

# The Impact of the Hepatocyte-to-Plasma pH Gradient on the Prediction of Hepatic Clearance and Drug-Drug Interactions for CYP2D6 Substrates<sup>S</sup>

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## ABSTRACT

The proton gradient from the intracellular space to plasma creates an unbound drug gradient for weak acids and bases that could modulate apparent drug clearance and drug-drug interactions. Cytochrome P450 intrinsic clearance and inhibitor potency are routinely determined in vitro at the plasma pH of 7.4 rather than the intrahepatocyte pH of 7.0. We determined the impact of pH on in vitro enzyme kinetic parameters and inhibition potency for substrates (bufuralol, dextromethorphan), reversible inhibitors (quinidine, amiodarone, desethylamiodarone, clozapine), and mechanism-based inhibitors (paroxetine, desethylamiodarone) of the major drug metabolizing-enzyme CYP2D6. The lower intracellular pH 7.0 compared with pH 7.4 resulted in a 60 and 50% decrease in intrinsic clearance for the substrates bufuralol and dextromethorphan, respectively. Reversible inhibition constants for three of the

four inhibitors tested were unaffected by pH, whereas for the inhibitor quinidine, a 2-fold increase in the inhibition constant was observed at pH 7.0. For time-dependent inhibitors desethylamiodarone and paroxetine, changes in time-dependent inhibition parameters were different for each inhibitor. These results were incorporated into physiologically based pharmacokinetic models indicating that the changes in in vitro parameters determined at pH 7.0 offset the effect of increased unbound intracellular concentrations on apparent clearance and extent of drug-drug interactions. However, this offset between concentration and enzyme activity cannot be generalized for all substrates, inhibitors, and enzymes, as the effect of a lower pH in vitro varied significantly; therefore, it would be prudent to determine in vitro enzyme parameters at the hepatocyte-appropriate pH 7.0.

## Introduction

Physiologically based pharmacokinetic (PBPK) models, of various types, are widely used to predict absorption, in vivo drug clearance, volume of distribution, and the “shape” of plasma and tissue concentration versus time curves using in vitro and/or preclinical in vivo data (Jones and Rowland-Yeo, 2013). In these models, the dependence of factors such as intestinal fluid solubility, apparent intestinal permeability, and tissue membrane partitioning on pH has been taken into account (Rodgers et al., 2005; Chen et al., 2012). The intracellular pH is more acidic than that of plasma and interstitial fluid (Frieden, 1984; Hall and Guyton, 2015), and consequently, the unbound intracellular concentration, consisting of ionized and un-ionized species, will differ from that in plasma for drugs that exist in ionized and un-ionized forms at physiologic pH values (Shore et al., 1957). The ratio of the intracellular unbound concentration to the unbound plasma concentration,  $K_{p_{uu}}$ , can be readily calculated using the Henderson-Hasselbalch relationship under the assumptions that the permeability of the cell membrane to ionized drug is negligible and the distribution of un-ionized drug is only passive (Berezhkovskiy, 2011; Mateus et al., 2013). However, the implications of the  $pK_a$ -dependent  $K_{p_{uu}}$  for prediction of in vivo clearance from in vitro data are poorly understood.

The ionization factor ( $F_I$ ) was developed to modify the in vitro-derived drug intrinsic clearance to account for the  $pK_a$ -dependent  $K_{p_{uu}}$  in the prediction of in vivo clearance (Berezhkovskiy, 2011). The use of  $F_I$  assumes that the only effect of the lower intracellular pH, relative to plasma, is to change the rate of elimination by modulating the product of unbound intracellular concentration and intrinsic clearance (Berezhkovskiy, 2011; Berezhkovskiy et al., 2012). However, this approach assumes that the in vitro intrinsic clearance of the eliminating pathway is estimated at the appropriate intracellular pH, or that intrinsic clearance is not affected by a pH over the range of 7.0–7.4. In addition, the  $F_I$  approach assumes that the rate of elimination is a function of the sum of the ionized and un-ionized forms of the unbound drug. Similarly, when the  $pK_a$ -dependent  $K_{p_{uu}}$  is used to modify the inhibition potency of a drug, it is assumed that the inhibitory constant is appropriately estimated, and that the sum of the ionized and un-ionized forms of the unbound drug is equally inhibitory.

