

# Genomic Testing in Oncology

Jessica N. Everett, MS, CGC Genetic Counselor Clinical Instructor, Internal Medicine

IOM Roundtable – February 3, 2014

## Two Contexts:

- Cancer Genetics Clinic all germline
- Michigan Oncology Sequencing
   Project tumor/germline dyads



# The Breadth of Cancer Genetic Testing in Clinical Practice

Conditions	Genes	Labs	Comprehensive Tests
21	31	15	3796

2820 New Patients 2002 – 2011



## Why Use a Large Scale Approach?

- Cost individually testing genes now available on panels >\$25,000
- Time for results as compared to step-wise testing approach
- Additional clinically useful information could be gained (e.g. families with more than one mutation, mosaicism)
- Occasional "diagnostic odyssey" patients, even in Cancer Genetics!



## Benefits of NGS/Panels in Cancer

- Expanding knowledge about phenotypic spectrum
- Potential to gain new information to better understand clinical utility of lower penetrance or less studied genes
- Generating data of research and/or academic interest without added cost



## Limitations of NGS/Panels in Cancer

- Identifying mutations where clinical utility is still unclear complicates risk assessment and clinical recommendations
- What exactly is the phenotype and who gets an "official diagnosis"?
- Generating data of research and/or academic interest on an individually small scale...need better ways to share for this to be useful



## Genomics in Oncology Care

 Tumor genome testing for understanding tumor biology, identifying targets for therapy

- "Genonemic? Genomic? No, I have no idea what it all means. No idea, really. Research maybe? It's about the genome?"



## Semantic Confusion in Somatic Testing

- 20/37 had some knowledge/understanding of genomic testing
- Among these, 10/20 thought it referred to or included constitutional/germline analysis
- "Although nobody told me this specifically, I thought the specimen might be used to find out whether or not there was risk of transmission to my children..."

Conclusion: "More attention should be paid to information issues in this field"



## MI-ONCOSEO

- Eligibility Phase I clinical trials (advanced refractory disease or rare cancer with no standard therapy)
- Whole exome and whole genome sequencing of tumor and germline DNA
- 4 week turn around (=standard wash out period)



AIP	C16orf57	DKC1	FANCF	HOXD4	MC1R	NOP10	PTEN	SDHC	THPO
AKT1	CASP8	ELANE	FANCG (XRCC9)	HRAS	MEN1	NRAS	PTPN11	SDHD	TINF2
ALK	CBL	EPHB2	FANCI (KIAA1794)	IGF1	MET	NSD1	PTPRJ	SH2D1A	TLR2
APC	CCND1	ERCC2 (XPD)	FANCL (PHF9/POG)	IGF2	MITF	ODC1	RAD50	SHOC2	TLR4
ATM	CDC73	ERCC3 (XPB)	FANCM (Hef)	JAK2	MLH1	PALB2 / FANCN	RAD51	SLC26A4	TMC8
ATR	CDH1	ERCC4 (XPF)	FAS	KIF1B	MLH3	PARK2	RAD51C	SMAD7	TMEM127
AURKA	CDK4	ERCC5 (XPG)	FASLG	KIT	MPL	PHB	RAD51D	SMARCB1	TP53
AXIN2	CDKN1B	EVER1	FH	KIT	MRE11A	PHOX2B	RAD54L	SOS1	TSC1
BAP1	CDKN1C	EVER2	FLCN	KRAS	MSH2	PLA2G2A	RAF1	SPRED1	TSC2
BARD1	CDKN2A	EXT1	G6PC3	LAMA3	MSH6	PMS1	RB1	STK11	VHL
BLM	CEBPA	EXT2	GALNT12	LAMB3	MSR1	PMS2	RECQL4	TERC	WAS
BMPR1A	CHEK2	FANCA	GATA2	LAMC2	MUTYH	POU6F2	RET	TERT	WRN
BRAF	COL17A1	FANCB	GFI1	MADH4	NBN	PPARG	RNASEL	TGFB1	WT1
BRCA1	COL7A1	FANCC	GPC3	MAP2K1	NF1	PRKAR1A	RUNX1	TGFBR1	XPA
BRCA2	CYP21A2	FANCD2	HAX1	MAP2K2	NF2	PRSS1	SBDS	TGFBR1	XPC
BRIP1 / FANCJ	DDB2 (XPE)	FANCE	HOXB13	MAX	NHP2	PTCH	SDHB	TGFBR2	PTCH2



