Delivery of Information: Implementation of Pharmacogenomics in Clinical Practice

Mary V. Relling

St. Jude Children's Research Hospital and PAAR4Kids, NIH Pharmacogenomics Research Network (PGRN)





At St. Jude, we can overcome (or ignore) many barriers to preemptive genotyping

- We cover all patient care costs
- We provide <u>all</u> medications for 5000 unique high-risk patients per year
 - ~ 80% have cancer
 - ~20% have sickle cell, HIV, and other lifethreatening diseases
- We have a team approach to pt care
- We have an integrated, comprehensive EMR (Cerner) with customized decision support





DMET array is CLIA-approved in at least one lab and allows for pre-emptive genotyping

- Affy DMET array: over 1 million features to interrogate 1900 polymorphisms in 225 genes
- For the same money we spend on 2 genes, we can interrogate 225---but what to do with the other 223 results?
- Need process for withholding/sharing results
- Need consent for:
 - Withholding results
 - Incidental findings

PG4KDS Protocol Clinical Implementation of Pharmacogenetics

Principal Investigator

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Ulrich Broeckel, M.D.

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PG4KDS: CLINICAL IMPLEMENTATION OF PHARMACOGENETICS at ST. JUDE

Goal: migrate pharmacogenetic tests from laboratory (array-based) into routine patient care, to be available preemptively

Which genes, which drugs should be used to inform the EMR?

- TPMT-thiopurines
- CYP2D6—codeine,?
- G6PD---rasburicase, Septra
- CYP2C9, VKORC1---warfarin
- CYP2C19---clopidogrel, ? Voriconazole
- DPYD---5FU
- HLA—abacavir
- HLA---carbamazepine
- HLA—phenytoin
- HLA---allopurinol
- UGT1A1---irinotecan

DMET array



Finding cures. Saving children. http://www.stjude.org/pg4kds

Patient Resources

Clinical Programs

Research

Ways to Help

Non-Therapeutic Protocol

PG4KDS: Clinical Implementation of

Pharmacogenetics

Type of Protocol/Clinical Study

Supportive Studies: Genetics

Description

Pharmacogenetics is the study of how genes affect a

person's response to drugs. This field combines pharmacology (the science of drugs) and genetics (the study of genes and their functions) with the goal of making medications safer and more effective by tailoring medications based on a person's genetic makeup.

Gene tests are used in pharmacogenetics. Over time, scientists are discovering which of these gene tests are so important that they should move from the research lab into the patient's medical record, where they would be available to the doctors and other care givers to see the test results, and to use the information when they give the patient the drug.

The process for deciding which tests to move from the research lab into the patient medical record

Related Topics

PG4KDS - Priority Genes

Video: PGEN4Kids Educational

Video

Mary V. Relling, PharmD

PG4KDS Objectives

The long term goal is to use proactive pharmacogenomic testing as the standard of care for St. Jude patients.

Primary Objective

Estimate the proportion of patients who have high-risk or actionable pharmacogenetic results entered in their electronic medical record (EMR) with decision support.

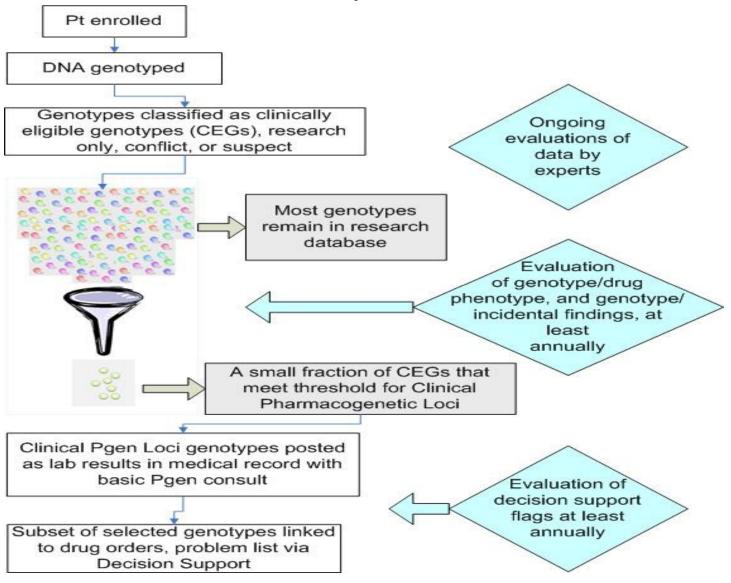
Secondary Objectives

Use systematic procedures to prioritize and migrate pharmacogenomic tests to post to the EMR.

Incorporate clinical decision support tools linking test results to medication use, and assess their level of use.

