In Vivo Information-Guided Prediction Approach for Assessing the Risks of Drug-Drug Interactions Associated with Circulating Inhibitory Metabolites

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ABSTRACT:
The in vivo drug-drug interaction (DDI) risks associated with cytochrome P450 inhibitors that have circulating inhibitory metabolites cannot be accurately predicted by conventional in vitro-based methods. A novel approach, in vivo information-guided prediction (IVIP), was recently introduced for CYP3A- and CYP2D6-mediated DDIs. This technique should be applicable to the prediction of DDIs involving other important cytochrome P450 metabolic pathways. Therefore, the aims of this study were to extend the IVIP approach to CYP2C9-mediated DDIs and evaluate the IVIP approach for predicting DDIs associated with inhibitory metabolites. The analysis was based on data from reported DDIs in the literature. The IVIP approach was modified and extended to CYP2C9-mediated DDIs. Thereafter, the IVIP approach was evaluated for predicting the DDI risks of various inhibitors with inhibitory metabolites. Although the data on CYP2C9-mediated DDIs were limited compared with those for CYP3A- and CYP2D6-mediated DDIs, the modified IVIP approach successfully predicted CYP2C9-mediated DDIs. For the external validation set, the prediction accuracy for area under the plasma concentration-time curve (AUC) ratios ranged from 70 to 125%. The accuracy (75–128%) of the IVIP approach in predicting DDI risks of inhibitors with circulating inhibitory metabolites was more accurate than in vitro-based methods (28–805%). The IVIP model accommodates important confounding factors in the prediction of DDIs, which are difficult to handle using in vitro-based methods. In conclusion, the IVIP approach could be used to predict CYP2C9-mediated DDIs and is easily modified to incorporate the additive effect of circulating inhibitory metabolites.

Introduction
Drug-drug interactions (DDIs) can result when one drug alters the pharmacokinetics (PKs) of another drug or its metabolites. According to the new FDA Draft Guidance for Industry (2012, http://www.fda.gov/downloads/Drugs/GuidanceComplianceRegulatoryInformation/Guidances/ucm292362.pdf), the PK interactions between an investigational new drug and other drugs should be defined during drug development, as part of an adequate assessment of the drug’s safety and effectiveness. Therefore, predicting clinically significant drug interactions during drug development is essential for the pharmaceutical industry and regulatory agencies. The large number of clinically significant DDIs due to the inhibition of cytochrome P450 (P450) substrate metabolism and the availability of in vitro, in vivo, and clinical methods for assessing P450 DDIs have made this a logical starting point for the development and validation of techniques to predict clinically significant DDIs.

There exists a broad consensus as to the common principles underlying prediction of the magnitude of an in vivo DDI from in vitro data. The increase in the area under the plasma concentration-time curve (AUC) of a substrate when coadministered in the presence of a reversible inhibitor of the substrate’s elimination pathway is a function of the ratio of the inhibitor concentration ([I]) to inhibition constant ($K_i$) (Ito et al., 1998; Shou, 2005; Brown et al., 2006; Obach et al., 2006; Einolf, 2007). A similar model involving $K_c$ (concentration of inhibitor required to achieve half-maximal inactivation) and $k_{inact}$ (maximal rate constant of enzyme inactivation) for DDIs associated with irreversible (mechanism-based) inhibitors has also been proposed (Obach et al., 2007). In addition, researchers have incorporated the fraction of substrate clearance mediated by the inhibited enzyme ($f_{uncYP}$), the plasma protein binding of the inhibitor (Shardlow et al., 2011), and fraction of absorbed substrate dose escaping gut metabolism by CYP3A ($F_c$) (Galetin et al., 2008) to improve predictions for certain drug classes.

