

Expanding From Basic Towards Systems Pharmacodynamic Models for Methylprednisolone

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The Glucocorticoids (GC)

- Steroid hormones that regulate development, metabolism, and immunity
- Produced endogenously from adrenal cortex; regulated by the HPA axis
- Exert biological effects upon binding the ubiquitously expressed glucocorticoid receptor (GR)



Light/Dark (Eyes)

Kassi and Chrousos, *Hormones* <u>12</u>: 172-191 (2013). Burns, CM, *Rheum Dis Clin N Am* <u>42</u>: 1-14 (2016). **Regulatory Signals from**

Upper Brain Centers

The Corticosteroids (CS)

- Synthetic analogues of the endogenous GC hormone
- Possess potent immunosuppressive efficacy widely prescribed
- Elicit adverse effects in multiple organs magnify normal GC functions



Hench PS et al. *Proc Staff Meet Mayo Clin* <u>24</u>:181-97 (1949). Kassi and Chrousos, *Hormones* <u>12</u>: 172-191 (2013). Burns, CM, *Rheum Dis Clin N Am* <u>42</u>: 1-14 (2016).

Pharmacogenomic Mechanisms of CS Action



Jusko WJ, *Toxicology* <u>102</u>: 189-196 (1995). Almon RR, DuBois DC, Jusko WJ, *Endocrinol* <u>148</u>: 2209-2225 (2007). Ayyar VS, Almon RR, DuBois DC, Sukumaran S, Qu J, Jusko WJ, *J Proteomics* <u>160</u>: 84-105 (2017). Ayyar VS, Sukumaran S, DuBois DC, Almon RR, Qu J, Jusko WJ, *J Pharmacokinet Pharmacodyn* <u>45</u>: 557–575 (2018). Ayyar VS, Sukumaran S, DuBois DC, Almon RR, Jusko WJ, *J Pharmacol Exp Ther* <u>367</u>: 168-183 (2018).

Components of Systems Models for Genomic Drug Actions

Quantitative Systems Pharmacology (QSP) aims to understand drugs at the levels of target engagement, changes in cellular biochemistry, impact on human pathophysiology, and optimal clinical use (Sorger et. al. 2011, NIH QSP Whitepaper).



Circadian Rhythms (Non-stationarity) Tolerance and rebound System variability (cell, tissue specificity) Biomarker dynamics (mRNA, protein, activity) Unbound drug at site of action Sex differences Others (disease, aging, DDI, genetic polymorphisms, epigenetics)

Circadian Rhythms – Relevance to PK/PD

- Occur in physiology at macroscopic (whole-body) to molecular (gene) levels
- Can affect the availability of target and/or effector molecules
- Add time-dependent complexities in PK and PD responses



Jusko WJ, *Toxicology* <u>102</u>: 189-196 (1995). Sukumaran S, Almon RR, DuBois DC, Jusko WJ *Adv Drug Deliv Rev* <u>62</u>: 904-917 (2010). Ballesta A, Innominato PF, Dallman R, Rand DA, Levi FA *Pharmacol Rev* <u>69</u>: 161-199 (2017).

GILZ as a Genomic Biomarker & Mediator of CS

The FASEB Journal • Review

Glucocorticoid-induced leucine zipper (GILZ): a new important mediator of glucocorticoid action

Emira Ayroldi¹ and Carlo Riccardi¹

Department of Clinical and Experimental Medicine, Section of Pharmacology, University of Perugia, Perugia, Italy

Identified in steroid-treated thymocytes (1997)

Factors making GILZ a favorable genomic marker:

- Expressed in multiple tissues
- Correlates, in part, to CS efficacy
- Exquisite sensitivity to regulation by CS

ARTHRITIS & RHEUMATISM Vol. 62, No. 9, September 2010, pp 2651–2661 DOI 10.1002/art.27566 © 2010, American College of Rheumatology

Glucocorticoid-Induced Leucine Zipper Is an Endogenous Antiinflammatory Mediator in Arthritis

Elaine Beaulieu,¹ Devi Ngo,¹ Leilani Santos,¹ Yuan Hang Yang,¹ Malcolm Smith,² Christian Jorgensen,³ Virginie Escriou,⁴ Daniel Scherman,⁴ Gabriel Courties,⁵ Florence Apparailly,³ and Eric F. Morand¹

