



Genes and the Environment: How they Affect Drug Metabolism and Response

A Study of CYP3A Enzymes

Ken Thummel, Department of Pharmaceutics
University of Washington

Rawls-Palmer Award Lecture – 03/10/16

1980: Age 24 and Considering Career Paths



Robert Vestal, MD



- 1981: Introduction to clinical pharmacology and pharmacokinetics at Boise VA
- Theophylline – drug interactions

Advised me to attend
graduate school –
Pharmaceutical Sciences
at UW

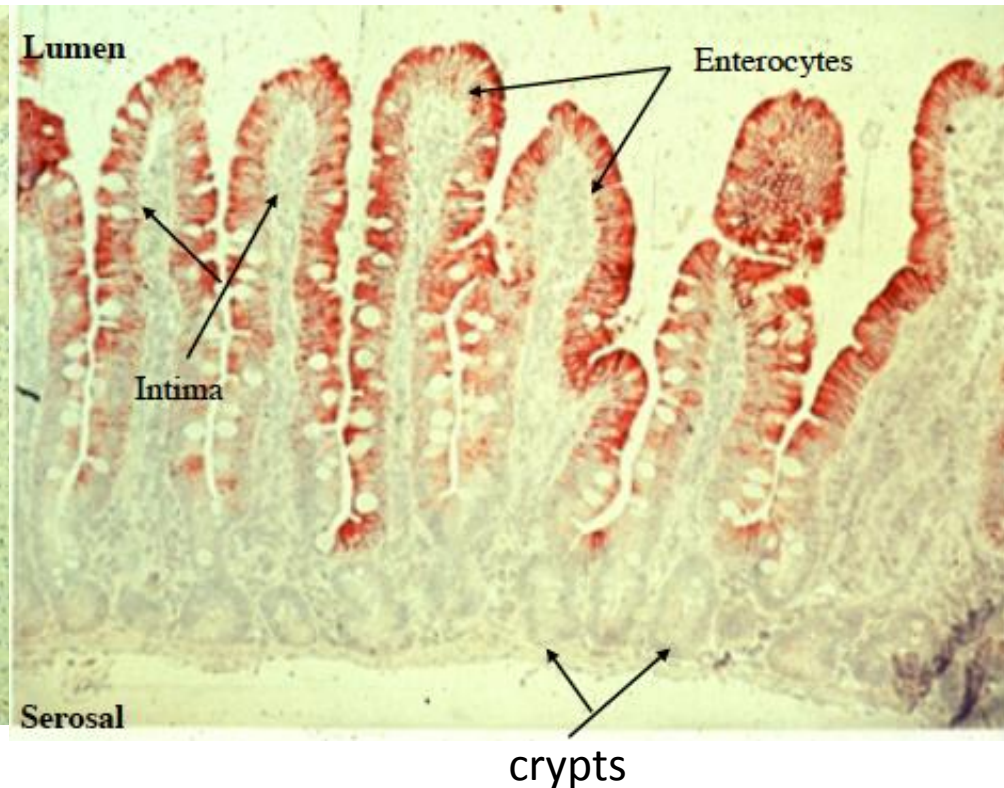
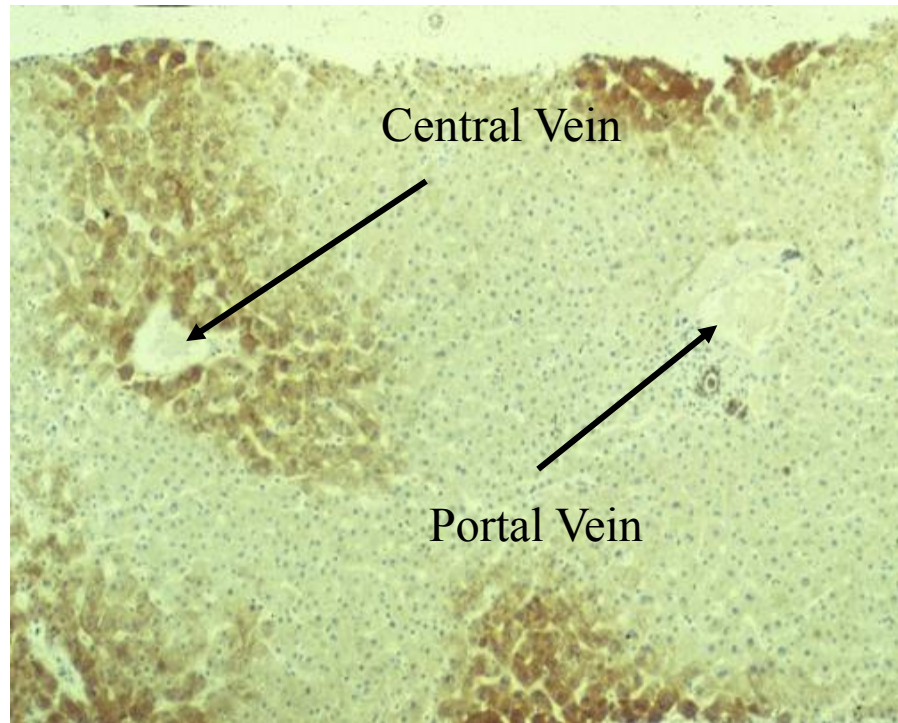
Early Training

- Graduate School (John Slattery)
 - DDIs and acetaminophen hepatotoxicity
- Post-doctoral Fellowship (John Schenkman)
 - cytochrome P450 biochemistry

Evolving research interest:

- Mechanism(s) of inter-individual differences in CYP3A-dependent drug metabolism and drug response

Hepatic and Intestinal CYP3A



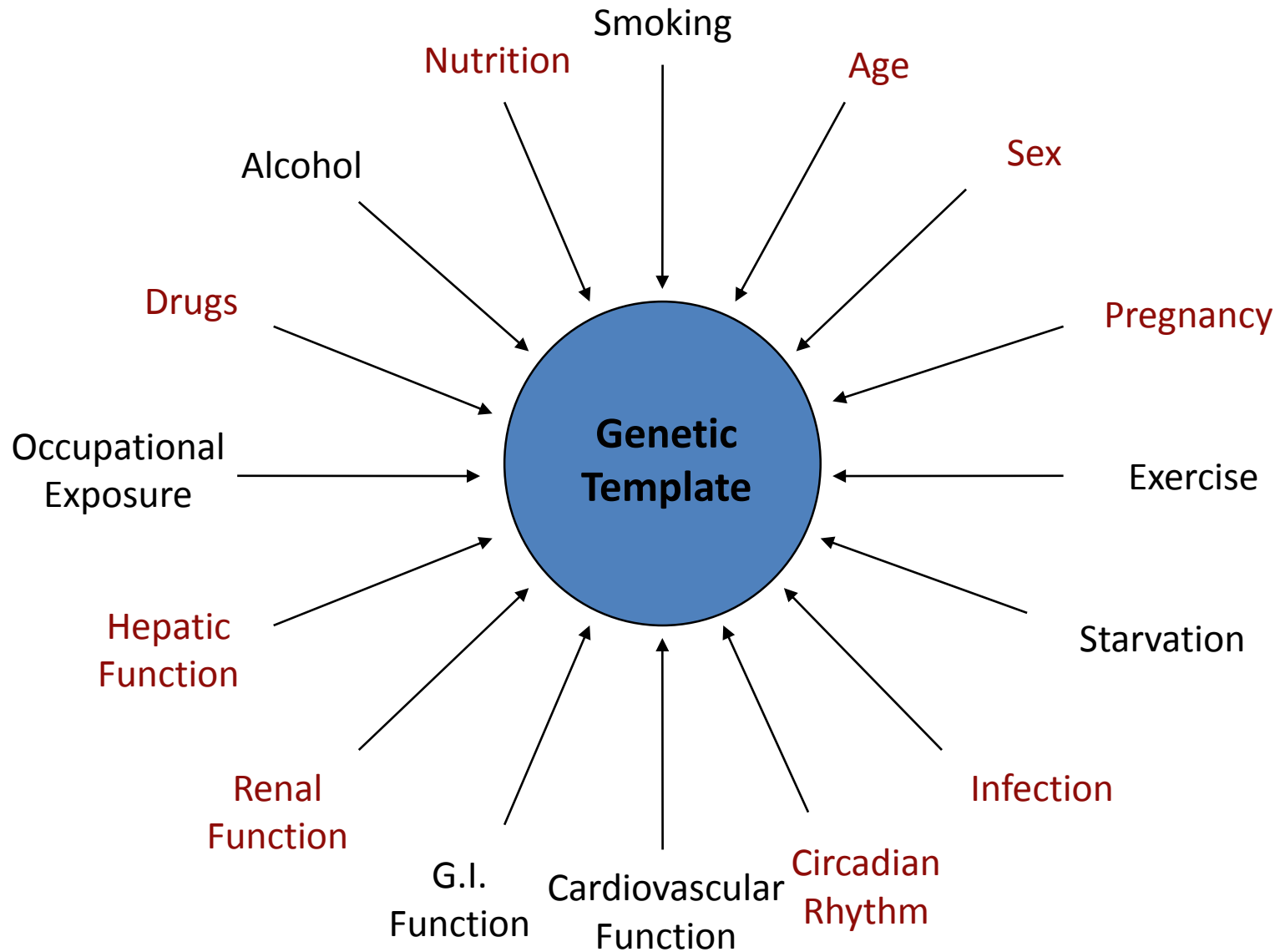
Hepatic CYP3A (brown) is predominantly pericentral; inter-individual differences reflect a variable number of CYP3A (+) pericentral hepatocytes.

(Thummel et al, JPET, 1994)

CYP3A (+) expression is confined to the “absorptive” enterocytes of the mucosal villi and shows high inter-individual variability.

(Courtesy of Paul Watkins)

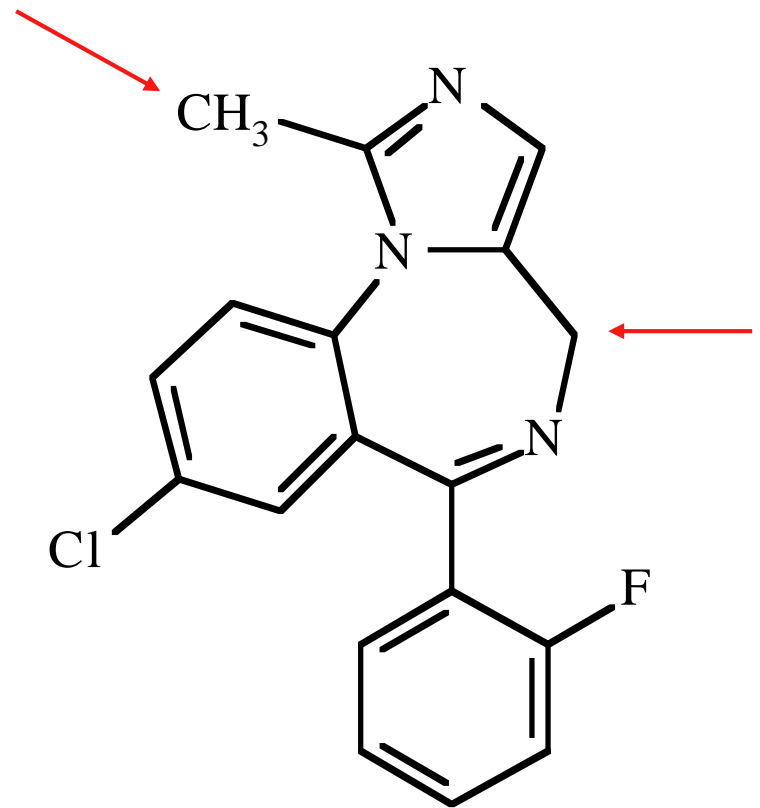
Sources of Interindividual Variability in P450 Expression



Adapted from E. Vesell, 1981

Identify a Selective, Sensitive Dual-Purpose *In Vitro* and *In Vivo* CYP3A Probe

- Cleared by oxidative metabolism, catalyzed exclusively by CYP3A4/5/
- Intermediate clearance (~240 mL/min), 30-45% oral bioavailability; very low renal clearance (< 1%)
- High plasma protein binding (~98%)
- 1'-OH MDZ formation dominates *in vivo*



Midazolam

Thummel et al. JPET, 1994

In Vitro to In Vivo Prediction of MDZ CL_H

$$\frac{V_{\max}(\text{liver})}{K_m} = Cl'_{\text{int}}(\text{liver}) \rightarrow \frac{(f_u \cdot Cl'_{\text{int}}) \cdot Q_H^P}{(f_u \cdot Cl'_{\text{int}}) + Q_H^P}$$

TABLE 3

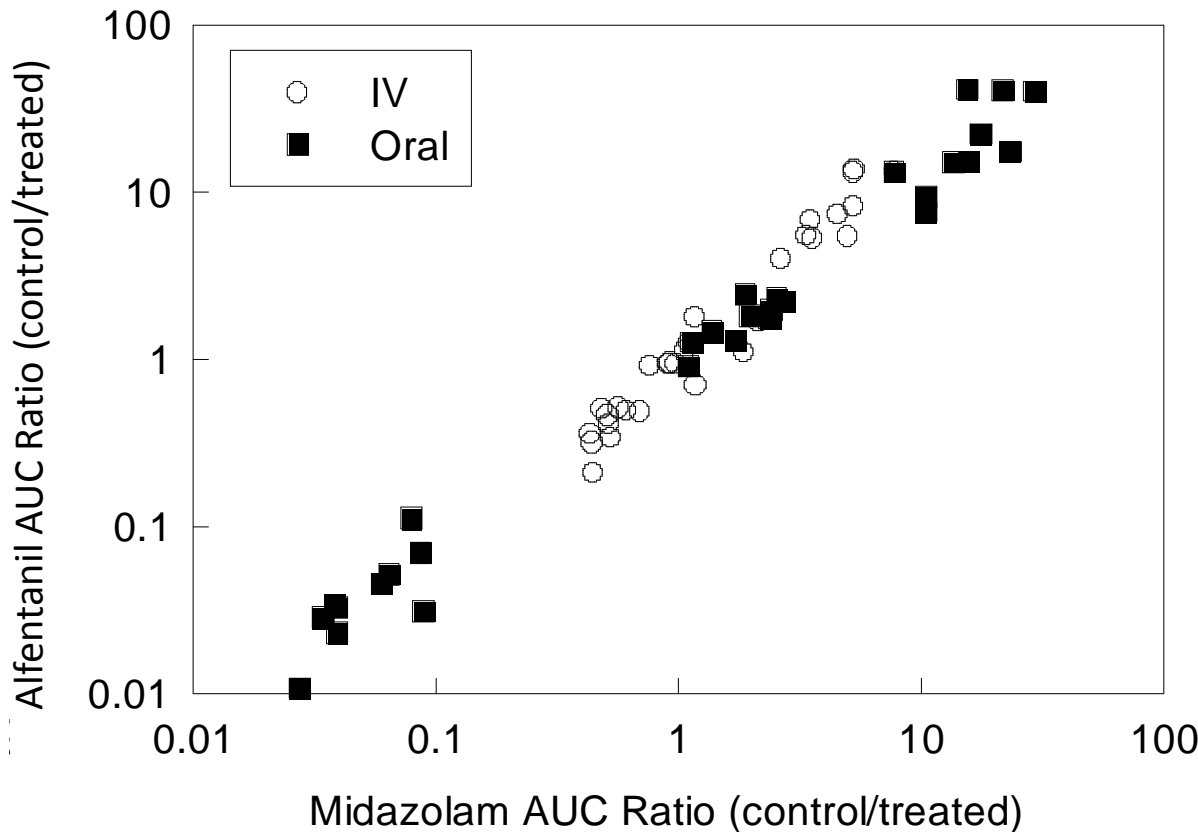
Predicted hepatic 1'-OH MDZ formation clearance

Subject	Donor Body Weight	Q_H^B ^a	Q_H^P ^b	Predicted $Cl_H^{1'-OH}$ ^c	Observed Cl_T ^d
	<i>kg</i>			<i>liter/min</i>	
R-2	80	1.73	1.21	0.28	0.67
R-6	80	1.73	1.12	0.21	0.15
R-7	64	1.38	0.99	0.44	0.68
R-19	73	1.58	1.07	0.58	0.68
R-22	106	2.29	1.60	0.58	0.79

^a Calculated as the product: body weight (kg) × 0.0216 liter/kg.

^b Calculated as the product: (1 - Hct) × (Q_H^B).

