

Database analyses for the prediction of *in vivo* drug–drug interactions from *in vitro* data

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Keywords

CYP2C9, CYP2D6, CYP3A4, drug interactions, prediction

Received

30 June 2003

Accepted

3 September 2003

Aims

In theory, the magnitude of an *in vivo* drug–drug interaction arising from the inhibition of metabolic clearance can be predicted using the ratio of inhibitor concentration ($[I]$) to inhibition constant (K_i). The aim of this study was to construct a database for the prediction of drug–drug interactions from *in vitro* data and to evaluate the use of the various estimates for the inhibitor concentrations in the term $[I]/K_i$.

Methods

One hundred and ninety-three *in vivo* drug–drug interaction studies involving inhibition of CYP3A4, CYP2D6 or CYP2C9 were collated from the literature together with *in vitro* K_i values and pharmacokinetic parameters for inhibitors, to allow calculation of average/maximum systemic plasma concentration during the dosing interval and maximum hepatic input plasma concentration (both total and unbound concentration). The observed increase in AUC (decreased clearance) was plotted against the estimated $[I]/K_i$ ratio for qualitative zoning of the predictions.

Results

The incidence of false negative predictions (AUC ratio > 2 , $[I]/K_i < 1$) was largest using the average unbound plasma concentration and smallest using the hepatic input total plasma concentration of inhibitor for each of the CYP enzymes. Excluding mechanism-based inhibition, the use of total hepatic input concentration resulted in essentially no false negative predictions, though several false positive predictions (AUC ratio < 2 , $[I]/K_i > 1$) were found. The incidence of true positive predictions (AUC ratio > 2 , $[I]/K_i > 1$) was also highest using the total hepatic input concentration.

Conclusions

The use of the total hepatic input concentration of inhibitor together with *in vitro* K_i values was the most successful method for the categorization of putative CYP inhibitors and for identifying negative drug–drug interactions. However this approach should be considered as an initial discriminating screen, as it is empirical and requires subsequent mechanistic studies to provide a comprehensive evaluation of a positive result.

Introduction

Inhibition of CYP-mediated drug metabolism by a concomitantly administered second drug is one of the major causes of drug–drug interactions in humans and can lead to serious toxicities. The use of *in vitro* data to predict

the inhibition potential of a drug is attractive because of the rapid and simple experimental procedures involved. Although there have been substantial technological advances in the conduct of *in vitro* studies, the interpretation of the parameters generated remains problematic

due to lack of a quantitative framework for the relationship between *in vitro* and *in vivo* data on drug–drug interactions [1].

Biochemical principles [2] state that when the metabolism of a drug (substrate) is reversibly inhibited by a second drug (inhibitor), the metabolic intrinsic clearance (CL_{int}) of substrate is decreased by a factor related to the inhibitor concentration available to the enzyme [I] and the inhibition constant, K_i (equation 1). The distinction between competitive and noncompetitive inhibition mechanisms is not relevant when the substrate concentration is much lower than the K_m value, the commonly encountered *in vivo* situation that results in linear kinetics.

$$CL_{int_I} = \frac{CL_{int}}{1 + [I]/K_i} \quad (1)$$

where subscript I represents the value in the presence of inhibitor.

This theory, and the suitability of equation 1 to describe *in vivo* data, has been confirmed in several animal studies under well defined, steady state conditions for various levels of inhibition achieved by intravenous infusions, for example, in the decrease in clearance of diazepam caused by omeprazole [3], of theophylline by enoxacin and ciprofloxacin [4] and of antipyrine by ketoconazole and fluconazole [5].

In human *in vivo* interaction studies, drug plasma concentration profiles are determined in the presence and absence of inhibitor (after multiple oral dosing) and the degree of interaction is expressed as the increase in the area under the plasma concentration–time curve (AUC) of substrate. If the substrate is eliminated by a single metabolic pathway that is subject to inhibition, the AUC ratio of orally administered substrate in the presence and absence of inhibitor reflects the ratio of clearances, provided that the conditions of the ‘well-stirred’ liver model are assumed and that the inhibitor does not affect either the intestinal absorption or plasma protein binding of the substrate:

$$\frac{AUC_I}{AUC} = \frac{F_a D_I}{F_a D} \times \frac{f_{u_B} CL_{int}}{f_{u_{BI}} CL_{int_I}} = \frac{CL_{int}}{CL_{int_I}} \quad (2)$$

where F_a is the fraction absorbed from gut into the portal vein, D is the dose, and f_{u_B} is the unbound fraction in blood. Therefore the ratio of AUCs is dependent on the $[I]/K_i$ ratio (equation 3) based on the assumptions mentioned above.

$$AUC \text{ ratio} = 1 + [I]/K_i \quad (3)$$

In recent years there has been much interest in the use of equation 3 to describe the degree of *in vivo* interaction

between two drugs [1, 6–12]. K_i values can be readily obtained from *in vitro* studies using human liver microsomes. However, it is not normally possible to measure the inhibitor concentration available to the hepatic enzyme *in vivo* in humans. Predictions have been attempted using various [I] values in equation 3, including the plasma total or unbound concentration or hepatic input concentration of the inhibitor [6, 8, 10, 12, 13]. However, most of these studies have dealt with particular combinations of drugs with only one dosage regimen for inhibitor and a general agreement has not been reached as to which concentration should be used for [I] in equation 3 [1, 14].

According to equation 3, interactions are regarded to be with low risk if the estimated $[I]/K_i$ ratio is less than 0.1, and high risk if it is greater than 1. Based on a plot of AUC ratio against $[I]/K_i$ (Figure 1), predictions can be categorized into four zones: true positives (AUC ratio > 2, $[I]/K_i > 1$), true negatives (AUC ratio < 2, $[I]/K_i < 1$), false positives (AUC ratio < 2, $[I]/K_i > 1$), or false negatives (AUC ratio > 2, $[I]/K_i < 1$). The threshold of two-fold increase in the AUC was selected based on a previous consensus report [1].

The aims of this study were 1) to extend previous analyses based on relatively small number of studies and to construct a database for the prediction of drug–drug interactions involving CYP inhibition from *in vitro* data, and 2) to evaluate the utility of the simple $[I]/K_i$ ratio by using various inhibitor concentrations *in vivo* to designate qualitatively CYP inhibition interaction predictions into zones.