## At Initial Study Visit...

- Take a 4 generation pedigree (cancer focused)
- Discuss sequencing of cancer genome vs. germline, reasons for doing both
- Respond to patient questions about family history or testing process
- Discuss consent for return of results, walk through flexible default plan



#### **Provisional Flexible-Default Informed Consent**

Disease Domain	Impact/ Significance	Default	Decline Results?	Description	
Cancer of Interest	Direct impact on care of current cancer	Disclose NOT flexible		Marketed treatment available Targeted clinical trial available	
	Significance for biological family	Disclose Flexible		Increased risk of cancer for biological family	
	Significance is unknown	NOT disclose	NOT flexible	Unknown mutation function or role	
Conditions OTHER than cancer of interest	Potential medical impact	Disclose	Flexible	Clinically significant relative risk of disease or outcomes	
	Significance for biological family	Disclose	Flexible	Significant implications for biological family decisions	
	Significance is unknown	NOT disclose	NOT flexible	Mutation function or role unknown	
Other	New or unanticipated issues	Determined by PMTB on case by case basis		Situations that do not readily fit into above categories PMTB may need to create new categories	

## Interest in Germline Findings

- Through April 31, 2013:
  - 167 adult patients consented
    - 162/167 (97%) opted to receive germline findings
  - 34 pediatric patients consented (57 through 1/31/14)
    - 30/34 (88%) opted to receive germline findings



## Germline Findings – Disclosure Categories

Germline analylsis completed for 179 patients

1	Previously reported pathogenic mutations in high penetrance cancer genes with known clinical utility (e.g. BRCA1/2, MLH1)	Disclose	8
2	Alleles associated with low to moderate cancer risk, clinical utility evolving or unknown (e.g. ATM, BARD1)	Case by case	7
3	Mutations associated with autosomal recessive conditions	Not disclose	11

#### Exceptions:

**ALL** germline findings relevant to current cancer (including carrier of AR condition, low to moderate penetrance alleles and possibly variants of uncertain significance)



#### Project 1 and 2

Project rand

**Project 3** 

Informed Consent Genetic Counseling





Aim 1

Eliciting
Patient
Preferences

Tumor Sequencing & Analysis





Precision Medicine Tumor Board



Aim 2

**Analyzing Board Decision-Making** 

Disclosure: Genomic Results



Aim 3

Developing
Communication
Tools

**Patient Responses** 

Aim 4

Examining Patient Responses

Mean
Time to
Disclosure

Impact on Decision making

Frequency of Informative genes

## **Genomic Sequencing** in Clinical Oncology

- § Informed Consent
- § Privacy
- § Translate, validate, and deliver results
- § Making decisions regarding which results are significant
- § Reporting results
- § Impact of sequencing



#### Acknowledgements

#### **MCTP**

Sameek Roychowdhury

Xuhong Cao Dan Robinson

Yimi Wu

Matthew Iver

Lee Sam

Bob Lonigro

Shanker K.-Sundaram

Alejandro Balbin

Mike Quist Catie Quist

Terry Barrette

Javed Siddiqui

Priya Kunju

Amy Gursky Scott Tomlins

Chandan Kumar

Nalla Palanisamy

Lynda Hodges

Phase I Team
/ Clinical Oncology

Moshe Talpaz Ken Pienta David Smith

Harry Erba Chris Lao Dale Bixby

Max <u>Wicha</u>

Pediatric Hem/Onc

Rajen Mody Ashley Carpenter Genetics

Jeff Innis

Jessica Everett Shanna Gustafson Victoria Raymond

Elena Stoffel Wendy Uhlmann

Radiology

Elaine Caoili Ellen Higgins

Anna Fox

**Bioethics** 

Scott Roberts

Scott Kim

Ray De Vries

Brian Zikmund-Fisher Michelle Gornick

Ad hoc STB

Dan Hayes

Greg Kalemkarian

M SPH

Mark Zalupski

Mark Kaminski

Maha Hussain







Supported by: NHGRI/NCI - CSER Prostate Cancer Foundation NIH, Prostate SPORE American Cancer Society Doris Duke Foundation Department of Defense

