ARTICLE

PBPK Model of Coproporphyrin I: Evaluation of the Impact of SLCO1B1 Genotype, Ethnicity, and Sex on its Inter-Individual Variability

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Coproporphyrin I (CPI) is an endogenous biomarker of OATP1B activity and associated drug-drug interactions. In this study, a minimal physiologically-based pharmacokinetic model was developed to investigate the impact of OATP1B1 genotype (c.521T>C), ethnicity, and sex on CPI pharmacokinetics and interindividual variability in its baseline. The model implemented mechanistic descriptions of CPI hepatic transport between liver blood and liver tissue and renal excretion. Key model parameters (e.g., endogenous CPI synthesis rate, and CPI hepatic uptake clearance) were estimated by fitting the model simultaneously to three independent CPI clinical datasets (plasma and urine data) obtained from white (n = 16, men and women) and Asian-Indian (n = 26, all men) subjects, with c.521 variants (TT, TC, and CC). The optimized CPI model successfully described the observed data using c.521T>C genotype, ethnicity, and sex as covariates. CPI hepatic active was 79% lower in 521CC relative to the wild type and 42% lower in Asian-Indians relative to white subjects, whereas CPI synthesis was 23% higher in male relative to female subjects. Parameter sensitivity analysis showed marginal impact of the assumption of CPI synthesis site (blood or liver), resulting in comparable recovery of plasma and urine CPI data. Lower magnitude of CPI-drug interaction was simulated in 521CC subjects, suggesting the risk of underestimation of CPI-drug interaction without prior OATP1B1 genotyping. The CPI model incorporates key covariates contributing to interindividual variability in its baseline and highlights the utility of the CPI modeling to facilitate the design of prospective clinical studies to maximize the sensitivity of this biomarker.

Hepatic uptake via OATP1B1 and 1B3 has been widely recognized as a rate-limiting step in the clearance of anionic drugs, such as statins.1,2 Considering the high degree of drug-drug interactions (DDIs) associated with OATP1B1 and therapeutic implications, regulatory agencies suggest elucidating factors that can change pharmacokinetics (PKs) of OATP1B1 substrates (https://www.fda.gov/media/134581/download, https://www.ema.europa.eu/en/documents/scientific-guideline/guideline-investigation-drug-interactions-revision-1_en.pdf). Genetic polymorphism of SLCO1B1

STUDY HIGHLIGHTS

WHAT IS THE CURRENT KNOWLEDGE ON THE TOPIC?
✔ Reduced activity of OATP1B1 in homozygous carriers of c.521T>C resulted in higher plasma concentration of coproporphyrin I (CPI), an endogenous biomarker of OATP1B. Women showed lower CPI plasma concentrations than men.

WHAT QUESTION DID THIS STUDY ADDRESS?
✔ To what extent do OATP1B1 c.521T>C, ethnicity, and sex affect CPI steady-state baseline and the extent of CPI-drug interaction? How does the assumption of CPI synthesis site affect model performance?

WHAT DOES THIS STUDY ADD TO OUR KNOWLEDGE?
✔ Modeling of CPI identified three covariates; decreased hepatic CPI uptake in 521CC relative to 521TT, Asian-Indians relative to white subjects, and lower CPI synthesis in women relative to men. These results were mostly unaffected by the assumption on CPI synthesis site in the model. Theoretical simulation evaluated the impact of each covariate on CPI-drug interaction risk.

HOW MIGHT THIS CHANGE DRUG DISCOVERY, DEVELOPMENT, AND/OR THERAPEUTICS?
✔ Modeling of CPI maximizes the sensitivity of this biomarker to evaluate OATP1B1 interaction potential as early as in first-in-human studies and to facilitate the design of prospective interaction studies with corresponding clinical probes.

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coding OATP1B1, is one of the factors affecting exposure of OATP1B1 substrates. Subjects with c.521T>C mutation (521CC), associated with reduced transporter activity, have higher exposure of OATP1B substrates relative to wild-type allele (521TT). In addition, 521CC subjects showed lower fold-change in the area under the plasma concentration-time curve ratio (AUCR) of statins in the presence of OATP1B inhibitors, likely due to reduced contribution of OATP1B1 to the elimination in these individuals. In addition, several studies reported increased exposure of statins in Asians (mainly Japanese) relative to whites, resulting in reduced starting dose of OATP1B substrates (e.g., rosvastatin) in this population. Increased exposure of statins in Japanese was attributed to the intrinsic ethnic variability in OATP1B activity, in addition to genetic polymorphism, although some studies have challenged this hypothesis. Recently, application of this assumption in letemovir physiologically-based PK (PBPK) modeling explained ethnic difference in the PKs of this drug.

Recent years have seen an increased application of endogenous biomarkers as novel tools to investigate transporter function in vivo, with the primary aim to de-risk transporter-mediated DDIs in early drug development. This trend has been particularly evident for OATP1B1. Coproporphyrin I (CPI), a byproduct of heme synthesis, is one of the most promising endogenous biomarkers of OATP1B1. It is a metabolically stable substrate of OATP1B1 and 1B3, as well as MRP2 and MRP3 transports. CPI-drug interactions reported so far in human and preclinical species suggest that this biomarker is expected to closely follow the perpetrator concentration–time profile. In contrast to other OATP1B1 biomarkers, circadian rhythm or food intake are not likely to cause interindividual variability in its plasma baseline.

