Treating Cancer in the Era of Omics

Effie Liakopoulou MD, PhD, FRCPath, CMM

Transforming Lives

Stem Cell Transplantation

Aim of treatment for Cancer

- To cure the disease
- Prolong survival
- Improve quality of life

Removal of T cells



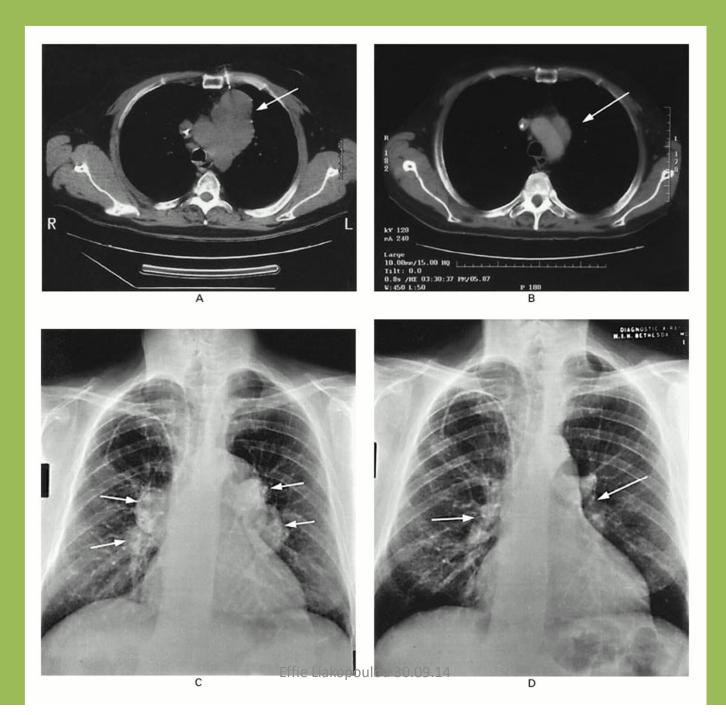


- GvHD
- Early mortality

- Infection
- Engraftment



Pre SCT



Day +276
Post SCT







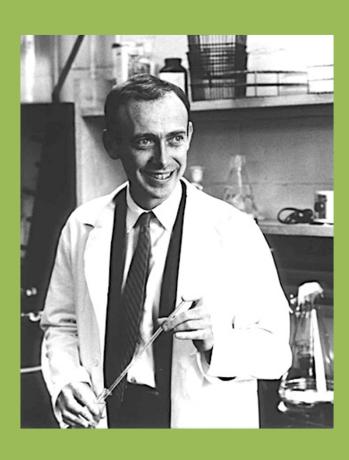


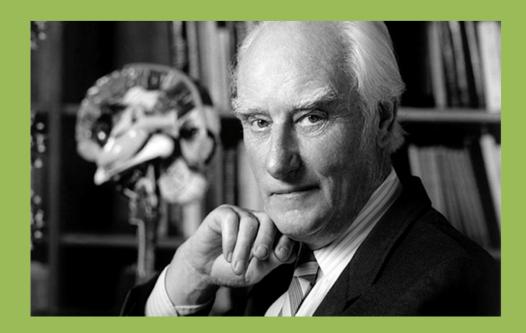
Effie Liakopoulou 30.09.14

2011: 40 Years War on Cancer



2012: 50 Years Genetic Revolution

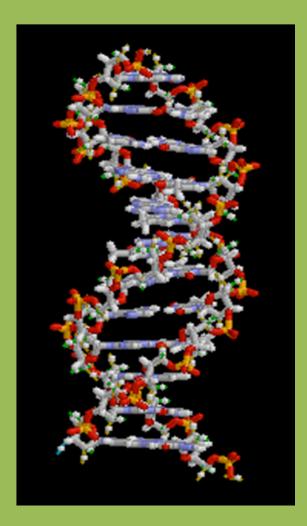




2012: National Science Award