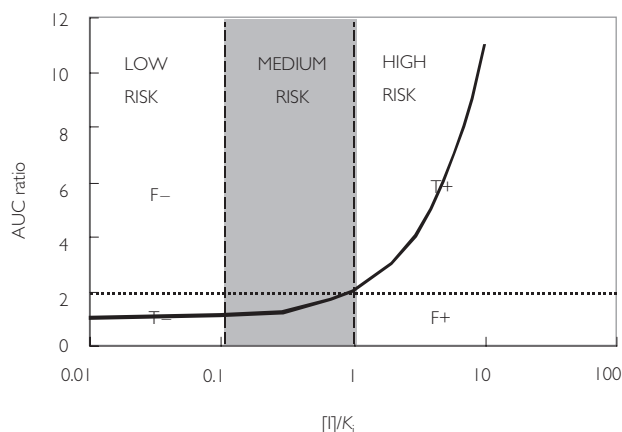


Figure 1

Qualitative zoning for the prediction of drug–drug interactions involving CYP inhibition. The curve represents the theoretical curve based on equation 1. F-: false negative, T-: true negative, F+: false positive, T+: true positive

Methods

Data collection

Three hundred and twenty-one *in vivo* drug–drug interaction studies involving inhibition of the CYP enzymes 3A4/5, 2D6 and 2C9 were obtained from the literature and collated as shown in Table 1. The degree of interaction in each study was expressed as a fold increase in the AUC of the substrate. For the interactions involving CYP2D6, the ratio of the plasma concentration at a single time point and the metabolic ratio (urinary excretion ratio of parent/metabolite(s)) were also used as *in vivo* metrics. As summarized in Table 1, relatively few studies reported the inhibitor concentration (either as an average, maximum, minimum, or particular time point concentration) in the same subjects.

In vitro K_i values for the CYP inhibitors involved in the above studies were also collected from the literature. Often *in vitro* data were available for the same substrate as used in the *in vivo* interaction studies (Table 1), and when several human liver microsomal studies had been conducted, average values were used. For CYP2C9 and 2D6, *in vitro* data from alternative, well accepted substrates were used in the absence of data from the first choice substrate. For interactions involving CYP3A4, K_i values for the same substrate as in the *in vivo* study were available in about half of the studies (Table 1) and for others, probe(s) were selected that belong to the same substrate subgroup class (S) as that in the *in vivo* study [15] as indicated in Table 1.

Information on inhibitor pharmacokinetics in humans (oral clearance (CL/F), half-life ($t_{1/2}$), and plasma

unbound fraction (f_u)) was obtained from the literature to calculate various concentrations as listed below.

Analyses

Various inhibitor concentrations were calculated for use in the analyses. For consistency these were estimated from literature pharmacokinetic parameters. Average systemic plasma concentration after repeated oral administration ($[I]_{av}$), maximum systemic plasma concentration after repeated oral administration ($[I]_{max}$), and maximum hepatic input concentration ($[I]_{in}$) [13] were calculated as follows:

$$[I]_{av} = \frac{D / \tau}{CL/F} \quad (4)$$

$$[I]_{max} = \frac{[I]_{av} k\tau}{1 - \exp(-k\tau)} \quad (5)$$

$$[I]_{in} = [I]_{av} + \frac{ka Fa D}{Qh} \quad (6)$$

where D and τ are the dose and the dosing interval, respectively, of inhibitor used in the *in vivo* interaction study, k is the elimination rate constant, ka is the absorption rate constant, Fa is the fraction absorbed from gut into the portal vein, and Qh is the hepatic blood flow rate. The values of ka , Fa , Qh , and R_B (blood-to-plasma concentration ratio) were assumed to be 0.1 min^{-1} , 1, 1610 ml min^{-1} , and 1, respectively. The corresponding unbound plasma concentrations after repeated oral administration (e.g. $[I]_{av,u}$) was calculated by multiplying the value of $[I]$ by f_u .

Table 1

Numbers of studies in the drug–drug interaction database

Category			Number of <i>in vivo</i> studies			Number of <i>in vitro</i> studies		
CYP	Metric	S class	Total	With C_{av}	With C_{max}	With other C	With same S	With unequivocal substitute S
2D6	AUC		58	6	6	13	25	33
	C_p		89	0	0	21	40	49
	MR		39	0	1	24	28	11
3A4	AUC	BZ	56	6	14	11	40	12
		TS	31	13	1	3	19	11
		NIF	14	1	3	0	0	0
		Other	8	1	2	1	0	0
2C9	AUC		26	3	3	3	22	4

BZ, benzodiazepines; TS, testosterone; NIF, nifedipine.

The $[I]/K_i$ ratio was calculated for each of the *in vivo* interaction studies using the various $[I]$ values described above. For inhibitors with a metabolite that also inhibits the same CYP enzyme, the $[I]/K_i$ ratio was calculated for both the parent drug and the metabolite and the values were added. The predictive performance using various $[I]$ values was compared using the chi-squared test.

Simulations

In a typical interaction study, the input term greatly exceeds the systemic term in equation 6. In order to assess the importance of the assigned values for ka , Fa (these two parameters appear as a product in equation 6), and Qh , the relationship between the AUC ratio and

$1/K_i$ was simulated based on the equations 3 and 6, using various values for $ka \times Fa$ (0.001, 0.01 and 0.1 min^{-1}) and Qh (805, 1610 and 3220 ml min^{-1}). For other parameters, values reported for quinidine were used ($D = 268 \text{ nmol}$, $\tau = 24 \text{ h}$, and $CL/F = 412 \text{ ml min}^{-1}$).

Results and discussion

Of the 321 *in vivo* interaction studies collated from the literature, 193 provided information on the increase in substrate AUC after repeated oral administration of inhibitor ($n = 58$ for CYP2D6, $n = 109$ for CYP3A4, and $n = 26$ for CYP2C9). Of these 94 and 99 studies reported AUC ratios greater and lesser than 2, respectively. Data are listed in Tables 2–4 as AUC ratios