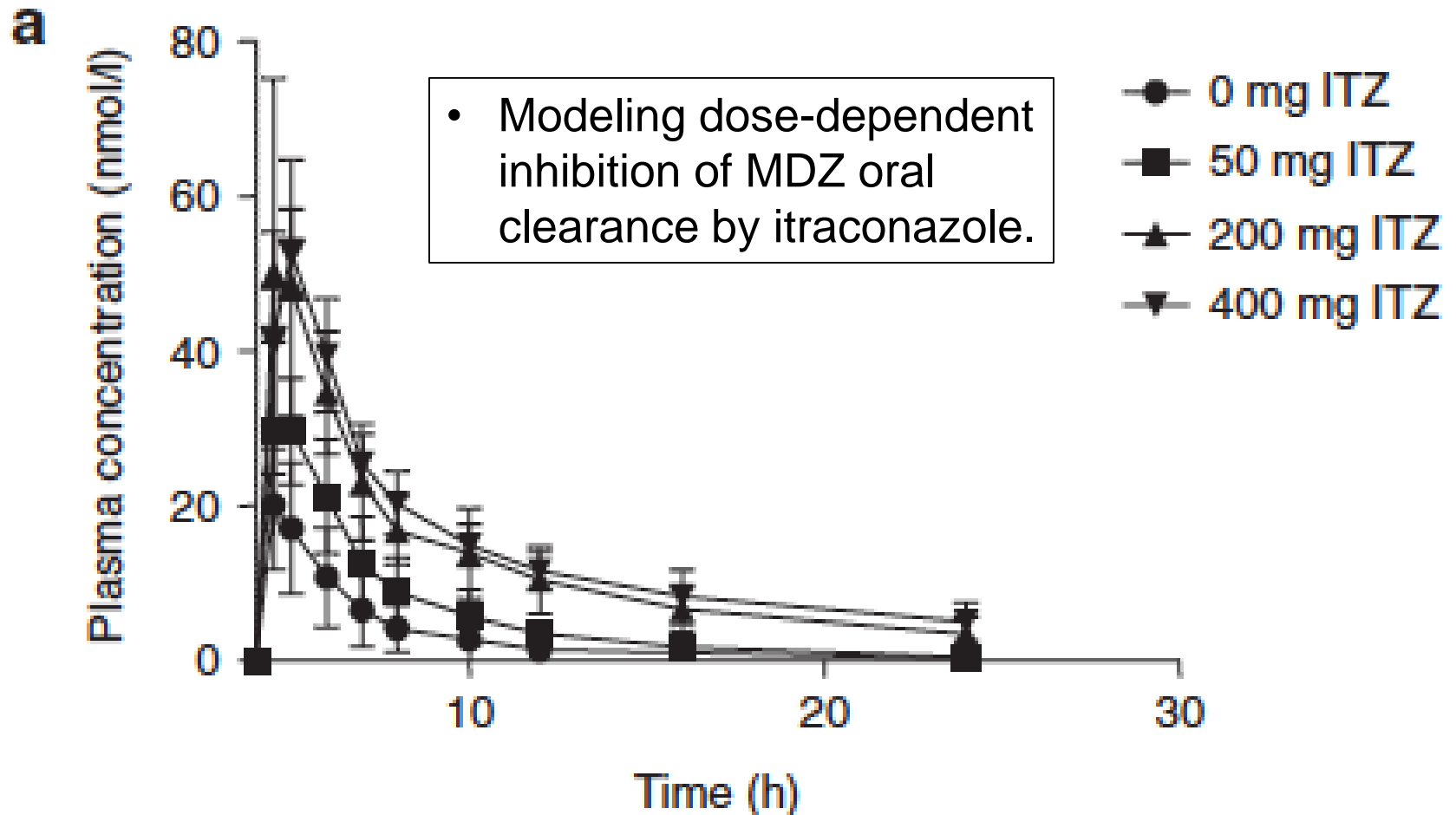
Midazolam Predicts the Disposition of Alfentanil when given with CYP3A Inducers and Inhibitors



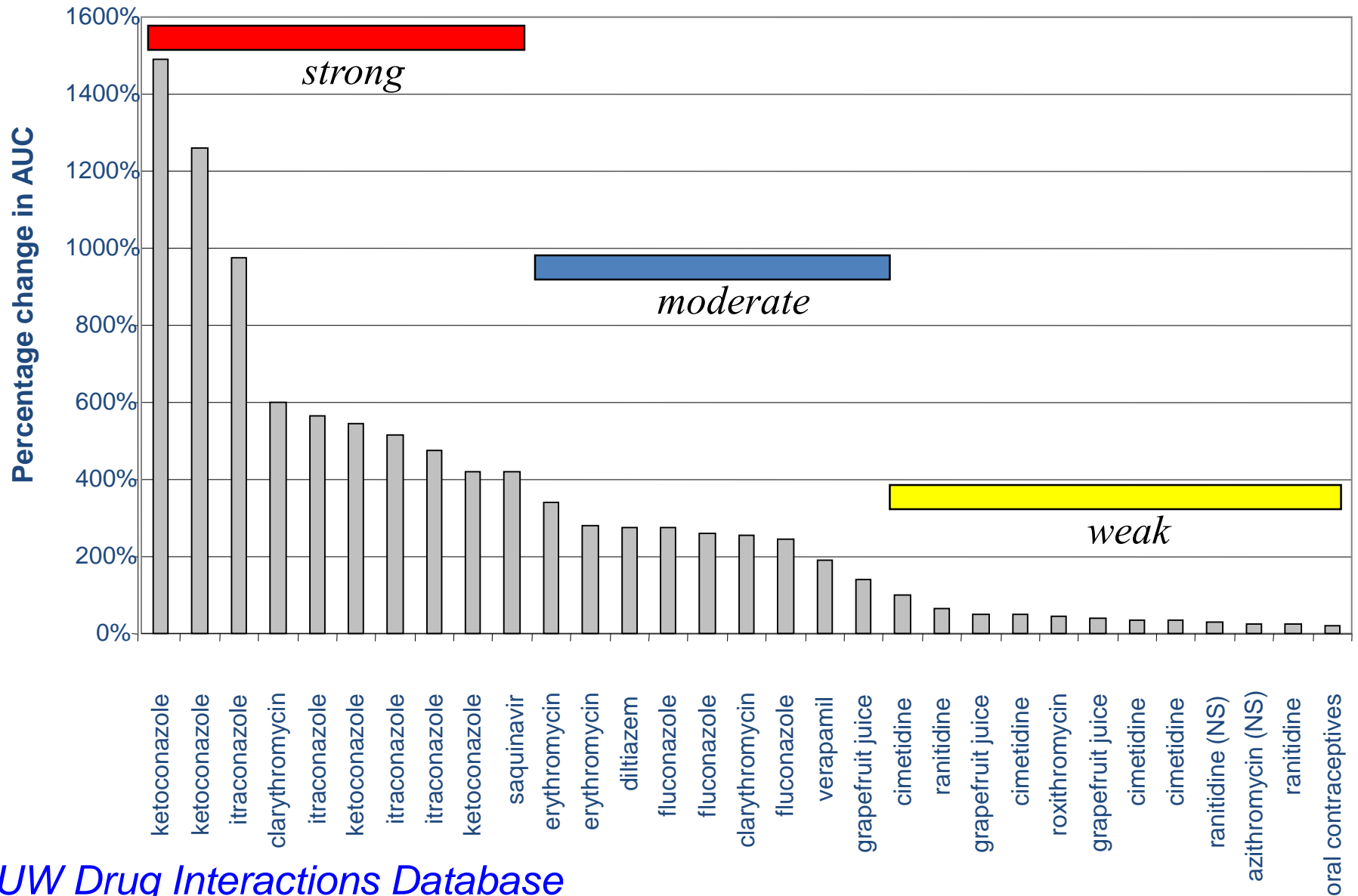
- Under control conditions, the clearance of alfentanil is predicted by the clearance of midazolam ($r^2 = 0.60$)
- Drugs were co-administered with rifampin, troleandomycin or grapefruit juice; rank order effect in different individuals is predictive.
- Both midazolam and alfentanil undergo intestinal metabolism and both are CYP3A5 substrates.

Kharasch et al., CPT, 2004; Proc Assoc Univ Anesthesiologists, 2005

Midazolam is a Sensitive Probe for Characterizing CYP3A Inhibition



Classifying Inhibitors of CYP3A Based on Inhibition of Oral Midazolam Elimination



Paul Watkins, MD

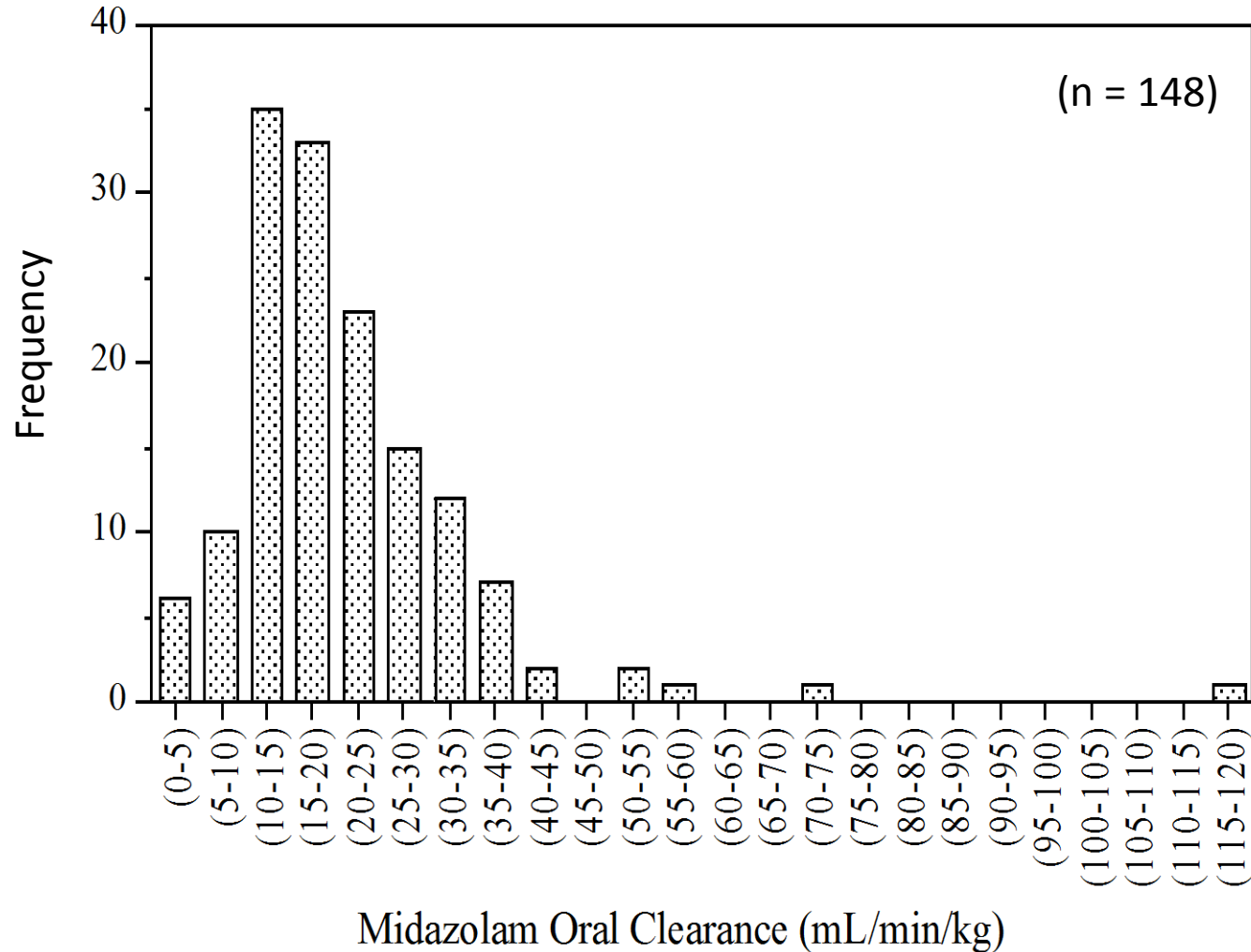


- Characterization of intestinal CYP3A4
- Development of ERMBT

Advised that the most interesting CYP3A science was going to be found in the intestine.

Population Distribution of Midazolam CL/F

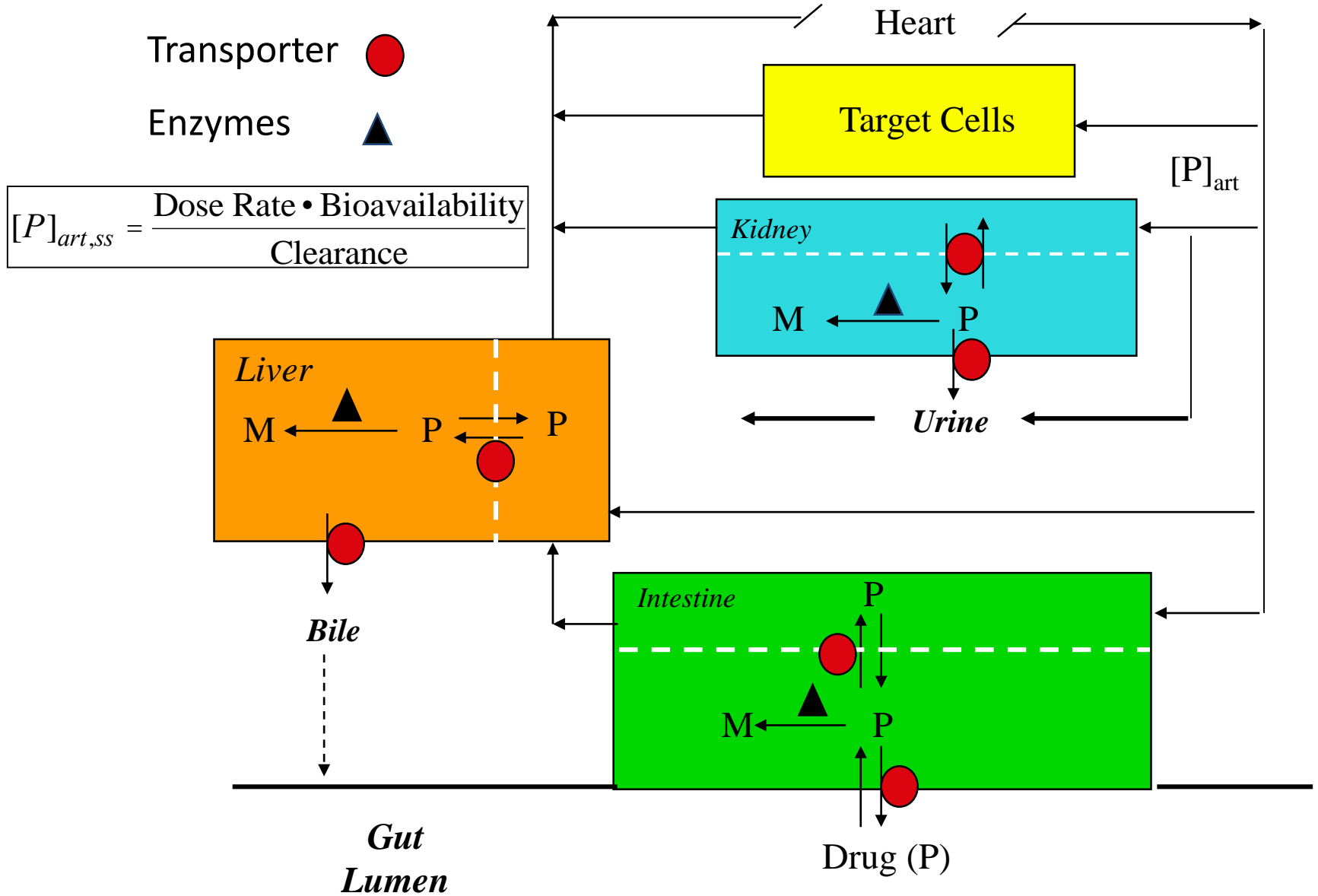
High Plasma Conc/Dose ————— Low Plasma Conc/Dose