Neurotherapeutics (2012) 9:210–225 DOI 10.1007/s13311-011-0084-7

Glucocorticoid-Induced Leucine Zipper (GILZ) Over-Expression in T Lymphocytes Inhibits Inflammation and Tissue Damage in Spinal Cord Injury

Emanuela Esposito · Stefano Bruscoli · Emanuela Mazzon · Irene Paterniti · Maddalena Coppo · Enrico Velardi · Salvatore Cuzzocrea · Carlo Riccardi The Journal of Clinical Investigation http://www.jci.org Volume 117 Number 6 June 2007

GILZ mediates the antiproliferative activity of glucocorticoids by negative regulation of Ras signaling

Emira Ayroldi, Ornella Zollo, Alessandra Bastianelli, Cristina Marchetti, Massimiliano Agostini, Rosa Di Virgilio, and Carlo Riccardi

Department of Clinical and Experimental Medicine, Section of Pharmacology, University of Perugia, Perugia, Italy.



Cell Death and Differentiation (2015) 22, 118–130 © 2015 Macmillan Publishers Limited All rights reserved 1350-9047/15

L-GILZ binds p53 and MDM2 and suppresses tumor growth through p53 activation in human cancer cells

E Ayroldi*,¹, MG Petrillo¹, A Bastianelli¹, MC Marchetti¹, S Ronchetti¹, G Nocentini¹, L Ricciotti¹, L Cannarile¹ and C Riccardi*,¹

¹Department Medicine, Section of Pharmacology, University of Perugia Medical School, Perugia, Italy

Basal GILZ Expression and Circadian Regulation



Ayyar VS, Almon RR, Jusko WJ, DuBois DC, Am J Physiol - Physiol Rep 6: e12382 (2015).

Enhancement of GILZ mRNA by MPL (IM dosing)

<u>Hypothesis</u>: A mechanistic PK/PD model of transactivation can characterize the multitissue dynamics of GILZ regulation upon MPL dosing



Ayyar VS, DuBois DC, Almon RR, Jusko WJ, J Pharmacol Exp Ther 363: 45-57 (2017).

Pharmacokinetic/Pharmacodynamic Model of Transactivation



Ramakrishnan R, DuBois DC, Almon RR, Pyszczynski NA, Jusko WJ, J Pharmacokinet Pharmacodyn 29: 1-24 (2002).

Krzyzanski W, Chakraborty A, Jusko WJ, *Chronobiol Int* <u>17</u>: 77-93 (2000). Hazra A, Pyszczynski N, DuBois DC, Almon RR, Jusko WJ, *Biopharm Drug Dispos* <u>28</u>: 263-73 (2007).

Glucocorticoid Receptor mRNA (Control & IM MPL)



Glucocorticoid Receptor mRNA (Control & IM MPL)

Parameter	Definition	Estimate (CV%)
$a_{0,GRm}$	Fourier coefficient for GR mRNA	2824° / 1055.9 ^d / 2216 ^{a,e}
$a_{1,GRm}$	Fourier coefficient for GR mRNA	6.8° / 162.2 ^d / -273.2 ^{a,e}
$a_{2,GRm}$	Fourier coefficient for GR mRNA	65.9 ^{a,e}
$b_{1,GRm}$	Fourier coefficient for GR mRNA	$185.6^{c} / -19.9^{d} / -10.9^{a,e}$
$b_{2,GRm}$	Fourier coefficient for GR mRNA	10.1 ^{a,e}
$k_{d,GRm}$ (h ⁻¹)	Degradation rate constant for GR mRNA	$0.26^{c} \left(15.4\right) / \left(0.28^{d} \left(29.9\right) / \left(0.31^{a,e}\right)\right)$
$k_{s,GR}$ (nM/h)(mol/ng) ⁻¹	Synthesis rate constant for receptor	$0.00025^c~(5.3)~/~0.00121^d~(34.5)~/~0.00196^{a,e}$
$IC_{50,GRm}(nM^{-1})$	Inhibition of GR mRNA production	15.6 ^b GR mRNA half-life:
$k_{d,GR}$ (h ⁻¹)	Degradation rate constant for receptor	0.05^{b} 2 – 3 hours
$k_{on} \left(\mathbf{n} \mathbf{M}^{-1} \cdot \mathbf{h}^{-1} \right)$	Association rate constant	0.016 ^b
f_{mpl}	Unbound fraction of MPL in plasma	0.23 ^b
k_{re} (h ⁻¹)	DR_n loss rate constant	1.31 ^b
R_{f}	Fraction recycled	0.93 ^b
k_T (h ⁻¹)	Translocation rate constant	58.3 ^b
$GR_{m,MPL}(0) \text{ (mol/ng RNA)}$	GR mRNA initial concentration (treatment)	3995^{c} / 1350^{d} (10.7) / $2200^{a,e}$
GR(0) (nM)	Free cytosolic receptor initial concentration	19.7° (5.3) / 32.7 ^d (34.5) / 86.2 ^{a,e}
DR(0) (nM)	Drug-receptor complex initial concentration	0 (fixed)
$DR_n(0)$ (nM)	Nuclear complex initial concentration	0 (fixed)