Watson, Crick & Wilkins Achievement

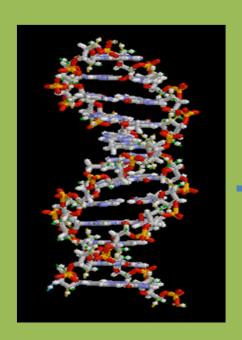


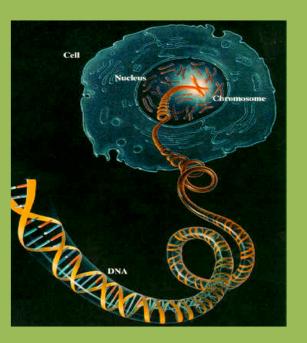
Molecular Structure of DNA

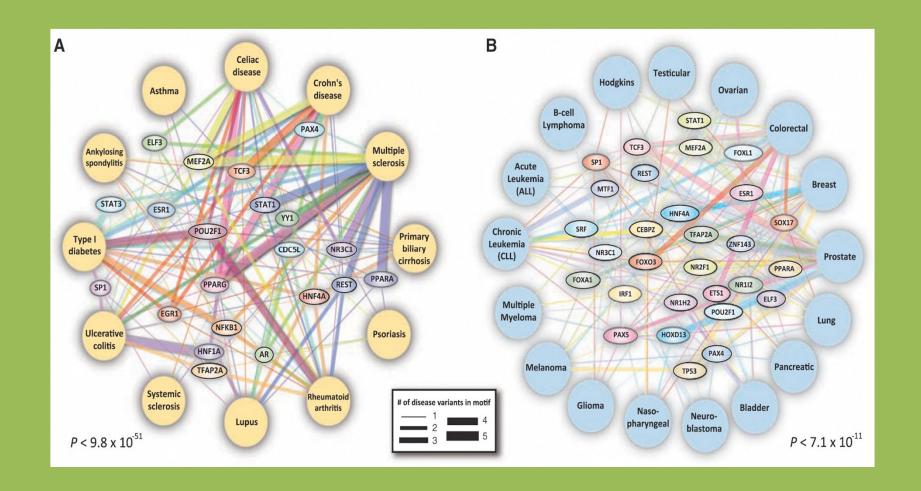
Hood's Achievement

DNA Molecular Structure

Structure of Human Genome







Encyclopedia of DNA Elements

ENCODE

ENCODE in Numbers

- 30 Km (22miles) long
- 16 m (48 ft) wide paper to print the data generated !!

There is No Junk!

Genetic Revolution

Will we need another 50 Years to make sense of the data?

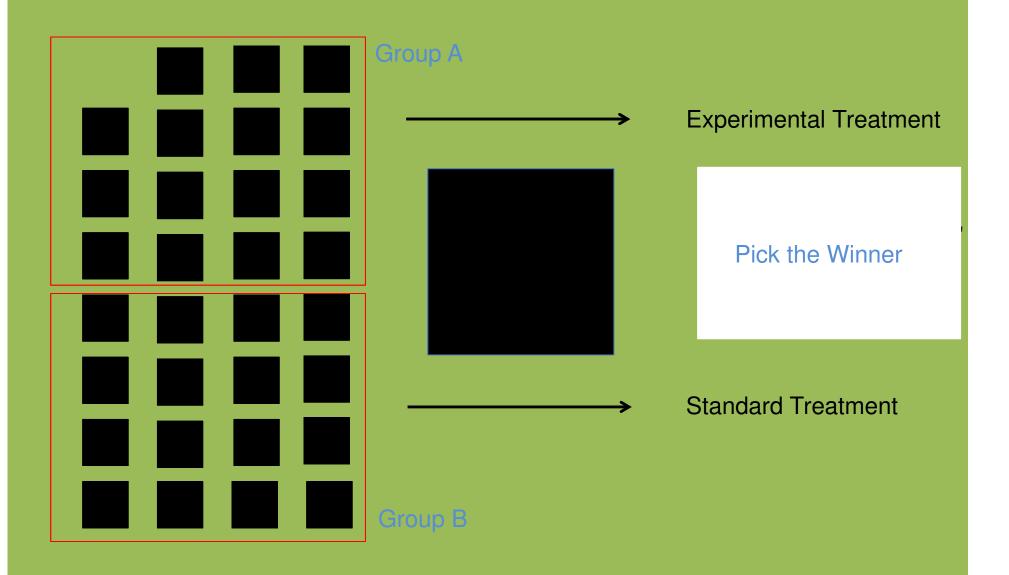
Genetic Revolution Will we need another 50 Years to make sense of the data?