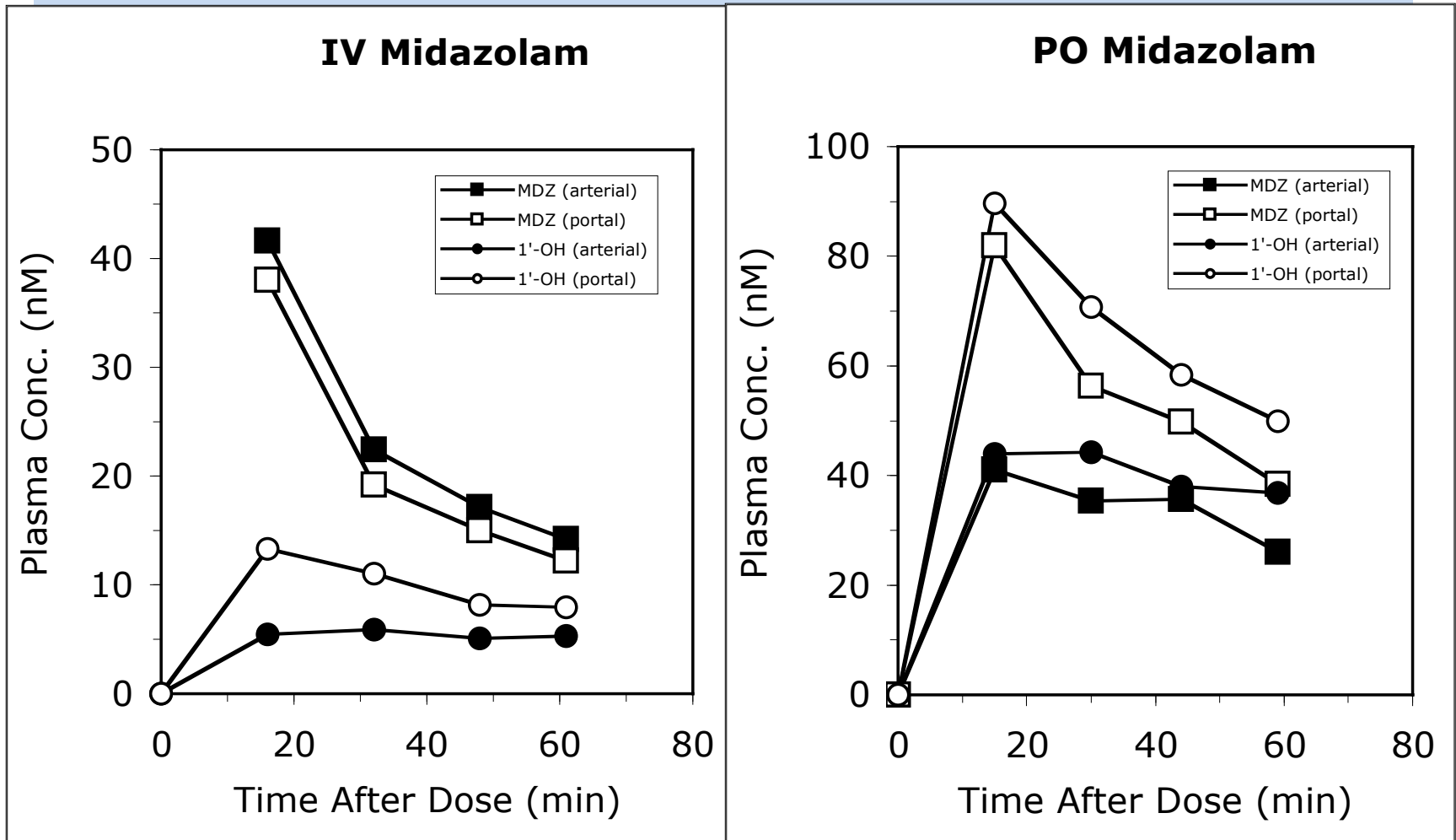
MDZ CL/F
depends on:

Hepatic CYP3A
Intestinal CYP3A

Oral Midazolam Disposition



In Vivo Intestinal Midazolam Metabolism



- 1 mg IV or 2 mg PO during anhepatic phase of a liver transplant operation (*Mary Paine et al., CPT, 1996*)

Intestinal Midazolam Extraction: Anhepatic Patients

<i>Intravenous Dose</i>		<i>Intraduodenal Dose</i>	
Subject	E (%)	Subject	E' (%)
3	11.1	1	40.5
4	25.6	2	45.1
6	8.5	5	57.1
7	-2.6	9	58.6
10	-1.8	11	13.6
<i>Mean</i>	8.2	<i>Mean</i>	43.0*
<i>S.D.</i>	11.5	<i>S.D.</i>	18.1

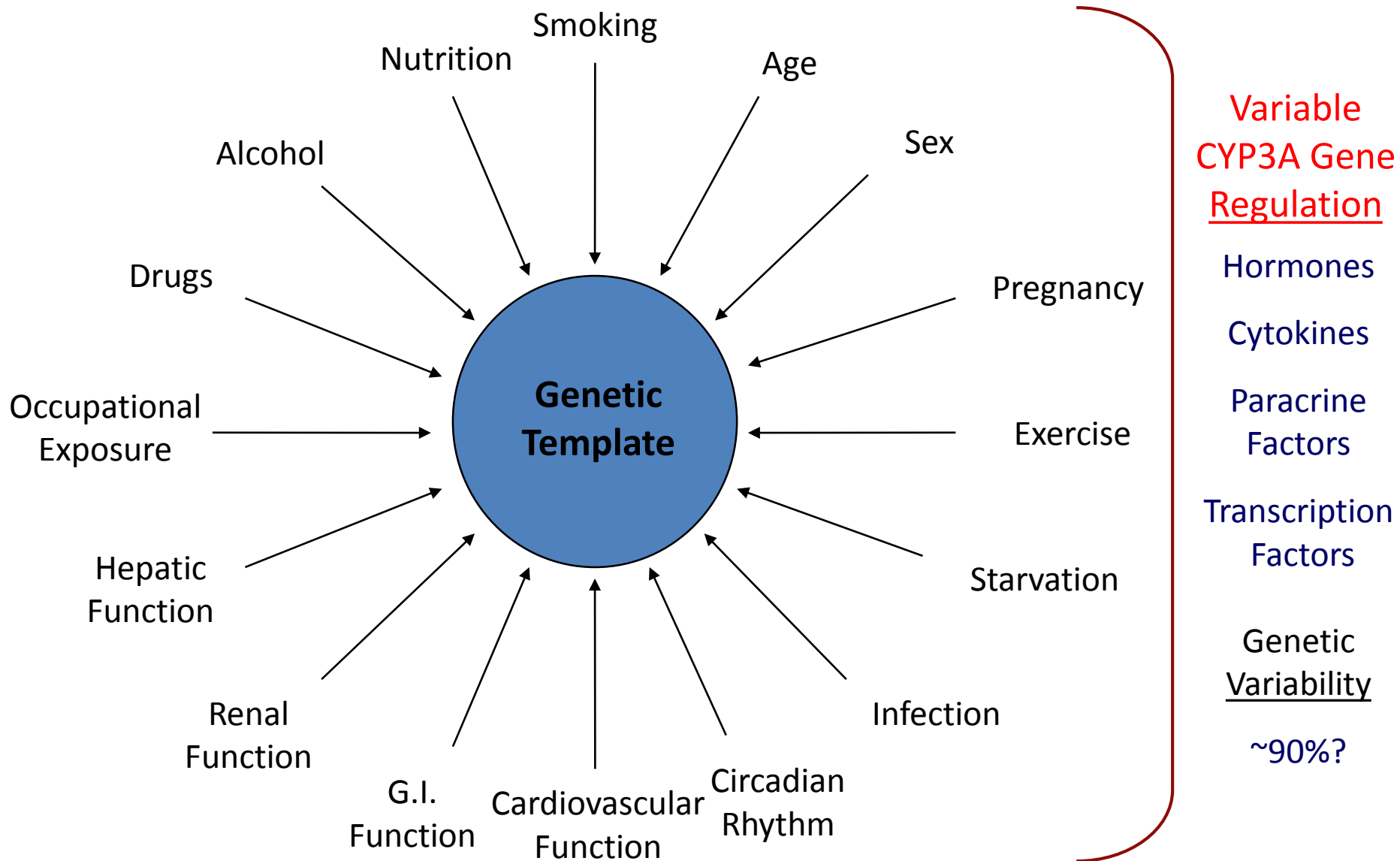
Mary Paine et al., CPT, 1996

CYP3A Substrates Suspected of Undergoing Extensive First-pass Gut Metabolism

Lovastatin	Cyclosporine	
Simvastatin	Tacrolimus	Felodipine
	Sirolimus	Verapamil
Midazolam		Nicardipine
Triazolam	Saquinavir	Diltiazem
	Ritonavir	

All have an oral bioavailability of < 50%.

Identifying Sources of Variable CYP3A Expression



Adapted from E. Vesell, 1981

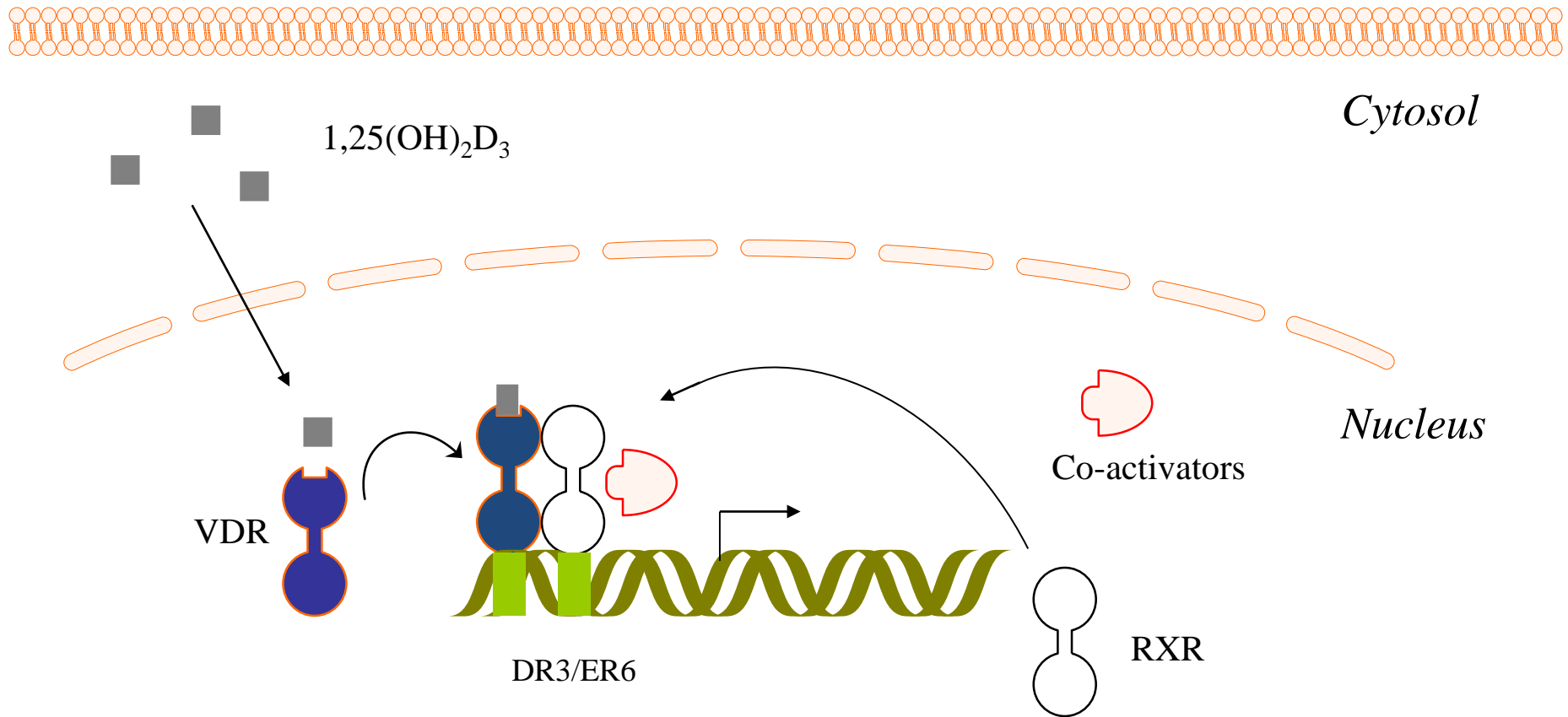
Erin Schuetz, PhD



- St Jude Children's Research Hospital
Sabbatical - 2000

Opportunity for research on the regulation of CYP3A4 by vitamin D and CYP3A gene variation

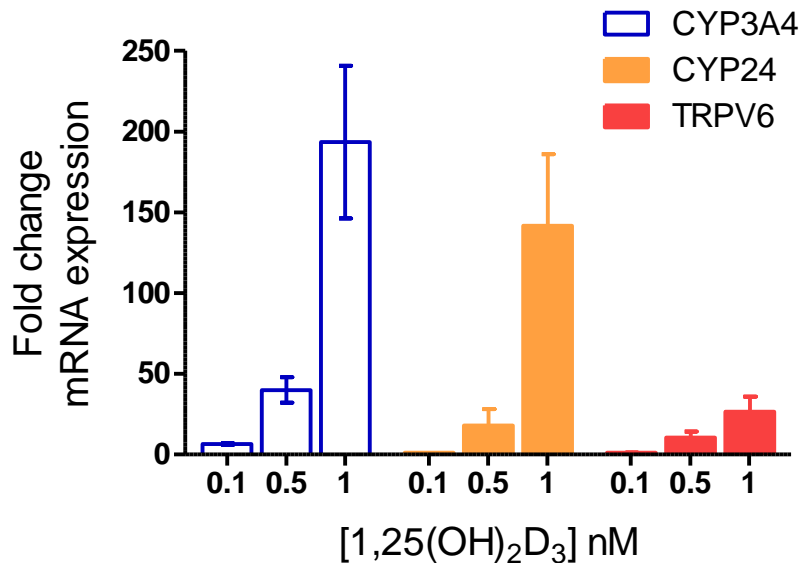
Regulation of Intestinal CYP3A4 by Vitamin D



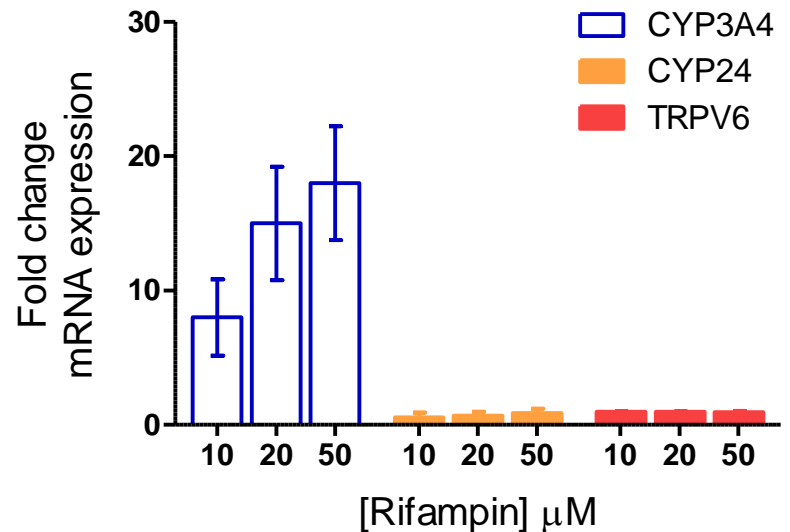
- 1,25(OH)₂D₃ induces CYP3A4 by a VDR-dependent process (Schmiedlen-Ren, *Jeannine Fisher, Mary Paine et al, Mol Pharmacol, 1997*; Thummel, *Tauri Senn et al, Mol Pharmacol, 2001*).

LS180 Cells: A Model for Human Enterocytes

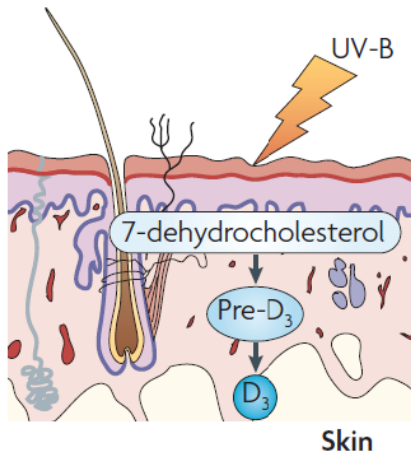
- LS180 cells contain relative high expression of hPXR, VDR, CYP3A4 and TRPV6, compared to Caco-2 cells (low PXR and minimal basal CYP3A4)



Very low dose 1,25(OH)₂D₃ induces all 3 VDR gene targets.

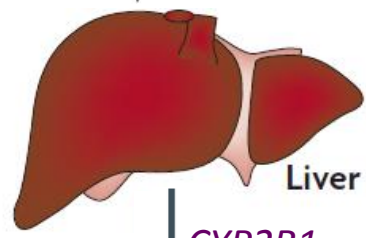
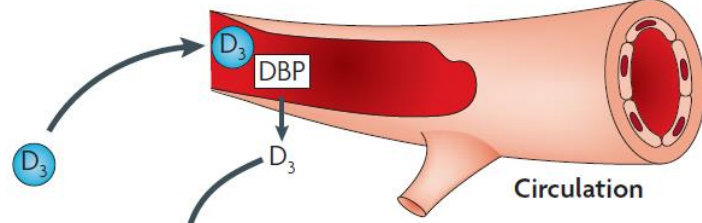


Rifampin is a selective CYP3A4 inducer.