Although in vitro-based models can quantitatively predict many in vivo DDIs with acceptable accuracy, the application of this model to the prediction of DDIs associated with P450 inhibitors that have inhibitory metabolites has not been successful (Yeung et al., 2011; McDonald et al., 2012). The prediction accuracy of in vitro models may be improved to some extent when data pertaining to metabolites...
were included in the model; however, prediction accuracy (35–188%) was still unsatisfactory for DDIs associated with 10 typical inhibitors that have inhibitory metabolites (Yeung et al., 2011). Another recent study found that prediction accuracy decreased when more inhibitory metabolites of amiodarone were taken into account (McDonald et al., 2012). A novel approach, in vivo information-guided prediction (IVIP), was recently introduced for CYP3A- and CYP2D6-mediated drug interactions (Ohno et al., 2007; Tod et al., 2011). This model relies primarily on in vivo data and uses two characteristic parameters: one for the substrate and the other for the inhibitor. This model has the potential to take into account inhibitory metabolites, different mechanisms of inhibition, and intestinal inhibition. Although information on the inhibitory metabolites can also be incorporated into an in vitro-based model, the IVIP approach has certain advantages compared with in vitro-based methods. Validation of the IVIP approach for the prediction of DDIs mediated by other CYP450 enzymes or the effects of inhibitory metabolites on DDIs is still lacking, because of the paucity of available data. Therefore, the aims of this study are to extend the IVIP approach to CYP2C9-mediated interactions and to validate the modified IVIP approach for prediction of DDIs associated with inhibitors that have inhibitory metabolites.

Materials and Methods
Extending the IVIP Approach to CYP2C9-Mediated Interactions. Medline, PubMed, and Embase databases (from 1975 until December 31, 2011) were searched using the terms “CYP2C9,” “inhibition,” and “pharmacokinetics.” Citations within the retrieved articles were used to search for additional relevant studies. Studies were included if 1) they were conducted in humans, 2) they provided the ratio between the AUC of the substrate when administered alone and when coadministered at the same dose with the inhibitor, 3) the dose of the inhibitor was within the therapeutic dose range, and 4) the inhibitor and substrate drugs were orally or intravenously administered to the subjects. Drug-drug interaction studies associated with herbal products, combination therapies, and oral contraceptives were excluded. Both reversible and irreversible inhibitors were included in the analysis.

An IVIP approach that has been described previously was modified and applied to the quantitative prediction of CYP2C9-mediated DDIs (Ohno et al., 2007; Tod et al., 2011). This modeling framework uses two characteristic parameters: the contribution ratio (CR) defined as the contribution of the specific enzyme to the oral clearance or total clearance (intravenous administration) of the drug whose metabolism is inhibited (victim) and the apparent inhibition ratio (IR) of the inhibiting drug (perpetrator). If reasonable estimates of CR (0 ≤ CR ≤ 1) and IR (0 ≤ IR ≤ 1) can be determined, then the ratio of the AUC of the presence (AUCI) and absence (AUC) of the inhibitor can be estimated using eq. 1 (Ohno et al., 2007; Hisaka et al., 2010; Tod et al., 2011):

\[
\frac{\text{AUCI}}{\text{AUC}} = 1 - \text{CR} \cdot \text{IR}
\]

(1)

In contrast to the complex derivation by previous studies (Ohno et al., 2007; Tod et al., 2011), eq. 1 is readily derived from the well-known in vitro-based model (reversible inhibition, intestinal metabolism ignored) below (eq. 2), where \( f_{\text{uCYPR}} \) is the contribution of the specific enzyme to the overall clearance.

\[
\frac{\text{AUCI}}{\text{AUC}} \frac{1}{f_{\text{uCYPR}}} = \left(1 - \frac{f_{\text{uCYPR}}}{1 + \frac{AUC1/AUCPM}{AUCEM}}\right)
\]

(2)

After defining \( f_{\text{uCYPR}} = \text{CR} \times \text{IR} = \frac{\text{IR}}{1 + \frac{AUC1/AUCPM}{AUCEM}} \), eq. 2 is transformed to eq. 1. The IR in this model relies on in vivo data, thus avoiding the confounding issues due to extrapolation from \( K_i \) or \( f_{\text{uind}}/K_i \) and does not require distinction between reversible and irreversible (mechanism-based) inhibitors.