- From Fragmented data Global information
- From Biological Mechanisms
 Medicines

From Sublime insight Infinite Library of Life

NEED
for technological applications
to facilitate progress

Cancer as a Black Box



The New York Times

Research

WORLD	U.S.	N.Y. / REGION	BUSINESS	TECHNOLOGY	SCIENCE	HEALTH	SPORTS	OPINION
Search Health 3,000+ Topics							Inside Health	
					Go	Res	search Fi	tness & Nutriti

TARGET CANCER

New Drugs Stir Debate on Rules of Clinical Trials



Monica Almeida/The New York Times Je

Two Cousins, Two Paths Thomas McLaughlin, left, was given a promising experimental drug to treat his lethal skin cancer in a medical trial; Brandon Ryan had to go without it.

By AMY HARMON

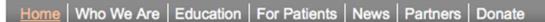
Published: September 18, 2010

Growing up in California's rural Central Valley, the two cousins spent summers racing dirt bikes and Christmases at their grandmother's on the coast. Endowed with a similar brash charm, they bought each other matching hardhats and sought iron-working jobs together. They shared a love for the rush that comes with hanging steel at dizzying heights, and a knack for collecting speeding tickets.

F RECOMMEND
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SEND TO PHONE
⊕ PRINT

Can we do better?







If everyone is thinking alike, then somebody isn't thinking.

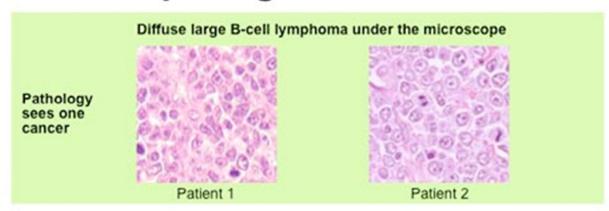
-George S. Patton

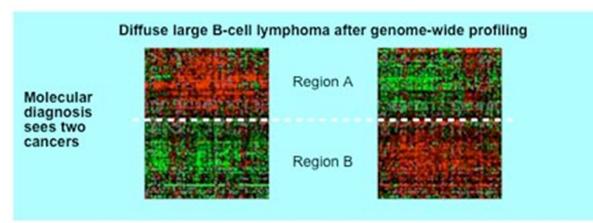
www.personaloncology.org

"It's far more important to know what person the disease has than what disease the person has."

Hippocrates

Can Genome-Wide Profiles Help Diagnose Cancer?







How Many Different Kinds of Lung Cancer?



How Many Different Kinds of Lung Cancer?