**U Michigan CCC** 

#### **UM Cancer Genetics Program**

Accelerating the world's most promising research

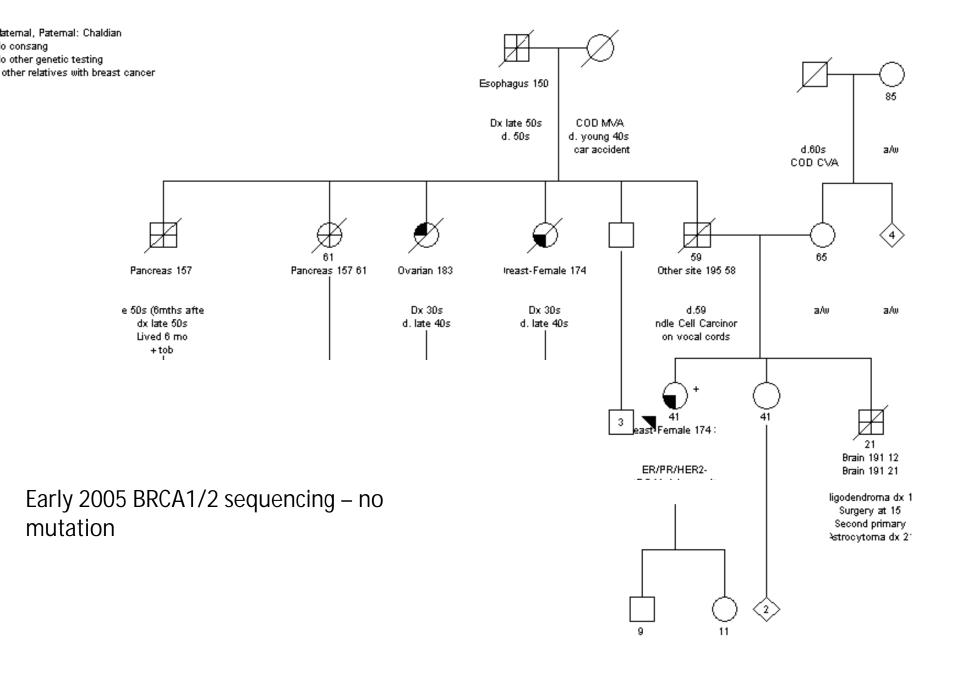
John Carethers Jenae Osborne

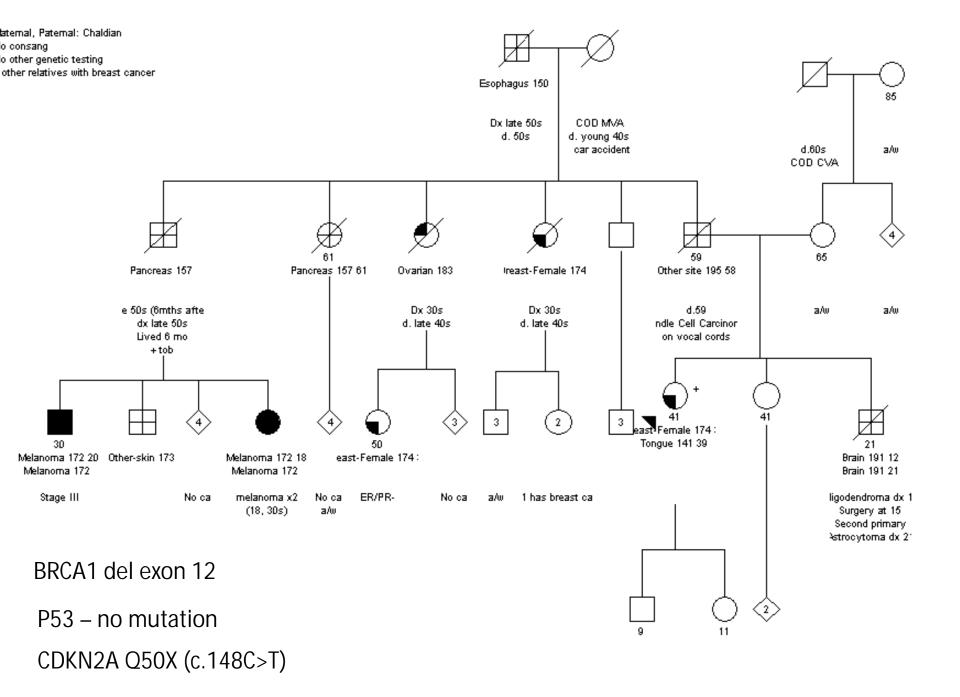
Tobias Else Victoria Raymond

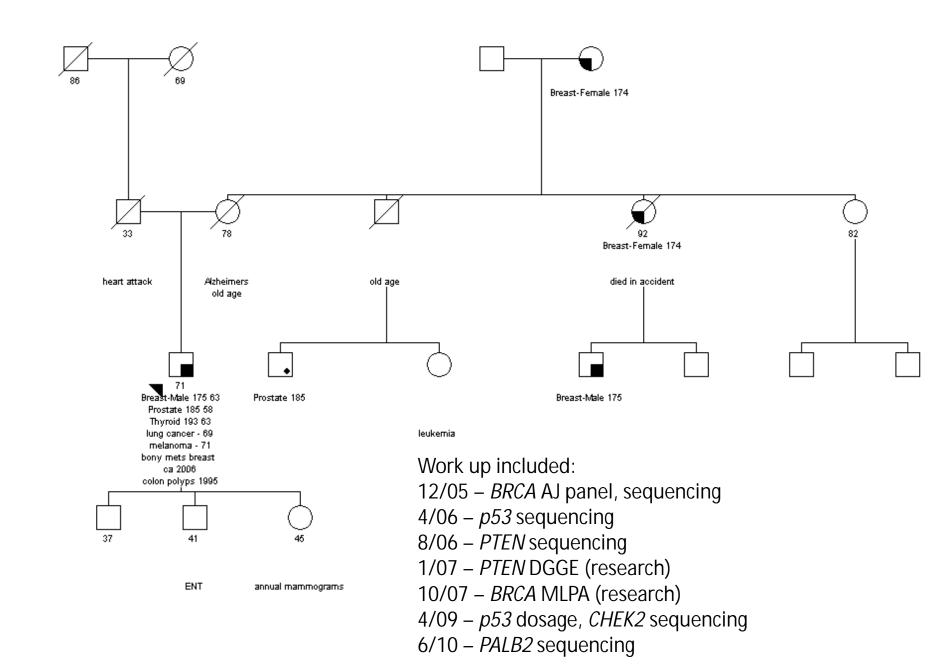
Ralph Stern Carmen Williams

Elena Stoffel







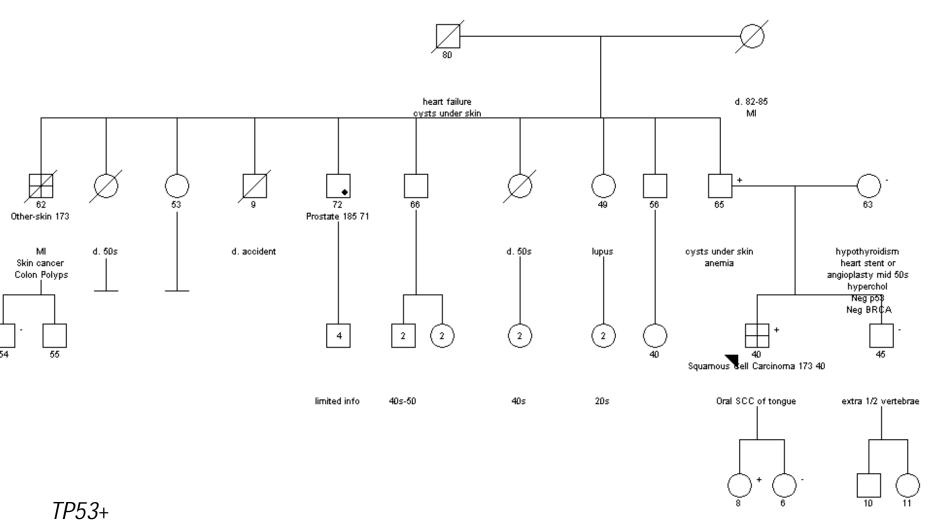


*TP53* p.R267Q Interpreted differently by different clinical labs rheumatoid arthritis Melanoma 172 46 Bladder 188 Breast-Female 174 Ovarian 183 90s uterine fibroids mild heart failure rheumatoid arthritis d. Alzheimers rheumatoid arthritis bladder caldx 60s 90s broken hip 90s breast caidx 40s ovarian vs cervical TAH-fibroids dx 70s ?B\$0 Breast-Female 174 57 Prostate 185 asthma depression no ca obese obese obese no contact depression hysterectomy for fibroids/cysts close contact 25 38 Adrenal 194.0 4

:hildhood heart conditior

Pituitary 194.3 27 prolactioma

juvenile rheumatoid arthritis



cyclic vomiting syndrome dx 4 anxiety blotchy, brittle nails born with "hole in heart" closed naturally