For the CYP2D6- and CYP3A-mediated DDIs, the CR values of most victim drugs can be estimated directly from in vivo data using the pharmacogenetic or drug interaction methods (Ohno et al., 2007; Tod et al., 2011). The pharmacogenetic method (Tod et al., 2011) allows determination of CR from eq. 3, where \( \text{AUC}_{\text{PM}} \) is the AUC in poor metabolizers and \( \text{AUC}_{\text{EM}} \) is the AUC in extensive metabolizers.

\[
\text{CR} = \frac{\text{AUC}_{\text{PM}}/\text{AUC}_{\text{EM}} - 1}{\text{AUC}_{\text{PM}}/\text{AUC}_{\text{EM}}}
\]

(3)

Estimation of CR using the interaction method (eq. 4) is based on transformation of eq. 1 using a known IR value of the inhibitor (IR was assumed to be 1.0 for a very strong inhibitor), where \( AUC_i \) is the AUC of the drug when the inhibitor is coadministered.

\[
\text{CR} = \frac{\text{AUC}_i/\text{AUC} - 1}{\text{AUC}_i/\text{AUC} \cdot \text{IR}}
\]

(4)

However, the IVIP approach developed for CYP2D6- and CYP3A-mediated DDIs cannot be directly extended to CYP2C9-mediated DDIs without modification. The CR values of CYP2C9 substrates cannot be reliably estimated by the pharmacogenetic method because relevant studies in CYP2C9 poor metabolizers are limited. Furthermore, the CR of most CYP2C9 substrates cannot be calculated by eq. 4 because of the absence of IR data (e.g., the IR value can be assumed to be 1 for a very strong P450 inhibitor, but no strong inhibitor of CYP2C9 has been found according to the new FDA Draft Guidance for Industry and a recent study (Polasek et al., 2011)). Therefore, the CR of CYP2C9 substrates was estimated using eq. 5, where \( f_{\text{u}} \) is the contribution of CYP2C9 to hepatic clearance (estimated in vitro by CYP2C9-specific inhibitor or functional neutralizing antibody) and \( f_i \) is the contribution of the hepatic clearance to the total clearance of the drug (estimated by the recovery of excreted CYP2C9 metabolites in urine, bile, and feces).

\[
\text{CR} = f_u \cdot f_i
\]

(5)

The CR values of most CYP2C9 substrates were estimated by the extrapolation method (CR = \( f_u \cdot f_i \) using literature data. A learning set (learning set 1) was selected to calculate the IR of CYP2C9 inhibitors. Only the DDIs associated with typical CYP2C9 substrates (S-warfarin, tolbutamide, diclofenac, and phenytoin) were included in this learning set. For the inhibitors with different levels of doses, IR values were estimated for each dose because IR should be dose-dependent. For the remaining few substrates whose CR could not be calculated by the extrapolation method (learning set 2), CR values were estimated by eq. 4 using the known IR of the inhibitors. An external validation of these estimates was performed by comparing the AUC ratios predicted by eq. 1 with the observed values from data not included in the preceding steps. An algebraic mean of the AUC increase was used in the calculation whenever results from multiple studies were available for a single combination of substrate and inhibitor (same dose of inhibitor was used in these studies).

Evaluation of the IVIP Approach in Predicting the DDI Risks of Various Inhibitors with Circulating Inhibitory Metabolites. The relevant data of clinical DDIs associated with P450 inhibitors that have inhibitory metabolites were mainly retrieved from a single recent report (Yeung et al., 2011), which is based on the University of Washington Metabolism and Transport Drug Interaction Database (MTDI database; http://www.druginteractions.org). Whenever available, additional data from the literature were included. In vivo DDIs were studied in our analysis only if they had been conducted with a reliable P450 probe. For CYP3A- and CYP2D6-mediated DDIs, only data from oral administration were included in the analysis. An algebraic mean of the AUC increase was used in the calculation when multiple studies were available for a single combination of victim drug and inhibitor (the same dose of inhibitor was used in these studies).