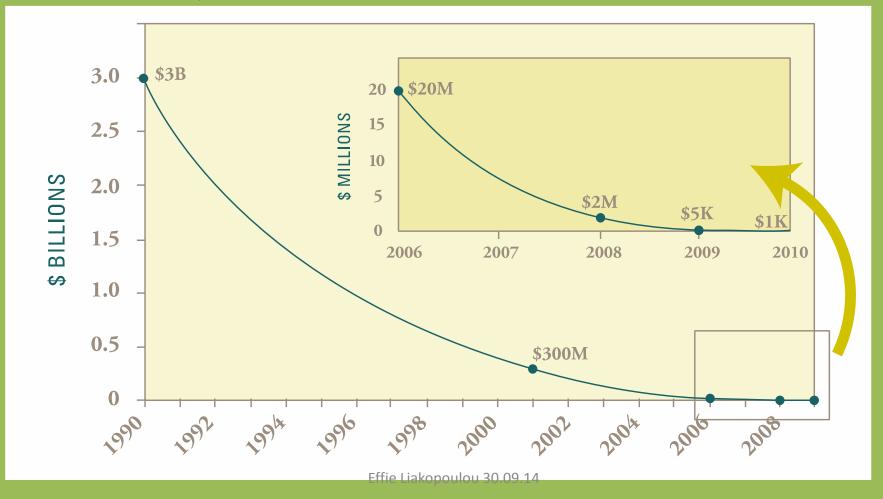


Transforming Medicine

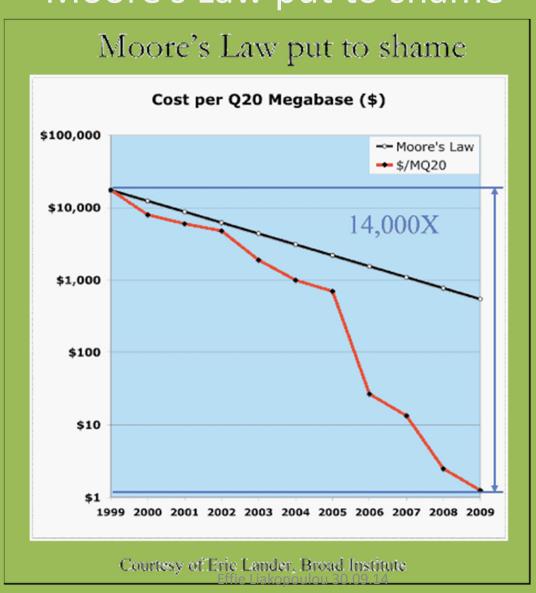
4 Main Drivers

Transforming Medicine #1 The Shrinking Cost of DNA Sequencing

Towards the \$1000 Genome



Transforming Medicine #1 Moore's Law put to shame



Every Cancer is Different

nature

Vol 456 6 November 2008 doi:10.1038/nature07485

ARTICLES

DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome

Timothy J. Ley^{1,2,3,4}*, Elaine R. Mardis^{2,3}*, Li Ding^{2,3}, Bob Fulton³, Michael D. McLellan³, Ken Chen³, David Dooling³, Brian H. Dunford-Shore³, Sean McGrath³, Matthew Hickenbotham³, Lisa Cook³, Rachel Abbott³, David E. Larson³, Dan C. Koboldt³, Craig Pohl³, Scott Smith³, Amy Hawkins³, Scott Abbott³, Devin Locke³, LaDeana W. Hillier^{3,8}, Tracie Miner³, Lucinda Fulton³, Vincent Magrini^{2,3}, Todd Wylie³, Jarret Glasscock³, Joshua Conyers³, Nathan Sander³, Xiaoqi Shi³, John R. Osborne³, Patrick Minx³, David Gordon⁸, Asif Chinwalla³, Yu Zhao¹, Rhonda E. Ries¹, Jacqueline E. Payton⁵, Peter Westervelt^{1,4}, Michael H. Tomasson^{1,4}, Mark Watson^{3,4,5}, Jack Baty⁶, Jennifer Ivanovich^{4,7}, Sharon Heath^{1,4}, William D. Shannon^{1,4}, Rakesh Nagarajan^{4,5}, Matthew J. Walter^{1,4}, Daniel C. Link^{1,4}, Timothy A. Graubert^{1,4}, John F. DiPersio^{1,4} & Richard K. Wilson^{2,3,4}

Acute myeloid leukaemia is a highly malignant haematopoietic tumour that affects about 13,000 adults in the United States each year. The treatment of this disease has changed little in the past two decades, because most of the genetic events that initiate the disease remain undiscovered. Whole-genome sequencing is now possible at a reasonable cost and timeframe to use this approach for the unbiased discovery of tumour-specific somatic mutations that alter the protein-coding genes. Here we present the results obtained from sequencing a typical acute myeloid leukaemia genome, and its matched normal counterpart obtained from the same patient's skin. We discovered ten genes with acquired mutations; two were previously described mutations that are thought to contribute to tumour progression, and eight were new mutations present in virtually all tumour cells at presentation and relapse, the function of which is not yet known. Our study establishes whole-genome sequencing as an unbiased method for discovering cancer-initiating mutations in previously unidentified genes that may respond to targeted therapies.