Table 2

In vivo database for the interactions involving CYP2D6

Substrate	Inhibitor	AUC ratio	K_i^* (μM)	$[I]_{av}/K_i$	$[I]_{av,u}/K_i$	$[I]_{max}/K_i$	$[I]_{in}/K_i$	Reference
Flecainide	Amiodarone	1.37	43 (20)	0.11	0.0023	0.11	0.57	2.01
Atenolol	Amitriptyline	1.24	30 (12)	0.13	0.0095	0.19	0.7	2.02
Metoprolol	Amitriptyline	1.44	30 (12)	0.13	0.0095	0.19	0.7	2.02
Propranolol	Chlorpromazine	1.69	4.8	0.11	0.004	0.13	2.2	2.03
Atenolol	Cimetidine	1.07	40	0.1	0.081	0.24	1.3	2.04
Metoprolol	Cimetidine	1.61	40	0.1	0.081	0.24	1.3	2.04
Propranolol	Cimetidine	1.91	40	0.1	0.081	0.24	1.3	2.04
Propranolol	Cimetidine	1.94	40	0.1	0.081	0.24	1.3	2.05
Propranolol	Cimetidine	1.47	40	0.12	0.097	0.28	2	2.06
Imipramine	Citalopram	1.15	24 (14)	0.015	0.0045	0.019	0.34	2.07
(Desipramine)	Citalopram	1.47	24 (14)	0.015	0.0045	0.019	0.34	2.07
Levomopromazine	Citalopram	0.74	24 (14)	0.015	0.0045	0.019	0.34	2.07
Atenolol	Diltiazem	1.07	150	0.0005	0.0001	0.001	0.03	2.08
Metoprolol	Diltiazem	1.33	150	0.0005	0.0001	0.001	0.03	2.08
Propranolol	Diltiazem	1.48	150	0.0005	0.0001	0.001	0.03	2.08
Propranolol	Diltiazem	1.33	150	0.0016	0.0003	0.003	0.091	2.09
Propranolol	Verapamil	1.42	16	0.0072	0.0007	0.013	1	2.09
Metoprolol	Diphenhydramine	1.61	10	0.056	0.012	0.076	1.2	2.10
R(+)-carvedilol	Fluoxetine	1.77	0.54 (0.58)	0.7	0.042	0.81	8.1	2.11
Desipramine	Fluoxetine	4.80	0.54 (0.58)	0.7	0.042	0.81	8.1	2.12
Desipramine	Sertraline	1.20	10 (24)	0.0071	0.0001	0.01	1	2.12
Desipramine	Fluoxetine	7.43	0.54 (0.58)	2.1	0.13	2.4	24	2.13
Imipramine	Fluoxetine	3.33	0.54 (0.58)	2.1	0.13	2.4	24	2.13
(Desipramine)	Fluoxetine	5.31	0.54 (0.58)	2.1	0.13	2.4	24	2.13
Propafenone	Fluoxetine	1.50	0.54 (0.58)	0.7	0.042	0.81	8.1	2.14
Ritonavir	Fluoxetine	1.19	0.54 (0.58)	2.1	0.13	2.3	13	2.15
Tolterodine	Fluoxetine	4.84	0.54 (0.58)	0.7	0.042	0.81	8.1	2.16
Desipramine	Fluvoxamine	1.14	5.8	0.055	0.013	0.09	3.4	2.17
Imipramine	Fluvoxamine	3.63	5.8	0.055	0.013	0.09	3.4	2.17
Metoprolol	Hydroxychloroquine	1.65	66	0.025	0.015	0.025	1.1	2.18
Imipramine	Labetalol	1.53	7	0.012	0.0062	0.026	5.4	2.19
(Desipramine)	Labetalol	2.27	7	0.012	0.0062	0.026	5.4	2.19
Metoprolol	Mexiletine HCl	1.82	30	0.095	0.035	0.13	1.5	2.20
Metoprolol (R)	Omeprazole	1.01	240	0.0003	<0.0001	0.008	0.03	2.21

Table 2 Continued

Substrate	Inhibitor	AUC ratio	K_i^* (μM)	$[\text{I}]_{\text{av}}/K_i$	$[\text{I}]_{\text{av,u}}/K_i$	$[\text{I}]_{\text{max}}/K_i$	$[\text{I}]_{\text{in}}/K_i$	Reference
Metoprolol (S)	Omeprazole	1.02	240	0.0003	<0.0001		0.03	2.21
Propranolol	Omeprazole	1.02	240	0.0002	<0.0001	0.004	0.015	2.22
Desipramine	Paroxetine	4.64	0.69	0.1	0.0051	0.16	5.6	2.23
Imipramine	Paroxetine	1.74	0.69	0.15	0.0076	0.24	8.4	2.24
(Desipramine)	Paroxetine	4.28	0.69	0.15	0.0076	0.24	8.4	2.24
Metoprolol (R)	Paroxetine	7.93	0.69	0.1	0.0051	0.13	2.8	2.25
Metoprolol (S)	Paroxetine	5.08	0.69	0.1	0.0051		2.8	2.25
Perphenazine	Paroxetine	6.96	0.69	0.1	0.0051	0.16	5.6	2.26
Desipramine	Paroxetine	5.21	0.69	0.1	0.0051	0.16	5.6	2.27
Desipramine	Sertraline	1.37	10 (24)	0.0065	0.0001	0.0091	1	2.27
Propranolol	Propafenone	2.13	0.55	19	0.95	30	93	2.28
Desipramine	Quinidine sulphate	7.50	0.082	5.5	0.72	16	210	2.29
Imipramine	Quinidine sulphate	1.54	0.082	5.5	0.72	16	210	2.29
Encainide	Quinidine sulphate	3.18	0.082	5.5	0.72	7.6	56	2.30
Encainide	Quinidine sulphate	11.40	0.082	5	0.64	7.5	66	2.31
Metoprolol	Quinidine sulphate	3.24	0.082	2.8	0.36	7.9	100	2.32
Mexiletine	Quinidine sulphate	1.32	0.082	5.5	0.72	7.6	56	2.33
Propafenone	Quinidine sulphate	2.70	0.082	4.1	0.54	6.2	55	2.34
Desipramine	Ritonavir	2.45	4.8	1.8	0.036	3.4	11	2.35
Desipramine	Sertraline	1.74	10 (24)	0.02	0.0002	0.027	3	2.36
Desipramine	Sertraline	1.54	10 (24)	0.02	0.0002	0.027	3	2.37
Imipramine	Sertraline	1.68	10 (24)	0.02	0.0002	0.027	3	2.37
(Desipramine)	Sertraline	2.29	10 (24)	0.02	0.0002	0.027	3	2.37
Metoprolol	Verapamil	1.33	16	0.0072	0.0007	0.013	1	2.38

* Numbers in parentheses represent the values for metabolites.

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Table 3*In vivo* database for the interactions involving CYP3A4

