Pharmacogenetics

You're at MD at urgent care...





Both need painkillers. You decide on codeine



Codeine is a very common painkiller and is on the list of the World Health Organization's Essential Medicines.

How much do you prescribe each of them?

Based on your codeine dose...



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Italian grandma is still in pain



Lebron is asleep, constipated, and wakes up only to vomit.



What do you do now?





Decreased dose for Lebron

Now, he's getting way less than what you prescribed for a 5year old yesterday, but:



Increased the dose for grandma...





Still in pain?

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Give grandma a very small dose of morphine



Codeine is a prodrug



Bioactivation by CYP2D6



Bioactivation by CYP2D6



Bioactivation by CYP2D6



Variation in CYP2D6 activity



1/Efficiency of metabolizing codeine

Nature Reviews | Genetics

Variation in CYP2D6 activity



1/Efficiency of metabolizing codeine

Nature Reviews | Genetics

dbSNP showing CYP2D6 region



- > 80 known CYP2D6 polymorphisms within coding and regulatory regions
 - includes SNPs, InDels, CNVs, and gene conversion events
- > 100 characterized CYP2D6 'star' alleles that can contain multiple polymorphisms
- Genotype analysis requires both SNP genoptyping and CNV analysis





CYP2D6 and codeine



Death of 3 children in 2012

Ultrametabolizers who take codeine may end up with 50% more morphine in their bodies than the average person taking the same dose

Kirchheiner 2007

Pharmacogenetic dream



в

You just performed a cesarean section...





24 hours later...



What may have happened?

24 hours later...







At least one baby has died from this in real life.

codeine — — morphine

Clinical Pharmacogenetics Implementation Consortium

Likely phenotype ^a	Activity score	Genotypes	Examples of diplotypes
Ultrarapid metabolizer (~1–2% of patients)	>2.0	An individual carrying more than two copies of functional alleles	*1/*1xN, *1/*2xN
Extensive metabolizer (~77–92% of patients)	1.0-2.0 ^b	An individual carrying two alleles encoding full or reduced function; or one full- function allele together with either one nonfunctional or one reduced-function allele	*1/*1, *1/*2, *2/*2, *1/*41, *1/*4, *2/*5, *1/*10
Intermediate metabolizer (~2–11% of patients)	0.5 ^b	An individual carrying one reduced-function and one nonfunctional allele	*4/*10, *5/*41
Poor metabolizer (~5–10% of patients)	0	An individual carrying no functional alleles	*4/*4, *4/*5, *5/*5, *4/*6

Table 1 Assignment of likely codeine metabolism phenotypes based on cytochrome P450 2D6 (CYP2D6) diplotypes

^aThe frequency estimates are based on data from Caucasians and may differ substantially for other ethnicities. See **Supplementary Data** online for estimates of phenotype frequencies among different ethnic/geographic groups. ^bNote that some investigators define patients with an activity score of 0.5 and 1.0 as intermediate metabolizers and those with an activity score of 1.5 and 2.0 as extensive metabolizers. Classifying patients with an activity score of 1.0 as extensive metabolizers in this guideline is based on data specific for formation of morphine from codeine in these patients.¹²

Phenotype	Implications for codeine metabolism	Recommendations for codeine therapy	Classification of recommendation for codeine therapy ^a
Ultrarapid metabolizer	Increased formation of morphine following codeine administration, leading to higher risk of toxicity	Avoid codeine use due to potential for toxicity.	Strong
Extensive metabolizer	Normal morphine formation	Use label-recommended age- or weight-specific dosing.	Strong
Intermediate metabolizer	Reduced morphine formation	Use label-recommended age- or weight-specific dosing. If no response, consider alternative analgesics such as morphine or a nonopioid.	Moderate
Poor metabolizer	Greatly reduced morphine formation following codeine administration, leading to insufficient pain relief	Avoid codeine use due to lack of efficacy.	Strong

Table 2 Codeine therapy recommendations based on cytochrome P450 2D6 (CYI

Pharmacogenetic testing is safer



CPIC

Guidelines

CPIC guidelines are designed to help clinicians understand HOW available genetic test results should be used to optimize drug therapy, rather than WHETHER tests should be ordered. A key assumption underlying the CPIC guidelines is that clinical high-throughput and pre-emptive (pre-prescription) genotyping will become more widespread, and that clinicians will be faced with having patients' genotypes available even if they have not explicitly ordered a test with a specific drug in mind. CPIC's guidelines, processes and projects have been endorsed by several professional societies – <u>read more</u>.



CPIC

HOW not WHETHER

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Cytochrome P450 family

Common theme: **Detoxification** of endogenous and environmental compounds. (hormones, drugs, carcinogenic compounds in food, plant chemicals).

One original cytochrome P450 from 2 billion years ago that has duplicated and divided into 14 families.

The recent 'burst' in new P450 genes appears to be the result of animal-plant warfare.

