachusetts General Hospital, focused on integrative genomic, proteomic, and metabolomic research on mitochondrial diseases.

Cambridge, MA

Click here for further information
(http://www.capconcorp.com/meeting/proteomic2008/)

Nov 2008

New Members Added to Ad-Hoc Program Coordinating Committee

Amanda G. Paulovich, MD, PhD, Fred Hutchinson Cancer Research Center
Leigh Anderson, PhD, Plasma Proteome Institute
Steven J. Skates, PhD, Massachusetts General Hospital
Bradford W. Gibson, PhD, Buck Institute of Age Research

Proteomic Reagents and Resources Core
March 2008

Antibody production begins

Three monoclonal antibodies are being developed per antigen

May 2008

Tissue Array Research Program at NCI Center for Cancer Research partnership is formed

Sept 2008

Harvard Institute of Proteomics collaboration is formed

Sept 2008

Human Protein Atlas collaboration is formed

Oct 2008

Antibodies are made available through Developmental Studies Hybridoma Bank at University of Iowa

Oct 2008

Reagent Data Portal is launched

Click here for access to portal (http://cpti.abcc.ncifcrf.gov/)

Public-Private Partnerships

Nov 2006

2007 SBIR Contract Proposals Solicited

Topic 238 - Development of Clinical Automated Multiplex Affinity Capture Technology for Detecting Low Abundance Cancer-related Proteins/Peptides
Topic 239 – Development of Alternative Affinity Capture Reagents for Cancer Proteomics Research

July 2007

2007 SBIR Contract Proposals Awarded

Topic 238:

Meso Scale Diagnostics
Sequenom Inc.
Quadraspec Inc.
Rules-Based Medicine Inc.

Topic 239:

Allele Biotechnology & Pharmaceuticals
Accacia International Inc.

Nov 2007

2008 SBIR Contract Proposals Solicited

253 – Advances in Protein Expression of Post-Translationally Modified Cancer Related Proteins
254 – Development of Clinical Quantitative Multiplex High-Throughput Mass Spectrometric Immunoassay for Detecting Low Abundance Cancer Related Proteins/Peptides in Bodily Fluids

Nov 2008

2009 SBIR Contract Proposals Solicited

268 - Novel Antibody Epitope Mapping Technologies
269 - Development of Novel Protein Expression Technologies for Glycosylated Cancer Related Proteins
270 - Peptide Aptamers: New Tools to Capture and Study Protein Interactions in Lieu of Immunological Reagents