Substrate	Inhibitor	AUC ratio	K_i^* (μM)	$[\text{I}]_{\text{av}}/K_i$	$[\text{I}]_{\text{av,u}}/K_i$	$[\text{I}]_{\text{max}}/K_i$	$[\text{I}]_{\text{in}}/K_i$	Reference
Midazolam	Azithromycin	0.87	30	0.0046	0.0033	0.0056	0.71	3.01
Midazolam	Azithromycin	1.19	30	0.0092	0.0066	0.011	1.4	3.02
Midazolam	Clarithromycin	3.57	57	0.0087	0.0047	0.024	0.37	3.02
Triazolam	Azithromycin	1.03	30	0.0092	0.0066	0.01	0.71	3.03
Triazolam	Clarithromycin	5.06	57	0.017	0.0094	0.048	0.74	3.03
Triazolam	Erythromycin	3.65	77	0.0068	0.0011	0.035	0.56	3.03
Midazolam	Azithromycin	1.27	30	0.0092	0.0066	0.011	1.4	3.04
Midazolam	Erythromycin	3.81	170	0.0046	0.0004	0.016	0.25	3.04
Alprazolam	Cimetidine	1.58	140	0.034	0.028	0.081	0.56	3.05
Triazolam	Cimetidine	1.54	99	0.048	0.039	0.11	0.8	3.05
Alprazolam	Cimetidine	1.73	140	0.028	0.023	0.067	0.38	3.06
Triazolam	Cimetidine	2.20	99	0.04	0.033	0.096	0.54	3.06
Midazolam	Cimetidine	2.02	180	0.022	0.0089	0.052	0.29	3.07
Midazolam	Ranitidine	1.66	170	0.0027	0.0012	0.011	0.17	3.07
Midazolam	Cimetidine	1.35	180	0.018	0.0071	0.074	0.56	3.08
Midazolam	Ranitidine	1.23	170	0.0027	0.0012	0.011	0.17	3.08
Nifedipine	Cimetidine	1.60	140	0.028	0.023	0.24	1.8	3.09
Nifedipine	Ranitidine	1.22	170	0.0027	0.0023	0.011	0.17	3.09
Nifedipine	Cimetidine	2.01	140	0.023	0.018	0.19	1.4	3.10
Nifedipine	Ranitidine	1.06	170	0.0055	0.0047	0.022	0.35	3.10
Nimodipine	Cimetidine	1.74	140	0.028	0.023	0.067	0.38	3.11
Nimodipine	Ranitidine	0.99	170	0.0027	0.0023	0.022	0.35	3.11
Nisoldipine	Cimetidine	1.49	140	0.028	0.023	0.067	0.38	3.12
Nitrendipine	Cimetidine	2.41	140	0.027	0.022	0.057	0.38	3.13
Triazolam	Cimetidine	1.55	99	0.048	0.039	0.11	0.8	3.14
Triazolam	Cimetidine	1.32	99	0.048	0.039	0.11	0.8	3.15
Midazolam	Clarithromycin	7.00	57	0.017	0.0094	0.048	0.74	3.16
Lovastatin	Cyclosporin	1.89	2	0.059	0.0041	0.11	3.7	3.17
Buspirone	Diltiazem	5.50	65	0.0024	0.0005	0.0047	0.14	3.18
Buspirone	Verapamil	3.40	16	0.0047	0.0005	0.0087	0.68	3.18
Cyclosporin	Diltiazem	1.49	63.0	0.0033	0.0007	0.0084	0.29	3.19
Cyclosporin	Diltiazem	1.57	63.0	0.0025	0.0006	0.0063	0.22	3.20
Cyclosporin	Ketoconazole	4.39	0.37	1.2	0.012	6.2	66	3.20
Lovastatin	Diltiazem	3.57	65	0.0032	0.0007	0.0081	0.28	3.21
Midazolam	Diltiazem	3.75	54	0.0029	0.0003	0.0056	0.17	3.22
Midazolam	Verapamil	2.92	13	0.0061	0.0003	0.011	0.87	3.22
Nifedipine	Diltiazem	2.22	65	0.0012	0.0003	0.0023	0.07	3.23
Nifedipine	Diltiazem	3.11	65	0.0036	0.0008	0.007	0.21	3.23
Simvastatin	Diltiazem	4.82	65	0.0032	0.0007	0.0081	0.28	3.24
Triazolam	Diltiazem	3.38	54	0.0029	0.0006	0.0056	0.17	3.25
Triazolam	Diltiazem	2.30	54	0.0029	0.0006	0.0056	0.17	3.26
Alprazolam	Erythromycin	2.47	120	0.005	0.0008	0.018	0.28	3.27
Buspirone	Erythromycin	5.90	110	0.0075	0.0012	0.027	0.41	3.28
Buspirone	Itraconazole	19.20	0.91 (2.2)	0.26	0.0005	0.32	9.9	3.28
Cerivastatin	Erythromycin	1.21	110	0.0075	0.0012	0.027	0.41	3.29
Cyclosporin	Erythromycin	2.22	66	0.0079	0.0013	0.022	0.33	3.30
Cyclosporin	Erythromycin	2.15	66	0.016	0.0025	0.044	0.66	3.31
Felodipine	Erythromycin	2.49	110	0.005	0.0008	0.014	0.21	3.32
Midazolam	Erythromycin	4.42	170	0.0046	0.0004	0.016	0.25	3.33
Quinidine	Erythromycin	1.19	110	0.005	0.0008	0.014	0.21	3.34
Quinidine	Itraconazole	2.58	0.91 (2.2)	0.13	0.0003	0.19	9.8	3.34
Simvastatin	Erythromycin	6.20	110	0.0075	0.0012	0.023	0.41	3.35
Simvastatin	Verapamil	4.60	16	0.0047	0.0005	0.0087	0.68	3.35