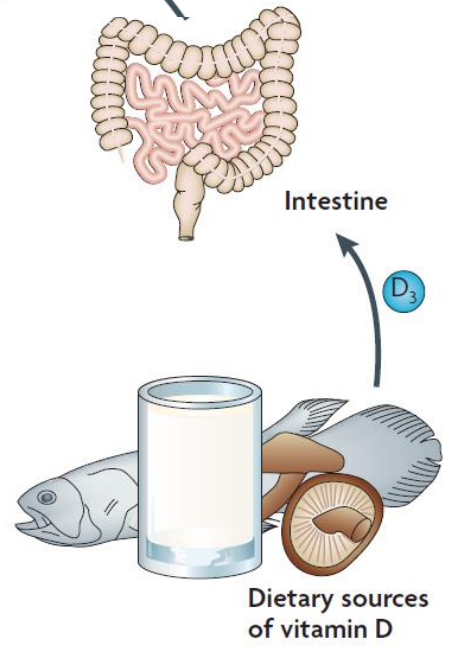
Vitamin D

DHCR7



25(OH)D₃

[DBP]



- Other Tissues**
- Skin
 - Immune cells
 - Vasculature
 - Colon

Kidney

CYP27B1

1,25(OH)₂D₃ [DBP]

VDR

Adapted from Deeb et al, 2007

Intracrine

Endocrine

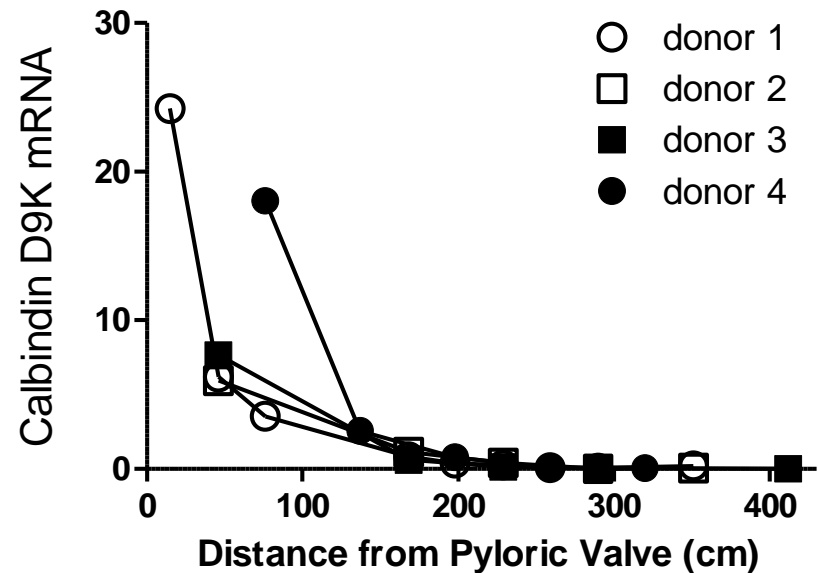
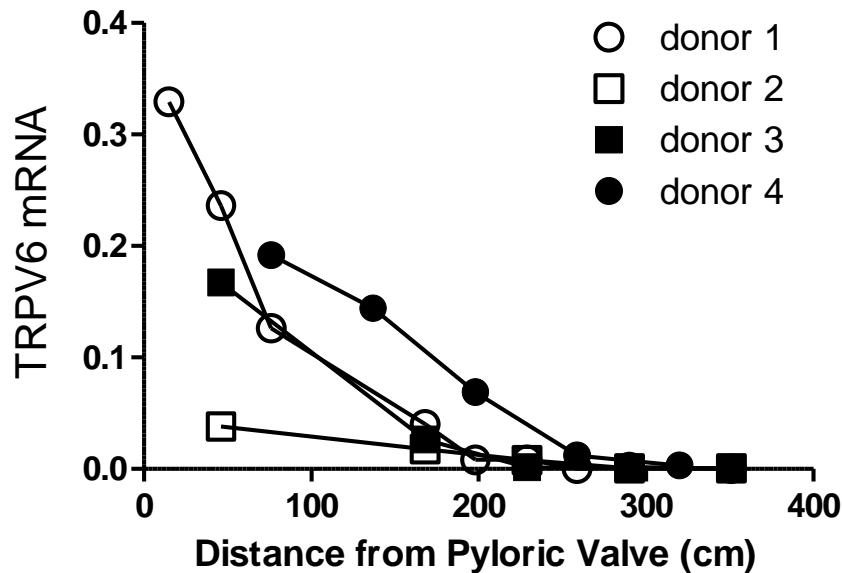
Immune cells
Induces cell differentiation

Kidney
Increases reabsorption of Ca²⁺ and Pi

Small Intestine
Increases absorption of Ca²⁺ and Pi, and CYP3A enzyme and activity

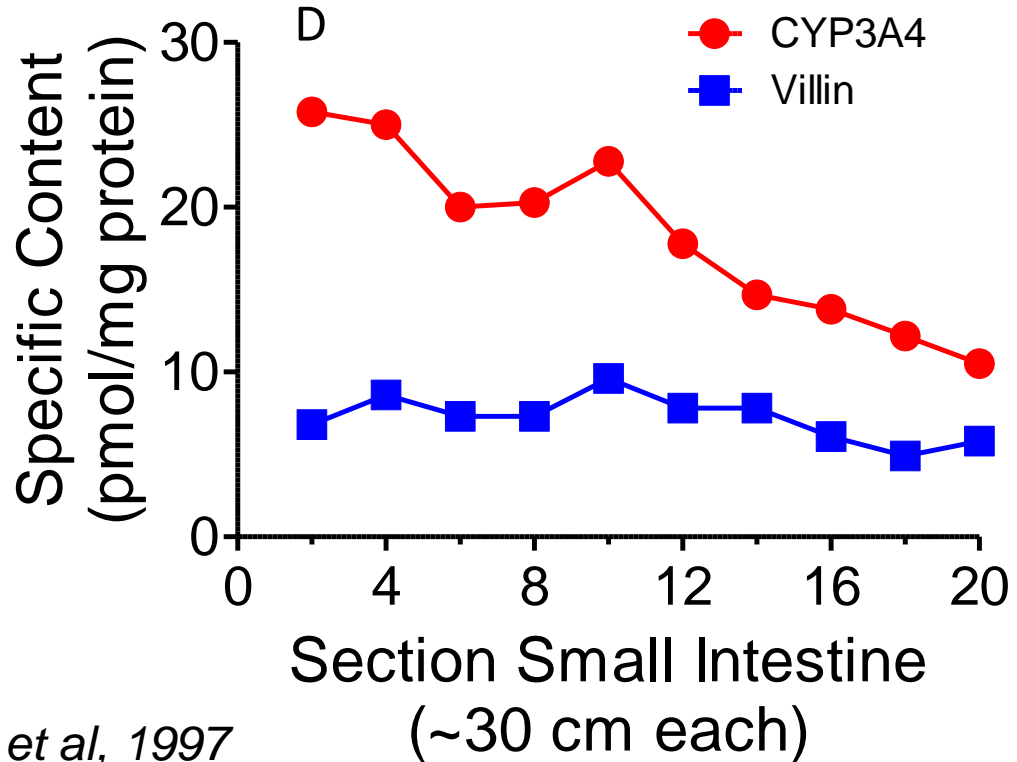
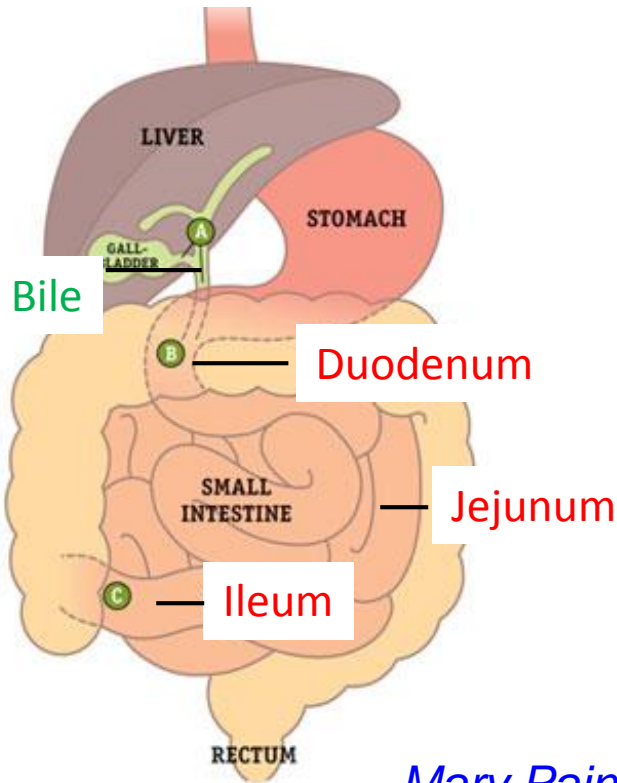
Bone
Mineralization and remodeling

Preferential Expression of VDR Target Genes in the Upper Small Intestine



- Heterogeneous expression pattern consistent with primary site of calcium absorption.

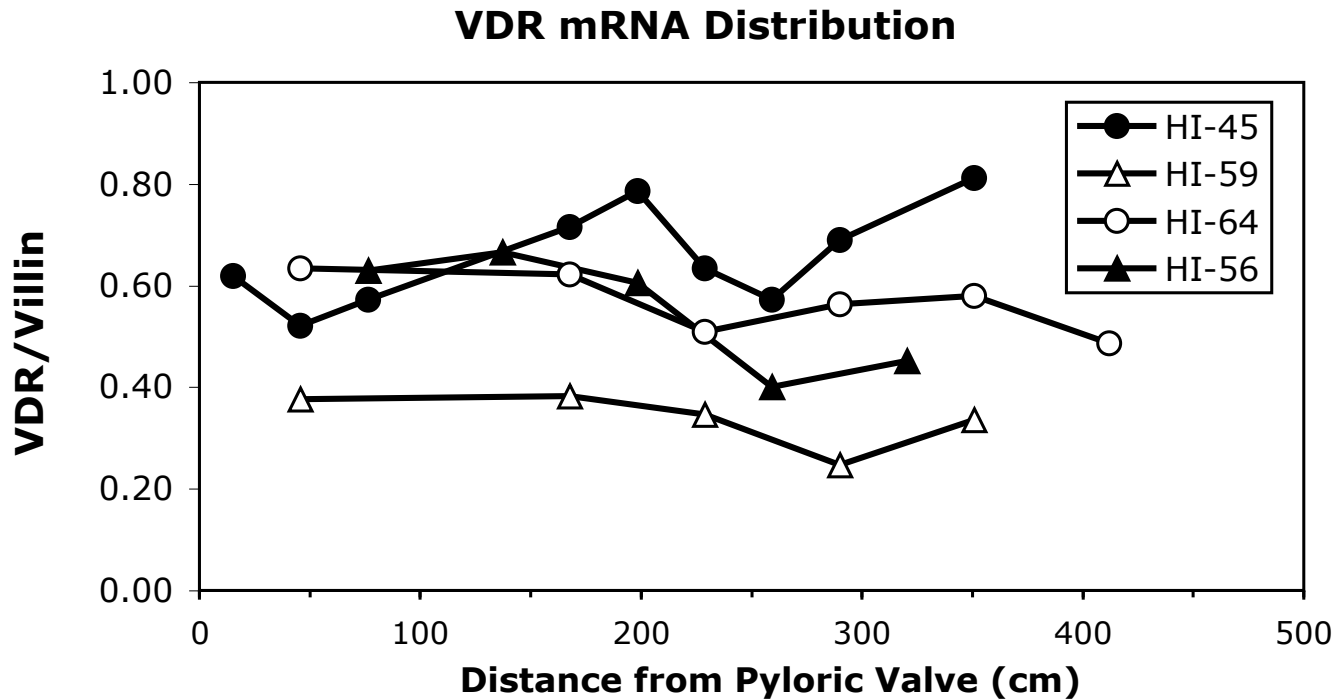
Heterogeneous Distribution of CYP3A4 Protein in Small Intestine



Mary Paine et al, 1997

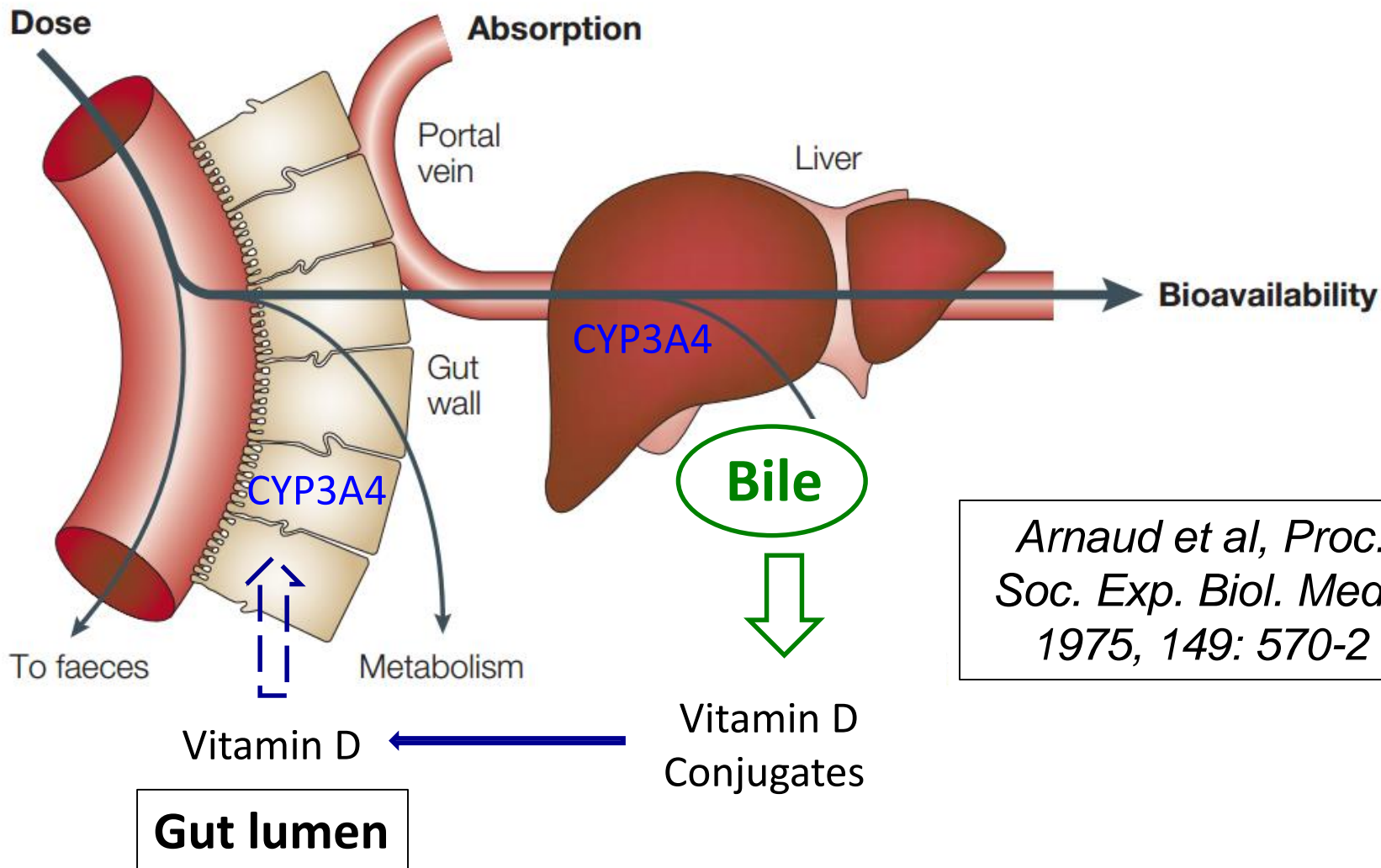
A common VDR signaling pathway for both calcium transport proteins (TRPV6, calbindin D9K) and CYP3A4?

VDR Expression is Relatively Constant Along the Length of the Small Intestine

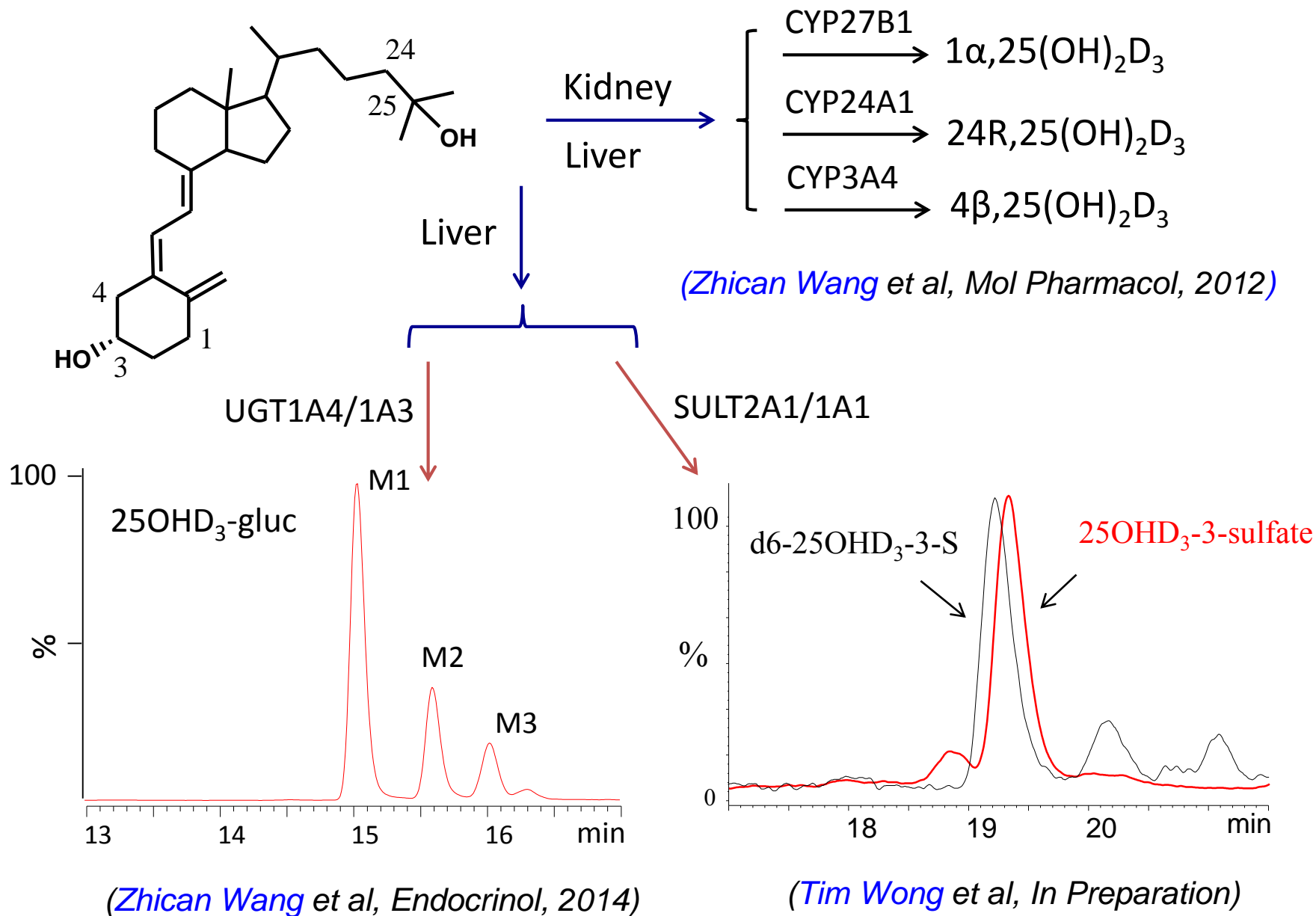


What about delivery of the ligand?