Assess attitudes and concerns of research participants and clinicians

The process

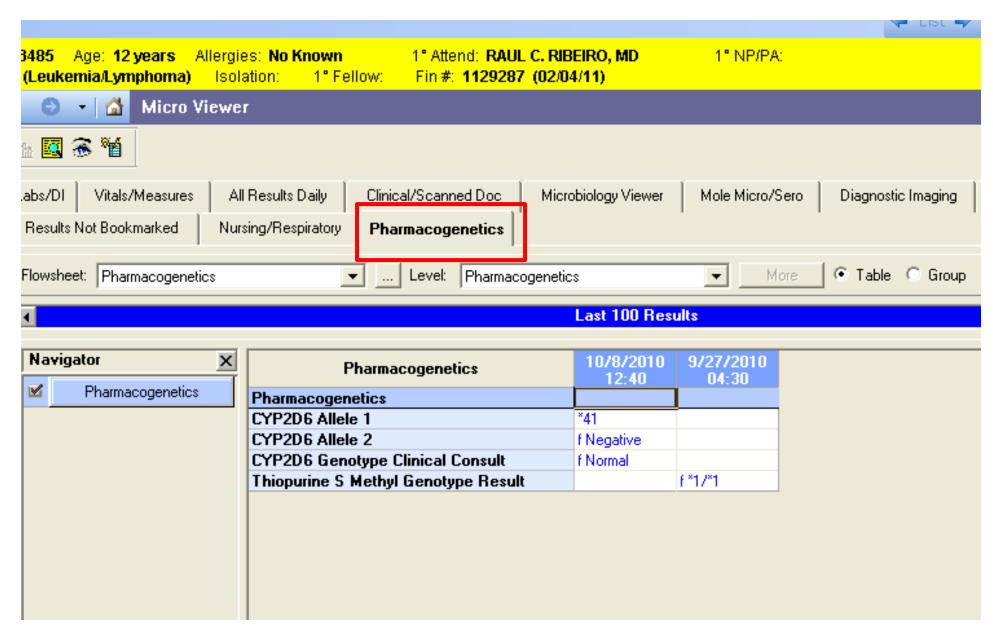


PG4KDS

Delivery of Genetic Information

- Posted to EMR
 - One gene at a time
 - As each gene is prioritized, it moves to EMR for all past and future pts
- All participants given choice as to whether to get a "letter" (one letter for each gene)
- Only those > 18 yrs of age given choice on "incidental" findings for disease risk
- General information and video on website

Pharmacogenetics tab added to EMR; all clinically eligible genotypes are entered with a gene-specific consult



Example Pharmacogenetics Consult - TPMT

Example TPMT Wild-type genotype consult:

Sample for *TPMT* genotype obtained 8/31/09.

Thiopurine S Methyl Transferase Genotype Result: *1/*1.

*1/*1 means that this patient's genotype is homozygous wild-type at the three most commonly polymorphic sites; i.e., nucleotides 238, 460, and 719. Wild-type means high (normal) TPMT activity. This result suggests that there is no reason to selectively adjust 6-mercaptopurine dose in this patient. If myelosuppression occurs, consult treatment protocol for dosing adjustments for chemotherapy agents.

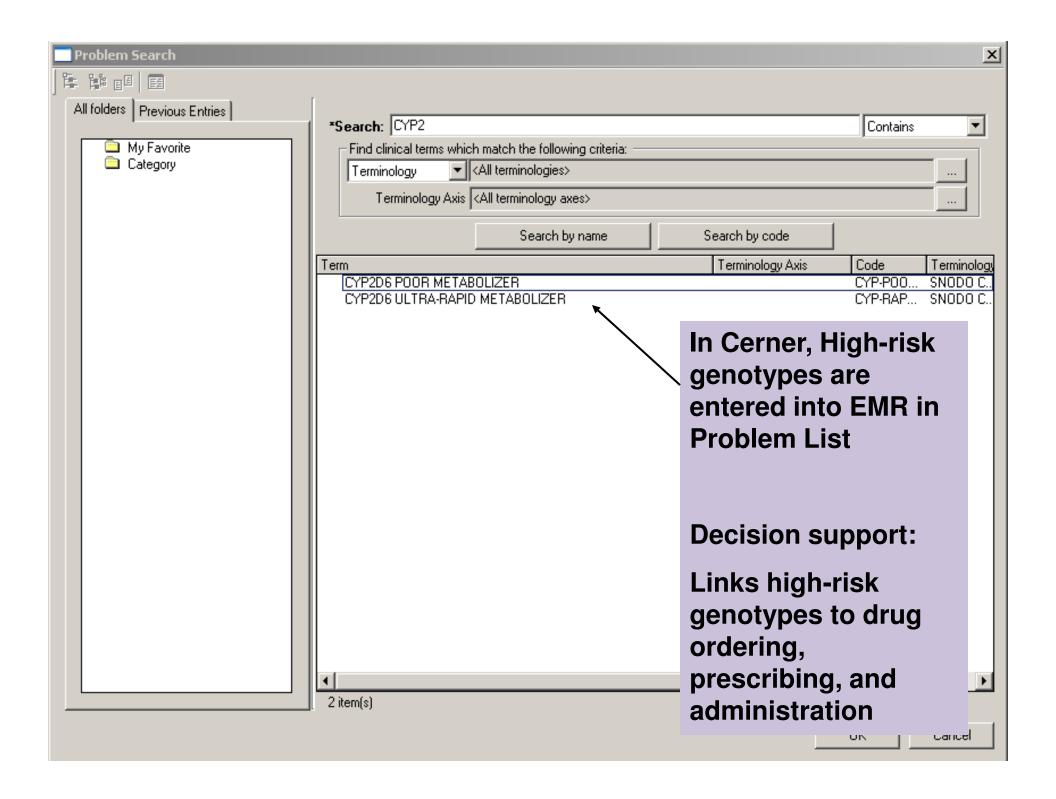
Time/Date of Consult: 0800/ 09/09/09

Kristine Crews, Pharm.D.