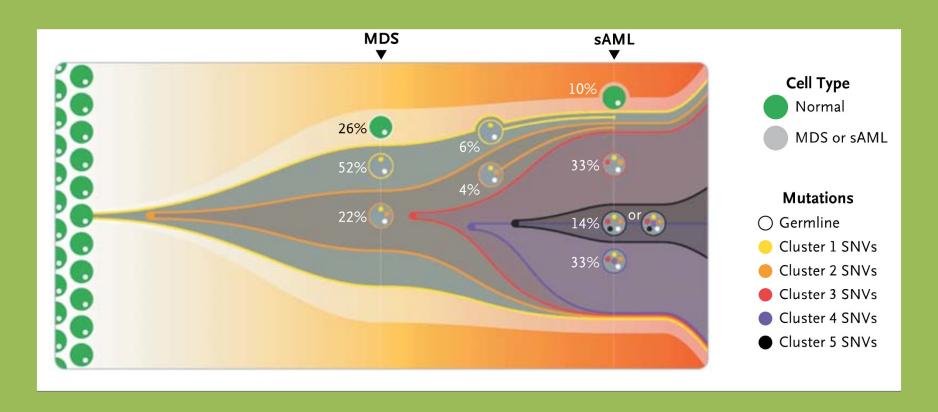
ORIGINAL ARTICLE

Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome

Elaine R. Mardis, Ph.D., Li Ding, Ph.D., David J. Dooling, Ph.D., David E. Larson, Ph.D., Michael D. McLellan, B.S., Ken Chen, Ph.D., Daniel C. Koboldt, M.S., Robert S. Fulton, M.S., Kim D. Delehaunty, B.A., Sean D. McGrath, M.S., Lucinda A. Fulton, M.S., Devin P. Locke, Ph.D., Vincent J. Magrini, Ph.D., Rachel M. Abbott, B.S., Tammi L. Vickery, B.S., Jerry S. Reed, M.S., Jody S. Robinson, M.S., Todd Wylie, B.S., Scott M. Smith, Lynn Carmichael, B.S., James M. Eldred, Christopher C. Harris, B.S., Jason Walker, B.A., B.S., Joshua B. Peck, M.B.A., Feiyu Du, M.S., Adam F. Dukes, B.A., Gabriel E. Sanderson, B.S., Anthony M. Brummett, Eric Clark, Joshua F. McMichael, B.S., Rick J. Meyer, M.S., Jonathan K. Schindler, B.S., B.A., Craig S. Pohl, M.S., John W. Wallis, Ph.D., Xiaoqi Shi, M.S., Ling Lin, M.S., Heather Schmidt, B.S., Yuzhu Tang, M.D., Carrie Haipek, M.S., Madeline E. Wiechert, M.S., Jolynda V. Ivy, M.B.A., Joelle Kalicki, B.S., Glendoria Elliott, Rhonda E. Ries, M.A., Jacqueline E. Payton, M.D., Ph.D., Peter Westervelt, M.D., Ph.D., Michael H. Tomasson, M.D., Mark A. Watson, M.D., Ph.D., Jack Baty, B.A., Sharon Heath, William D. Shannon, Ph.D., Rakesh Nagarajan, M.D., Ph.D., Daniel C. Link, M.D., Matthew J. Walter, M.D., Timothy A. Graubert, M.D., John F. DiPersio, M.D., Ph.D., Richard K. Wilson, Ph.D., and Timothy J. Ley, M.D.

N ENGL J MED 361;11 NEJM.ORG SEPTEMBER 10, 2009

Clonal Evolution from MDS to sAML



One Size Does Not Fit All

PATIENTS CAN RESPOND D	IFFERENTLY	Y TO THE SAME MEDICINE				
ANTI-DEPRESSANTS (SSRI's)	38%	†††††††				
ASTHMA DRUGS	40%	ŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢ				
DIABETES DRUGS	43%	ŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢ				
ARTHRITIS DRUGS	50%	ŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢ				
ALZHEIMER'S DRUGS	70%	ŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢ				
CANCER DRUGS	75%	ŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢ				
Percentage of the patient population for which a particular drug in a class is ineffective, on average						

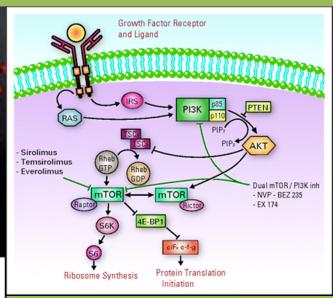
Source of data: Brian B. Spear, Margo Heath-Chiozzi, Jeffrey Huff, "Clinical Trends in Molecular Medicine, Volume in Kopy 12001, Pages 201-204.

Transforming Medicine #2 Targeted Therapies

EGFR

Geftinib -Geftinib -Growthib -Canertinib -Neratinib -Erses -BIBW2992 Protein synthesis: Cell survival Cell proliferation