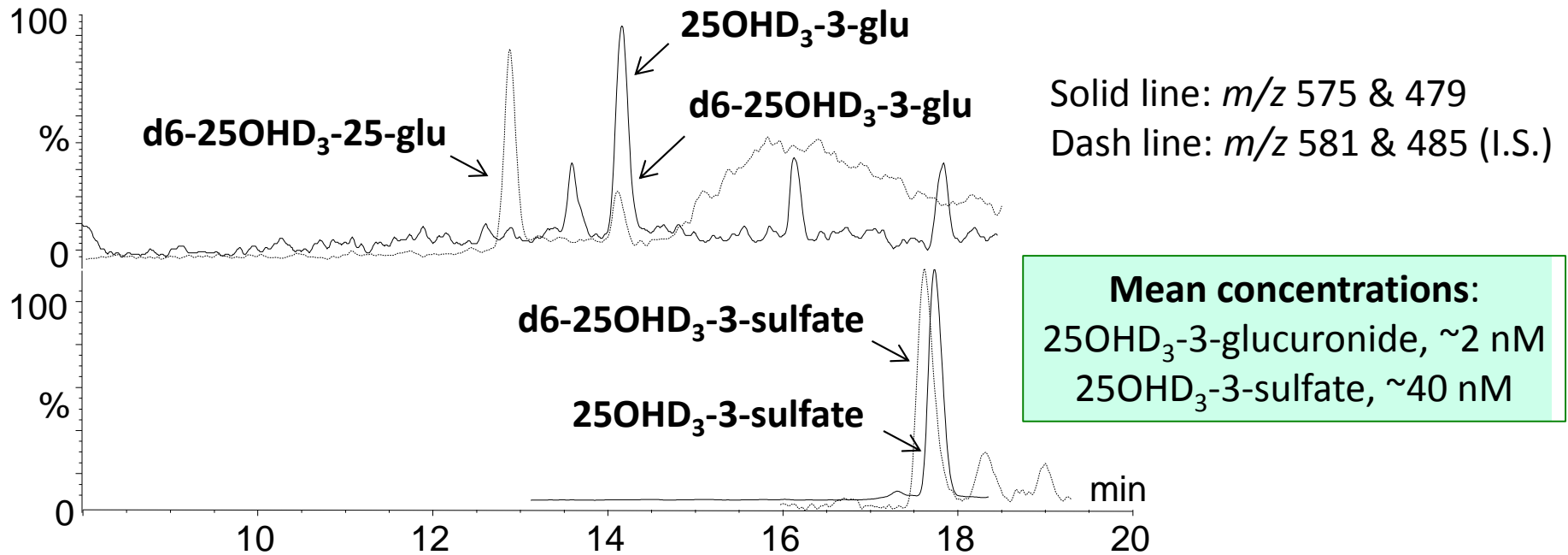
Hypothesis: Biliary Vitamin D Conjugates Regulate Intestinal *CYP3A4* Expression



Major Metabolic Pathways of 25OHD₃

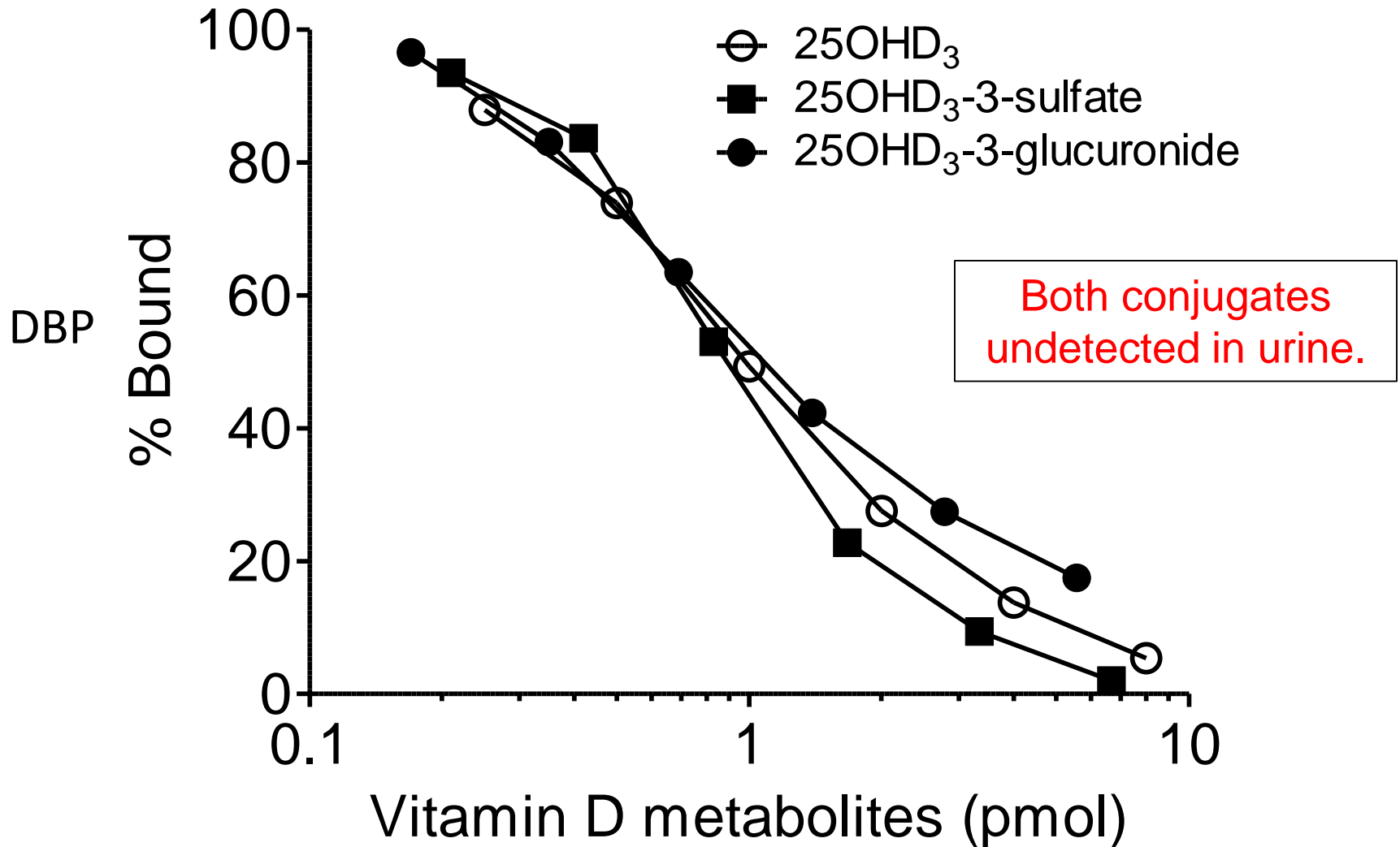


25OHD₃ Conjugates in Human Plasma



Conditions	25OHD ₃ nM	24R,25(OH) ₂ D ₃ nM (M/P ratio)	25OHD ₃ -3-sulfate nM (M/P ratio)
Healthy Control (n = 21)	52.3 ± 25.2	3.8 ± 2.8 (0.11 ± 0.02)	46.2 ± 21.1 (1.07 ± 0.73)
Liver Disease (n = 20)	40.6 ± 21.8	2.9 ± 1.9 (0.11 ± 0.03)	42.5 ± 30.2 (1.33 ± 0.95)
Kidney Disease (n = 15)	26.5 ± 18.5	1.1 ± 0.4 (0.05 ± 0.02)	28.0 ± 19.0 (1.06 ± 0.39)

Circulating 25OHD₃ Conjugates Tightly Bind to Vitamin D Binding Protein (DBP)



25OHD Glucuronides in Human Bile

Diluted human bile

Hexane extraction

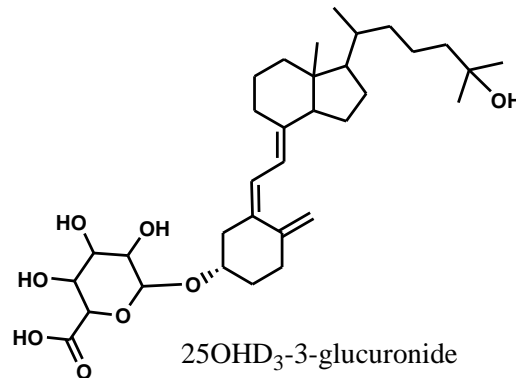
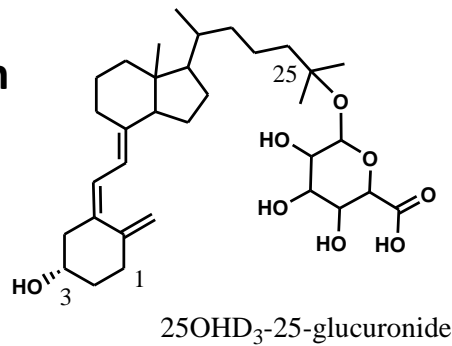
Aqueous solution

Buffered,
sodium acetate
(pH 4.0)

Mixture

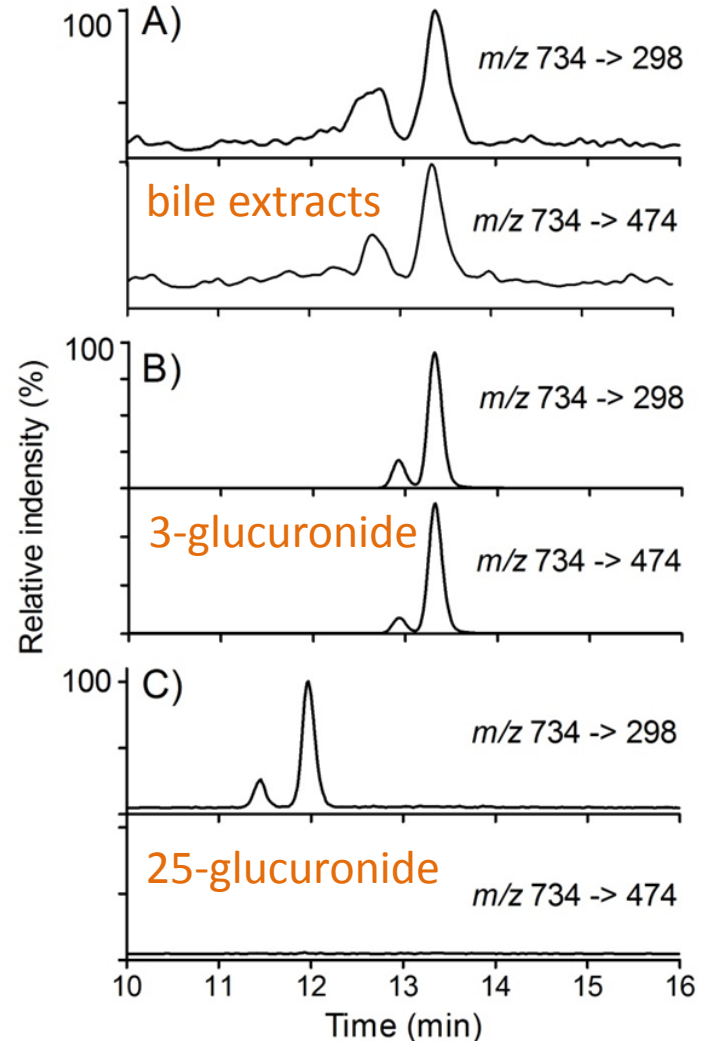


Dried
Derivatization



ESI-LC-MS/MS

Mass spectra of 25OHD-3-glucuronide in human bile

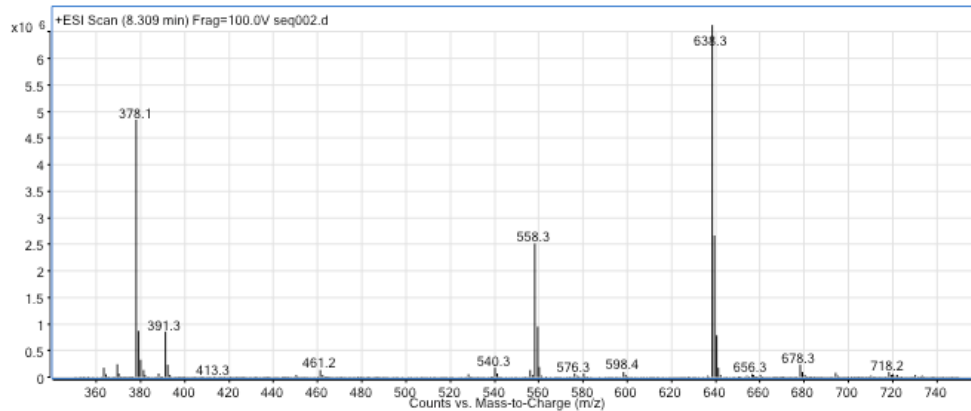


Anion exchange SPE

Zhican Wang et al, *Endocrinology*, 2014

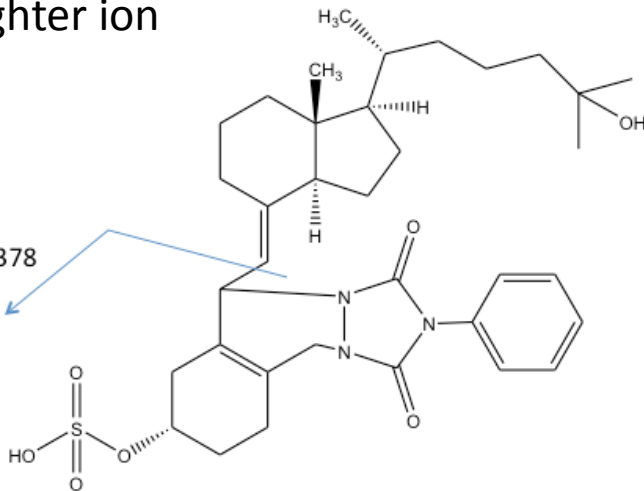
25OHD₃-3-O-Sulfate in Human Bile

Precursor ion Scan: 25OHD-3-S-PTAD



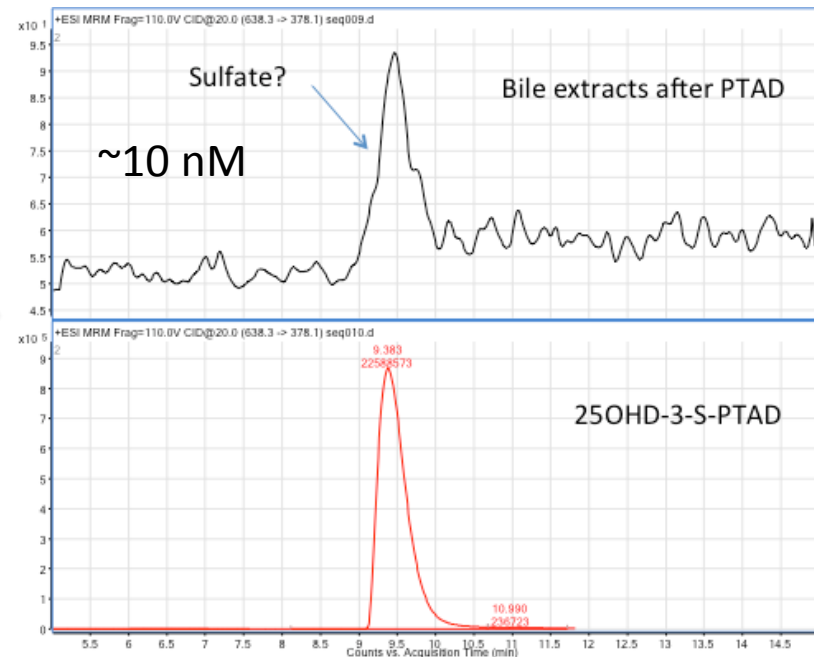
diagnostic
daughter ion

m/z 378



MRM

- similar daughter ion scans for bile extract and standard (not shown) suggest the presence of the 3-sulfate metabolite in bile.