^a Parameter values fixed from Sukumaran et al. 2011

^b Parameter values fixed from Hazra et al. 2007a

^c Lung; ^d Muscle; ^e Adipose tissue

GILZ mRNA (Control & IM MPL)





Simulation of Tissue-specific GILZ – SC Infusion



Chronic MPL PK and tissue-specific parameters for GR and GILZ employed to <u>predict</u> the dynamic behavior of GILZ under chronic dosing

Measurements in tissues from male Wistars given 0.3 mg/kg/h SC infusion of MPL for 7 days

Ayyar VS, DuBois DC, Almon RR, Jusko WJ, J Pharmacol Exp Ther 363: 45-57 (2017).

Modeling Circadian Removal of PD Responses

Ayyar VS, Krzyzanski W, Jusko WJ, J Pharmacokinet Pharmacodyn 46: 89-101 (2019).

$$\frac{dR}{dt} = k_{in} \cdot (1 + H_1(t)) - k_{out}(t) \cdot (1 + H_2(t)) \cdot R(t)$$

$$\frac{dR}{dt} = k_{in} \cdot (1 + H_1(t)) - k_{out}(t) \cdot (1 + H_2(t)) \cdot R(t)$$

$$k_{out}(t) = \frac{k_{in} + \frac{2\pi}{T} R_a sin(\frac{2\pi}{T}(t - t_p))}{R_m + R_a cos(\frac{2\pi}{T}(t - t_p))}$$

Applicable physiology and PD biomarkers:

- Renal excretion (GFR) Uric acid
- Transporter activity [Dopamine] brain, ECF
- Glymphatic clearance [Amyloid-β] brain



Ferris, MJ et al., Proc Nat Acad Sci 111: E2751-E2759 (2014).



Overarching goals:

- Characterize temporal dynamics of MPL-regulated transcripts and proteins in liver
- Examine quantitative relationships between hepatic <u>transcripts and proteins</u>
- Develop a mechanistic model that <u>connects gene/protein-mediated signaling to physiological</u> <u>PD endpoints</u>



Study Design – 'omics' Measures and Bioinformatics Analyses



- 22% 24% 6% 14% 2%
 - Immune regulation
 - Drug/Xenobiotic metabolism
 - Drug/Xenobiotic transport
 - Energy metabolism
 - Other

Cluster 1 Cluster 2 Hafia Hepatocyte auckar: factor 1, homeobox A

Jin JY et al., J Pharmacol Exp Ther <u>307</u>: 93-109 (2003). Nouri-Nigjeh E et al., Anal Chem <u>86</u>: 8149-57 (2014). Ayyar VS, Almon RR, DuBois DC, Sukumaran S, Qu J, Jusko WJ, J Proteomics <u>160</u>: 84-105 (2017). Ayyar VS, Sukumaran S, DuBois DC, Almon RR, Jusko WJ J Pharmacol Exp Ther 367: 168-183 (2018).