Only when a high-risk drug collides with a high-risk (priority) genotype do decision-support-based alerts fire

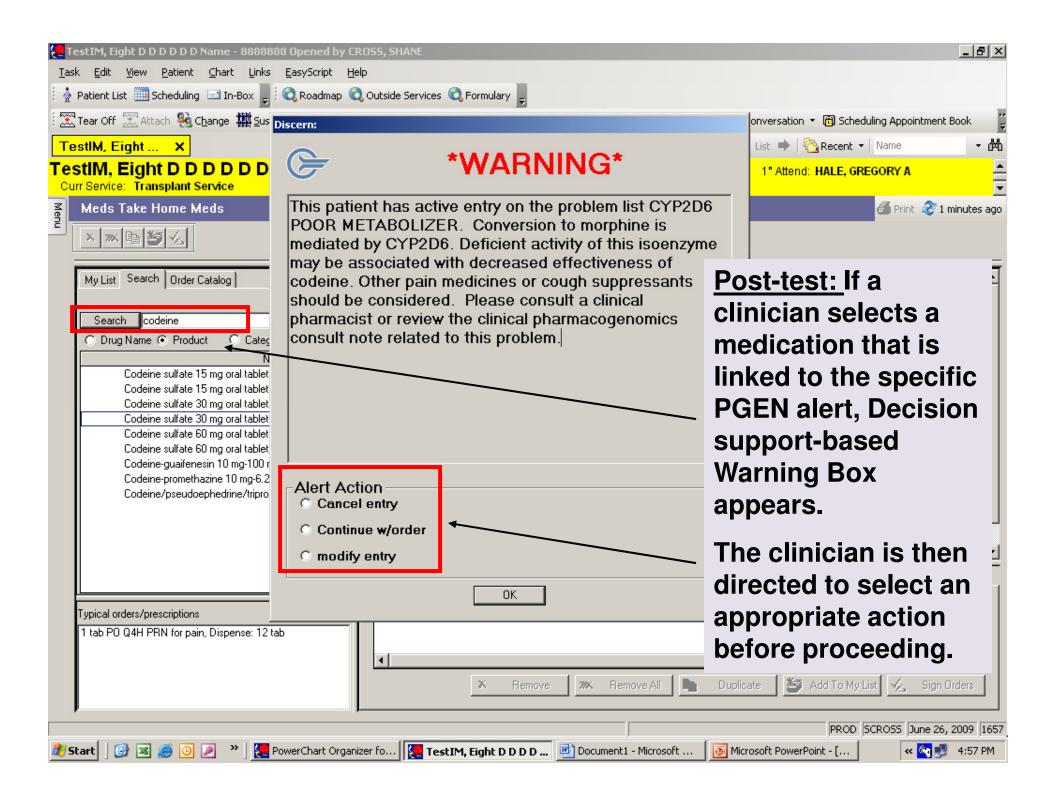
Patients with high-risk genotype: e.g. *CYP2D6* UM or PM; *CYP2C19* PM; *TPMT* heterozygote

Patients with high-risk drugs: e.g. codeine, amitriptyline; clopidogrel azathioprine



Two types of decision support warnings

- Post-pgen test—already have high-risk genotype in EMR
- Pre-pgen test---no test results yet in EMR





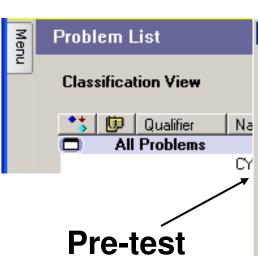
WARNING

This patient has an active entry on the problem list CYP2D6 ULTRA-RAPID METABOLIZER. Ultra-rapid metabolizers of codeine are expected to experience a higher incidence of side effects from codeine than normal. Other pain medicines or cough suppressants should be considered. Please consult a clinical pharmacist or review the clinical pharmacy consult note related to this problem.

Alert Action

- Cancel entry
- Continue w/order
- modify entry

ÖΚ



Discern:



WARNING

You have ordered a medication for which genetic testing may be important, but test results are not yet available. Please consult with a clinical pharmacist or PK research nurse to obtain pharmacogenetic tests.

Change View
ification Ranking Life Cycle St...
cal Active

Alert Action

- Cancel entry
- Continue w/order
- modify entry

OΚ

PG4KDS - Priority Genes

Updated May 2011

Thiopurine Methyltransferase (TPMT)

Thiopurine methyltransferase (TPMT) is an enzyme that breaks down (metabolizes) thiopurines. Thiopurines include

three medications: 6- mercaptopurine (6-MP), 6-thioguanine (6-TG), and azathioprine. 6-MP and 6-TG are often used to treat leukemia or lymphoma. Like many drugs, their effectiveness and side effects can vary from person to person. One of the reasons why this difference occurs is because each person's ability to metabolize thiopurines is different based on variations in the TPMT gene.

dose of 6-MP and 6-TG for the different genotype groups. By changing the dose based on a patient's genotype, there are fewer side effects (due to low blood counts).

Every person can be classified into one of 3 possible genotype groups. We use a different starting

Priority genotypes

- Heterozygous variant (intermediate activity) means there is one normal, functioning copy of the gene and one non-functioning copy of the gene. Patients have reduced TPMT activity and may require reduced doses of thiopurine medications to avoid side effects. About 1 in 10 people have this genotype.
- Homozygous variant (low or deficient activity) means there are two copies of the non-functioning gene and there is no normal TPMT enzyme. These patients are at a very high risk of experiencing toxicity (low blood counts) from 6-MP or 6-TG or azathioprine. Patients should receive substantially lower doses than normal to avoid side effects of low blood counts. About 1 in 400 people have this very high risk priority genotype.

Related Topics

Mary V. Relling, PharmD

Protocol: PG4KDS

Video: PGEN4Kids Educational

Video

We can deliver genetic information to our EMR, we can deliver it directly to the pt...

 ...but until we have a universal lifetime EMR, the same fragmentation that affects all of health care will affect genomic medicine as well.

Some challenges in implementation.....