Table 3 Continued

Substrate	Inhibitor	AUC ratio	K_i^* (μM)	$[\text{I}]_{\text{av}}/K_i$	$[\text{I}]_{\text{av,u}}/K_i$	$[\text{I}]_{\text{max}}/K_i$	$[\text{I}]_{\text{in}}/K_i$	Reference
Triazolam	Erythromycin	2.06	120	0.0042	0.0007	0.015	0.23	3.36
Quinidine	Felodipine	1.07	11	0.0003	<0.0001	0.0005	0.15	3.37
Quinidine	Nifedipine	1.15	17	0.0047	0.0002	0.022	0.21	3.37
Cyclosporin	Fluconazole	1.84	40	0.54	0.48	0.69	1.55	3.38
Midazolam	Fluconazole	3.60	6	3.6	1.6	4.6	10	3.39
Midazolam	Itraconazole	6.64	0.92 (6.3)	0.18	0.0004	0.26	19	3.39
Rifabutin	Fluconazole	1.82	12	1.8	1.6	2.3	5.2	3.40
Triazolam	Fluconazole	1.63	1.8	2.9	2.6	3.8	8.5	3.41
Triazolam	Fluconazole	2.05	1.8	5.9	5.2	7.6	17	3.41
Triazolam	Fluconazole	4.42	1.8	12	10	15	34	3.41
Triazolam	Fluconazole	2.46	1.8	5.9	5.2	7.6	17	3.42
Triazolam	Terbinafine	0.81	100	0.012	<0.0001	0.02	0.55	3.42
Alprazolam	Fluoxetine	1.34	65 (10)	0.088	0.0053	0.1	0.27	3.43
Alprazolam	Fluoxetine	1.26	65 (10)	0.059	0.0035	0.063	0.12	3.44
Triazolam	Fluoxetine	1.02	26 (5.4)	0.14	0.0085	0.16	0.61	3.45
Alprazolam	Fluvoxamine	1.96	9.2	0.035	0.0080	0.057	2.2	3.46
Buspirone	Fluvoxamine	2.35	11	0.029	0.0066	0.048	1.8	3.47
Quinidine	Fluvoxamine	1.41	11	0.029	0.0066	0.048	1.8	3.48
Triazolam	Isradipine	0.80	17	0.0001	<0.0001	0.0003	0.043	3.49
Triazolam	Mibefradil	8.97	2.5	0.25	0.001	0.39	2.8	3.49
Alprazolam	Itraconazole	2.66	0.95 (2.2)	0.26	0.0005	0.37	19	3.50
Astemizole	Itraconazole	2.77	0.91 (2.2)	0.52	0.001	0.63	20	3.51
Atorvastatin	Itraconazole	3.64	0.91 (2.2)	0.26	0.0005	0.38	20	3.52
Buspirone	Itraconazole	14.50	0.91 (2.2)	0.26	0.0005	0.38	20	3.53
Cerivastatin	Itraconazole	1.15	0.91 (2.2)	0.26	0.0005	0.38	20	3.54
Felodipine	Itraconazole	6.34	0.91 (2.2)	0.26	0.0005	0.38	20	3.55
Lovastatin	Itraconazole	22.10	0.91 (2.2)	0.26	0.0005	0.38	20	3.56
Lovastatin	Itraconazole	15.40	0.91 (2.2)	0.13	0.0003	0.19	9.8	3.57
Midazolam	Itraconazole	7.97	0.92 (6.3)	0.18	0.0004	0.26	19	3.58
Midazolam	Itraconazole	5.75	0.92 (6.3)	0.089	0.0002	0.13	9.7	3.59
Midazolam	Itraconazole	10.80	0.92 (6.3)	0.36	0.0007	0.52	39	3.60
Midazolam	Ketoconazole	15.90	0.088	5	0.025	26	270	3.60
Quinidine	Itraconazole	2.42	0.91 (2.2)	0.26	0.0005	0.38	20	3.61
Simvastatin	Itraconazole	18.60	0.91 (2.2)	0.26	0.0005	0.38	20	3.62
Triazolam	Itraconazole	27.10	0.16 (0.2)	2.2	0.0044	3.2	110	3.63
Triazolam	Ketoconazole	22.40	0.022	41	0.41	210	2200	3.63
Alprazolam	Ketoconazole	3.98	0.061	15	0.15	40	400	3.64
Triazolam	Ketoconazole	13.70	0.022	41	0.41	110	1100	3.64
Cyclosporin	Ketoconazole	5.15	0.36	2.5	0.025	6.7	67	3.65
Cyclosporin	Ketoconazole	5.31	0.36	1.2	0.012	6.2	66	3.66
Midazolam	Ketoconazole	16.00	0.088	10	0.051	28	280	3.67
Nisoldipine	Ketoconazole	24.40	0.099	4.5	0.045	23	240	3.68
Tacrolimus	Ketoconazole	2.88	8	0.056	0.0006	0.28	3	3.69
Triazolam	Ketoconazole	9.16	0.022	31	0.31	110	1100	3.70
Alprazolam	Nefazodone	1.41	1.2	0.98	0.0089	2	24	3.71
Triazolam	Nefazodone	3.90	1.2	0.98	0.0089	2	24	3.72
Cyclosporin	Nifedipine	0.88	10	0.008	0.0003	0.037	0.36	3.73
Cyclosporin	Verapamil	1.45	24	0.0036	0.0004	0.0066	0.51	3.73
Quinidine	Nifedipine	0.98	17	0.0071	0.0003	0.023	0.21	3.74
Nifedipine	Quinidine sulphate	1.37	160	0.019	0.0025	0.029	0.26	3.74
Midazolam	Ranitidine	1.66	170	0.0027	0.0012	0.011	0.17	3.75
Alprazolam	Ritonavir	2.48	0.065	71	1.4	120	340	3.76
Midazolam	Roxithromycin	1.47	110	0.061	0.0012	0.19	0.26	3.77
Midazolam	Saquinavir	5.14	3.5	0.12	0.0012	0.15	32	3.78
Quinidine	Verapamil	1.47	16	0.0047	0.0005	0.0087	0.68	3.79
Quinidine	Verapamil	1.50	16	0.0071	0.0007	0.013	1	3.79

Table 3 Continued

*Numbers in parentheses represent the values for metabolites.

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Table 4*In vivo* database for the interactions involving CYP2C9

Substrate	Inhibitor	AUC ratio	K_i (μM)	$[\text{I}]_{\text{av}}/K_i$	$[\text{I}]_{\text{av,u}}/K_i$	$[\text{I}]_{\text{max}}/K_i$	$[\text{I}]_{\text{in}}/K_i$	Reference
S-Warfarin	Amiodarone	2.11	95	0.033	0.0014	0.033	0.23	4.01
S-Warfarin	Amiodarone	1.27	95	0.024	0.001	0.025	0.31	4.02
Phenytoin	Amiodarone	1.40	95	0.016	0.0006	0.016	0.21	4.03
S-Warfarin	Benzbromarone	2.15	0.0085	550	0.55	960	1400	4.04
S-Warfarin	Bucolome	3.29	20	1.9	0.19	2.4	5.3	4.05
S-Warfarin	Fluconazole	2.84	7.5	6.2	5.5	8	17	4.06
Tolbutamide	Fluconazole	2.09	16	0.73	0.65	0.94	2	4.07
Phenytoin	Fluconazole	1.75	7.5	3.2	2.8	4.1	8.6	4.08
Phenytoin	Fluconazole	1.33	7.5	6.2	5.5	8	17	4.09
Losartan	Fluconazole	1.69	13	1.8	1.6	2.4	5	4.10
Losartan	Fluconazole	1.27	13	1.8	1.6	2.4	5	4.11
Fluvastatin	Fluconazole	1.84	13	1.8	1.6	2.4	5	4.12
Glimepiride	Fluconazole	2.38	13	1.8	1.6	2.4	5	4.13
Diclofenac	Fluvastatin	1.25	0.18	0.32	0.0032	7.1	31	4.14
Tolbutamide	Fluvastatin	1.23	0.25	0.23	0.0032	5.1	22	4.15
Tolbutamide	Ketoconazole	1.77	8.1	0.65	0.0065	3.3	3.5	4.16
Phenprocoumon	Lornoxicam	1.13	12	0.1	0.001	0.24	0.22	4.17
R-Acenocoumarol	Lornoxicam	1.06	10	0.12	0.0012	0.28	0.26	4.18
S-Warfarin	Miconazole	4.72	0.5	0.54	0.054	0.75	33	4.19
Phenytoin	Sertraline	1.19	33	0.013	0.0001	0.018	1.1	4.20
Tolbutamide	Sertraline	1.19	33	0.005	<0.0001	0.0065	1.1	4.21
Tolbutamide	Sulphamethizole	1.62	75	0.0012		0.004	3.1	4.22
Tolbutamide	Sulphaphenazole	5.28	0.32	220	70	320	530	4.23
Tolbutamide	Sulphaphenazole	3.10	0.32	220	70	320	530	4.24
S-Warfarin	Sulphinpyrazone	1.70	230	0.018	0.0004	0.042	0.15	4.25
S-Warfarin	Sulphinpyrazone	1.93	230	0.018	0.0004	0.042	0.15	4.26

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together with *in vitro* K_i values and four $[\text{I}]/K_i$ parameters, based on average systemic total drug plasma concentration ($[\text{I}]_{\text{av}}$), average systemic unbound drug plasma concentration ($[\text{I}]_{\text{av,u}}$), maximum systemic plasma concentration ($[\text{I}]_{\text{max}}$), and maximum hepatic

input concentration ($[\text{I}]_{\text{in}}$). The latter represents the theoretical maximum drug concentration entering the liver, which is the sum of the hepatic artery and portal vein concentrations during the absorption process.