Kamisoglu K et al., OMICS 19: 80-91 (2015). Ayyar VS et al., J Pharmacol Exp Ther 367: 168-183 (2018).

Fold-change

Time (hour)

General PK/PD Paradigm for Genomic Drug Effects



<u>General Hypothesis</u>: Genomic regulation by CS occurs at the mRNA and protein levels via mechanisms affecting key turnover processes.

Temporal Modeling of Transcriptomic and Proteomic Patterns

Ayyar VS, Sukumaran S, DuBois DC, Almon RR, Jusko WJ, J Pharmacol Exp Ther 367: 168-183 (2018).



Temporal Modeling of Transcriptomic and Proteomic Patterns

Ayyar VS, Sukumaran S, DuBois DC, Almon RR, Jusko WJ, J Pharmacol Exp Ther 367: 168-183 (2018).



Temporal Modeling of Transcriptomic and Proteomic Patterns

Ayyar VS, Sukumaran S, DuBois DC, Almon RR, Jusko WJ, J Pharmacol Exp Ther 367: 168-183 (2018).



Systems PK/PD Model for MPL in Liver

Ayyar VS, Sukumaran S, DuBois DC, Almon RR, Qu J, Jusko WJ, J Pharmacokinet Pharmacodyn 45: 557-575 (2018).



Direct, transcription-mediated mechanism

MPL Pharmacokinetics and Receptor Dynamics



Parameter (units)	Definition	Est (%CV)
MPL Pharmacokinetics		
CL(L/h/kg)	Clearance	2.93 (0.89)
$CL_D(L/h/kg)$	Distribution clearance	2.51 (1.94)
$V_c(L/kg)$	Central volume of distribution	0.803 (0.97)
$V_T(L/kg)$	Peripheral volume of distribution	0.974 (1.51)
F	Bioavailability	0.2 (0.94)
Fr	Fraction absorbed by k_{a1}	0.725 (fixed)
$k_{a1}(h^{-1})$	Absorption rate constant	1.82 (2.8)
$k_{a2}(h^{-1})$	Absorption rate constant	0.54 (4.1)
Glucocorticoid Recept	for Dynamics ^a	
$k_{s,GRm}(fmol/g/h)$	Synthesis rate constant for GR mRNA	3.2
$k_{d,GRm}(h^{-1})$	Degradation rate constant for GR mRNA	0.12
k _{s,GR} (nM/h)(fmol/g) ⁻¹	Synthesis rate constant for receptor	0.84
$IC_{50,GRm}(nM)$	DR_n for 50% inhibition of GR mRNA synthesis	123.7
$k_{d,GR}(h^{-1})$	Degradation rate constant for receptor	0.04
$k_{on} (nM^{-1} \cdot h^{-1})$	Association rate constant	0.019
f_{mpl}	Unbound fraction of MPL	0.23
$k_{re} (h^{-1})$	DR _n loss rate constant	0.402
R_{f}	Fraction recycled	0.69
$k_T(h^{-1})$	Translocation rate constant	58.2
$GR_m(0)$ (fmol/g)	GR mRNA initial concentration	25.8
GR(0) (nM)	Free cytosolic receptor initial concentration	540.7
DR(0) (nM)	Drug-receptor complex initial concentration	0
$DR_n(0)$ (nM)	Nuclear complex initial concentration	0

^a Parameter values obtained from Hazra et al [36]

Ayyar VS, Sukumaran S, DuBois DC, Almon RR, Qu J, Jusko WJ, J Pharmacokinet Pharmacodyn 45: 557–575 (2018).

Modeling TAT mRNA, Protein, and Activity



Parameter (units)	Definition	Estimate (% CV)
Tyrosine aminotransferase dynamics		
$k_{d,TATm}(h^{-1})$	Degradation rate constant for TAT mRNA	0.22 (66.6)
$S_{DRn}^{TATm}(nM^{-1})$	Stimulation constant for TAT mRNA	0.002 (48.1)
$k_{d,TAT}(h^{-1})$	Degradation rate constant for TAT protein	0.29 (73.6)
γ ₁	Amplification factor for TAT protein	4.5 (34.9)
$k_{d,TAT}(h^{-1})$	Degradation rate constant for TAT activity	2.0 (96.0)
γ_2	Amplification factor for TAT activity	1.67 (11.8)
$TAT_m(0)$	Baseline TAT mRNA	0.87 (12.0)
TAT(0)	Baseline TAT protein	0.88 (12.8)
$TAT_a(0)$ (activity/mg)	Baseline TAT activity	0.041 (7.3)



Time (hour)

Modeling MPL-Induced Hyperglycemia



Ayyar VS, Sukumaran S, DuBois DC, Almon RR, Qu J, Jusko WJ, J Pharmacokinet Pharmacodyn 45: 557–575 (2018).