- Lack of consensus guidelines on what to recommend for high-priority/high risk diplotypes
- Must be able to update information (e.g. add drugs to genes as data accumulate)
- Many diplotypes are ambiguous
- Interpretation of diplotypes is complex and will change
- Must be mechanism for QC, sample identity and genotype reproducibility

Clinical Pharmacogenetics Implementation Consortium Guidelines for Thiopurine Methyltransferase Genotype and Thiopurine Dosing

MV Relling¹, EE Gardner¹, WJ Sandborn², K Schmiegelow^{3,4}, C-H Pui⁵, SW Yee⁶, CM Stein⁷, M Carrillo⁸, WE Evans¹ and TE Klein⁸

Clin Pharmacol Ther. 2011 89:387-91



Clinical Pharmacogenetics Implementation Consortium Guidelines for Cytochrome P450-2C19 (*CYP2C19*) Genotype and Clopidogrel Therapy

SA Scott¹, K Sangkuhl², EE Gardner³, CM Stein^{4,5}, J-S Hulot^{6,7}, JA Johnson^{8,9,10}, DM Roden^{11,12}, TE Klein² and AR Shuldiner^{13,14}

CLINICAL PHARMACOLOGY & THERAPEUTICS

www.pharmgkb.org

Some challenges in implementation.....

- Lack of consensus guidelines on what to recommend for high-priority/high risk diplotypes
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CYP2D6 metabolizes several drugs---codeine is the only one with "flag" currently

- TCAs (nortriptyline, amitriptyline)
- SSRIs (fluoxetine, paroxetine)
- Atomoxetine
- Tamoxifen
- Beta blockers (metoprolol)
- Anti-arrhythmics (propafenone, flecainide)
- Ondansetron

Some challenges in implementation.....

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DMET Diplotypes from 240 patients: many results are ambiguous

	CYP2C19	CYP2C9	CYP2D6	DPYD	TPMT	UGT1A1	VKORC1
# No Calls	1	0	5	0	0	1	3
% No Calls	0.4%	0%	2%	0% 0%		0.4%	1%
# Ambiguous	43	37	5	35	22	40	1
% Ambiguous	18%	16%	2%	15%	9%	17%	0.4%
% Called: Non- Ambiguous	81.6%	84%	96%	85%	91%	83%	98.6%

- >What are the reasons for ambiguous diplotype assignments?
- ➤ Are there phenotype differences between the ambiguous diplotypes?
- ➤ Can PHASE select the most probable diplotype?

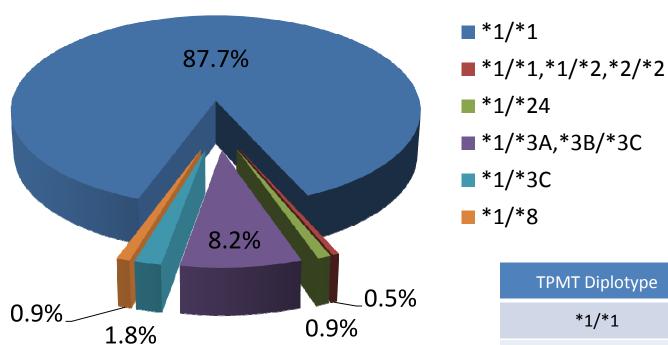
PHASE Improves Non-Ambiguous Diplotypes to Over 98% for top 7 Genes of Interest

	CYP2C19	CYP2C9	CYP2D6	DPYD	TPMT	UGT1A1	VKORC1
# No Calls	1	0	5	0	0	1	3
% No Calls	0.4%	0%	2%	0%	0%	0.4%	1%
# Ambiguous	43	37	5	35	22	40	1
% Ambiguous	18%	16%	2%	15%	9%	17%	0.4%
% Called: Non- Ambiguous	81.6%	84%	96%	85%	91%	82.6%	98.6%
PHASE Adjusted Non-Ambiguous Calls		100%	98%	100%	100%	99.6%	99%

Some challenges in implementation.....

- Lack of consensus guidelines on what to recommend for high-priority/high risk diplotypes
- Must be able to update information (e.g. add drugs to genes as data accumulate)
- Many diplotypes are ambiguous
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TPMT: diplotypes observed in 240 pts

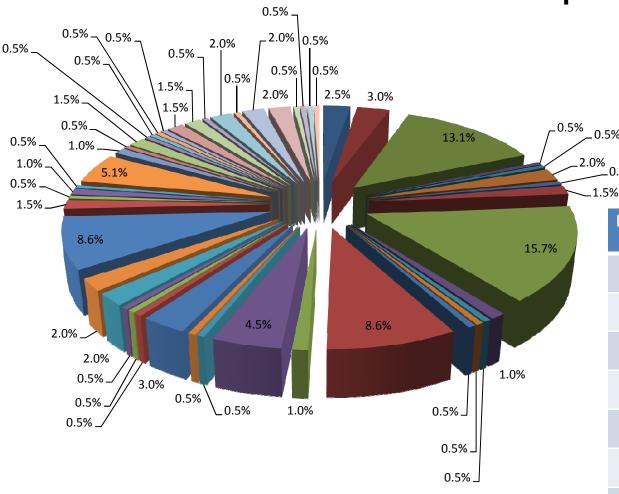


TPMT Diplotype	% Observed
*1/*1	87.7%
*1/*1,*1/*2,*2/*2	0.5%
*1/*24	0.9%
*1/*3A,*3B/*3C	8.2%
*1/*3C	1.8%
*1/*8	0.9%

Link *TPMT* diplotypes to internal review status, prioritization, lab result entry, consult template, and DS

Diplotype	Freque ncy	Internal Flag	EMR	Rx Consult	Link to Consult
*1/*1	193	Pass	Routine	Wild Type	wild-type
*1/*1,*1/*2,*2/*2	1	Review	Priority	Unknown	Probable wild-type
*1/*24	2	Pass	Routine	Wild Type	wild-type
*1/*3A,*3B/*3C	18	Review	Priority	Heterozygous	Heterozygous with caveat
*1/*3C	4	Review	Priority	Heterozygous	heterozygous
*1/*8	2	Pass	Routine	Wild Type	wild-type

CYP2D6: 48 diplotypes observed in first 240 pts



Diplotype & CN	% Observed
*1/*2(x2)	15.66%
*1/*1(x2)	13.13%
*1/*4(x2)	8.59%
*2/*2(x2)	8.59%
*2/*4(x2)	5.05%
*1/*41(x2)	4.55%
*1/*1(x1)	3.03%
*1/*9(x2)	3.03%

0.5%

0.5%

CYP2D6:

- 1. Generate score based on alleles called and CN
- 2. All "new" diplotypes must be manually reviewed
- 3. Translate score into phenotype

From CYP2D6 DMET results, e.g. (*1/*10)3N, the program will generate all possible combinations, e.g. (*1/*1/*10) and (*1/*10/*10).