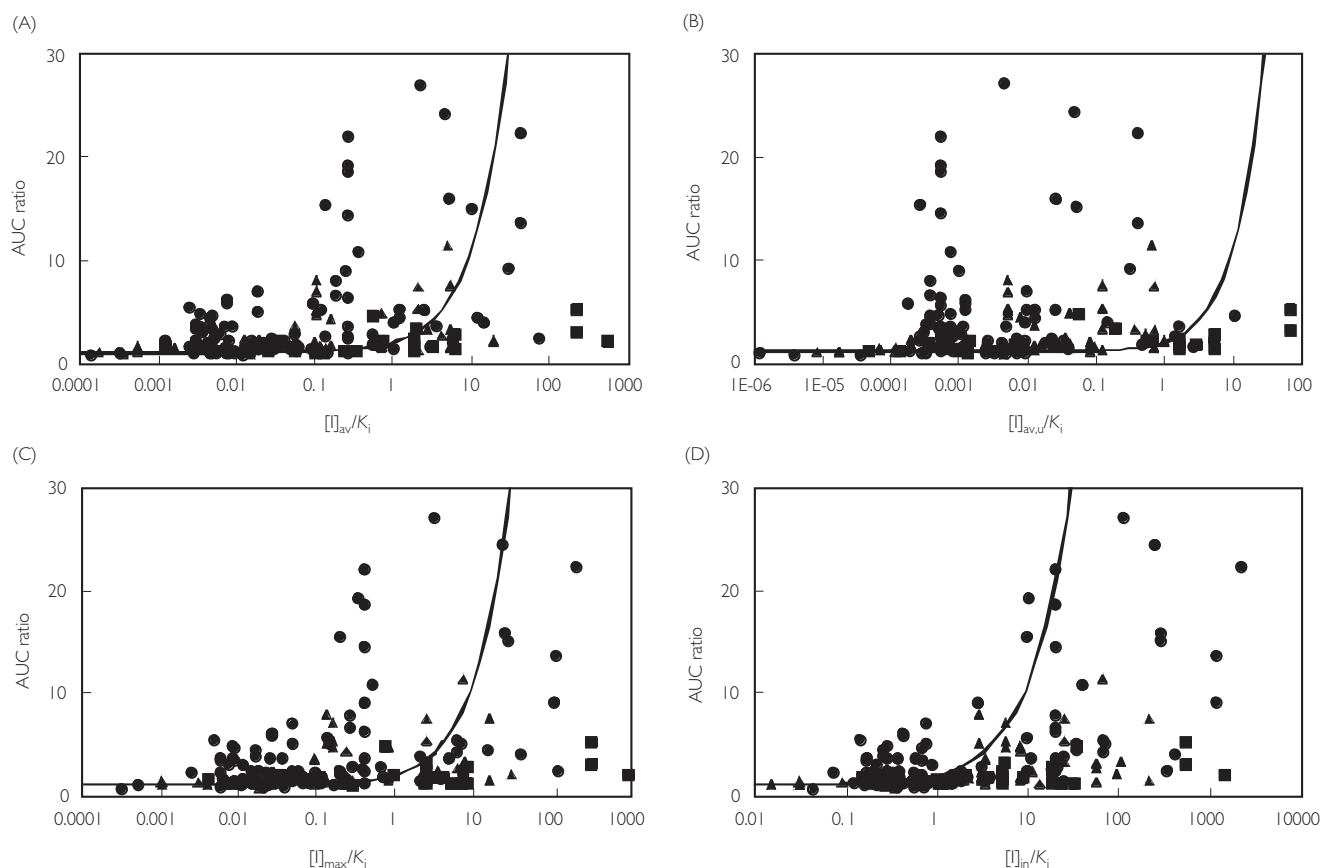


Figure 2

Relationship between the observed AUC ratio and the various $[I]/K_i$ ratios for drug-drug interactions involving CYP3A4 (●), CYP2D6 (▲) or CYP2C9 (■). The curves represent the theoretical curves based on equation 1 using average systemic total drug plasma concentration ($[I]_{av}$ – panel A), average systemic unbound drug plasma concentration ($[I]_{av,u}$ – panel B), maximum systemic plasma concentration ($[I]_{max}$ – panel C), and maximum hepatic input concentration ($[I]_{in}$ – panel D)

Table 5

Summary of the predictions of drug-drug interactions based on the various values for $[I]$. The studies were designated according to the qualitative zoning shown in Figure 1

	CYP3A4				CYP2D6				CYP2C9			
	$[I]_{av}$	$[I]_{av,u}$	$[I]_{max}$	$[I]_{in}$	$[I]_{av}$	$[I]_{av,u}$	$[I]_{max}$	$[I]_{in}$	$[I]_{av}$	$[I]_{av,u}$	$[I]_{max}$	$[I]_{in}$
True positive	16	5	17	36	10	0	10	15	6	4	6	8
True negative	31	31	30	24	33	36	33	13	12	11	9	6
False positive	2	2	3	9	3	0	3	23	5	5	8	11
False negative	23	34	22	3	5	15	5	0	3	5	3	1
Total	72	72	72	72	51	51	51	51	26	25	26	26

In Figure 2, the observed values of AUC ratio are plotted against the values of $[I]/K_i$ ratio estimated using each of the four $[I]$ above. The average degree of *in vivo* interaction was largest for CYP3A4 (4.5-fold), intermediate for CYP2D6 (2.6-fold) and smallest for CYP2C9

(2.0-fold). *In vitro* K_i values differed over five orders of magnitude. The use of $[I]_{av}$ (panel A) gave an approximate description of the data with 78% and 22% of the inhibitors with $[I]/K_i$ ratios below and above 1, respectively. Table 5 provides a breakdown of the number of

studies within the true positives ($AUC \text{ ratio} > 2$, $[I]/K_i > 1$), true negatives ($AUC \text{ ratio} < 2$, $[I]/K_i < 1$), false positives ($AUC \text{ ratio} < 2$, $[I]/K_i > 1$), or false negatives ($AUC \text{ ratio} > 2$, $[I]/K_i < 1$) zones.

Using $[I]_{av,u}$ (panel B) shifted all the points to the left compared with $[I]_{av}$, resulting in substantial underprediction for most of the studies, whereas the use of $[I]_{max}$ (panel C) appears little different from $[I]_{av}$. In contrast, the points shifted to the right using $[I]_{in}$ (panel D), leading to a more convincing zoning of negatives and positives.

Among the inhibitors involved in CYP3A4 interaction studies, macrolide antibiotics (erythromycin, clarithromycin, etc.) and some of the calcium channel blockers (diltiazem, verapamil and mibefradil) are reported to be mechanism-based inhibitors of CYP3A4 that cause irreversible inhibition by forming an inactive complex with the enzyme [16–18]. In addition, paroxetine has recently been reported to be a mechanism-based inhibitor of CYP2D6 [19]. Since equation 1 is only applicable for reversible inhibition, the interactions involving mechanism-based inhibitors were identified. Once these are excluded, there is a marked improvement in zoning with almost no false negative predictions (see Figure 3 using $[I]_{in}$).