Several endogenous factors can affect the disposition of CPI. Hepatic uptake via OATP1B1 is the main elimination route of CPI (> 85%) and increased CPI baseline was recently reported in OATP1B1 521CC patients, whereas other genetic mutations of OATP1B1 (e.g., c.388A>G) showed no effect. Higher proportion of CPI in urine in patients with MRP2 mutations (Dubin–Johnson syndrome) were reported, with no strong evidence of altered plasma CPI concentrations. Ethnic differences in baseline CPI were not highlighted in previous studies including white and Asian subjects. However, these studies did not consider OATP1B1 genotype in conjunction with ethnicity as a covariate. Changes in CPI synthesis may also alter CPI baseline. Increased urinary and fecal excretion of CPI was observed when hemoglobin is triggered by anemia or hemolysis. In addition, lower CPI baseline was reported in Japanese female subjects relative to male subjects, with no sex-related differences in exposure of other OATP1B1 markers or probes, suggesting reduced CPI synthesis in women.

Several groups, including us, have reported CPI models with different complexities, ranging from a turnover model to more complex description of the processes in the liver, developed with the aim to facilitate quantitative understanding of CPI disposition. In all modeling examples, hepatic and nonhepatic routes were considered, but there were inconsistencies in terms of CPI synthesis site; it was assumed to occur either in the blood (central) compartment or liver, with no clear consensus.

This study aimed to evaluate quantitatively the impact of genetic polymorphism of SLC01B1 c.521T>C, ethnicity, and sex on interindividual variability in CPI baseline using the largest clinical dataset so far. To estimate the effect of these covariates and to account for the mechanistic description of hepatic transporter processes, the CPI model was extended from our previous work. Parameter estimation was implemented by fitting the model simultaneously to three independent CPI clinical datasets, including white (n = 16, men and women) and Asian-Indian (n = 26, neb) subjects and included all SLC01B1 c.521T>C variants (521TT, TC, and CC). Comprehensive literature search on the available biological information related to CPI synthesis was performed and the impact of different assumptions of the CPI synthesis site was assessed by parameter sensitivity analysis using the extended CPI model. Finally, the impact of the covariates on CPI-drug OATP1B-mediated interaction potential was simulated to support optimal design of prospective clinical studies.

### METHODS

#### Individual CPI clinical data

Individual CPI data were obtained from three clinical studies (Table 1). Shen et al. (study 1) conducted in 14 healthy male Asian-Indians (521TT; n = 13, 521TC; n = 1) and CPI baseline plasma concentrations were measured over 24 hours (Supplementary Material Section S1). Yee et al. (study 2) was conducted in 16 healthy Caucasians (521TT; n = 8, 521TC; n = 6, and 521CC; n = 2); only CPI concentration in plasma was measured on 1 occasion over 12 hours. Lai et al. (study 3) was conducted in 12 healthy male Asian-Indians (all 521TT) subjects and CPI concentrations in plasma and urine were measured over 24 hours on 3 occasions; 2 occasions involved interaction with rifampicin. Data on three main covariates (SLCO1B1 c.521T>C status, ethnicity, and sex) investigated here were available for all 42 subjects.

#### CPI population PBPK model

The CPI model structure was based on our CPI model published previously, but included a mechanistic description of the liver compartment (Figure 1). The model consists of five compartments, including blood (central), urine, liver vascular, liver tissue, and bile compartments. The ordinary differential equations describing the concentration/amount in these compartments are:

\[
\frac{dC_{\text{blood}}}{dt} = \left(k_{\text{syn}} - CLR \cdot C_{\text{blood}} + Q_H \cdot (C_{\text{LV}} - C_{\text{blood}})\right) \cdot \frac{1}{V_c} \tag{1}
\]

\[
\frac{dC_{\text{LV}}}{dt} = \left(Q_H \cdot (C_{\text{blood}} - C_{\text{LV}}) + CL_{\text{passive,LT}} \cdot (C_{LT} - fu_{LT}) - CL_{\text{active,LT}} \cdot C_{LV} \cdot fu_{LT}\right) \cdot \frac{1}{V_L} \tag{2}
\]

\[
\frac{dC_{LT}}{dt} = \left(CL_{\text{passive,LT}} \cdot (C_{LV} \cdot fu_{LT}) - CL_{\text{LT}} \cdot C_{LT} \cdot C_{LT} \cdot fu_{LT} + CL_{\text{active,LT}} \cdot C_{LV} \cdot fu_{LT} - CL_B \cdot C_{LT} \cdot fu_{LT}\right) \cdot \frac{1}{V_L} \tag{3}
\]

\[
\frac{dA_{\text{urine}}}{dt} = CL_B \cdot C_{LT} \cdot fu_{LT} \tag{4}
\]
Identification of Covariates for Coproporphyrin I