With use of the above retrieved data, in vivo DDIs associated with inhibitory metabolites were predicted by the fully validated IVIP approach. To avoid “self-prediction,” the data in the learning set were not included in the validation set and vice versa. The learning sets for CYP2D6- and CYP3A-mediated DDIs were selected according to the following criteria: 1) the dose of the inhibitor in the learning set is the same as in the validation set, 2) the regimen of the inhibitor in the learning set and the validation set are both multiple-dose or single-dose regimen, and 3) the victim drug is a known probe or a substrate with a relatively high CR value.
These retrieved data were also used to predict in vivo DDIs by each of the in vitro-based methods. The steady-state concentrations \([I]\) of the inhibitors were estimated in two ways: 1) total systemic \(C_{\text{max}}\) and 2) unbound hepatic inlet concentration (UHI) defined by eq. 6, where \(k_a\) is the absorption rate constant [0.03/min, an assumed average value (Obach et al., 2006)], \(F_u\) is the fraction absorbed (assumed to be 1), \(D\) is the dose of the inhibitor, \(Q_L\) is the liver blood flow (1498 ml/min), and \(f_u\) is the unbound fraction of drug in plasma. This equation assumes that metabolism of the inhibitor in the gut is negligible.

\[
[I]_{\text{hepatic, init}} = f_u \cdot \left( C_{\text{max}} + \frac{k_a \cdot F_u \cdot D}{Q_L} \right)
\]

For reversible inhibitors of CYP2C9 and CYP2D6, eq. 7 was used to predict the clinical DDI. The effect of multiple inhibitors was accounted for by summing the \([I]/K_i\) ratios (Yeung et al., 2011). It should be pointed out that both \(f_u\) and \(K_i\) (in vitro-based model) and CR (IVIP model) indicate the contribution ratio of the target metabolizing enzyme to the clearance of a substrate drug after oral absorption or intravenous administration, so the same value is used in our analysis.

![TABLE 1](image)

<table>
<thead>
<tr>
<th>Substrates</th>
<th>CR</th>
<th>(f_u)</th>
<th>References for (f_u)</th>
<th>(f_u)</th>
<th>References for (f_u)</th>
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<td>0.95</td>
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<td>0.99</td>
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<td>0.69</td>
<td>Zgheib et al., 2007</td>
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<td>Tse et al., 1992</td>
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<td>S-Buprofen</td>
<td>0.50</td>
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<td>Hämman et al., 1997</td>
<td>0.70</td>
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<td>Meloxicam</td>
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<td>Schmid et al., 1995</td>
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<td>0.99</td>
<td>Miners and Birkett, 1998; Komatsu et al., 2000a</td>
<td>0.85</td>
<td>Madsen et al., 2001</td>
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<td>0.96</td>
<td>Yamazaki et al., 1998a,b</td>
<td>0.72</td>
<td>Toon et al., 1986; Heimark et al., 1992</td>
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</table>

Calculating by the extrapolation method (eq. 5).
The contribution of CYP2C9 to hepatic clearance.
The contribution of the hepatic clearance to the total clearance of the drug.

The references are only shown in Supplemental Material 3.
in vivo DDI studies were identified by the literature search. The estimated values of CR for CYP2C9 substrates determined by the extrapolation method are listed in Table 1. Calculated IR values of all CYP2C9 inhibitors and CRs of the remaining four substrates (whose CR cannot be estimated by the extrapolation method) are shown in Table 2, which comprises learning sets 1 and 2.

References for the DDI studies involving CYP2C9 that were used for the external validation are shown in Table 3. A total of 19 AUC ratios were available. The relationship between the observed and predicted AUC ratios is plotted in Fig. 1A. All the points are inside the range of acceptable predictions (50–200%). The prediction accuracy of AUCi/AUC ranged from 70 to 125% (Fig. 1B). The predictive sensitivity and specificity were both 93%. The predictive error and precision were −0.09 and 0.29, respectively.