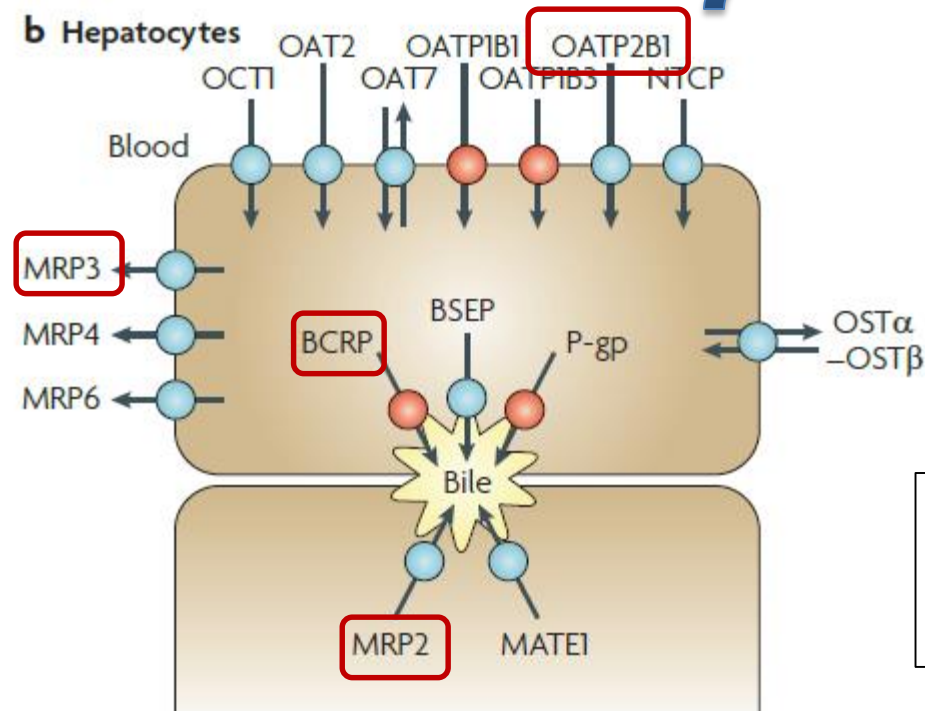
Chunying. Gao et al, Unpublished

Identification of Hepatic Vitamin D Conjugate Transporters

Uptake of 25(OH)D₃-3-sulfate: OATP2B1

Efflux of 25(OH)D₃-3-sulfate: BCRP

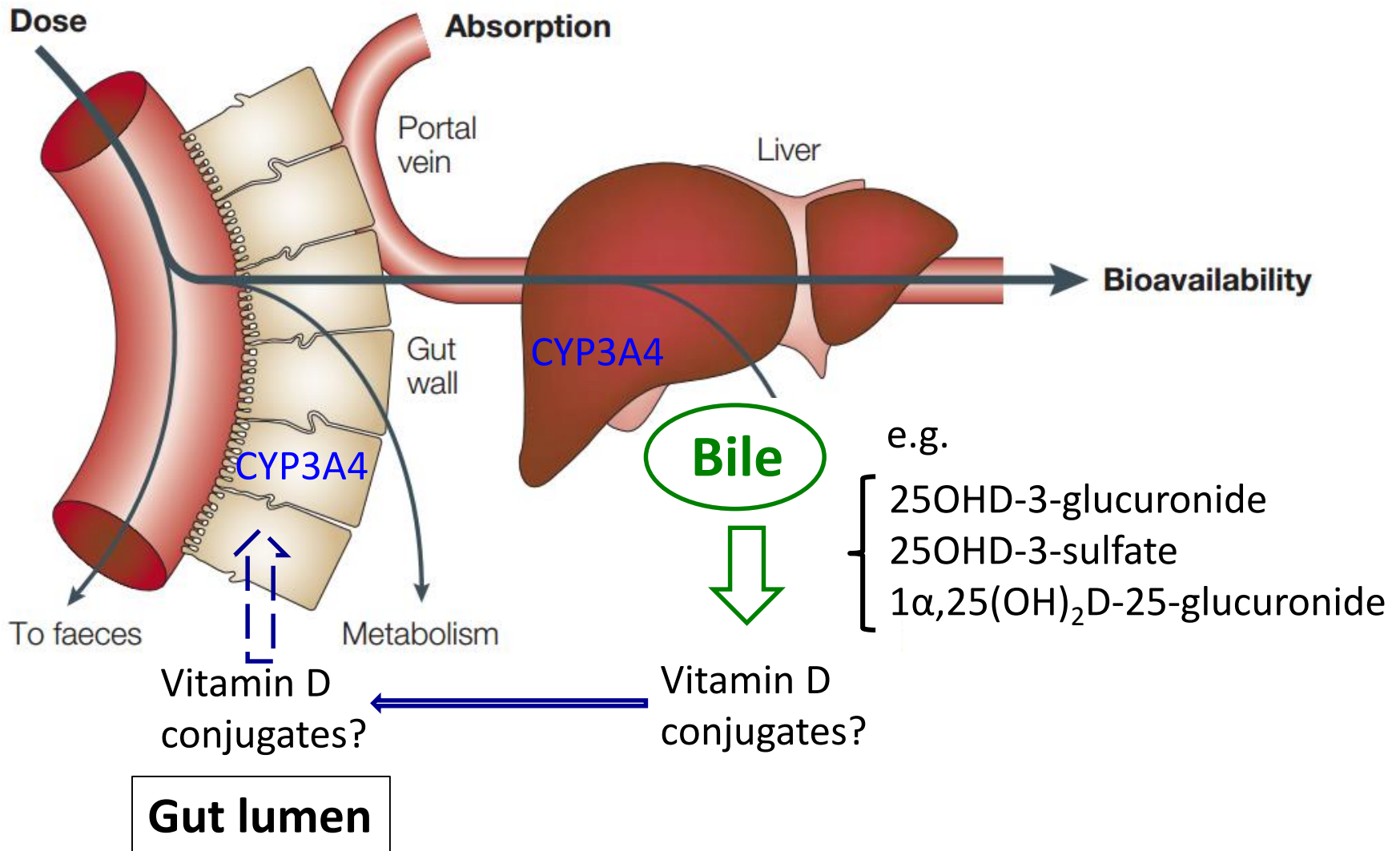
Efflux of 25(OH)D₃-3-glucuronide: MRP2, MRP3



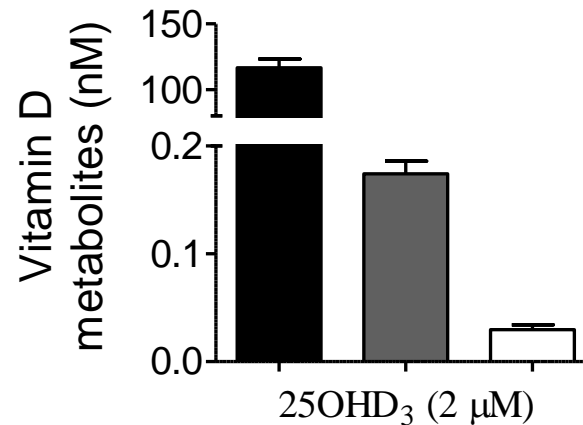
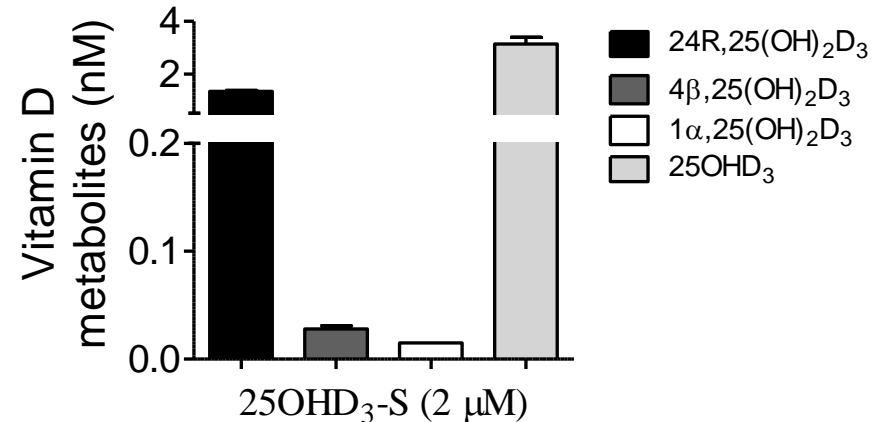
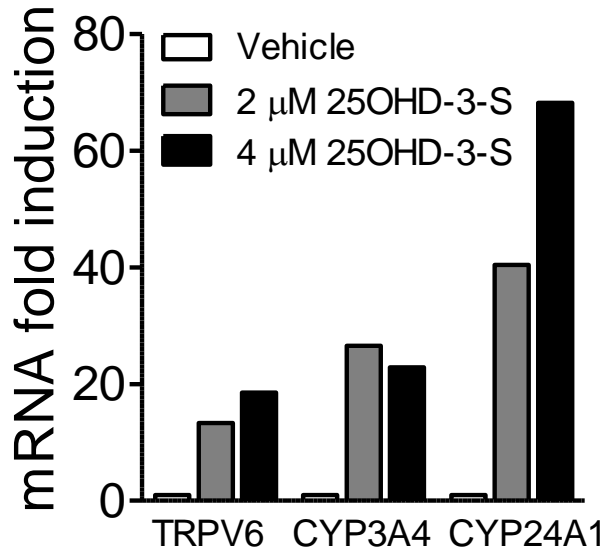
Also expressed
on the apical
surface of
enterocytes.

Chunying Gao
Qingcheng Mao
Unpublished Results

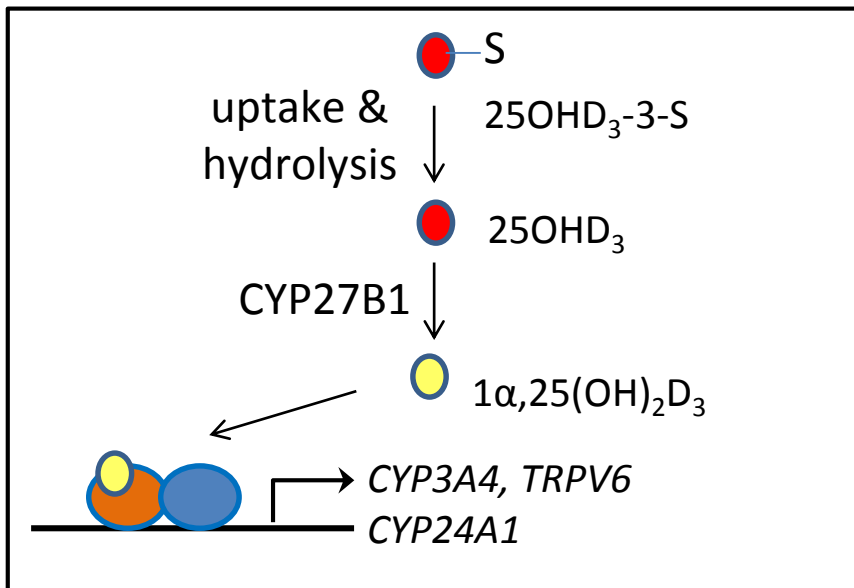
Hypothesis: Biliary Vitamin D Metabolites Regulate Intestinal *CYP3A4* Expression



25OHD₃-3-sulfate Regulates VDR-responsive Gene Expression in Intestinal LS180 Cells

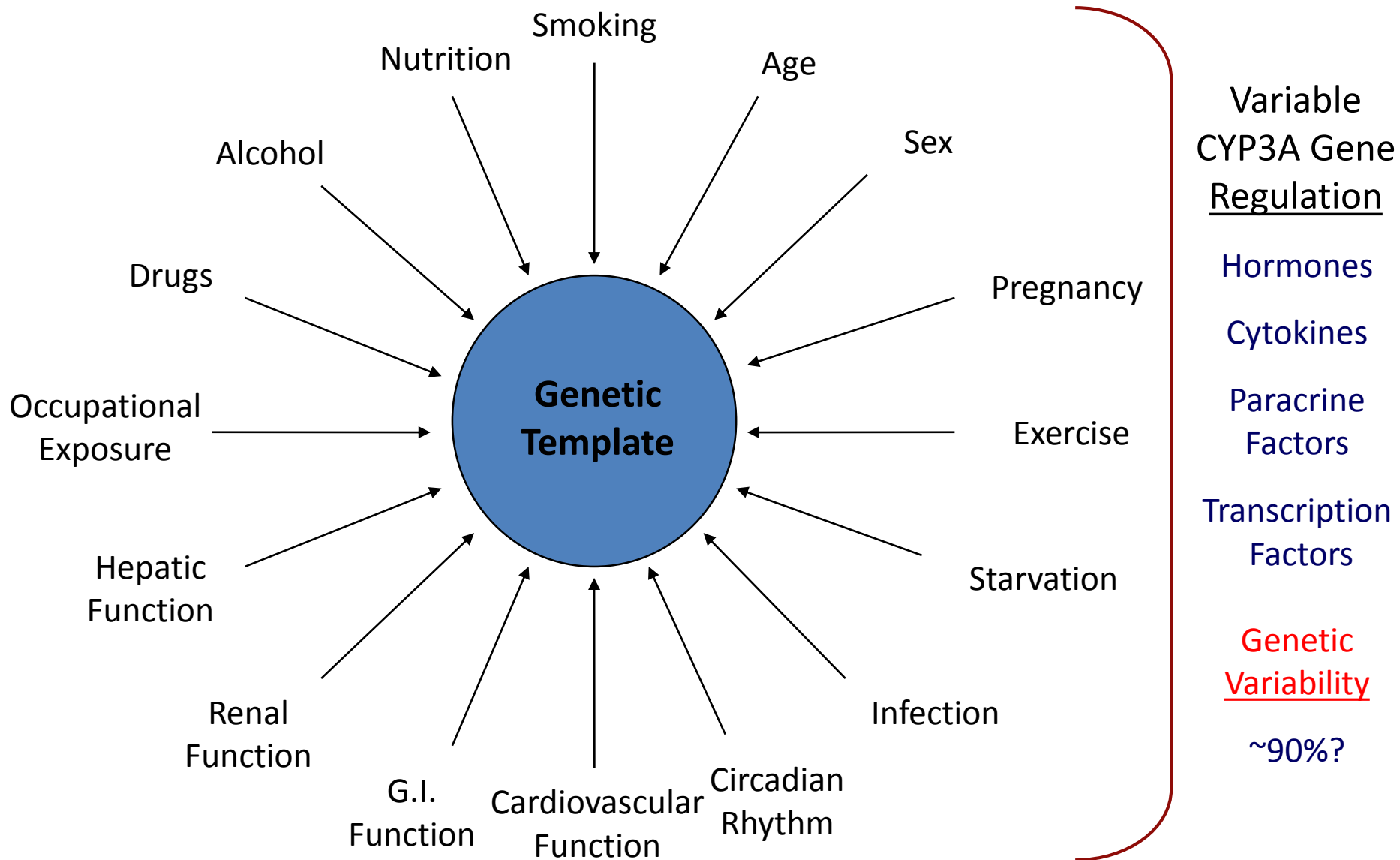


*Zhican Wang
Brian Chapron
Unpublished*



Cells were treated with 25OHD₃ or 25OHD₃-S (2 μM, 4 μM) for 24 hrs, cell lysates were collected for mRNA analysis. The culture media were collected for LC-MS/MS analysis.