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Table 1 Clinical data used in CPI population PBPK model development

<table>
<thead>
<tr>
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<tr>
<td>Ethnicity</td>
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<td>Caucasian</td>
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</tr>
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<td>Sex</td>
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<td>Female</td>
</tr>
<tr>
<td>Study duration</td>
<td>24h</td>
<td>12h</td>
<td>12h</td>
</tr>
<tr>
<td>SLCO1B1 c.521 Genotype</td>
<td>TT (n = 13), TC (n = 1)</td>
<td>TT (n = 4), TC (n = 3), CC (n = 1)</td>
<td>TT (n = 4), TC (n = 3), CC (n = 1)</td>
</tr>
<tr>
<td>Occasions; treatment</td>
<td>Occ 1; Predose</td>
<td>Occ 1; Pravastatin</td>
<td>Occ 1; Pravastatin</td>
</tr>
<tr>
<td>No. plasma samples</td>
<td>Occ 1; 155 (TT) and 12 (TC)</td>
<td>(TT); 58</td>
<td>(TT); 57</td>
</tr>
<tr>
<td>No. urine samples</td>
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<td>0</td>
</tr>
<tr>
<td>C_{ave,base}, nM</td>
<td>TT; 1.07 ± 0.26</td>
<td>TT; 0.66 ± 0.11</td>
<td>TT; 0.54 ± 0.05</td>
</tr>
<tr>
<td></td>
<td>TC; 1.86</td>
<td>CC; 1.74</td>
<td>CC; 1.37</td>
</tr>
</tbody>
</table>

C_{ave,base} = coproporphyrin I concentration in plasma over whole study period in occasions without rifampicin treatment; CPI, coproporphyrin I; Occ, occasion.

\[
\frac{dA_{\text{ urine}}}{dt} = \frac{C_{\text{ R}} \cdot C_{\text{ blood}}}{V_{\text{c}}}
\]

where \( C_{\text{ blood}} \), \( C_{\text{LV}} \), \( C_{\text{LT}} \), \( A_{\text{ urine}} \), and \( A_{\text{ urine}} \) are the concentration (C) or amount (A) of CPI in the blood (central), liver vascular, liver tissue, bile, and urine compartments, respectively. The parameters \( k_{\text{ syn}} \), \( Q_{\text{ R}} \), \( V_{\text{ R}} \cdot V_{\text{LT}} \cdot CL_{\text{R}} \cdot CL_{\text{ passive,u}} \cdot CL_{\text{ active,u}} \cdot CL_{\text{B}} \cdot f_{u,b} \) and \( f_{u,LT} \) are rate of CPI synthesis, hepatic blood flow, volume of blood (central) compartment, volume of liver vascular, volume of liver tissue, renal clearance, hepatic passive clearance (unbound), hepatic active uptake clearance (unbound), biliary clearance, fraction unbound in blood, and fraction unbound in liver tissue, respectively. Due to lack of corroborating evidence of CPI enterohepatic recirculation\(^{29}\) and low bioavailability of labeled CPI in monkeys,\(^{30}\) this process was assumed to be insignificant for the PK of CPI and was not considered in the current model development.

Competitive inhibition of OATP1B-mediated \( CL_{\text{ active,u}} \) by rifampicin was described by Eqs. 6 and 7.

\[
\frac{dC_{\text{LV}}}{dt} = \left( Q_{\text{ R}} \cdot (C_{\text{ blood}} - C_{\text{LV}}) + CL_{\text{ passive,u}} \cdot ((C_{\text{LT}} \cdot f_{u,LT}) - (C_{\text{LV}} \cdot f_{u,b})) \right)
\]

\[
\left( \frac{CL_{\text{ active,u}} \cdot C_{\text{LV}} \cdot f_{u,b}}{1 + \frac{C_{\text{LV}}}{K_{i}}} \right) \left( \frac{1}{V_{\text{LV}}} \right)
\]

\[
\frac{dC_{\text{LT}}}{dt} = \left( CL_{\text{ passive,u}} \cdot ((C_{\text{LV}} \cdot f_{u,b}) - (C_{\text{LT}} \cdot f_{u,LT})) \right)
\]

\[
\left( \frac{CL_{\text{ active,u}} \cdot C_{\text{LV}} \cdot f_{u,b}}{1 + \frac{C_{\text{LV}}}{K_{i}}} \right) - CL_{\text{B}} \cdot C_{\text{LT}} \cdot f_{u,LT} \left( \frac{1}{V_{\text{LT}}} \right)
\]

where \( C_{\text{ R}} \) is total rifampicin plasma concentration and \( K_{i} \) is the inhibition constant for OATP1B-mediated \( CL_{\text{ active,u}} \). \( C_{\text{ R}} \) was predicted using individual parameter estimates (posthoc) obtained during development of a population PK model for rifampicin, as reported previously.\(^{18}\)