A comparison of the success of qualitative zoning of the inhibition predictions (excluding mechanism-based inhibitions) according to the four $[I]$ values are summarized in Table 5. Results based on $[I]_{av}$ and $[I]_{max}$ were similar to each other for all of the CYP enzymes, with a high proportion of ‘true’ predictions (the sum of ‘true positives’ and ‘true negatives’). The incidence of false negative prediction was largest using the $[I]_{av,u}$ and smallest using the $[I]_{in}$ for any of

the CYP enzymes, a difference that was statistically significant ($P < 0.001$). These findings are consistent with a previous study [14], which showed a high possibility of false negative predictions based only on the systemic concentration of inhibitor. The use of $[I]_{in}$ resulted in the highest incidence of true positive predictions (Table 5), though the number of false positive predictions was also the highest of the four values for $[I]$. There was a significant difference between the use of $[I]_{in}$ and the other three $[I]$ values ($P < 0.001$).

The inhibitors used in the interaction studies involving CYP3A4 and CYP2D6 are identified in Figures 4 and 5, respectively. Most of the interactions involving major effects on CYP3A4 were caused by azoles, par-

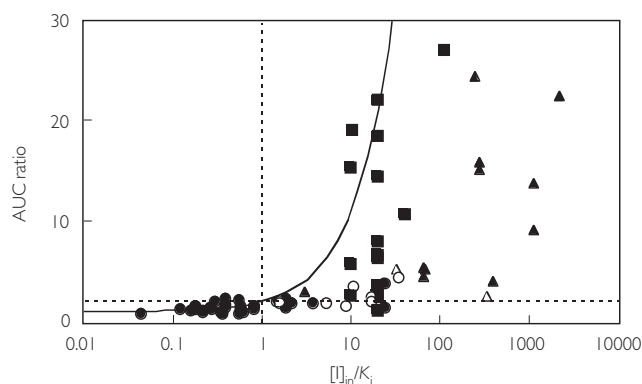


Figure 4

Data from studies involving CYP3A inhibitors. Fluconazole ($n = 7$) (○), itraconazole ($n = 17$) (■), ketoconazole ($n = 11$) (▲), HIV protease inhibitors ($n = 2$) (△), others ($n = 35$) (●)

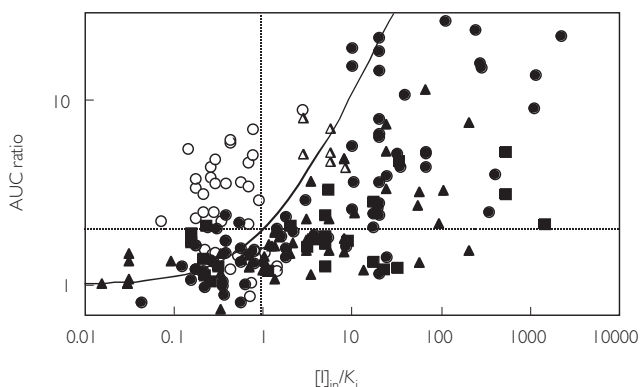


Figure 3

Identifying drug–drug interaction studies involving either reversible (closed symbols) or mechanism-based inhibition (open symbols). CYP3A4 (●), CYP2D6 (▲), CYP2C9 (■). Note, ordinate has a logarithmic scale.

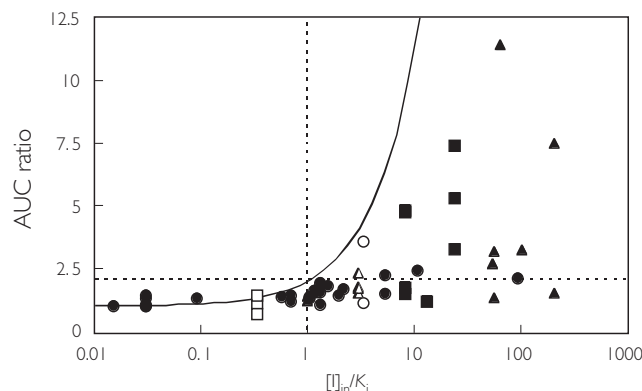


Figure 5

Data from studies involving CYP2D6 inhibitors. Quinidine ($n = 7$) (▲), citalopram ($n = 3$) (□), fluoxetine ($n = 8$) (■), fluvoxamine ($n = 2$) (○), sertraline ($n = 6$) (△), others ($n = 25$) (●)