The AUCi/AUC ratios of 180 possible interactions between the 12 substrates and the 15 inhibitors listed in Tables 2 and 3 were calculated (Fig. 1C). Only a small proportion (21%) of all possible combinations between substrates and inhibitors had been studied in vivo.

Evaluation of the IVIP Approach in Predicting the DDI Risks of Various Inhibitors with Circulating Inhibitory Metabolites. The details of the data and calculation are provided as Supplemental Material 1. A total of 14 different combinations of in vivo DDI studies (including 12 inhibitors with inhibitory metabolites) were identified (Table 4). Two inhibitors (diltiazem and erythromycin) and their metabolites have been shown to possess both reversible and irreversible inhibitory effects on CYP3A (Zhang et al., 2009a). However, both the reversible and irreversible in vitro models could not accurately predict the AUC ratios (Table 4). In general, the predictive performance of the model incorporating unbound UHI was not superior to the model that used total systemic Cmax (Fig. 2). The predictive error of the three in vitro-based models was 6.62 (parent drug, [I] = Cmax), 9.81 (parent drug and metabolites, [I] = Cmax), and 1.77 (parent drug and metabolites, [I] = UHI), respectively. The precision of these in vitro-based models was 24.9, 35.4, and 8.06, respectively.

### Results

Extending the IVIP Approach to CYP2C9-Mediated Interactions. A total of 44 different combinations (substrate and inhibitor) of

<table>
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<tr>
<th>Substrates</th>
<th>Inhibitor</th>
<th>Dose and Regimen</th>
<th>IR</th>
<th>CR</th>
<th>Predicted AUCi/AUC</th>
<th>Accuracy</th>
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<td>1.40</td>
<td>1.30</td>
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<td>0.47</td>
<td>1.67</td>
<td>1.90</td>
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<td>Losartan</td>
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<td>Phenytoin</td>
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<td>0.50</td>
<td>2.01</td>
<td>1.43</td>
<td>71 Hynninen et al., 2006</td>
</tr>
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</table>

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*a* Milligrams per day, the daily doses of the inhibitors; days, the duration of the multiple dosing before administration of substrates.

*b* The AUCi/AUC was predicted by eq. 1.

*c* The references are only shown in Supplemental Material 3.

*d* 400 mg on the first day.

*e* 800 mg on the first day.

*f* An algebraic mean of the observed AUCi/AUC was used if multiple studies are reported for a single combination of substrate and inhibitor (same dose of inhibitor was used in these studies).
In contrast, the predictive error (0.10), precision (0.57), and absolute accuracy (75–128%) of the IVIP approach were significantly better. The predictive sensitivity of the in vitro model could be improved to some extent, when data pertaining to metabolites were included in the model (57% versus 79%). The IVIP approach could successfully identify 12 of 14 positive DDIs (86%). For the two failures, the observed versus predicted AUC ratios were 1.28 versus 1.17 and 1.59 versus 1.24, respectively. The predictive specificities of all three in vitro-based models and the IVIP approach were 86, 71, 86%, and 100%, respectively.

Discussion

There were two primary findings of this study. The first finding is that the modified IVIP approach can be extended to the prediction of CYP2C9-mediated DDIs. For the external validation set, the prediction accuracy for AUC ratios ranged from 70 to 125%. The second finding is that the accuracy of the IVIP approach in predicting DDI risks of 12 inhibitors with circulating inhibitory metabolites was more accurate than in vitro-based methods.