Parameter estimation and covariate analysis

To improve the parameter identifiability, some CPI model parameters were fixed to in vitro determined or physiological values, namely in vitro \( CL_{\text{ passive,u}} \) was scaled to in vivo \( CL_{\text{ passive,u}} \) using hepatocellularity of \( 120 \times 10^6 \) cells/g of liver,\(^{26}\) and \( f_{u,LT} \) was estimated from in vitro CPI uptake studies in human hepatocytes (Supplementary Material Section S2). \( f_{u,b} \) was calculated from experimentally determined fraction unbound in plasma (\( f_{u,p} \)), with labeled CPI measured in this study (Supplementary Material Section S2), and reported blood-to-plasma ratio (Table S4). \( Q_{\text{ R}} \) and volumes of compartments (with the exception of the central compartment) were fixed to the physiological values reported previously.\(^{38}\)

Remaining model parameters were estimated using mixed-effects modeling in NONMEM version 7.42 using ADVAN13 and first-order conditional estimation with interaction method. The CPI model was fitted to all individual plasma and urine data simultaneously using combined proportional and additive residual error models for the residual unexplained variabilities of both plasma and urine data; simulated CPI blood concentrations were converted to plasma concentrations using blood-to-plasma ratio. Between subject variability (BSV) was estimated for \( k_{\text{ syn}} \), \( CL_{\text{B}} \), \( CL_{\text{R}} \), and \( V_{\text{ c}} \), assuming log-normal distribution of the parameters; between occasion variability (BOV) was estimated only for \( CL_{\text{B}} \) because inclusion of BOV for other parameters did not improve model performance.
Three covariates were investigated in the CPI model using log-likelihood ratio tests at a significance level of \( p < 0.05 \): the effects of \( \text{SLCO1B1} \) c.521T>C and/or ethnicity on \( CL_{\text{active,u}} \), and the effect of sex on \( k_{\text{syn}} \), \( CL_{\text{active,u}} \) in 521TT subjects was represented as the reference value (\( CL_{\text{active,0}} \)), and the fractional change for polymorphic TC and CC allelic variants (\( \text{COV GEN} \)) were represented as follows:

\[
CL_{\text{active,u}} = CL_{\text{active,0}} \cdot (1 - \text{GEN} \cdot \text{COV GEN})
\]  

where \( \text{GEN} \) is a dummy variable that takes values: \( \text{GEN} = 0 \) (521TT), 0.5 (521TC), and 1 (521CC). Here, the fractional change in 521TC was assumed to be half of the value for 521CC (an additive genetic effect). To keep \( \text{COV GEN} \) between 0 and 1, \( \text{COV GEN} \) was estimated indirectly using a surrogate variable of genetic effect (\( \text{FRAX} \)) shown in Eq. 9:

\[
\text{COV GEN} = 1 / (1 + \text{FRAX})
\]

where \( \text{FRAX} \) can have any positive real value.

The effect of ethnicity on \( CL_{\text{active,u}} \) was also introduced as follows:

\[
CL_{\text{active,u}} = CL_{\text{active,0}} \cdot (1 - \text{RACE} \cdot \text{COV RACE}) \cdot (1 - \text{GEN} \cdot \text{COV GEN})
\]

where \( CL_{\text{active,0}} \) is for Caucasian subjects with 521TT genotype (reference group), \( \text{COV RACE} \) is the fractional change in \( CL_{\text{active,u}} \) in Asian-Indians relative to Caucasians, and \( \text{RACE} \) is a dummy variable that takes the value of 0 for Caucasians and 1 for Asian-Indians.

The effect of sex on CPI synthesis rate (\( k_{\text{syn,sex}} \)) was described as follows:

\[
k_{\text{syn,sex}} = k_{\text{syn,male}} \cdot (1 - \text{SEX} \cdot \text{COV SEX})
\]

where \( \text{COV SEX} \) is the fractional change in \( k_{\text{syn}} \) in women relative to men, and \( \text{SEX} \) is a dummy variable that takes the value of 0 for men and 1 for women.

Data exploration and goodness-of-fit (GOF) plots were produced using MATLAB (R2017a version 9.2.0). GOF plots, such as observed data vs. population predicted (PRED) or individual PRED, conditionally weighted residual vs. TIME or population prediction were used to assess possible model misspecification. Visual predictive check (VPC) based on 5,000 simulated individuals using the covariate demographics (\( \text{SLCO1B1} \) c.521T>C, ethnicity, and sex) was used to assess final model performance.