PI3K/AKT/mTOR



VEGF-R₁ NRP₁₂ R₂ Sunitinib Sorafenib -Sorafenib -Vandetanib

-Vatalanib

-Axitinib -Semaximab -AMG 706

AFlibercept

Bevacizumab

HuMV833

Lymphangiogenesis

Other RTKs

Effie Liakopoulou 30.09.14

and angiogenesis

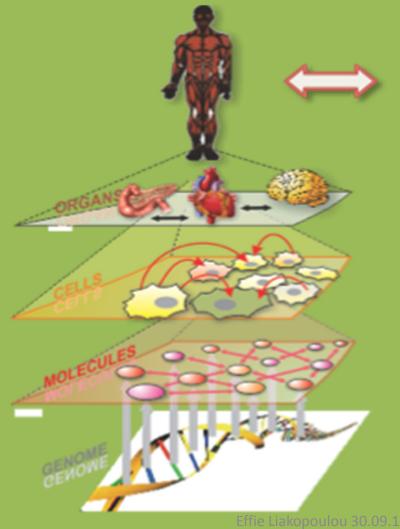
Some Rationally Designed Cancer Therapies

- Chronic myelogenous leukemia (Bcr-Abl)
- c-Kit positive gastrointestinal stromal tumor
- Her2 positive breast cancer
- EGFR mutated lung and colorectal cancer
- Alk mutated lung cancer
- BRAF mutated melanoma

Transforming Medicine #3:

Systems Biology

The Network of Networks



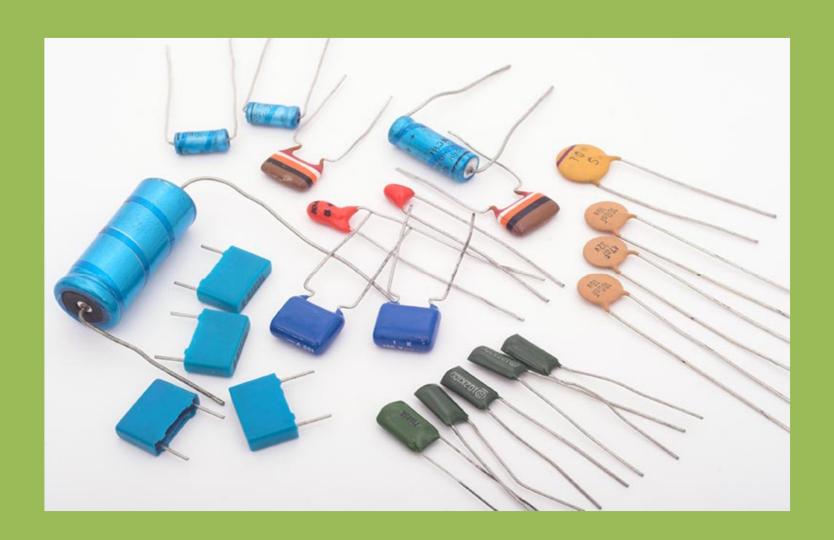


Networks organize, integrate and model data to enormously increase the signal to noise