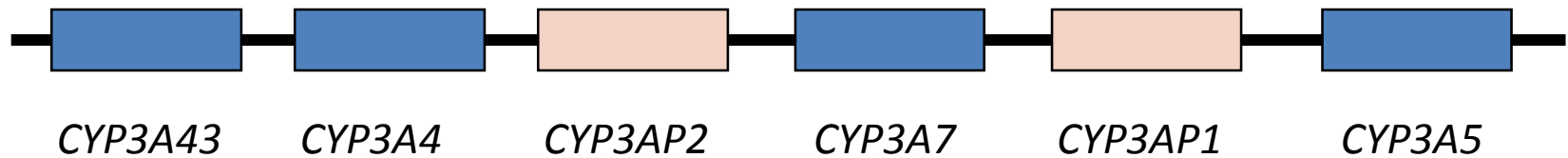
Sources of Variable P450 Expression



Adapted from E. Vesell, 1981

Human *CYP3A* Gene Locus on Chromosome 7q

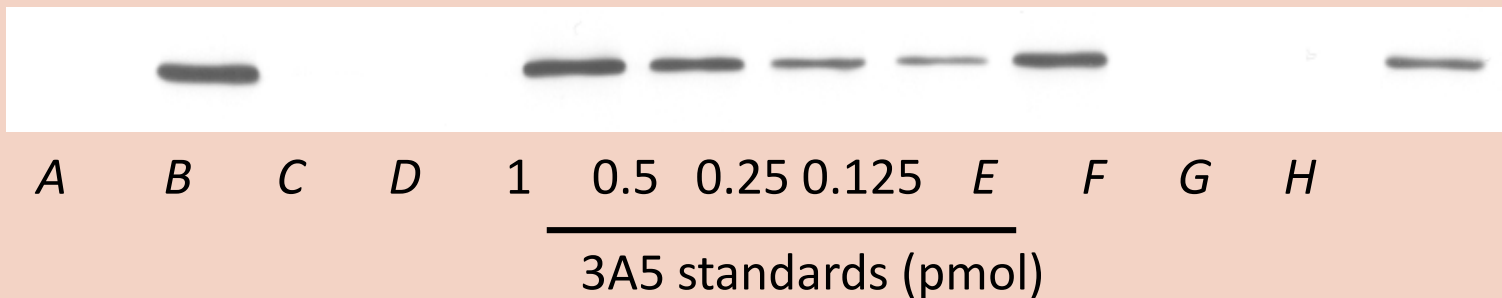
Adapted from: Finta & Zaphiropoulos; Gene 260:13-23, 2000



- *CYP3A4* > *CYP3A5* > *CYP3A7* are the most important for drug metabolism in the adult
- all three *CYP3A* enzymes are subject to genetic and environmental sources of variability
 - *CYP3A5* exhibits the most obvious polymorphic behavior

Immunodetection of Hepatic CYP3A5

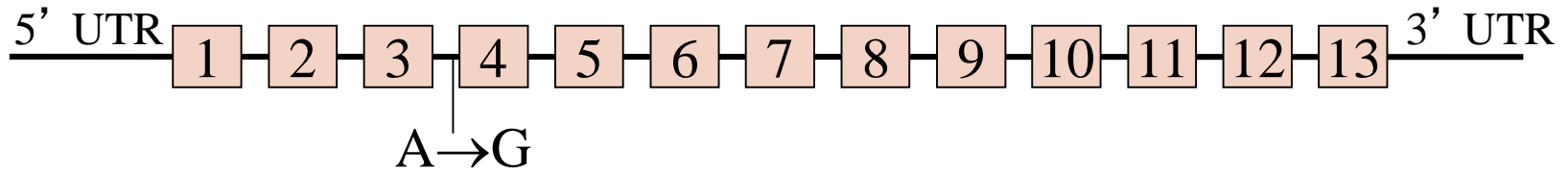
Anti-CYP3A5



Analysis of microsomes from different human livers (A-H) indicates marked inter-individual variability in specific enzyme content

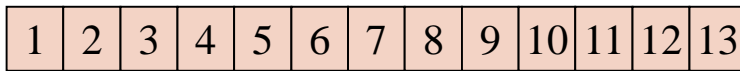
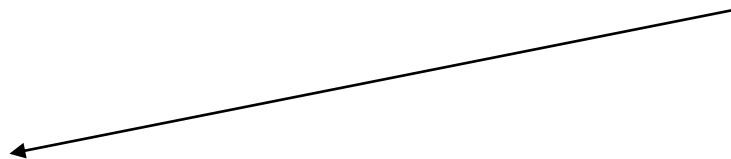
Mary Paine et al., JPET, 1997

CYP3A5*3 Variant Allele

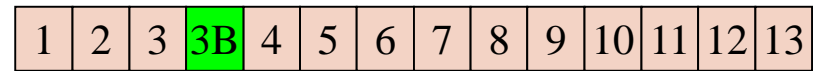


*CYP3A5*1* (A)

*CYP3A5*3* (G)



(*wt-CYP3A5 mRNA*)



(*SV1-CYP3A5 mRNA*)



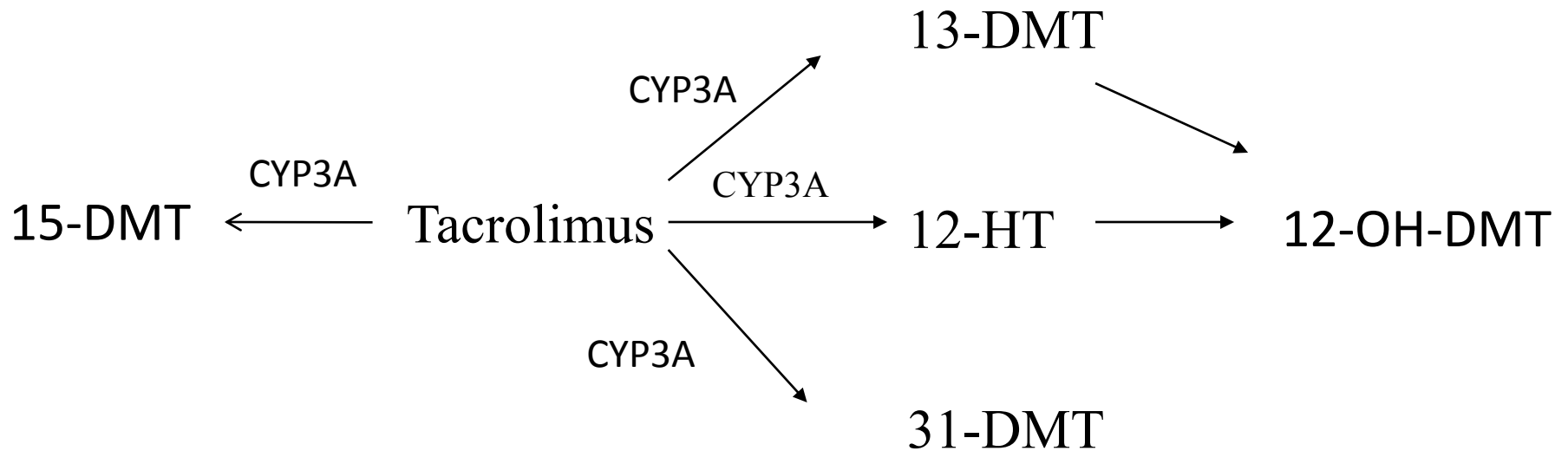
CYP3A5
protein



truncated, inactive protein

Kuehl, *Yvonne Lin et al.*, *Nature Genetics*, 2001;
Yvonne Lin et al., *Mol Pharmacol*, 2002

Metabolic Fate of Tacrolimus



- Tacrolimus is used to prevent grafted organ rejection (immune suppressant)
- CYP3A5 is one of 2 enzymes (also CYP3A4) that metabolically clear tacrolimus from the body
- CYP3A5 makes all 4 primary metabolites, but preferentially the major one (13-DMT), 12-HT and, 31-DMT

Contribution of CYP3A5 to Hepatic Tacrolimus Metabolism

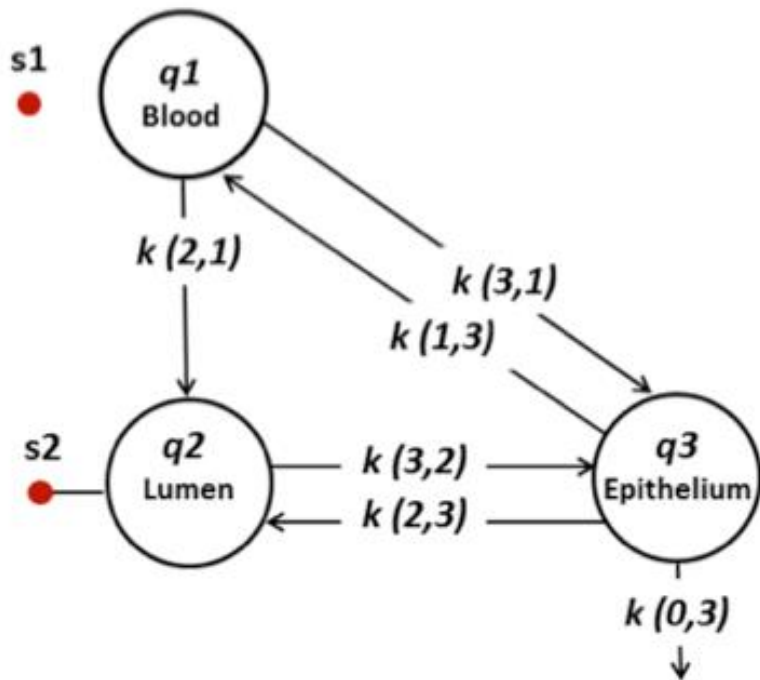
	13-DMT Formation	Human Liver Microsomes	Tacrolimus Disappearance (nmol/min/mg)
CYP3A4			
K_m (μM)	0.21		
V_{max} (nmol/min/nmol)	8.0	CYP3A4	6.1 (3.6)
Cl_{int} (ml/min/nmol)	38		
CYP3A5			
K_m (μM)	0.21	CYP3A4 + CYP3A5	15.9 (9.8)
V_{max} (nmol/min/nmol)	17.0		
Cl_{int} (ml/min/nmol)	82		

Unbound K_m and Cl_{int} calculated after correction for nonspecific binding).

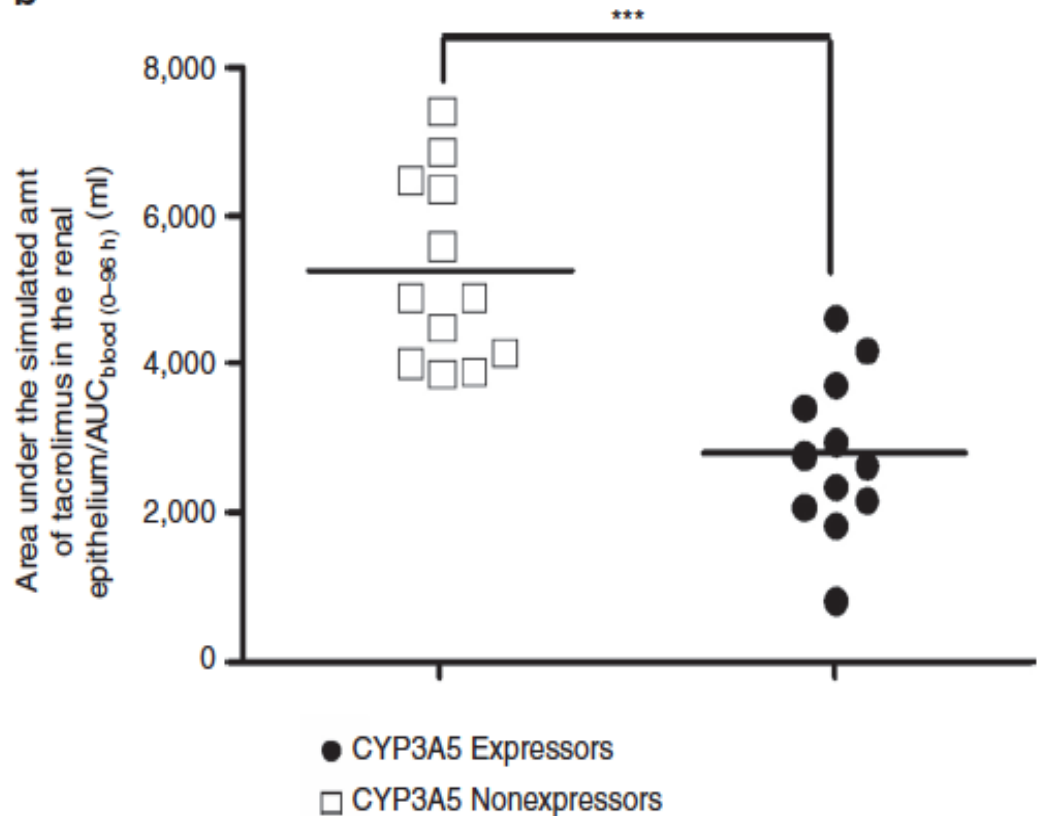
The CYP3A4 content for the 10 matched microsomal preparations represented in each group was equivalent. The nominal initial tacrolimus conc was 0.2 μM ; unbound conc determined after measurement of nonspecific binding.

*CYP3A5**1 Affects Intra-Renal Tacrolimus Accumulation

Semi-Physiological Renal Compartmental Model of Tacrolimus Disposition



b



Ben Zheng et al, CPT, 2012

Simulated renal tacrolimus exposure for CYP3A5 expressors was **53%** of that for CYP3A5 nonexpressors

Wylie Burke, MD, PhD



- Director, Center for Genomics and Healthcare Equality, UW

Pursue genomic research for those not represented in the literature – AI/AN communities in Alaska and Montana

NWA-PGRN Principal Investigators Ken Thummel & Wylie Burke

Collaborative Site Lead Investigators

- **Allan Rettie**
University of Washington
- **Bert Boyer**
Center for Alaska Native Health Research/
Yukon-Kuskokwim Health Corporation
- **Denise Dillard**
Southcentral Foundation, Anchorage
- **Erica Woodahl**
University of Montana, Missoula/
Confederated Salish-Kootenai Tribes
- **Denise Boudreau**
Group Health Research Institute



Challenge of Conducting Genetic Research with Indigenous Communities

- Tribes perceive that past health research has provided little benefit to indigenous populations
- Tribes often mistrust academic research due to historical and current trauma inflicted in the name of “knowledge for the greater good”, and unequal control over the research process and data or samples

Concept of Collaborative Stewardship

- Mutual recognition among stakeholders
 - Listening to each other's voices
- Dialogue
 - Sustained engagement
 - Accept and work through conflicts
- Negotiate accommodation
 - “What touches all should be agreed to by all”
(James Tully)

*Wylie A, Promise and perils of an ethic of stewardship, in Embedding Ethics,
Eds Meskell & Pels 2005*

The Yup'ik People of Alaska

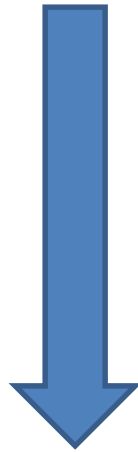


- Communities along the Yukon-Kuskokwim Delta
- >20,000 indigenous people across 50 remote Alaskan communities
- Traditional diet is high in fish and marine animals that are rich in **ω -3 polyunsaturated fatty acids** and **vitamin D₃**
- Living at 60° 47' N, they experience significant seasonal changes in sunlight exposure and vitamin D₃ synthesis

Study Design

Recruited 1000 Yup'ik study participants

- Collect 5 ml blood: fractionate for DNA, plasma, RBC
- Distribute samples to UA Fairbanks, UW Medicinal Chemistry, UW Laboratory Medicine, UW Genome Sciences

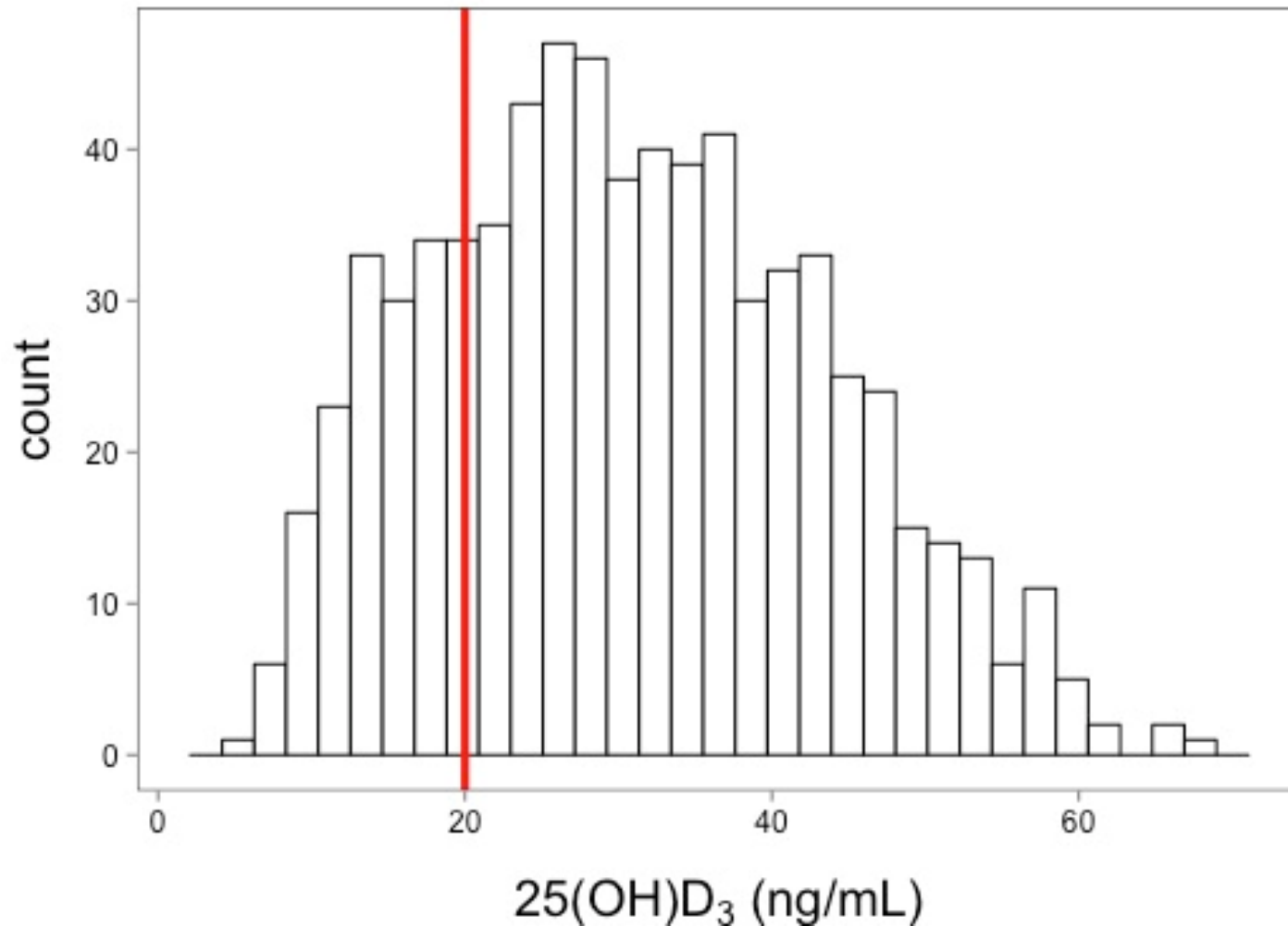


Measure vitamin D status
(serum 25OHD₃)