**Location of CPI synthesis**

The plausibility of the conflicting hypotheses on the site of the CPI synthesis (blood or liver) was assessed by comprehensive literature search. In addition to collation of biological evidence, the impact of the CPI synthesis site was evaluated by comparing estimated parameter values in modified CPI models when assuming different fractions of CPI synthesis in the liver (\( FL_{\text{syn}} \) ranged from 0 to 1; i.e., 0–100% of \( k_{\text{syn}} \) in the liver).

\[
\frac{dC_{\text{blood}}}{dt} = ((1 - FL_{\text{syn}}) \cdot k_{\text{syn}} - CL_{\text{R}} \cdot C_{\text{blood}} + Q_{\text{H}} \cdot (C_{\text{LV}} - C_{\text{blood}})) \cdot \frac{1}{V_{c}}
\]

\[
\frac{dC_{\text{LT}}}{dt} = (FL_{\text{syn}} \cdot k_{\text{syn}} + CL_{\text{passive,u}} \cdot (f_{\text{u,LT}} - (C_{\text{LT}} - f_{\text{u,LT}})) + CL_{\text{active,u}} \cdot C_{\text{LV}} - f_{\text{u,LT}})) \cdot \frac{1}{V_{c}}
\]

**Theoretical simulation of CPI-drug interaction with different \( CL_{\text{active}} \) and \( k_{\text{syn}} \)**

CPI PK parameters (baseline, AUCR, maximum concentration (\( C_{\text{max}} \)) observed, and time of maximum concentration observed (\( T_{\text{max}} \)) were simulated with hypothetical OATP1B
inhibitors using the developed CPI population PBPK model. Inhibitors were assumed to have the same PK as rifampi-
cin, but varying OATP1B $K_i$ (up to 10-fold lower potency in
inhibition). $CL_{\text{active}}$ and $k_{\text{syn}}$ in the model ranged from 10–
125% or 50–125% relative to those in male Caucasians with
521TT, respectively, to capture the covariates estimated in
this study. AUCR was calculated as a ratio of AUC$_{\text{no-drug}}$
with and without inhibitor. To evaluate changes derived from al-
tered CPI disposition, PK of the inhibitor was assumed to be
independent of the covariates.

Statistical analysis
CPI concentration in plasma over whole study period on
occasions without rifampicin treatment ($C_{\text{ave,base}}$) was cal-
culated for each subject, and mean and SD of $C_{\text{ave,base}}$
were calculated for each subpopulation. All occasions
without rifampicin were treated as baseline conditions
because co-administration of clinical probes (furosemide)
without rifampicin were treated as baseline conditions
were calculated for each subpopulation. All occasions
without rifampicin treatment ($C_{\text{ave,base}}$) was cal-
tered CPI disposition, PK of the inhibitor was assumed to be
independent of the covariates.

RESULTS
Clinical studies evaluating CPI in different OATP1B1
genotype and ethnicity
Men with 521TC (1.86 nM) showed higher $C_{\text{ave,base}}$ than
521TT (1.07 ± 0.26 nM) in study 1; the same tendency
was also observed in men (TT 0.66 ± 0.11 nM (n = 4), TC
1.08 ± 0.14 nM (n = 3), and CC 1.74 nM (n = 1)) and women
(TT 0.54 ± 0.05 nM (n = 4), TC 0.69 ± 0.13 nM (n = 3), and
CC 1.37 nM (n = 1)) in study 2. Female subjects showed
lower $C_{\text{ave,base}}$ than men regardless of OATP1B1 geno-
type. $C_{\text{ave,base}}$ of male Caucasian subjects with 521TT
(0.66 ± 0.11 nM in study 2) was lower than those in Asian-
Indians with 521TT genotype (1.07 ± 0.26 nM in study 1 and
0.87 ± 0.16 nM in study 3). $C_{\text{ave,base}}$ in male Asian-Indians
with 521TT was comparable between study 1 and study 3.

Development of CPI population PBPK model with
multiple covariates
The value of $CL_{\text{passive,u}}$ and $f_{u,L^T}$ were fixed to those
measured in vitro in human hepatocytes (scaled $CL_{\text{passive,u}} = 8$ L/h or equivalent to 0.76 µL/min/10$^6$
cells, and $f_{u,L^T} = 0.19$, details of in vitro studies in
Supplementary Material Section S2). Experimentally
determined CPI $f_{u,p}$ was 0.069. With these parameters fixed,
population PBPK CPI model, accounting for the mechanistic liver description and the three covariates,
successfully estimated all parameters with acceptable
uncertainty (< 35% relative standard error except for ad-
ditive residual error for CPI in urine; Table 2). The VPC
showed adequate coverage of the data, with most of the
data within acceptable range in GOF plots, despite mod-
erately smaller conditionally weighted residual for higher
PRED (plasma and urine; Figures 2 and 3).

Active process was a major contributor (> 99%) to CPI hepatic uptake; estimated $CL_{\text{active},0}$ (for the reference 521 TT
group) was 1,397 L/h (equivalent to 137 µL/min/10$^6$
cells), which was 175-fold or 517-fold higher than $CL_{\text{passive,u}}$ or $CL_R$
(2.7 L/h), respectively. Estimated $CL_{\text{active},0}$ was 2-fold higher
than the CPI $CL_{\text{active}}$ obtained in vitro (64.8 µL/min/10$^6$ cells,

Table S2). $CL_d$ (6.24 L/h) was lower than previously esti-
mated (12.3 L/h); however, this finding is not surprising
considering the more mechanistic description of CPI hepatic
disposition in this analysis, with the inclusion of $CL_{\text{active,u}}$.
The estimated total rifampicin OATP1B $K_i$ (0.93 µM, equiv-
alent to 0.10 µm as unbound $K_i$ calculated with rifampicin
$f_{u,p}$ of 0.11$^{28}$) was consistent with our previous analysis
(1.15 µM). BSV of $k_{\text{syn}}, CL_d, CL_R$, and $CL_{\text{active,u}}$ were < 40%.