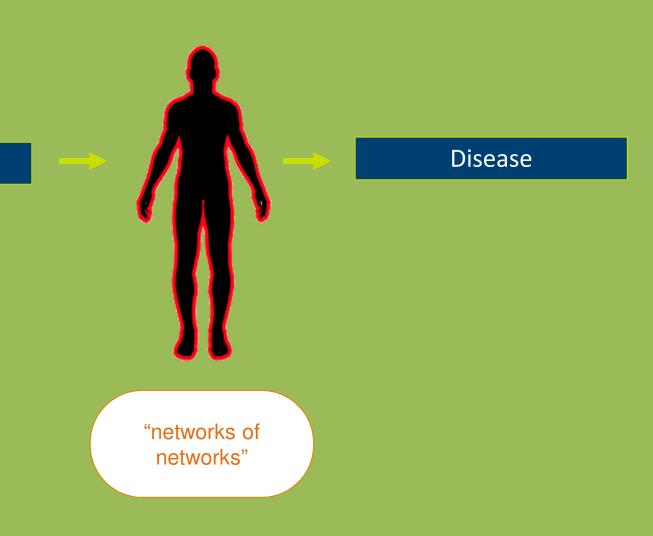


Radio Waves

Sound Waves



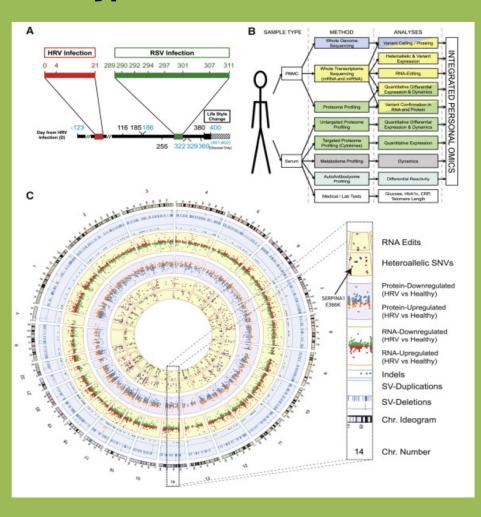




Health

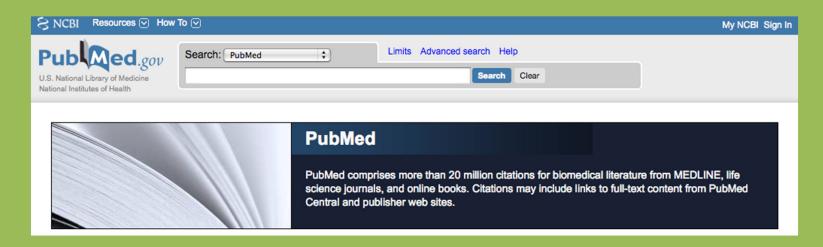
Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes

1 Patient, 400 days, 3 billion data points



Transforming Medicine #4: The Internet







Targeted Therapy Finder - Melanoma

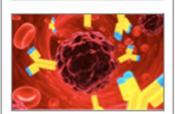
Questions? Feedback? Problems?





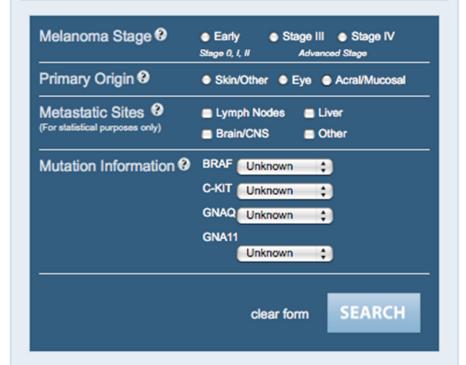
Learn More:
Patients | Physicians

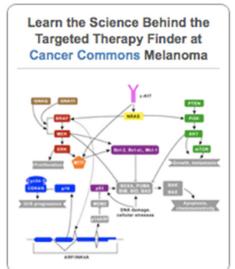
Breaking News: Ipilimumab/Yervoy Approved for Melanoma



Ipilimumab/Yervoy, an

Provide Melanoma Information













Keith T Flaherty MD

Partners in Personal Oncology



Tony Blau



Greg Foltz



Effie Liakopoulou



Marty Tenenbaum



Lee Hood



Brian Druker



Mike Bisesi



Houda Hachad



Bruce Avolio



Sibel Blau

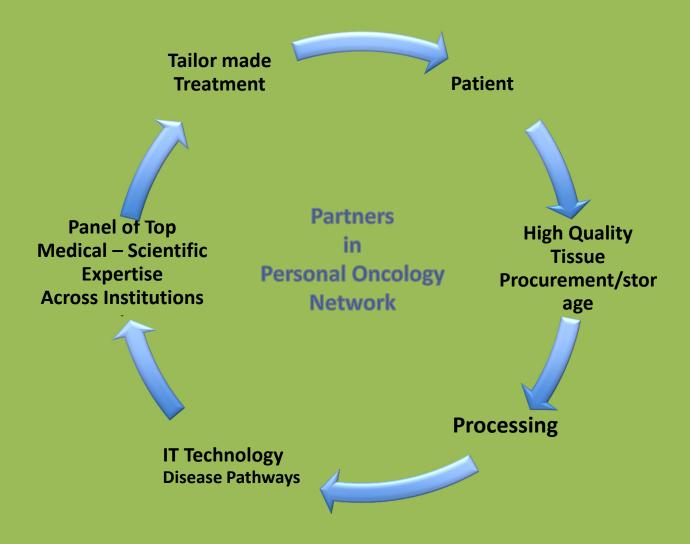


David Beatty



Robin Jones

Partners in Personal Oncology



How to Deconstruct Cancer One Patient at a time T. Blau & E. Liakopoulou

Trends in Genetics 2013 &

Cell Press Reviews: Cancer Therapeutics, 2014

Fundamental Idea of Personalized Medicine

Coupling established clinical—pathological indexes

with

State-of-the-art molecular profiling

to create

 Diagnostic, prognostic, and therapeutic strategies precisely tailored to patient's requirements



Two Clinical Trials

Triple Negative Breast Cancer

AML (Pam Becker)

- Enroll patients with cancers not generally considered curable.
- Seek to better match patients to drugs.
- To do this, both use HTS and Omics.
- Both represent grass roots efforts.

