

An AACR Special Conference on

Translation of the Cancer Genome: Scientific, Clinical, and Operational Challenges

October 15-18, 2011

Hyatt Regency San Francisco

San Francisco, CA

Saturday, October 15

1:00 p.m.-4:00 p.m.

Educational Session

Grand Ballrooms B&C

Chairperson: Tona M. Gilmer, GlaxoSmithKline, Research Triangle Park, NC

Challenges in analyzing cancer genomes for clinical decisions

Gad Getz, Broad Institute, Cambridge, MA

Cancer genomics in the TCGA, TARGET, and ICGC projects

David Haussler, Howard Hughes Medical Institute, Santa Cruz, CA

Determinants of response and resistance in drug discovery and development

Tona M. Gilmer

Bridging the gap between cancer genomics and drug discovery

Giulio F. Draetta, University of Texas MD Anderson Cancer Center, Houston, TX

Applying massively parallel sequencing technology to the study of cancer genomes

Elaine Mardis, Washington University School of Medicine, St. Louis, MO

6:00 p.m.-8:00 p.m.

Session 1: Biology and Genomics of Cancer Evolution

Grand Ballrooms B&C

Chairperson: Elaine Mardis, Washington University School of Medicine, St. Louis, MO

Genomic compartmentalization of epigenetic alterations in cancer

Peter W. Laird, University of Southern California, Los Angeles, CA

Evolution of the cancer genome

Elaine Mardis

Dealing with intra- and intertumoral heterogeneity

Gordon B. Mills, University of Texas MD Anderson Cancer Center, Houston, TX

Exome sequencing and integrative mutational profiling of lethal castrate-resistant prostate cancer*

Catherine Grasso, Michigan Center for Translational Pathology, Ann Arbor, MI

Genome-wide translocation sequencing reveals mechanisms of chromosome breaks and rearrangements in B cells*

Yu Zhang, Harvard Medical School, Boston, MA

*Short talks from proffered papers

Sunday, October 16

8:00 p.m.-9:30 p.m. **Welcome Reception**
Garden Room A&B

7:00 a.m.-8:00 a.m. **Continental Breakfast**
Market Street Foyer

8:00 a.m.-9:00 a.m. **Keynote Presentation 1**
Grand Ballrooms B&C

Organizing large projects across boundaries: The particle physics experience
Pier J. Oddone, Fermilab, Batavia, IL

9:00 a.m.-11:00 a.m. **Session 2: Functional Genomics I**
Grand Ballrooms B&C
Chairperson: Scott W. Lowe, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY

Functional genomics to decipher cancer dependencies and mechanisms
William C. Hahn, Dana-Farber Cancer Institute, Boston, MA

Constructing and deconstructing cancer using mouse models and RNA interference
Scott W. Lowe

Target discovery through functional genomics
Timothy Heffernan, Dana-Farber Cancer Institute, Boston, MA

From cancer genomes to tumors: Polygenic validation of human cancer mutations by in vivo tumorigenesis*
Su Kit Chew, Wellcome Trust Sanger Institute, Hinxton, United Kingdom

Exome sequencing identifies frequent mutation of ARID1A in molecular subtypes of gastric cancer*
Suet Leung, University of Hong Kong, Hong Kong, China

*Short talks from proffered papers

11:00 a.m.-11:15 a.m. **Break**
Market Street Foyer

11:15 a.m.-12:45 p.m. **Session 3: Functional Genomics II**
Grand Ballrooms B&C
Chairperson: David A. Largaespada, University of Minnesota, Minneapolis, MN

Uncovering cancer genes and pathways using unbiased, forward genetic screens
David A. Largaespada

Translational genomics using population-based tumor models
Murray O. Robinson, AVEO Pharmaceuticals, Inc., Cambridge, MA

Characterization of BRAF and NRAS models of zebrafish melanoma through exome sequencing*
Jennifer Yen, Wellcome Trust Sanger Institute, Hinxton, United Kingdom

Cancer genome-based multigenic models of colon cancer in Drosophila*
Erdem Bangi, Mount Sinai School of Medicine, New York, NY

12:45 p.m.-2:30 p.m. **Lunch on own/Free time**

2:30 p.m.-4:30 p.m. **Session 4: Functional Genomics III**
Grand Ballrooms B&C
Chairperson: Lynda Chin, University of Texas MD Anderson Cancer Center, Houston, TX

Measuring the modeling life-death decisions in single cells
Peter K. Sorger, Harvard Medical School, Boston, MA

Translating the cancer genome
Lynda Chin

Genetic mining of the cancer genome: New entry points for anticancer therapy
Thomas (Trey) F. Westbrook, Baylor College of Medicine, Houston, TX

Optimizing molecularly targeted cancer therapy using functional genomics*
Trevor Bivona, University of California, San Francisco, CA

A Sleeping Beauty transposon mutagenesis screen suggests involvement of the imprinted Dlk1-Dio3 domain in hepatocellular carcinoma development*
Jesse Riordan, University of Iowa, Iowa City, IA