For each possible combination, it will add up the scores; (in this case *1=1, *10=0.5; hence [*1/*1/*10] = 2.5; [*1/*10/*10] = 2) For each possible score, it will check the threshold to assign PM, IM, EM, UM. (in the above case, would be UM [2.5] or EM [2]; now look at it these rules should be part of the file as well, but it's hard coded right now...)

if score > 2 : phenotype = 'UM'

if score >= 1 and score <= 2 : phenotype = 'EM'

if score >= 0.5 and score < 1 : phenotype = 'IM'

if score < 0.5 and score >= 0 : phenotype = 'PM'

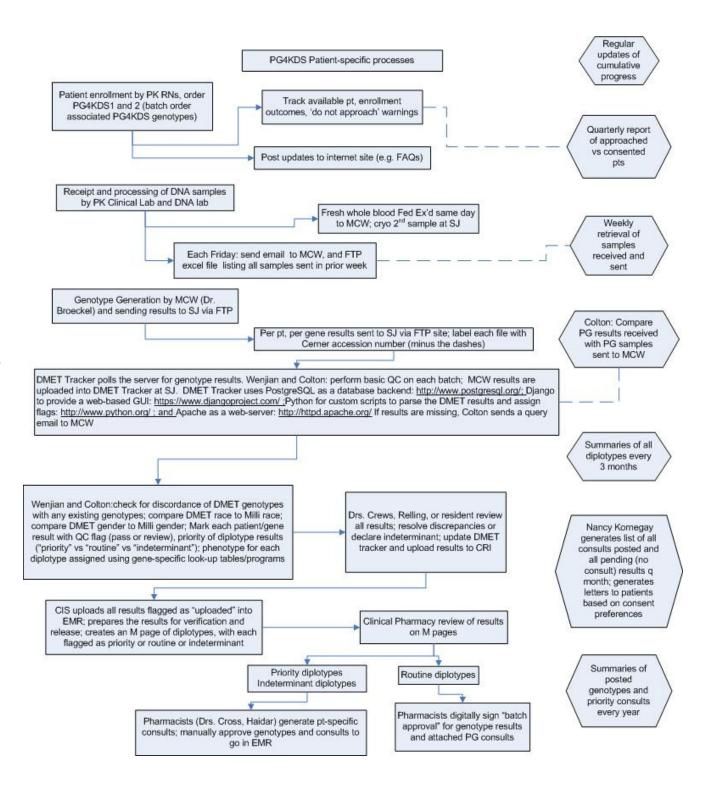
Haplotypes	Activity Score
*1	1
*2	1
*3	0
*4	0
*5	0
*6	0
*7	0
*8	0
*9	0.5
*10	0.5
*11	0
*12	0
*14A	0
*14B	0.5
*15	0
*17	0.5
*18	0
*19	0
*20	0
*21	0
*29	0.5
*38	0
*40	0
*41	0.5
*42	0
*44	0
*56A	0
*56B	0
*64	NA
*39	1
*5	0
*31	0
*36	NA
*45	1
*46	1
*49	0.5
*59	0.5
*60	0
*66	0

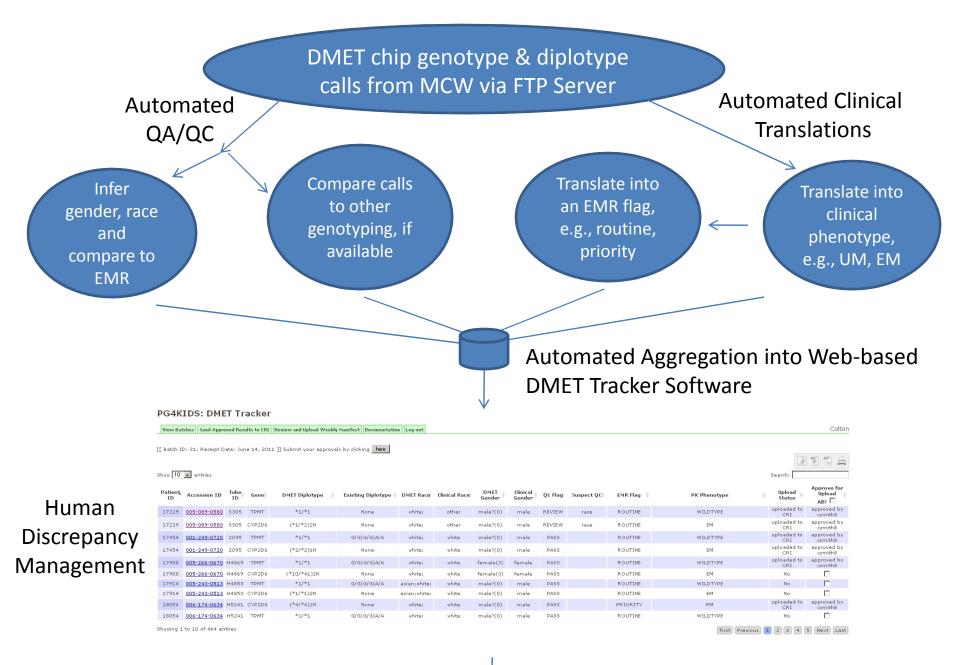
Some challenges in implementation.....