Protocol 8132: ITOMIC-001: Intensive Trial of OMics In Cancer

October 28, 2013: Trial Launch

Highlights:

- 1) Multiple samplings from multiple different sites of disease.
- 2) Standardized protocols for tissue acquisition, handling, and storage.
- 3) Coordinate analyses across multiple different labs, platforms & institutions.
- 1) Convene ITOMIC tumor board (X4).
- 2) Respond rapidly to a change in a patient's clinical status.
- 3) Obtain data from all patients examined thus far.
- 4) Prepare reports.
- 5) Assist with accessing drugs.
- 6) Perform repeated biopsies.
- 7) Culture tumor cells, test in drug screen (1 patient).
- 8) Serially monitor circulating tumor cells (CTCs) (1 patient).
- 9) Patient Surveys

AML - A Practical Approach

- Examining the relationship between gene expression and sensitivity to chemotherapy.
- Immediately address drug sensitivity, with treatment based on high throughput drug sensitivity testing.

UNIVERSITY OF WASHINGTON

Institute for Stem Cell & Regenerative Medicine

QUELLOS HIGH THROUGHPUT SCREENING CORE

ABOUT THE CORE



The Quellos High Throughput Screening (HTS) Core specializes in Functional Genomics as well as Drug Discovery and Small-Molecule Optimization through chemical screening. It is located within the UW's Institute for Stem Cell and Regenerative Medicine at the South Lake Union Campus of the University Of Washington School Of Medicine serving Academic Institutions (e.g., Fred Hutchinson Cancer Research Center) as well as BioTechs and Pharma organizations in Washington State and nationwide. A team with industrial and academic experience is available to aid investigators in their assay optimization and screening activities. The Quellos HTS Core was created to provide "state of the art" high throughput and lab automation approaches that were once only available in large pharmaceutical organizations.

AML Trial

HTS Screen

160 Drugs - 45 FDA Approved, 115 Investigational

Ability to use cryopreserved cells

Use of adherent culture conditions

14 AML cell lines, 30 patient samples



Sensitive

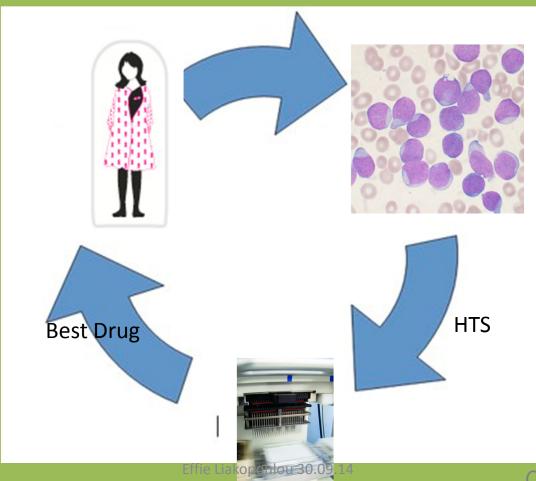
Each patient exhibits unique result. Clustering of similar drugs.

Resistant



AML Trial

Collect Leukemia Cells



Courtesy Dr. Tony Blau

AML Trial

Primary Objective: Demonstrate feasibility of the assay as a potential means to predict response

Secondary Objective: Cytoreduction with chosen drugs

<u>Subjects:</u> Multiply relapsed or refractory AML patients Declines in blast count in all 11 patients treated.

Actual: Drug sensitivity test results 5-7d (mean 5.2d).

All pts treated within 7-21 days.

Take Home Message

Recent biotechnological advances have led to an explosion of dis-ease-relevant molecular information, with the potential for greatly advancing patient care.

Personalized Medicine

No longer a blip on the horizon

Brings new challenges and success is based:

- establishing frameworks for regulating,
- compiling, and
- interpreting the in- flux of information that can keep pace with rapid scientific developments

2nd international Conference on Hematology and Blood Disorders

Session 4: 10.20, 1 October 2014

Whole genome methodology for in silico quantification of intra tumor heterogeneity: Model for clinical applications in the treatment of patients with hematological malignancies



Tony Blau



Greg Foltz



Tony Blau Effie Liakopoulou 30.09.14

Thank you