The parameter estimation revealed 79% lower $CL_{\text{active,u}}$
in 521CC relative to 521TT, which was slightly lower than
in vitro-estimated genotype effect based on comparison of
CPI uptake in donors with 521TT and 521CC genotype
(85.6 ± 6%; Table S3). Estimated $CL_{\text{active,0}}$ in Asian-Indians
was 42% lower than that in Caucasians. Estimated CPI $k_{\text{syn}}$
in female subjects was 23% lower than that in male subjects.

Location of CPI synthesis
Our comprehensive literature search on the location of CPI
synthesis was not conclusive because of supportive informa-
tion for both assumptions (details in Supplementary Material
Section S4). In brief, CPI synthesis in blood was qualitatively
suggested based on the parallel change in urinary CPI ex-
cretion and erythropoiesis activity in the blood.\textsuperscript{33,34} Partial
contribution of hepatic CPI synthesis seemed possible be-
cause an administered radiolabeled precursor of CPI, which
is selectively taken into the hepatic heps synthesis pathway,
was partially converted to CPI in humans.\textsuperscript{38}

Considering uncertainties above, parameter estimations
with different values assumed for $FL_{\text{syn}}$ (from 0 to 1) were
investigated. VPC with each set of estimated parameters
were visually indistinguishable (estimated values and VPC
with $FL_{\text{syn}} = 0$ (synthesis in blood) and $FL_{\text{syn}} = 1$ (synthesis in
liver) are shown in Table 2 and Figure S7 and S8, respec-
tively). The model with CPI synthesis in the liver showed
comparable parameter estimates to the model assum-
ing CPI synthesis in the blood (central); moderate relative
changes in $k_{\text{syn}}$ (+80%), $CL_{\text{active},0}$ (−33%), $K_i$ (+55%), BSV in
$k_{\text{syn}}$ (−50%) and $CL_d$ (−82%), and BOV in $CL_d$ (−83%) were
evident, with marginal changes in other parameters (±30%).
Estimated parameters in the models with different contribu-
tion of CPI synthesis in liver ($FL_{\text{syn}}$ = 0.25, 0.5, or 0.75) were
between those estimated with $FL_{\text{syn}} = 0$ and 1 assumptions
(Figure S9).

Theoretical simulation of CPI-drug interaction in
different covariate groups
CPI baseline and $C_{\text{max}}$ increased with decreasing $CL_{\text{active,u}}$
(the effect of 521T>C or ethnicity), whereas opposite trend
was seen with decrease in $k_{\text{syn}}$ (the effect of sex; Figure 4
and Figure S10). Simulated AUCR with OATP1B inhibitor
equivalent to rifampicin decreased with lower initial trans-
porter activity ($CL_{\text{active}}$), whereas AUCR was insensitive
to differences in $k_{\text{syn}}$. The effect of 521T>C genotype on CPI
AUCR (25–40% decrease in 521CC relative to 521TT in white
and Asian-Indian subjects, respectively) was more evident
than that of ethnicity (2–22% decrease in Asian-Indian rel-
tive to Caucasian subjects in 521TT and CC, respectively).
Moderate-to-weak OATP1B inhibitors showed the same
trends, although the degree of interaction was smaller (de-
tails in Figure S11).
Identification of Covariates for Coproporphyrin I

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DISCUSSION

Utility of model-informed drug development with CPI model

Mechanistic modeling has been increasingly used to improve quantitative understanding of the formation and elimination mechanisms of endogenous biomarkers for drug transporters; these efforts are more advanced for CPI/OATP1B in comparison to other endogenous biomarkers/transporters. One of the key applications of modeling approaches is to guide optimal design of OATP1B-mediated interaction studies.\textsuperscript{18,35,36} To that end, modeling and simulation studies have provided adequate information on the sample size to identify weak-to-moderate OATP1B inhibitors\textsuperscript{18} and used estimated \textit{in vivo} \(K_i\) based on CPI data to simulate the DDI between rifampicin/new inhibitors and statins.\textsuperscript{35,36,40} One of the key advantages of CPI as an endogenous biomarker of OATP1B function \textit{in vivo} is its relatively stable baseline in contrast to other biomarkers (e.g., fatty or bile acids and their conjugates).\textsuperscript{15} Recent clinical studies have provided evidence of the effect of OATP1B1 genetic polymorphism\textsuperscript{25,28,31} on CPI plasma concentration. Therefore, this study aimed to expand our previous CPI model\textsuperscript{18} to incorporate multiple covariates on CPI disposition and investigate their impact on the evaluation of CPI-drug interaction risk.