- Lack of consensus guidelines on what to recommend for high-priority/high risk diplotypes
- Must be able to update information (e.g. add drugs to genes as data accumulate)
- Many diplotypes are ambiguous
- Interpretation of diplotypes is complex and will change
- Must be mechanism for QC, sample identity and genotype reproducibility (over a lifetime)

PG4KDS

Multiple steps are involved in processing pt-specific results, from lab to EMR





To the EMR

DMET Tracker: place to flag genotype, race, or gender mismatches; review priority or indeterminant diplotypes; track upload from research database to clinical warehouse

]		
entries												Search: [
Accession ID	Tube ID	Gene	DMET Diplotype	Existing Diplotype	DMET Race	Clinical Race	DMET Gender	Clinical Gender	QC Flag	Suspect QC	EMR Flag	PK Phenotype 🖣	Upload Status	Approve for Upload All?
005-089-0580	S305	TPMT	* 1/* 1	None	white;	other	male?(0)	male	REVIEW	race	ROUTINE	WILDTYPE	uploaded to CRI	approved by csmith8
005-089-0580	S305	CYP2D	(*1/*2)2N	None	white;	other	male?(0)	male	REVIEW	race	ROUTINE	EM	uploaded to CRI	approved by csmith8
001-249-0720	2095	TPMT	* 1/* 1	G/G G/G A/A	white;	white	male?(0)	male	PASS		ROUTINE	WILDTYPE		approved by csmith8
001-249-0720	2095	CYP2D6	(*2/*2)1N	None	white;	white	male?(0)	male	PASS		ROUTINE	EM	uploaded to CRI	approved by csmith8
005-266-0670	H4869	TPMT	* 1/* 1	G/G G/G A/A	white;	white	female(3)	female	PASS		ROUTINE	WILDTYPE		approved by csmith8
005-266-0670	H4869	CYP2D6	(*10/*41)2N	None	white;	white	female(3)	female	PASS		ROUTINE	EM	No	
005-243-0513	H4853	TPMT	* 1/* 1	G/G G/G A/A	asian; white;	white	male?(0)	male	PASS		ROUTINE	WILDTYPE	No	
005-243-0513	H4853	CYP2D6	(*1/*1)2N	None	asian; white;	white	male?(0)	male	PASS		ROUTINE	EM	No	
006-174-0634	H5241	CYP2D6	(*4/*4)2N	None	white;	white	male?(0)	male	PASS		PRIORITY	PM	uploaded to CRI	approved by csmith8
006-174-0634	H5241	TPMT	* 1/* 1	G/G G/G A/A	white;	white	male?(0)	male	PASS		ROUTINE	WILDTYPE	No	
006-349-0465	H5503	TPMT	* 1/* 1	G/G G/G A/A	white;	multiple race (nos)	female(3)	female	REVIEW	race	ROUTINE	WILDTYPE	No	
006-349-0465	H5503	CYP2D6	(*1/*2)3N	None	white;	multiple race (nos)	female(3)	female	REVIEW	race	PRIORITY	UM	No	
					1.1.	1.5	1 -/->							_

Some challenges in implementation.....

- Who's going to pay?
- Cheaper, faster, easier, more effective to genotype pre-emptively---before you even think about prescribing the drug.....

PGRN Translational Pharmacogenetics Program (TPP)

- Complete more CPIC guidelines and apply them clinically
- Measure common outcomes across clinical sites
 - accuracy of genetic testing, turn around times
 - methodologies to report results
 - suggested treatment algorithms
 - Educational programs
 - Frequency of actions taken



SJ Pharmaceutical	SJ Hartwell Center	St. Jude	PGRN 🚫
Wenjian Yang	Geoff Neale	Ching-Hon Pui	Teri Klein PGRN
Jun Yang	Yiping Fan	Dario Campana	Nancy Cox
Jitesh Kawedia		James Downing	Paul Scheet
Laura Ramsey	SJ Biostatistics	Susana Raimondi	Russ Altman
Christian Fernandez	Cheng Cheng	Sue Kaste	Dick Weinshilboum
Shane Cross	Stan Pounds	Sima Jeha	Alan Shuldiner
Cheng-cheng Liu	Deqing Pei	Scott Howard	Julie Johnson
Carl Panetta	Xueyuan Cao	Jerry Shenep	Rachel Tyndale
Kris Crews			MCW
James Hoffman	St. Juda Children's		Uli Broeckel
William Evans	St. Jude Children's Research Hospital ALSAC - Danny Yhonas, Fonder Rinding curses Souing children		

Finding cures. Saving children.