To our knowledge, this is the first proof-of-concept study demonstrating that the IVIP approach is a useful tool for the prediction of drug interaction risks associated with P450 inhibitors that have circulating inhibitory metabolites. The IR in IVIP model relies on in vivo data, thereby avoiding the confounding issues due to extrapolation from in vitro $K_i$ (or $k_{inact}/K_i$). The IVIP approach accommodates important confounding factors (inhibitory metabolites, different mechanisms of inhibition, and intestinal inhibition) in the prediction of DDIs, which are difficult to handle by in vitro-based methods. The theoretical basis for the versatility of the IVIP approach is provided in Supplemental Material 2. In brief, the versatility of the IVIP approach is dependent on the IR of the inhibitors. The underlying meaning of the IR is different for different confounding factors. For instance, the IR reflects the total extent of inhibition occurring in the liver and intestines, if intestinal inhibition exists. In cases in which there are multiple inhibitors that act via independent inhibition mechanisms, the IR reflects the combined inhibitory effects of all inhibitors present.

Another advantage of the IVIP approach is that it is easy to use and does not require statistical or pharmacokinetic simulation software to perform the analysis.

Although the IVIP approach was developed on the basis of previous methods (Ohno et al., 2007; Tod et al., 2011), some differences merit discussion. In the current study, only the well known CYP2C9 probes (5-warfarin, tolbutamide, diclofenac, and phenytoin) were eligible for the learning set used to calculate the IR values of various inhibitors. This criterion is likely to minimize the possibility of introducing misleading CR information. In addition, the IR values of the inhibitors that are calculated on the basis of reliable CYP2C9 probes will only reflect the inhibition of CYP2C9 rather than other inhibitory mechanisms (such as transporter-mediated inhibition). In the current study, the CR values of most CYP2C9 substrates cannot be directly estimated from in vivo information because relevant data for CYP2C9 are limited. To overcome this difficulty, estimation of CR values was mainly based on the extrapolation method, using in vitro data. This modified approach was demonstrated to be accurate and reliable, suggesting that the extrapolation method is a reasonable alternative for estimation of CR values. The data from both oral and intravenous administration were included in our prediction of CYP2C9-mediated DDIs because the activity of CYP2C9 in the intestine is only 4% of the activity in the liver (Galetin and Houston, 2006).

The IVIP model for CYP2C9-mediated DDIs was also used to forecast the magnitude of a large number of drug interactions that have not been studied. The most potent CYP2C9 inhibitors are predicted to be bucalome and miconazole. Respectively, they caused 6.25- and 6.25-fold increases in the plasma AUC values of the CYP2C9 probe tolbutamide (Fig. 1C). According to the FDA classifications of strong, moderate, or weak inhibitors (FDA Draft Guidance for Industry, 2012), these perpetrators may be strong inhibitors of CYP2C9. However, no strong inhibitor of CYP2C9 was listed in the new FDA draft guidance and a recent criteria-based assessment of perpetrators (Polasek et al., 2011). Although these three perpetrators have limited clinical application, they may serve as useful tools for drug metabolism studies. With regard to...
the moderate (amiodarone, benz bromarone, sulfaphenazole, and fluconazole) and weak (voriconazole, sulfipyrazone, and fluvoxamine) inhibitors of CYP2C9, our predictions are consistent with the FDA DDI guidance.