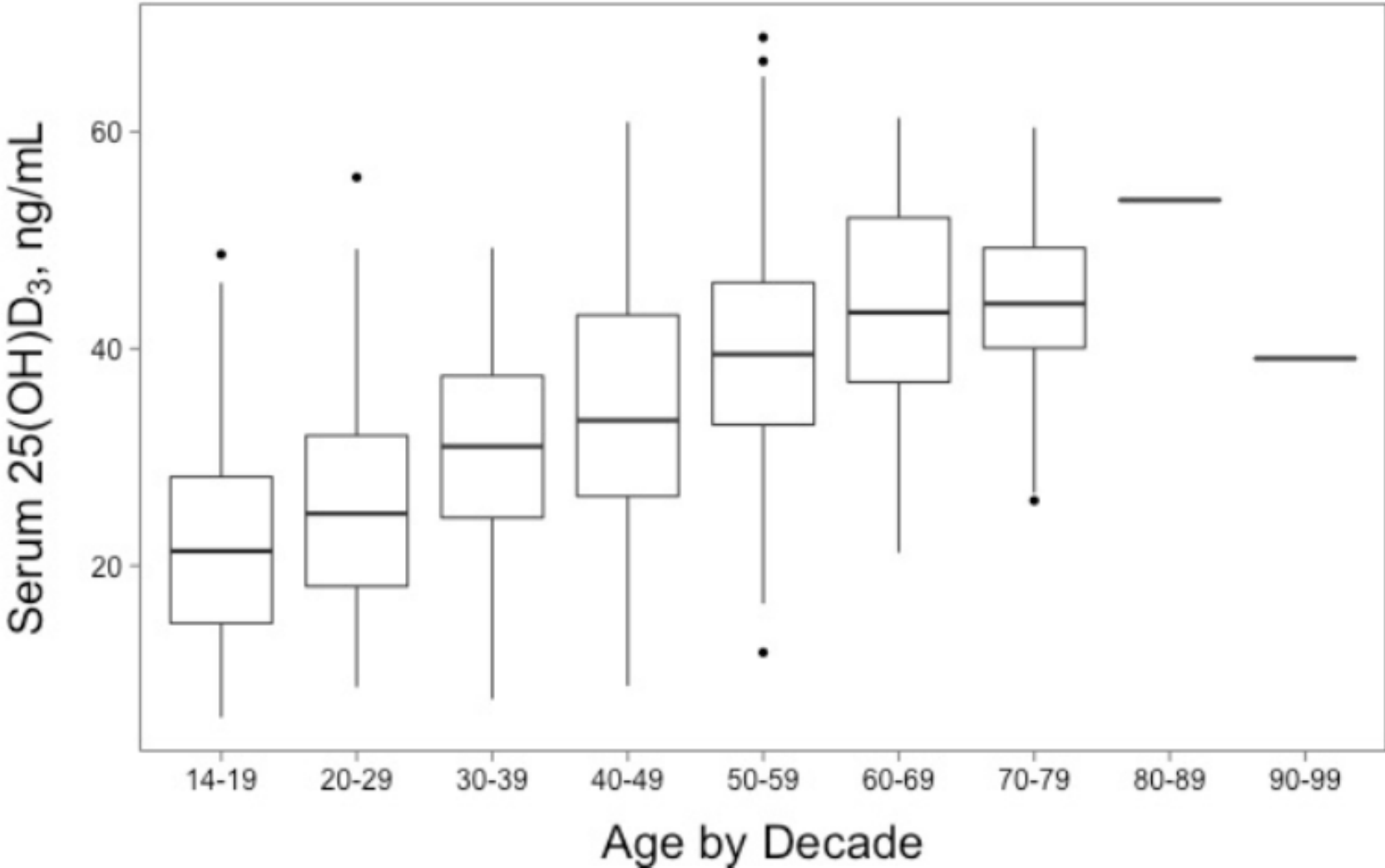
Determine association with:

Age, gender, BMI, *CYP2R1*, *DHCR7* and *DBP* genotypes, dietary ω 3 PUFA biomarker ($\delta^{15}\text{N}$), season of blood draw

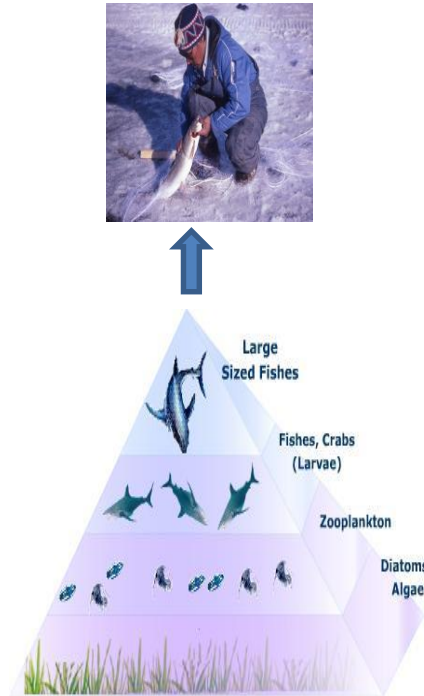
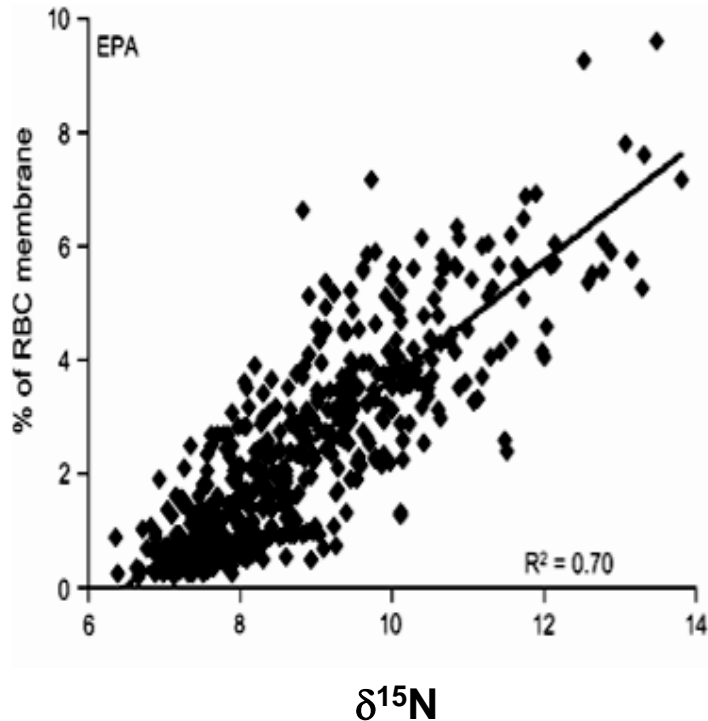
Serum 25(OH)D₃ Concentrations



Distribution of Serum 25(OH)D₃ Level by Age



Assessment of Dietary ω 3 PUFA Intake – ^{15}N Enrichment ($\delta^{15}\text{N}$)



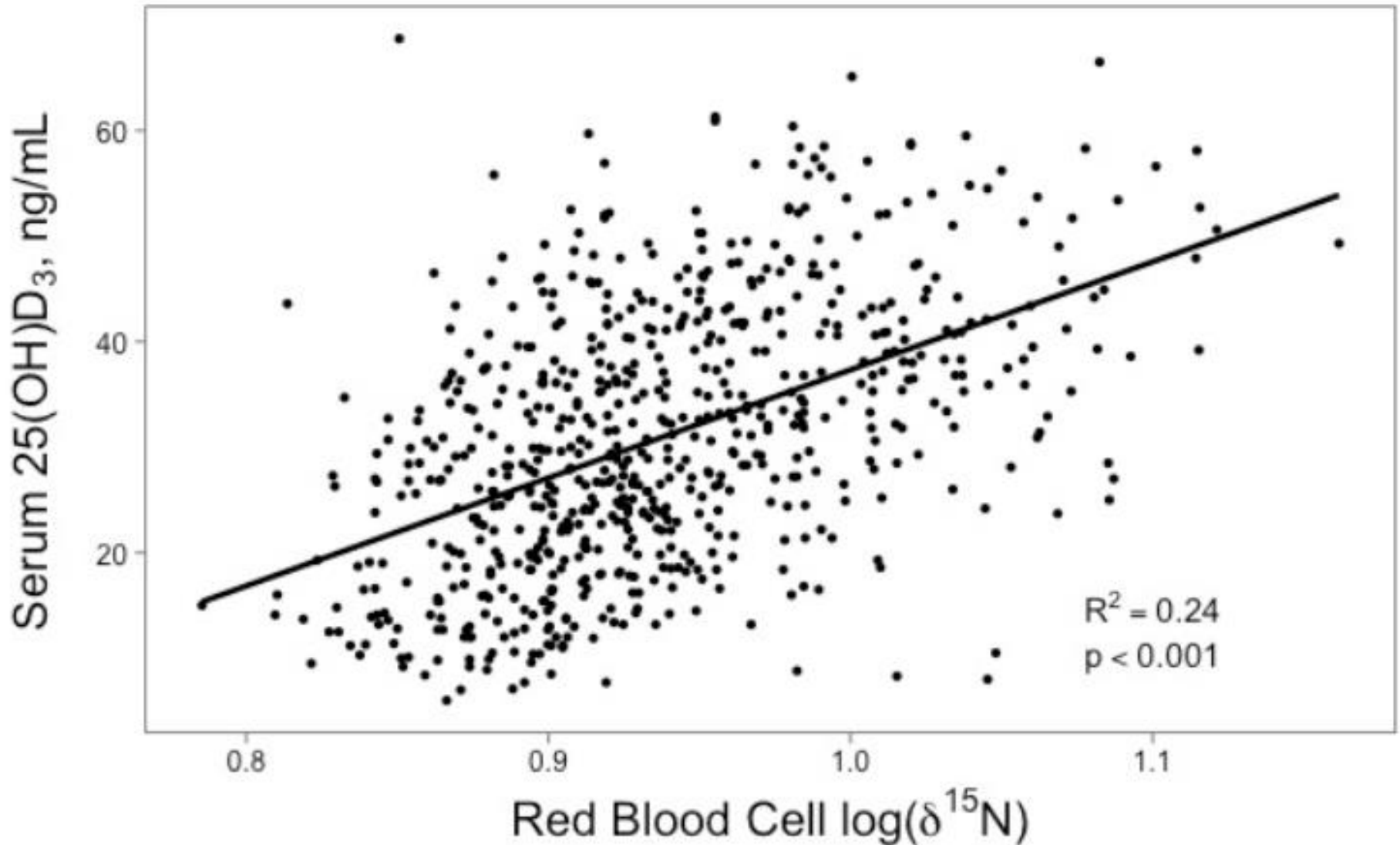
$$\delta^{15}\text{N} = \frac{(R_{\text{sample}} - R_{\text{standard}})}{R_{\text{standard}}} \times 1000\text{‰}$$

- $R = (^{15}\text{N}/^{14}\text{N})$
- Standard = atmospheric N_2 , where % abundance of $^{15}\text{N} = 0.37\%$

- Continuous-flow isotope mass spectrometry
- Surrogate marker of ω 3 PUFA consumption
- Marine environments have more ^{15}N → reflects the length of food chain in predatory fish

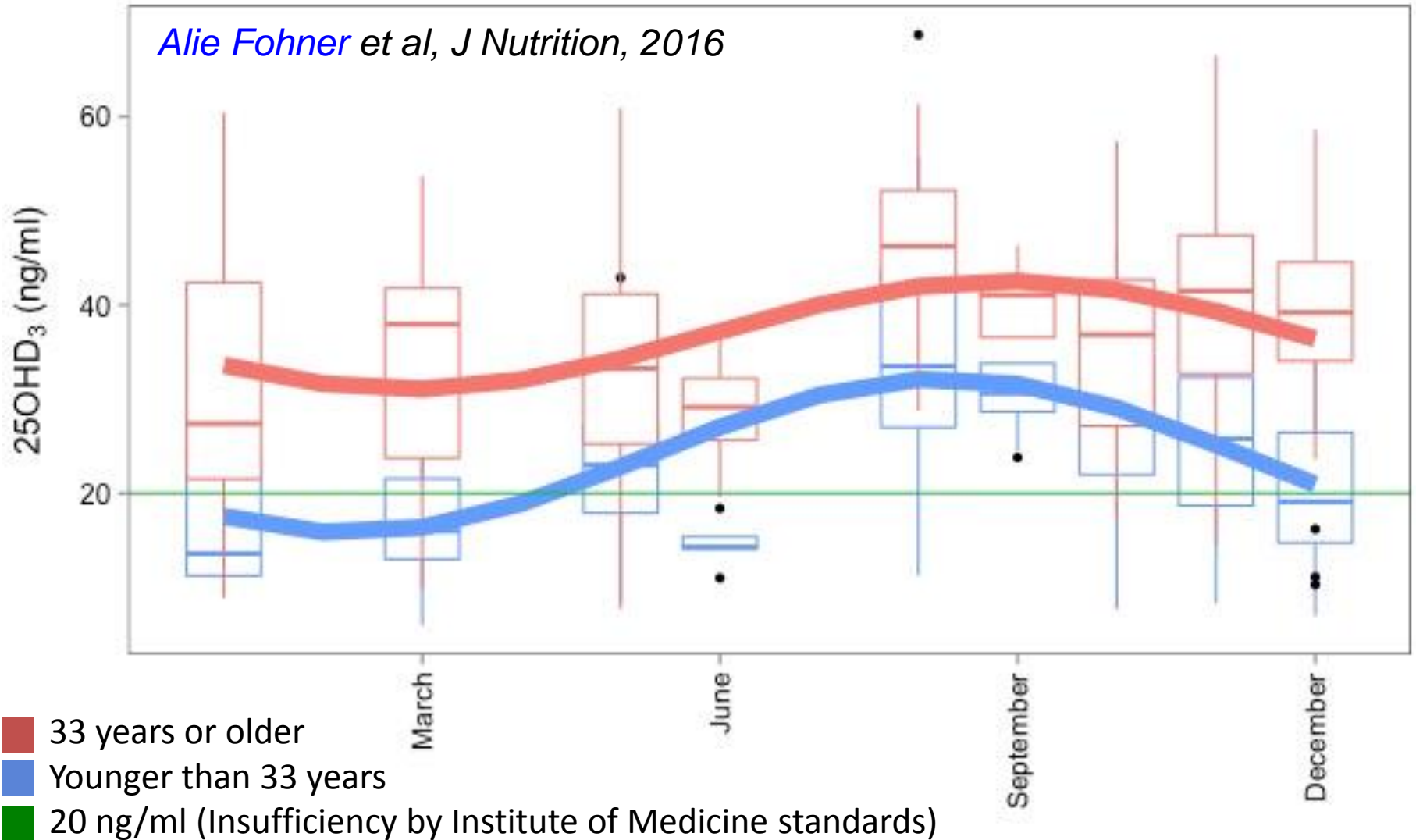
*O'Brien DM, et al.
J Clin Nutr. 2009*

Correlation of 25(OH)D₃ with log($\delta^{15}\text{N}$)



Sinusoidal Model of Annual Variation

Alie Fohner et al, J Nutrition, 2016



Unrelated Subset Multiple Regression

Covariate	N	Significance in full model	Variability explained (R ²)
Fully adjusted model	526	p < 0.001	(0.528)
Age (younger vs older than 33)		p < 0.001	(0.365)
Season		p < 0.001	(0.091)
Log₁₀(δ¹⁵N value)		p < 0.001	(0.205)
Gender		p = 0.007	(0.00)
Village location (Coastal vs Inland)		p < 0.001	(0.063)
BMI		p = 0.041	(0.006)
CYP2R1 rs11023374		p = 0.016	(0.011)
GC rs4588 (TA haplotype)		p < 0.001	(0.028)
Age and log₁₀(δ¹⁵N value)			(0.386)

- 58% of the variability explained by demographic, diet, season and genetic factors; what explains for the rest?

Conclusions from 25 Years of Studying CYP3A

Demographic factors, concomitant medications, diet, season, and genetic variation in CYP3A genes and vitamin D regulatory genes are all likely to contribute to inter-individual differences in CYP3A function.

Precision Medicine testing must capture both **genomic** and **environmental** variation to fully deliver on its promise.

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Trainees (1992-2016)