Modeling Combined Lymphocyte Trafficking & Apoptosis



Ayyar VS, Sukumaran S, DuBois DC, Almon RR, Qu J, Jusko WJ, J Pharmacokinet Pharmacodyn 45: 557–575 (2018).

Simulation of MPL Responses

Data from Jin JY and Jusko, WJ, *Biopharm Drug Dispos* <u>30</u>: 21-34(2009). Data from Ramakrishnan R et al, *J Pharmacol Exp Ther* <u>300</u>: 245-256 (2002).

TAT Dynamics – 7-day 0.3 mg/kg/h SC infusion



Insulin / Glucose Dynamics – 5 mg/kg IV bolus



Time (hour)

Sex Differences in PK/PD - Why is This Important?

PRECLINICAL RESEARCH

Sex Matters for Mechanism

Jayne S. Danska

Some funding agencies now require consideration of sex and gender in preclinical research, a policy that heralds opportunities and challenges for researchers.



NIH to balance sex in cell and animal studies

Janine A. Clayton and Francis S. Collins unveil policies to ensure that preclinical research funded by the US National Institutes of Health considers females and males.



Pharmacology studies include five times as many male animals as females!

Danska JS, Sci Transl Med 6: 258fs40 (2014).

Beery AK and Zucker I, Neurosci and Biobehav Rev 35: 565-572 (2011). Clayton JA and Collins SC, Nature 509: 282-283 (2014).

Sex Effects on Methylprednisolone PK/PD in Humans



"Although women are more sensitive to methylprednisolone as <u>measured by cortisol suppression</u>, they eliminate the drug more quickly, generally producing a similar net response."

DEX-inducible GILZ is Antagonized by Estradiol in vitro



Whirledge S and Cidlowski JA, *Endocrinol* <u>154</u>: 499-510 (2013).

Estrous Cycle & Sex Hormone Regulation in Female Rats

32



Methylprednisolone PK/PD Studies – Sex and Estrous Stage

Hazra A, Pyszczynski N, DuBois DC, Almon RR, Jusko WJ, J Pharmacokinet Pharmacodyn 28: 263-73 (2007).



All animals dosed between 1.5 – 3 h after lights ON



Daily vaginal lavages in females performed from 8 – 11 weeks of age to stage estrous cycle

Sex Differences in Plasma and Hepatic PK: 50 mg/kg IM

Ayyar VS, DuBois DC, Nakamura T, Almon RR, Jusko WJ, J Pharmacol Exp Ther Accepted (2019b).



No statistically significant difference found in females per estrous stage



~ 3-fold higher plasma exposure in females

Sex	$AUC_{0-\infty}(h \cdot ng/mL)$	CL/F (mL/h/kg)
Male	$2901 \pm 185^{\mathrm{b}}$	17,232 ± 1099
Female	$9751\pm482^{\mathrm{b}}$	5128 ± 252

^a Bailer's Method applied to compute area-under-curve (AUC)

^b Standard error

Steroid Assay: Normal-phase HPLC

No Sex Differences in Plasma Protein Binding of MPL and Glucocorticoid Receptors in Tissues

Ayyar VS, Song D, DuBois DC, Almon RR, Jusko WJ, J Pharmacol Exp Ther Accepted (2019a).



No difference in hepatic GR mRNA in males and E-females



Previous report indicates no difference in <u>hepatic</u> GR protein density and binding in rats

Duma D and Cidlowski JA, Sci Signaling <u>3</u>: ra74 (2010).