CPI population PBPK model was based on several assumptions. Certain parameters (e.g., \(CL_{\text{passive,}u}\) and \(f_u,LT\)) were fixed to the values measured \textit{in vitro} to improve parameter identifiability (Supplementary Material Section S2). Enterohepatic circulation of CPI was not considered in our model, supported by the recent studies.\textsuperscript{29,30} For pragmatic reasons, concentration of rifampicin in the central compartment was used as inhibitory concentration affecting CPI \(CL_{\text{active,}u}\); any potential rifampicin concentration gradient between blood and hepatic inlet was not considered. This assumption may potentially underestimate rifampicin OATP1B1 inhibition constant (equivalent to 0.10 \(\mu\)M as unbound \(K_i\) calculated with rifampicin \(f_u,LT\) of 0.11); \(k_{\text{syn}}\), rate of coproporphyrin I synthesis; PBPK, physiologically-based pharmacokinetic; \(V_c\), volume of blood (central) compartment.

Residual unexplained variabilities

\(\sigma_{\text{prop}}\), proportional residual error; \(\sigma_{\text{add}}\), additive residual error; BOV, between occasion variability; BSV, between subject variability; \(CL_p\), biliary clearance; \(CL_{\text{in}}\), renal clearance; \(CL_{p,\text{active,}u}\), hepatic active uptake clearance (\(CL_{\text{active,}u}\)) in white men with SLCO1B1 521TT genotype; COV\(_{\text{GEN}}\), fractional change in \(CL_{\text{active,}u}\) in SLCO1B1 521CC genotype; COV\(_{\text{RACE}}\), fractional change in \(CL_{\text{active,}u}\) in Asian-Indian subject; COV\(_{\text{sex}}\), fractional change in \(k_{\text{syn}}\) in women relative to men; CPI, coproporphyrin I; \(F_{\text{syn}}\), fraction CPI synthesis in the liver; FRAX, surrogate variable of genetic effect; \(K_i\), total rifampicin OATP1B1 inhibition constant (equivalent to 0.10 \(\mu\)M as unbound \(K_i\) calculated with rifampicin \(f_u,LT\) of 0.11); \(k_{\text{syn}}\), rate of coproporphyrin I synthesis; PBPK, physiologically-based pharmacokinetic; \(V_c\), volume of blood (central) compartment.

*aThe population (fixed effect) parameters. Values within parentheses represent relative standard errors (RSE, %). bEstimated BSV (%) and its RSE (%). cEstimated BOV (%) and its RSE (%). dCalculated based on the population (fixed effect) parameter estimate of FRAX.

Covariates affecting CPI hepatic active uptake clearance

In our study, OATP1B1 521T>C was considered a sole allelic variant that affects CPI disposition, due to limited clinical evidence of the effect of other polymorphisms (e.g., c.388A>G).\textsuperscript{26,31} The implementation of the genetic effect in...
the model was based on relatively small number of subjects with c.521T>C mutation (9 subjects with 521TC or CC), but the overall trends are in line with a recently published study. The 521CC has resulted in 79% lower CPI CL\text{active,u}, relative to 521TT, in agreement with clinical OATP1B1 probes. The 521CC effect was slightly lower compared with in vitro evaluation (80–92%; Table S3). This slight discrepancy can be rationalized by large interindividual differences in protein expression of OATP1B1 and small number of hepatocyte donors used in the in vitro evaluation. Considering

**Figure 2** Visual predictive check (VPC) for mechanistic population PBPK modeling of CPI plasma and urine data. Symbols, solid lines, and grey areas represent observed data, median population prediction, and 95% prediction intervals (n = 5,000), respectively. Simulations were performed for each subgroup, including subjects with different sex or SLCO1B1 c.521 (OATP1B1 transporter) genotype (521TT (TT), 521TC (TC), and 521CC (CC)) in three clinical studies. The CPI model with $k_{\text{syn}}$ in the blood (central) compartment was used for the simulation. CPI, coproporphyrin I; PK, pharmacokinetic.
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available dataset, this genetic effect on CPI exposure was mainly based on the data reported in Caucasians. Ethnic differences in the degree of genetic effect are not likely considering comparable effects of 521T>C mutation reported for clinical OATP1B probes between Caucasians and Asians.41

The literature evidence of ethnic differences in the activity of OATP1B relative to Caucasians was reported for Japanese,11 but not for Asian-Indians due to limited number of clinical studies in this population. Two clinical studies reported higher (up to 63%) AUC of rosuvastatin in Asian-Indians relative to Caucasians7,8; however, BCRP 421G>A status of those subjects was not reported. Therefore, those results require careful interpretation, as rosuvastatin is a substrate of OATP1B1 and BCRP and genetic polymorphism of both transporters affects its plasma exposure.7-8,41 Birmingham et al.9 reported moderately (> 26%) higher rosuvastatin AUC in Asian-Indians relative to Caucasians regardless of OATP1B1 and BCRP genotype, implying the existence of intrinsic ethnic variability in OATP1B activity between the two populations. Therefore, the ethnicity effect in the CPI model was assumed on CLactive,u and 42% lower CLactive,u was estimated for Asian-Indians relative to Caucasians.42 suggesting minimal differences in CPI synthesis rate between these two populations. Reported mean CPI Cave,base in Japanese (men, 521TT) of 0.63–0.77 nM26,31 is comparable to Caucasians (Table 1) and in contrast to the proposed ethnic differences in OATP1B activity between Japanese and Caucasians.11 Lower hemoglobin has been reported in Japanese relative to Caucasians, which may imply lower CPI synthesis in Japanese.46