INITIAL PLANS FOR TRANSLATIONAL PHARMACOGENETICS PROJECT for PGRN

PGRN Group	Platform	Variant(s)	Application	Timing	Comments
PAAR 4 Kids (St. Jude) Relling		TPMT and CYP2D6 now; soon CYP2C19, CYP2C9, VKORC1, DYPD, G6PD	pediatric patients receiving multiple therapies	any time while active patient at St. Jude	part of a research protocol; purpose is to develop process to move results into medical records for clinical use
PEAR (U. of FL) Johnson	Illumina ADME Core Panel	CYP2C19	cardiac catheterization laboratory; anticipating percutaneous coronary intervention (PCI)	hours to influence decision before, or	additional genotypes will be stored in integrated data repository (part of CTSI and UF EMR, but not in EMR); can be pulled in as additional gene/drug pairs are added to the Personalized Medicine Program, as approved by the P&T subcommittee
PAPI (U. MD) Shuldiner	Nanosphere Verigene (point-of-care) for CYP2C19; broader panels, e.g., Illumina ADME planned	CYP2C19; more planned	cardiac catheterization laboratory	at presentation to cath lab; or earlier (if elective PCI)	
PAT (Vanderbilt) Peterson/ Roden	Illumina VeraCode ADME Core Panel	CYP2C19	preparation for angiography, anticipating percutaneous coronary	drawn concurrent	additional genotypes obtained stored electronically in secure repository separate from EMR; when appropriate drug prescribed for a drug-genome interaction, the genome is made visible in the EMR
PPI (Mayo) Pereira/ Weinshilbou m	Nanosphere Varigene (point-of-care) CYP2C19 platform	CYP2C19	cardiac catheterization laboratory	I ⁻	first bolus clopidogrel dose without genotype, second dose randomized to either "standard care" with clopidogrel or assignment to clopidogrel or prasugrel based on genotype; CYP2C19 information will be stored in the Mayo EMR
XGEN (OSU) Sadee	Autogenomics Infinity System at Nationwide Children's Hospital in Columbus; future use of Ilumina ADME planned	1.) CYP2C19 first; 2.) later phase in CYP2C9 and VKORC1	1.) cardiac catheterization lab of Ross Heart Hospital, anticipating PCI; 2.) subsequently, begin recruitment of orthopedic patients as part of pre-op visit	app lab with results available prior to surgery - goal is to have genotype information available when drug choice and dosing are to be	1.) results posted to EMR (EPIC) w/ alert tags & genotype compared with functional assay of clopidogrel test doses; 2.) warfarin dosing for the orthopedic population will use website with plans to incorporate algorithms directly into EMR; 3.) additional genotype information (with Illumina ADME panel) will go into OSUMC Information Warehouse, a secure depository

Related Projects

Rex Chisholm	Northwestern	Using pharmacogenomics evidence (from GWA genotyping) to guide prescriptions in primary care and assess risk for other conditions such as HFE/hemochromatosis
Geoff Ginsburg	Duke	 Computer-based family hx collection and CDS tool with 1-yr follow-up for perceptions, attitudes, behaviors related to thrombosis and breast, ovarian, and colon cancer SLCO1B1*5 genotyping and statin adherence Effect of genetic risk info on anxiety and adherence in T2DM
David Ledbetter	Geisinger	 Selection for gastric bypass surgery vs other wt loss means based on genetic variants predictive of long-term benefit from surgery IL28B variants and response to hepatitis C treatment KRAS and BRAF mutational analysis in thyroid cancer patients
Cathy McCarty	Marshfield	Choice of intra-ocular pressure lowering agent based on genotype
Dan Roden	Vanderbilt	Pre-emptive PGx genotyping for clopidogrel, warfarin, or high-dose simvastatin
Alan Shuldiner	U Maryland	Develop and apply evidence-based gene/drug guidelines that allow clinicians to translate genetic test results into actionable medication prescribing decisions
Dick Weinshilboum	Mayo	 PGx driven selection/dosing of antidepressants CYP2C19 genotyping for antiplatelet rx post PCI

Ability to genotype at lots of loci on CLIAapproved array is coming here and allows for pre-emptive genotyping

- Affy DMET array: over 1 million features to interrogate 1900 polymorphisms in 225 genes
- For the same money we spend on 2 genes, we can interrogate 225 genes
 - Makes pre-emptive genotyping a possibility

How to provide useful advice to clinicians on top gene/drug pairs?



Consortia

Click on the acronym for each consortium to learn more about research goals.

Project Acronym	Publications	Host Institute
CPIC		Clinical Pharmacogenetics Implementation Consortium
INSINC		International Severe Irinotecan Neutropenia Consortium
ITPC		International Tamoxifen Pharmacogenomics Consortium
IWPC		International Warfarin Pharmacogenetics Consortium
IWPC-GWAS		International Warfarin Pharmacogenetics Consortium - Genome Wi

CPIC: Clinical Pharmacogenetics Implementation Consortium of the Pharmacogenomics Research Network

MV Relling¹ and TE Klein²

- Rationale
- Format
- Grading schemes for
 - strength of recommendations
 - levels of evidence

Clinical Pharmacogenetics Implementation Consortium Guidelines for Thiopurine Methyltransferase Genotype and Thiopurine Dosing