Sex Differences in Pharmacodynamics - GILZ in Liver



Sex Differences in Pharmacodynamics - GILZ in Uterus



General Schematic of Mechanism-Based Modeling Approach

<u>Objective</u>: To develop a quantitative model that integrates mechanisms controlling steroid disposition and pharmacodynamics across sex, reproductive stage, and tissue type



mPBPK / PD Model for MPL in Males and Females



- Model implemented using ADAPT 5
- Stepwise modeling approach employed
- Sources of parameter values:
- i) Prior in-house experiments (data re-fit or estimated values fixed)
- ii) Literature (data fitting, directly obtained, or calculated from *in vitro* studies)
- iii) Fitting of obtained in vivo data
- Model assessed jointly across all groups

Ayyar VS, DuBois DC, Almon RR, Jusko WJ, J Pharmacol Exp Ther Accepted (2019c).

CST

Mechanistic Considerations: Sex and Hepatic Metabolism



Fig. 4. High performance liquid chromatograms from microsomal incubations of ³HDEX (1 μ M) with microsomes from (a) male rat and (b) female rat.

Mechanistic Considerations: Tissue Binding of MPL in vivo vs. in vitro vs. in silico Differences

Ayyar VS, Song D, DuBois DC, Almon RR, Jusko WJ, J Pharmacol Exp Ther Accepted (2019a).

Tissue ultrafiltration methods were developed and validated for analysis of MPL binding *in vitro*

^a Model estimated value from IM data (corrected for hepatic CL_{int})

^bCalculated from steady-state infusion PK in male rats

^c Unbound fraction corrected for single tissue dilution using Kalvass-Maurer equation

^d Computed using method of Rogers and Rowland (J Pharm Sci, 2006)

Kalvass JC and Maurer TS, Biopharm Drug Dispos 23: 327-38 (2002).

Step 1: MPL Pharmacokinetics (mPBPK Approach)

^d Fixed from *in vitro* experiments

Step 2: Dynamics of Corticosterone (CST) Suppression

Time (hour after lights ON)

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Step 3: Glucocorticoid Receptor Binding and Dynamics

Step 3: Glucocorticoid Receptor Binding and Dynamics

Liver data from Hazra A et al., J Pharmacokinet Pharmacodyn 28: 263-73 (2007).

Time (hr from 00:00 on Day 1 or 8)

Step 3: Glucocorticoid Receptor Binding and Dynamics

Parameter	Definition	Estimate (CV%)
a _{0,GRm,liver}		14.3
a _{1,GRm,liver}		-1.53
a2,GRm,liver	Fourier coefficient for liver GR mRNA ^a	0.554
b _{1,GRm,liver}		-3.04
b _{2,GRm,liver}		1.18
$k_{d,GRm}(h^{-1})$	Degradation rate constant for GR mRNA	0.14 (17.0)
IC _{50,GRm} (fmol/mg)	Half-maximal inhibition of GR mRNA production	15.2 ^a
$ au_{GRm}(h)$	Transduction delay for mRNA rebound	15.6 ^a
IC _{50,TC2} (fmol/mg)	Half-maximal inhibition of GR mRNA removal	60.5 ^a
$k_{d,GR}(h^{-1})$	Degradation rate constant for receptor	0.05 ^a
$k_{on,MPL} (nM^{-1} \cdot h^{-1})$	Association rate constant for MPL	0.016 ^a
$k_{on,CST} (nM^{-1} \cdot h^{-1})$	Association rate constant for CST	0.001 (fixed)
fup,mpl	Unbound fraction of MPL in plasma	0.4 ^b
fu,liv,mpl	Unbound fraction of MPL in liver	0.032 (calculated as $K_{p,hep}/f_{u,p}$)
fu,cst	Unbound fraction of CST in plasma	0.017 ^a
$k_{re} (h^{-1})$	DR _N loss rate constant	1.31 ^a
R_f	Fraction recycled	0.93 ^a
$k_T(h^{-1})$	Translocation rate constant	58.3 ^a
GR(0) (fmol/mg protein)	Free cytosolic receptor initial concentration	476.0 ^a (liver) ; 320.0 (uterus) ^c

^a Fixed from Hazra et al. (2007)