Induction of expression by environmental exposures.



Cytochrome P450 Enzymes (IV)

The metabolism of endogenous substances (xenobiotics) is carried out predominately by CYP 3A4, CYP 2D6, and CYP 2C9.



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Annotated Drugs

Curated Pathways Clinical Guideline Annotations

Cytochrome P450s and genetic variation



Cytochrome P450s and genetic variation



Grapefruit and CYP3A4 inhibition





Types of pharmacogenetic variation

Metabolizer enzymes (like the Cytochrome P450s)

Transporter proteins (control flow of molecules through membranes)

Allergic reactions (like abacavir and HLA-B*15:02 hypersensitivty)

Pharmacodynamic effects (the mechanism of action like ivacaftor in cystic fibrosis)

Warfarin (Coumadin) - anticoagulant





Thrombus causing partial obstruction



Thrombus causing total obstruction



Thrombus travels, embolus



Warfarin (Coumadin) - anticoagulant





Did ya hear Rodney's on the rat poison?

Better him than me.

Narrow therapeutic window

Therapeutic window



Intensity of anticoagulation (INR)





Table vs Algorithm. Genetics and warfarin dose

	CYP2CS	9							
	*1/*1	*1/*2	*1/*3	*2/*2	*2/*3	*3/*3			
VKORC1									
GG	5-7 mg	5- 7 mg	3-4 mg	3-4 mg	3-4 mg	0.5-2 mg		CYP2C9	
GA	5-7 mg	3-4 mg	3-4 mg	3-4 mg	0.5-2 mg	0.5-2 mg	S-Warfa	rin 7-OH-warfarin	
AA	3-4 mg	3-4 mg	0.5-2 mg	0.5-2 mg	0.5-2 mg	0.5-2 mg	VKORC	1	
			1					CYP4F2	
						Vitam oxid	nin K lized	Vitamin K	Hydro Vitam
							Gamma-glu carboxyla	tamyl	
						1			
						Actic	ive factors	Hypo-functional clotting factors	

Genetic variation and warfarin dose in Caucasians

The CYP2C9*2 and CYP2C9*3 alleles explain **12%** of dose variability.

Two SNPs in VKORC1 explain **30%** of dose variability.

How we can get these values of proportions explained?

Warfarin daily dose algorithm (Caucasian only)

Coefficients	Estimate	Standard error	Р
Intercept	9.468	0.118	< 2 × 10 –16
<i>VKORC1</i> rs9923231 A/G	-0.901	0.049	< 2 × 10 –16
rs9923231 A/A	-2.018	0.067	< 2 × 10 –16
<i>CYP2C9</i> <u>*</u> 1/ <u>*</u> 1 (no *2 or *3 variant)	0		
<u>*</u> 1/ <u>*</u> 2	-0.508	0.058	< 2 × 10 -16
<u>*1/*</u> 3	-0.975	0.070	< 2 × 10 -16
<u>*2/*</u> 2	-1.102	0.197	3.0 × 10-8
<u>*2/*</u> 3	-1.747	0.203	< 2 × 10 -16
<u>*</u> 3/ <u>*</u> 3	-3.400	0.330	< 2 × 10 -16
Age, y	-0.036	0.001	< 2 × 10 -16
sexF	-0.276	0.046	4.2 × 10 -9
Interaction × number of drugs that increase INR <u>+</u>	-0.069	0.018	.001

Warfarin daily dose algorithm (Caucasian only)

Variants don't all do the same thing!

Coefficients	Estimate	Standard error	Р
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CYP2C9 variation globally

Frequencies ^a o	f CYP2C9 allel	les in major ra	ce/ethnic grou					
CYP2C9 allele ^c	African Allele Frequency	African American Allele Frequency	Caucasian (European + North American) Allele	Middle Eastern Allele Frequency	East Asian Allele Frequency	South/Central Asian Allele Frequency	Americas Allele Frequency	Oceanian Allele Frequency
			Frequency					
*1 ^d	86.420	86.700	80.010	76.910	96.570	78.900	88.920	96.620
*2	2.356	2.304	12.602	13.211	0.064	10.738	6.625	0.882
*3	1.033	1.170	7.083	9.312	3.365	10.165	3.254	2.502
*5	1.231	1.284	0.000	0.067	0.000	0.000	0.500	n/a
*6	0.960	0.772	0.000	0.000	0.000	0.000	0.150	n/a
*8	5.020	6.662	0.143	0.500	0.000	0.100	0.338	n/a
*11	2.700	1.386	0.167	0.000	0.003	0.100	0.213	n/a

pharmGKB allele frequency tables



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to guide precision medicine.