Covariates affecting CPI synthesis rate
In Caucasian subjects, lower Cave,base was observed in women relative to men regardless of OATP1B1 genotype (Table 1). Comparable exposure of other endogenous biomarkers of OATP1B (e.g., fatty acids) between men and women in the same subjects (data not shown) suggested no sex effect on CLactive,u, but reduced CPI synthesis in women. These findings are supported by the comparable protein expression of hepatic OATP1B between men and women42 and lower blood hemoglobin in women.47 Although this study used all the available individual CPI data, it is worth noting that small sample size in some subpopulations in this study (e.g., 521CC) may bias the estimation of covariates, as suggested by power calculations in previous studies.18 Further studies with larger sample size, including different demographics (e.g., OATP1B1 genotype, ethnicity, or sex) would address these questions and validate/confirm assumptions made here with regard to CPI synthesis or intrinsic ethnic differences in OATP1B activity.

Prospective application of the developed CPI model
As CPI is a surrogate marker of OATP1B functional activity in vivo, the population PBPK model developed here
provides a powerful and informative tool for the prospective evaluation of OATP1B-mediated interaction risk. This approach is particularly valuable for exploration of interaction risk in subpopulations that are often not considered in clinical studies or in populations with multiple co-existing covariates. Simulations of such what-if scenarios are where a model-informed drug development approach exploits its true potential. Theoretical simulations of CPI-drug interactions illustrated complex interplay between biomarker synthesis and OATP1B-mediated uptake, with high sensitivity of AUCR to changes in CL-active,u, but not to k-syn (Figure 4). Decrease in CL-active,u reduces the proportion of CPI eliminated via OATP1B, which is compensated by increased elimination of CPI into urine (data not shown), resulting in decreased AUCR. Relatively greater effect of 521T>C genotype on CL-active,u (∼79% in 521CC relative to 521TT) than that of ethnicity (∼42% in Asian-Indian relative to white subjects) results in more pronounced impact of the genetic effect on the CPI interaction (AUCR). Simulated decreased AUCR in 521CC is consistent with data reported with clinical OATP1B probes and suggests the risk of underestimation of the magnitude of transporter-mediated interaction if these subjects are included in a CPI-drug interaction study, which is more likely to happen in clinical studies performed without prior genotyping (e.g., first-in-human study) or in populations with higher prevalence of 521CC. In contrast, any changes in CPI synthesis did not affect fraction transported via OATP1B and simulated AUCR, highlighting no risk of underestimation of the OATP1B interaction magnitude if female subjects are included in the study. As exemplified here, the modeling of CPI gives us prospective insights of clinical output and enables optimal clinical design to increase likelihood of success. Furthermore, the physiological description of the liver processes in the CPI model enables the extension of the model to other special populations (e.g., evaluation of the changes in OATP1B activity in the chronic kidney disease population).

In conclusion, this study evaluated the impact of the genotype of OATP1B1 c521T>C, ethnicity, and sex on CPI baseline and its OATP1B-mediated interaction potential. For the first time, this revised CPI population PBPK model implemented reduced active uptake due to OATP1B polymorphism, ethnic differences in active uptake between Asian-Indians and Caucasians, and reduced CPI synthesis in women. Modeling highlighted that assumption of the CPI synthesis site (blood, liver, or both) has marginal impact on the simulated plasma exposure of this

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**Figure 4** Theoretical simulation of CPI-drug interaction across different CPI hepatic uptake clearance and synthesis rate. Simulation of CPI baseline and AUCR caused by the rifampicin equivalent OATP1B1 inhibitor with varying CPI hepatic uptake clearance and endogenous synthesis rate, represented as relative values (CL-active,u,relative and k-syn,relative) to those in male Caucasians with 521TT (yellow star), respectively. Symbols on surface plots represent subpopulations simulated with the population (fixed effect) parameters of each subpopulation; men (filled) and women (open), 521TT (red) and 521CC (blue), Caucasians (square), and Asian-Indians (circle). Yellow and blue arrows indicate effects of three covariates on male white subjects with 521TT. AUCR, fold change in CPI AUC; CL-active,u, hepatic active clearance; CPI, coproporphyrin I; k-syn, zero-order synthesis.
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endogenous biomarker; availability of liver concentrations would be necessary to allow differentiation of these sites. The CPI PBPK model proposed here aims to facilitate the design of prospective clinical studies with OATP1B perpetrator drugs to maximize the sensitivity of this biomarker.

Supporting Information. Supplementary information accompanies this paper on the CPT: Pharmacometrics & Systems Pharmacology website (www.psp-journal.com).

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