^b Fixed from Ayyar et al. (2019a)

^c Fixed from Izawa et al. (1984)

Step 4: Estrous Variation of Plasma 17β-Estradiol in Rats

Step 4: Estrous Variation of Plasma 17β-Estradiol in Rats

Parameter	Definition	Estimate (%CV) or Value (Source)
Estrogen Receptor Binding &	& Dynamics	
f _{up,E2}	Unbound fraction of estradiol in plasma	0.053 (Plowchalk and Teeguarden, 2002)
B _{max,ER(liv)} (fmol/mg protein)	Estrogen receptor content in liver	24.5 (Dickson and Eisenfeld, 1979; Aten et al., 1978)
B _{max,ER(uterus)} (fmol/mg protein)	Estrogen receptor content in uterus	560 (Notides, 1970)
K _{D,ER(liv)} (pM)	ER Binding Constant in liver	140 (Dickson and Eisenfeld, 1979)
K _{D,ER(uterus)} (pM)	ER Binding Constant in uterus	100 (Branham et al., 2002)
$\mathbf{k}_{t} (\mathbf{h}^{-1})$	Translocation rate constant	58.3 (Assumed equal to GR translocation)

Ayyar VS, DuBois DC, Almon RR, Jusko WJ, J Pharmacol Exp Ther Accepted (2019c).

Step 5: Pharmacodynamic Regulation of GILZ

Step 5A: Pharmacodynamic Regulation of GILZ in Liver

Step 5A: Pharmacodynamic Regulation of GILZ in Liver

Parameter	Definition	Estimate (% CV)
$k_{d,GILZm}$ (h ⁻¹)	Degradation rate constant for GILZ mRNA	7.5 (21.8)
S _{max, GILZm}	Maximal stimulatory capacity by DR_N	7.5 (fixed)
SC _{50, DRn, GILZm} (fmol/mg)	DR _N producing half maximal stimulation	558 (5.5)
K _{i, ERn, GILZm} (fmol/mg)	ER_N producing half maximal inhibition of GILZ mRNA	62.1 (fixed based on uterine data)
$GILZ_m(\theta)$ (molecules/ng RNA)	GILZ mRNA initial concentration	1893 (M) ; 2051 (E) ; 2538 (PE)

Step 5B: Pharmacodynamic Regulation of GILZ in Uterus

Step 5B: Pharmacodynamic Regulation of GILZ in Uterus

Ayyar VS, DuBois DC, Almon RR, Jusko WJ, J Pharmacol Exp Ther Accepted (2019c).

Time (hours from 00:00 - Day 1)

Parameter	Definition	Estimate (% CV)
$k_{d,GILZm}$ (h ⁻¹)	Degradation rate constant for GILZ mRNA	1.9 (27.5)
S _{max, GILZm}	Maximal stimulatory capacity by DR_N	7.5 (fixed)
SC _{50, DRn, GILZm} (fmol/mg)	DR _N producing half maximal stimulation	672 (19.2)
K _{i, ERn, GILZm} (fmol/mg)	ER_N producing half maximal inhibition of GILZ mRNA	62.1 (68.6)
GILZ _m (0) (molecules/ng RNA)	GILZ mRNA initial concentration	3245 (E); 2400 (PE)

Antagonism of Glucocorticoid Signaling by Estrogens: Implications for CS Efficacy and Individualized Therapy?

SUMMARY & CONCLUSIONS

- Early PK/PD models of methylprednisolone were evolved into more mechanistic and global systems models.
- Mechanistic modeling of GILZ integrated circadian rhythms and receptor-mediated steroid pharmacogenomics to capture and predict tissue-specific responses.
- Systems modeling offers a mechanistic bridge to connect drug exposure to relevant PD endpoints via indirect (receptor/gene/protein-mediated) mechanisms.
- Time- (estrous cycle) and estrogen receptor-dependent antagonistic co-regulation by estradiol explained sex differences in genomic steroid response.
- The combined systems (experimental and modeling) approach revealed a unique pharmacodynamic interaction of multi-receptor signaling *in vivo*.
- The fundamental array of mechanism-based PK/PD models serve as building blocks for developing global and mechanistic systems pharmacology models.

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