In the present study, the predictive performances of three in vitro-based models were compared with the IVIP approach. These in vitro data-based mathematical models require an assumption of the perpetrator concentration available to the enzyme (II) for the prediction of DDIs. This elusive value is not easy to determine for human P450 drug metabolism. Therefore, alternative assumptions have been explored to optimize a static value for II, including systemic Cmax, Cavg, and estimated hepatic inlet concentrations. However, as present in the study there is no consensus on the in vivo inhibitor concentration that should be used. For instance, the FDA DDI guidance advocates that a clinical DDI study be conducted if the II/Ki ratio > 0.1, where II = total systemic Cmax. It has also been reported that different estimates work better for different classes of inhibitors; for example, unbound systemic concentration has been used for predicting DDIs caused by irreversible inhibition, whereas the estimated unbound hepatic inlet concentration has been the preferred value for reversible inhibition (Obach, 2009). In a recent study, Shardlow et al. (2011) observed that unbound hepatic inlet concentration allowed the accurate prediction of DDIs for the drugs in their data set (including different types of inhibitors). Therefore, both total systemic Cmax and estimates of unbound hepatic inlet concentrations were used as surrogates for the inhibitor concentration in our analysis. Furthermore, in vitro-based models differentiated reversible and irreversible inhibition and also considered the contribution of intestinal metabolism for CYP3A substrates.
The IVIP approach is validated to be accurate in the prediction of AUC ratios. When applied to the data set of the present study, the IVIP model was shown to predict the AUC ratios with a high degree of accuracy. The dotted red lines represent 50 to 200% ranges of the prediction accuracy. For the inhibitors diltiazem and erythromycin, only the predicted AUC ratios based on the irreversible inhibition model were shown. In vitro (P), only the data of the parent drugs were included in the in vitro-based prediction approach and total systemic C_{max} was used to estimate the perpetrator concentration available to the enzyme; in vitro (P+M), total systemic C_{max} for the parent drug and metabolites were used in the in vitro-based prediction approach; in vitro UHI (P+M), unbound hepatic inlet concentrations of parent drug and metabolites were used to estimate the perpetrator concentration available to the enzyme.

**References**


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**Authorship Contributions**

Participated in research design: Hu, Parker, and Laizure.

Conducted experiments: Hu.

Performed data analysis: Hu.

Wrote or contributed to the writing of the manuscript: Hu, Parker, and Laizure.

The limitations of the present study need to be considered. It is noteworthy that the value of IR is dose-dependent (as shown in Table 2) because it is estimated from specific in vivo study and the exposure of the perpetrator has already been considered with the certain relationship with K_{i} or k_{i}/k_{r}. Therefore, to accurately predict a certain clinical DDI, the dose and regimen of the perpetrator in the learning set should not be significantly different from that of the same perpetrator in this clinical DDI study. In addition, in its present form, the IVIP is not applicable to inhibitors that can inhibit both P450 enzymes and transporters such as P-glycoprotein. Failing to account for the interaction with P-glycoprotein may result in underprediction of the interaction caused by changes in cytochrome P450 activity using in vivo information. *J Pharmacol Exp Ther* 318:1220–1229.

Further studies are underway in our laboratory to apply the model to transporter-mediated DDIs.

The IVIP approach is validated to be accurate in the prediction of CYP2C9-mediated DDIs and is a useful tool for the prediction of drug interaction risks associated with P450 inhibitors that have inhibitory metabolites. The prediction was based on four different models. The dotted red lines represent 50 to 200% ranges of the prediction accuracy. For the inhibitors diltiazem and erythromycin, only the predicted AUC ratios based on the irreversible inhibition model were shown. In vitro (P), only the data of the parent drugs were included in the in vitro-based prediction approach and total systemic C_{max} was used to estimate the perpetrator concentration available to the enzyme; in vitro (P+M), total systemic C_{max} for the parent drug and metabolites were used in the in vitro-based prediction approach; in vitro UHI (P+M), unbound hepatic inlet concentrations of parent drug and metabolites were used to estimate the perpetrator concentration available to the enzyme.

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The development after the result of the first clinical DDI study is available.

Inhibitory metabolites. This approach can be used in new drug development. The limitations of the present study need to be considered. It is noteworthy that the value of IR is dose-dependent (as shown in Table 2) because it is estimated from specific in vivo study and the exposure of the perpetrator has already been considered with the certain relationship with K_{i} or k_{i}/k_{r}. Therefore, to accurately predict a certain clinical DDI, the dose and regimen of the perpetrator in the learning set should not be significantly different from that of the same perpetrator in this clinical DDI study. In addition, in its present form, the IVIP is not applicable to inhibitors that can inhibit both P450 enzymes and transporters such as P-glycoprotein. Failing to account for the interaction with P-glycoprotein may result in underprediction of the interaction caused by changes in cytochrome P450 activity using in vivo information. *J Pharmacol Exp Ther* 318:1220–1229.


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