MV Relling¹, EE Gardner¹, WJ Sandborn², K Schmiegelow^{3,4}, C-H Pui⁵, SW Yee⁶, CM Stein⁷, M Carrillo⁸, WE Evans¹ and TE Klein⁸

```
DMET 8170 CYP2D6 translation.txt - Notepad
 File Edit Format View Help
#SJAccession=08-155-0435B
#PatientName=>>>>>>
#DMETfile=DMET_8170.dmet_GT.txt
                                                 One file per patient sample per gene
#TubeNumber=8170
#PatientID=(0000)02XXXX
#SampleType=PGEN DNA
#TranslationFile=DMET_Plus.v1.20101104DRAFT.full.translation
#AnnotationFile=DMET_Plus.v1.20090910.dc_annot.csv
#ReporterBuild=0.8.5
#VerifiedList=VerifiedbyAffy_Nov08 marker list.txt
PharmGKB link http://www.pharmgkb.org/do/serve?objId=PA128&objCls=Gene
Independent Copy Number 2
 <del>Called Interpretation Code</del>
                                  UNIQ+UN
Called Diplotypes Possible
                                 *1/*41
                                          *2/UNK
called novel piplotypes Possible
Copy Number Corrected Alleles
Number Non-reference Probe Sets 5
                 Affy Verified
Probe Set ID
                                 Genome Position dbSNP RS ID
                                                                  Genotype
                                                                                   Call
                                                                                           Contributes To Alleles Descri
AM_12261
                         Ch22:40853887
                                         rs16947 C/T
                                                          Ref/Var *2, *8, *11, *12, *14A, *14B, *17, *19, *20, *21, *29, *40, *41, *4
AM_12257
                         ch22:40853749
                                         rs28371725
                                                          G/A
                                                                  Ref/Var *41
                                                                                   CYP2D6*41_2988G>A(SpliceDefect)
AM_15502
                         ch22:40858512
                                                          G/A
                                                                  Ref/Var -
                                                                                   CYP2D6_-1770G>A
                                         rs1080983
AM_12277
                                                                                   CYP2D6_1661G>C(V136V)
                                                          G/C
                         ch22:40855076
                                         rs1058164
                                                                  Ref/Var -
                                                          G/C
                                                                  Ref/Var 5486T
AM_12247
                         Ch22:40852557
                                         rs1135840
                                                                                   CYP2D6_4180G>C(S486T)
Number Reference only Probe Sets
                                         25
Probe Set ID
                 Affy Verified Genome Position dbSNP RS ID
                                                                                           Contributes To Alleles Descri
                                                                  Genotype
                                                                                   Call
AM_12285
                                                                  Ref/Ref *4,*10,*14A,*56B,*64
                         Ch22:40856638
                                         rs1065852
                                                          C/C
                                                                                                   CYP2D6_100C>T(P345)
                                                                                   CYP2D6*12_124G>A(G42R)
AM_12284
                                                                  Ref/Ref *12
                         ch22:40856614
                                         rs5030862
                                                          G/G
                                                          T/T
AM_12283
                         Ch22:40856600
                                         rs72549357
                                                                  Ref/Ref *15
                                                                                   CYP2D6*15_137insT
AM_12281
                         ch22:40855856
                                         rs5030863
                                                          G/G
                                                                  Ref/Ref *11
                                                                                   CYP2D6*11_883G>C(SpliceDefect)
                                                                  Ref/Ref *17, *40. *64
AM 12280
                         ch22:40855716
                                         rs28371706
                                                          c/c
                                                                                           CYP2D6_1023C>T(T107I)
AM 12278
                                                          G/G
                                                                  Ref/Ref *29
                                                                                   CYP2D6*29_1659G>A(V136I)
                 Ν
                         Ch22:40855078
                                         rs61736512
AM_12276
                                         rs5030655
                                                                                   CYP2D6*6_1707delT
                 Υ
                         ch22:40855030
                                                          T/T
                                                                  Ref/Ref *6
AM 12275
                                                          rs5030865
                                                                                   Ref/Ref *14A, *14B, *8
                         Ch22:40854979, Ch22:40854979
                                                                          G/G
                                                                                                            CYP2D6*14or*8
AM_12274
                                                                  Ref/Ref *4
                                                                                   CYP2D6*4_1846G>A(SpliceDefect)
                 Υ
                         Ch22:40854891
                                         rs3892097
                                                          G/G
AM_12272
                                                          -/-
                                                                                   CYP2D6*40_1863ins(TTTCGCCCC)2
                         ch22:40854873
                                         rs72549356
                                                                  Ref/Ref *40
AM_12270
                         ch22:40854763
                                                                  Ref/Ref *20
                                                                                   CYP2D6*20 _1973insG
                                         rs72549354
                                                          -/-
AM_12268
                 Υ
                         ch22:40854195
                                         rs72549353
                                                          AACT/AACT
                                                                           Ref/Ref *19
                                                                                           CYP2D6*19_2539delAACT
AM 12267
                 Υ
                         Ch22:40854188
                                         rs35742686
                                                          A/A
                                                                  Ref/Ref *3
                                                                                   CYP2D6*3 2549delA
AM_12266
                         ch22:40854157
                                         rs72549352
                                                          -/-
                                                                  Ref/Ref *21
                                                                                   CYP2D6*21 2573insC
AM_12265
                                                                                           CYP2D6*38_2587delGACT
                                                          GACT/GACT
                         Ch22:40854147
                                         rs72549351
                                                                           Ref/Ref *38
                                                          AGA/AGA Ref/Ref *9
AM_12264
                         Ch22:40854120
                                         rs5030656
                                                                                   CYP2D6*9 2615delAAG
AM_12259
                                                                  Ref/Ref *7
                 Υ
                         ch22:40853802
                                         rs5030867
                                                          A/A
                                                                                   CYP2D6*7_2935A>C(H324P)
AM_12258
                 Υ
                                                                  Ref/Ref *44
                         Ch22:40853787
                                         rs72549349
                                                          G/G
                                                                                   CYP2D6*44_2950G>C(SpliceDefect)
AM_12255
                         Ch22:40853554
                                                          G/G
                                                                  Ref/Ref *29
                                                                                   CYP2D6*29_3183G>A(V338M)
                                         rs59421388
AM_12254
                         ch22:40853536
                                                          c/c
                                                                  Ref/Ref *56A, *56B
                                                                                           CYP2D6*56_3201C>T(R344X)
                                         rs72549347
AM_12252
                                                                  Ref/Ref *42
                                                                                   CYP2D6*42_3259insGT
                         Ch22:40853477
                                         rs72549346
                                                          -/-
                                                          T/T
AM_12248
                 Υ
                         ch22:40852603
                                         rs1135836
                                                                  Ref/Ref *18
                                                                                   CYP2D6*18_4125dupGTGCCCACT
                                                                  Ref/Ref -
AM_15506
                         Ch22:40858920
                                         rs28360521
                                                          G/G
                                                                                   CYP2D6_-2178G>A
AM 15503
                         ch22:40858703.ch22:40858703
                                                                           Ref/Ref -
                                                                                           CYP2D6 -1961C>G>A
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Translate phenotypes into EMR priority status

CYP2D6

<u>phenotype</u>	CYP2D6 EMR flag
UM	priority
EM	routine
IM	routine
PM	priority
EM, IM	routine
others	marked for review