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PharmVar Publications

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Knowledge of variant function

CVP2C9*3		PV00539	4261445C (13591)		decreased function
<u>0172075</u>		1 1 00 3 3 3			<u>~</u>
<u> </u>	CYP2C9*3A	PV00058	<u>-1911T>C, -1885C>G, -1537G>A, -981G>A, 442614A>C</u> (I359L), <u>50298A>T</u>	Lim	<u>Kidd et al, 1999</u> <u>Shintani et al, 2001</u> <u>Romkes et al, 1991</u> <u>Haining et al, 1996</u> <u>Sullivan-Klose et al, 1996</u> <u>Aithal et al, 1999</u> <u>Takanashi et al, 2000</u> <u>Blaisdell et al, 2004</u> <u>King et al, 2004</u>
<u> </u>	CYP2C9*3B	PV00057	- <u>1911T>C, -1885C>G, -1537G>A, -1188T>C, -981G>A, #42614A>C</u> (I359L), <u>50298A>T</u>	Def	deposited by Gaedigk et al <u>Shintani et al, 2001</u> <u>Blaisdell et al, 2004</u> <u>King et al, 2004</u>
CYP2C9*4		PV00540	<u>42615T>C</u> (I359T)		possibly decreased
<u> CYP2C9*4.001 </u>	CYP2C9*4	PV00024	<mark>142615T≻C</mark> (I359T)	Lim	<u>lmai et al. 2000</u>
CYP2C9*5		PV00541	<u>42619C>G</u> (D360E)		possibly decreased
<u> <u> CYP2C9*5.001</u> </u>	CYP2C9*5	PV00025	- <u>1188T>C</u> , <u>42619C>G</u> (D360E)	Def	deposited by Gaedigk et al <u>Dickman et al., 2001</u> <u>Allabi et al, 2004</u> <u>Allabi et al, 2005</u>
CYP2C9*6		PV00542	10601delA (273frameshift)		no function
<u>CYP2C9*6.001</u>	CYP2C9*6	PV00027	1 <u>10601delA</u> (273frameshift)	Lim	<u>Kidd et al, 2001</u> <u>Allabi et al, 2004</u> <u>Allabi et al, 2005</u>

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Knowledge of variant function

CYP2C9*3



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nonosibly dependent

Knowledge of variant function

CYP2C9*4

CYP2C9*5

CYP2C9*6

	possibly decreased
L _{im})	<u>lmai et al, 2000</u>
	possibly decreased
	× 4
Def	deposited by Gaedigk et al <u>Dickman et al., 2001</u> <u>Allabi et al, 2004</u> <u>Allabi et al, 2005</u>
	no function
	×
Lim	<u>Kidd et al, 2001</u> <u>Allabi et al, 2004</u> <u>Allabi et al, 2005</u>

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VKORC1 More SNPs, more precision?

rs2359612 explained 33.3% ($P = 5.78 \times 10^{-73}$) of dose variability

rs9923231 explained 32.8% (*P* = 3.97 × 10⁻⁷²)

Included together, they explain 34% of variability.

Why?

Let's look up our SNPs on LDpop

https://ldlink.nci.nih.gov/?tab=ldpop

rs9923231 and rs2359612 (use r²) Look at CEU, YRI, CHB and JPT.



Let's look up our SNPs on LDpop

https://ldlink.nci.nih.gov/?tab=ldpop

rs9923231 and rs2359612 CEU: 1.0 YRI: 0.13 CHB: 1.0 JPT: 1.0

Let's look up our SNPs on LDpop

https://ldlink.nci.nih.gov/?tab=ldpop

rs9923231 and rs2359612 CEU: 1.0 YRI: 0.13 In A CHB: 1.0 JPT: 1.0

In African Americans, VKORC1 genotype still matters, but results in ½ the effect size as in these other populations

African American as a variable

	β	% Dose change (95% CI)	Р
Intercept	1.4564		
African American	-0.0992	-9.44 (-13.57 to -5.11)	<.001
Age, y	-0.0068	-0.68 (-0.81 to -0.54)	<.001
BSA, per m^2	0.4219	52.48 (41.3 to 64.55)	<.001
Current smoker	-0.0022	-0.22 (-6.12 to 6.06)	.94
VTE	0.0512	5.26 (0.85 to 9.86)	.02
Amiodarone	-0.2245	-20.1 (-25.11 to -14.76)	<.001
<i>CYP2C9[*]2</i>	-0.1929	-17.54 (-21.54 to -13.34)	<.001
$CYP2C9^{*}3^{\parallel}$	-0.4183	-34.19 (-38.5 to -29.57)	<.001
VKORC1	-0.3016	-26.03 (-28.45 to -23.54)	<.001

Summary

- Genetics can change drug response by altering drug target, drug metabolism, and drug transport, and by triggering allergies. Using genetic information can improve toxicity and efficacy of drugs.
- These variants only matter when faced with an external substance.
- Frequencies of variants vary greatly across the world.
- Genetic tests can inform treatment but are based incomplete information (complex biological systems and limited understanding of functional effects of variants).