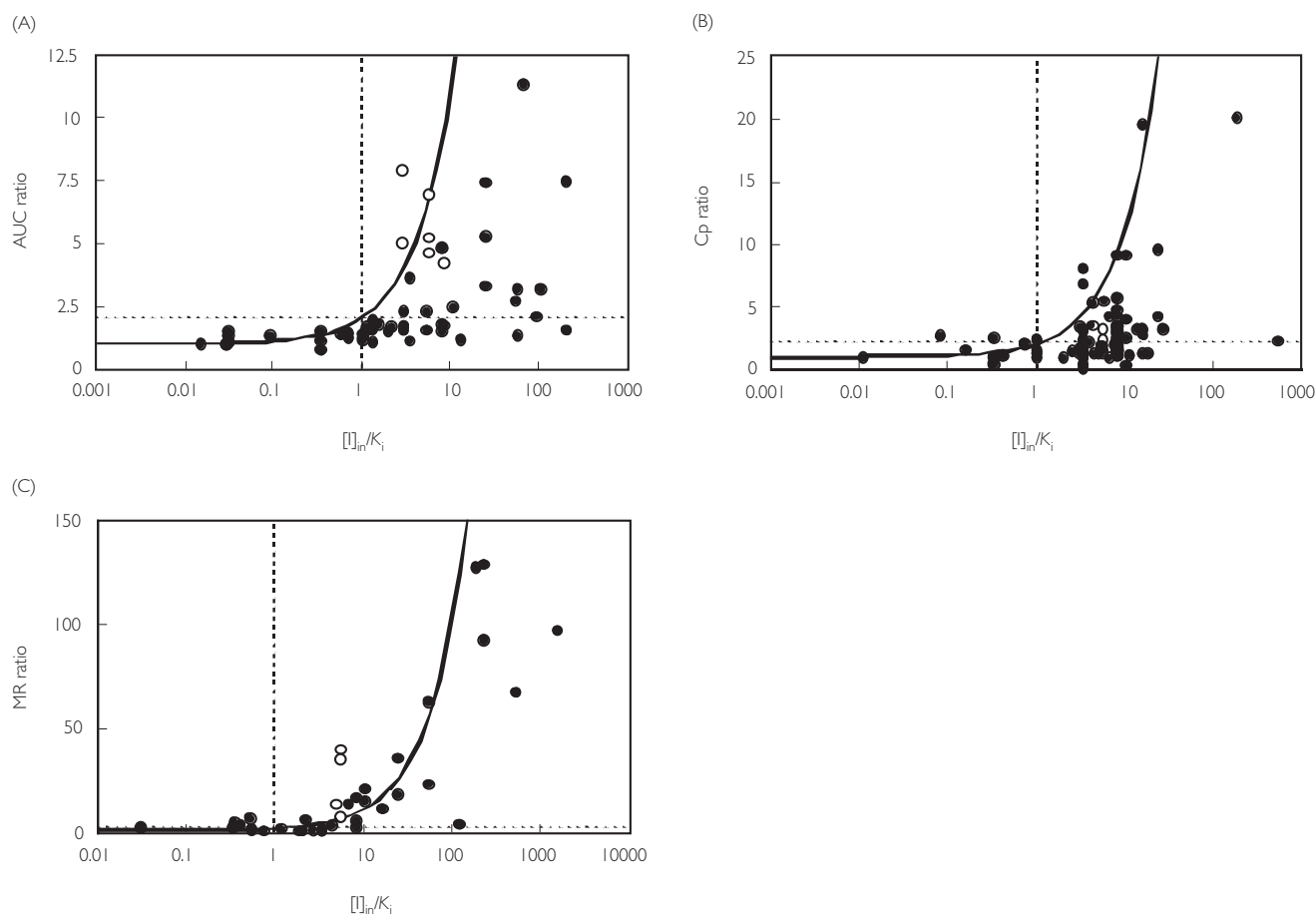


Figure 6

Comparison of the use of three *in vivo* metrics for interactions involving CYP2D6 inhibition. The ordinates show the observed ratio of AUC (A), plasma concentration at a single time point (B), or metabolic ratio (C) for the substrate in the presence and absence of inhibitor. Open symbols represent studies involving paroxetine.

ticularly itraconazole and ketoconazole. For CYP2D6 interactions, more than half of the studies involved quinidine or SSRI antidepressants (fluoxetine, fluvoxamine, etc.) as inhibitors.

Figure 6 shows the comparison of the three *in vivo* metrics (AUC ratio, Cp ratio and MR ratio) used in CYP2D6 interaction studies. All three gave similar patterns as illustrated by $[I]_{in}$.

The use of $[I]_{in}$ relies on an input term for the hepatic portal vein plasma concentration calculated from the inhibitor absorption rate constant, the fraction absorbed, the dose and the hepatic blood flow (equation 6). One possible limitation of this equation is the use of theoretical maximum values of 0.1 min^{-1} and 1 for the inhibitor k_a and F_a , respectively [8]. Therefore the effect of lowering the values of the inhibitor $k_a \times F_a$ product was simulated (see Figure 7A). Since the input term (the second term in equation 6) is larger than $[I]_{av}$ (as illustrated for quinidine), the simulated AUC ratio was

affected largely by the value of k_a (or indeed F_a). This results in a shift of the theoretical line to the right. Quinidine represents an intermediate case where the input term exceeds the systemic term by 37-fold. Within the database the mean differential observed is 73-fold (87% studies had an input term of more than 10 times the systemic term). Although it is generally not easy to obtain accurate values for k_a (or, to a lesser extent F_a), estimations of these values for each inhibitor would provide more precise predictions. In contrast the hepatic blood flow term appears far less important, since a four-fold difference in the Q_h value resulted in only a small difference in the simulated value of AUC ratio (Figure 7B). The dose of inhibitor is the major determinant of the $[I]_{in}$.

In conclusion, qualitative zoning of CYP inhibition interactions can be achieved from the $[I]/K_i$ ratio using *in vitro* kinetic parameters and the hepatic input concentration of inhibitor. True negatives can be identified and,

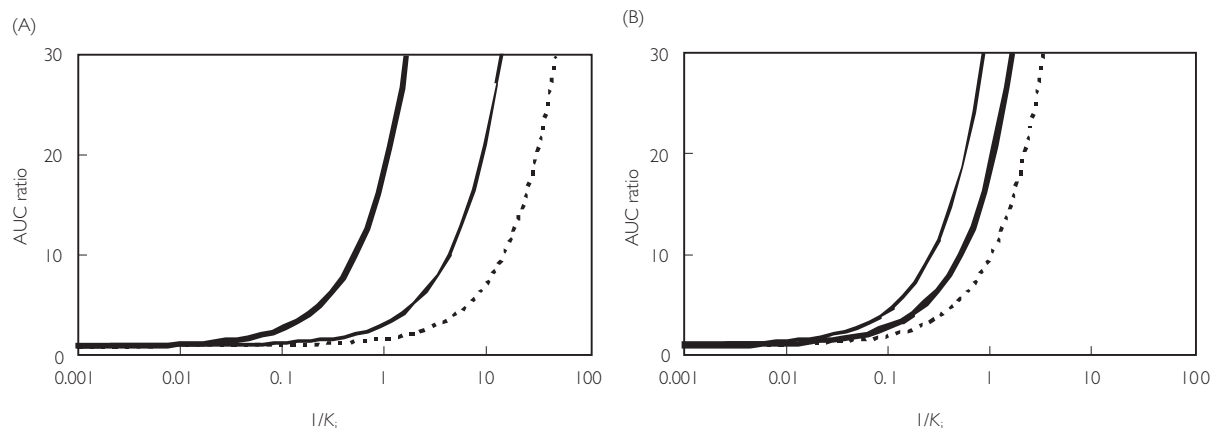


Figure 7

Simulation of the effects of changing the rate of absorption of the inhibitor (A) or liver blood flow (B). The AUC ratio was calculated as $1 + [I]_{in}/K_i$ and plotted against $1/K_i$. The following parameter values for inhibition by quinidine were used, $D = 268$ nmol, $\tau = 24$ h, & $CL/F = 412$ ml min^{-1} in equations 4 and 6

A—: $k_a F_a = 0.1$ min^{-1} , —: $k_a F_a = 0.01$ min^{-1} , ...: $k_a F_a = 0.001$ min^{-1}

B—: $Q_h = 1610$ ml min^{-1} , —: $Q_h = 805$ ml min^{-1} , ...: $Q_h = 3220$ ml min^{-1}

in contrast to the use of other values for $[I]$, false negatives are eliminated. True positives are also predicted well and, although the incidence of false positive predictions is quite high, the use of hepatic input concentration is recommended. This approach would be particularly valuable in drug screening, where false negative predictions need to be avoided. However, it is important to appreciate that the present analysis is empirical, and must be regarded as an initial step in the prediction of CYP inhibition interactions, since it ignores the interactions related to gut metabolism and specific substrate/inhibitor properties. The likely importance of these individual characteristics is evident from the number of true positives that are quantitatively over-predicted in this global analysis. Factors such as the role of hepatic uptake transporters, the existence of more than one metabolic/elimination pathway, the influence of multisite kinetics for CYP3A4/5 and the nonlinear kinetics of substrates, will require consideration in addition to the $[I]/K_i$ ratio in order to progress the prediction of CYP inhibition interactions towards a quantitative basis.

HSB was financially supported by a Bristol Myers Squibb studentship. The authors would like to thank Dr Rene H. Levy for permission to use the Drug Interaction Database of the University of Washington to obtain some of the published articles used in this data base and Dr Aleksandra Galetin for valuable discussion.

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