4:30 p.m.-6:30 p.m. **Poster Session A/Reception**
Bayview A&B

*Short talks from proffered papers

Monday, October 17

7:00 a.m.-8:00 a.m. **Continental Breakfast**
Market Street Foyer

8:00 a.m.-9:00 a.m. **Keynote Presentation 2**
Grand Ballrooms B&C

Genomic determinants of malignant progression in pancreatic cancers
Douglas Hanahan, Swiss Institute for Experimental Cancer Research, Lausanne, Switzerland

9:00 a.m.-11:00 a.m. **Session 5: Target Validation and Biology**
Grand Ballrooms B&C
Chairperson: Frank McCormick, University of California, San Francisco, CA

Recurrent gene fusions in prostate cancer: Implications for personalized medicine
Arul M. Chinnaiyan, University of Michigan, Ann Arbor, MI

Targeting the undruggable: Lessons from Ras
Frank McCormick

Identification of high-value targets for oncology drug discovery
Markus Warmuth, H3 Biomedicine, Cambridge, MA

Functional characterization of WAC, a candidate tumor suppressor gene identified by transposon-based genetic screens for intestinal tumors in mice*
Caitlyn Conboy, University of Minnesota, Minneapolis, MN

Viability screens in leukemic and breast cancer cells with pooled lentiviral shRNA libraries identify potential therapeutic targets and synergistic lethal interactions*
Alex Chenchik, Celecta, Inc., Mountain View, CA

11:00 a.m.-1:00 p.m. **Lunch on own/Free time**

*Short talks from proffered papers

1:00 p.m.-3:00 p.m.

Session 6: Hot Topics

Grand Ballrooms B&C

Chairperson: Kornelia Polyak, Dana-Farber Cancer Institute, Boston, MA

Chemical and mechanical cues regulate signaling to drive malignancy

Valerie M. Weaver, University of California, San Francisco, CA

Diversity in breast cancer: Mechanisms and clinical relevance

Kornelia Polyak

Variants in the germline genome that confer large risk of several cancers, including ovarian cancer and gliomas

Kári Stefánsson, deCODE genetics Reykjavik, Iceland

RetroSeq: A tool to discover somatic insertion of retrotransposons*

Elena Helman, Harvard-MIT Health Sciences & Technology, Cambridge, MA

Selection of somatic mtDNA mutations in cancer development*

Estella Chen-Quin, Kennesaw State University, Kennesaw, GA

3:00 p.m.-3:30 p.m.

Break

Market Street Foyer

3:30 p.m.-5:00 p.m.

Session 7: Defining the Clinical Path Hypothesis

Grand Ballrooms B&C

Chairperson: Joe W. Gray, Oregon Health & Science University Knight Cancer Institute, Portland, OR

Models and processes to facilitate preclinical to clinical translation

Joe W. Gray

Developing genomic signatures into clinically actionable markers: Lessons from glioblastoma

Cameron W. Brennan, Memorial Sloan Kettering Cancer Center, New York, NY

Phase II study of therapy selected by molecular profiling in patients with previously treated metastatic pancreatic cancer: SU2C-001*

Michael Barrett, Translational Genomics Research Institute, Phoenix, AZ

Next-generation diagnostics: Expanding clinical actionability of the cancer genome*

Alex Parker, Foundation Medicine Inc., Cambridge, MA

5:00 p.m.-7:00 p.m.

Poster Session B/Reception

Bayview A&B

*Short talks from proffered papers

Tuesday, October 18

7:00 a.m.-8:00 a.m. **Continental Breakfast**
Market Street Foyer

8:00 a.m.-9:00 a.m. **Keynote Presentation 3**
Grand Ballrooms B&C

The genetic basis for cancer therapeutics: The opportunity and the challenge
William R. Sellers, Novartis Institutes for BioMedical Research, Cambridge, MA

9:00 a.m.-11:00 a.m. **Session 8: Genomics in Clinical Trial Design**
Grand Ballrooms B&C
Chairperson: William R. Sellers, Novartis Institutes for BioMedical Research, Cambridge, MA

Clinical trials in early-stage cancer patients: Future opportunities and challenges
Peter Blume-Jensen, Metamark Genetics, Inc., Cambridge, MA

The ALK story: A new paradigm for the development of targeted therapies in NSCLC
Alice T. Shaw, Massachusetts General Hospital Cancer Center, Boston, MA

Integrated “omics” profiles for patient stratification
Anne-Lise Børresen-Dale, Institute for Cancer Research, Oslo, Norway

Personalized oncology through integrative high-throughput sequencing: A pilot study*
Sameek Roychowdhury, University of Michigan, Ann Arbor, MI

Identification of predictive biomarkers and development of patient stratification assay for co-targeting mTOR and AKT*
Theresa Zhang, Merck, Boston, MA

11:00 a.m. **Departure**

*Short talks from proffered papers