Determination of the Michaelis-Menten constant ( $K_m$ ), maximum rate of reaction ( $V_{max}$ ), intrinsic clearance ( $CL_{int}$ ), and inhibition constants [inhibitory constant for reversible inhibitors ( $K_i$ ), inhibitory constant for time-dependent inhibition ( $K_I$ ), and maximum rate of enzyme inactivation ( $k_{inact}$ )] for cytochrome P450 (P450)-catalyzed reactions is routinely performed at pH 7.4 despite in vitro and in vivo observations that hepatocyte intracellular pH, including the cytosol and endoplasmic reticulum, is 7.0 (Park et al., 1979; Pollock, 1984; Bonventre and

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**ABBREVIATIONS:** AUC, area under the plasma concentration-time curve; DDI, drug-drug interaction; HLM, human liver microsomes; LC-MS/MS, liquid chromatography-tandem mass spectrometry; P450, cytochrome P450; PBPK, physiologically based pharmacokinetic; PK, pharmacokinetic; QD, every day; TDI, time-dependent inhibition.

Cheung, 1985; Andersson et al., 1987; Fitz et al., 1992; Durand et al., 1993; Strazzabosco et al., 1995; Gerweck and Seetharaman, 1996; Kim et al., 1998; Vidal et al., 1998). Ionizable groups within P450 enzymes have the potential to modulate catalytic and inhibitory parameters as pH varies, and the relative affinity of the active site for ionized and un-ionized drug is unclear (Denisov et al., 2005). Berezhkovskiy et al. (2012) investigated the difference in fraction unbound and intrinsic clearance, through parent degradation, in rat liver microsomes at pH 7.0 and pH 7.4 for a set of seven proprietary compounds. Although differences were detected between the pH values, it was concluded that the results were within assay variability, and that the prediction of hepatic clearance using  $F_1$  could be used with intrinsic clearance values determined at pH 7.4. However, this interpretation was based on a small chemical space and unknown elimination pathways, and therefore, extending this conclusion to all in vitro metabolism studies is not presently justified.

The current study was undertaken to establish the impact of pH on these in vitro determinations for one of the major drug-metabolizing enzymes, CYP2D6. Enzyme kinetic parameters used for clearance ( $K_m$ ,  $V_{max}$ ,  $CL_{int}$ ) were determined by metabolite formation in human liver microsomes (HLM) using two prototypical probe substrates, bufuralol and dextromethorphan. The inhibitory potential for reversible and time-dependent inhibitors ( $K_i$ ,  $K_I$ , and  $k_{inact}$ ) toward these substrates was also investigated. The in vitro findings were incorporated into PBPK models to predict exposure and drug-drug interactions (DDIs) in an effort to understand the significance of pH dependence of enzymes in the in vitro system in combination with the  $F_1$  correction.

## Materials and Methods

**Materials.** Chemical reagents were obtained commercially: dextromethorphan, NADPH, quinidine, amiodarone, clozapine, paroxetine, and metoclopramide (Sigma-Aldrich, St. Louis, MO); bufuralol, 1'-hydroxybufuralol, and desethylamiodarone (Toronto Research Chemicals Inc., Toronto, Canada); dextrorphan (Cerilliant, Round Rock, TX); and sodium phosphate monobasic, sodium phosphate dibasic, phosphoric acid, and sodium hydroxide (Fisher Scientific, Pittsburgh, PA). A single lot of HLM pooled from 150 individuals (UltraPoolTM, lot #38290, equal proportion male and female; Corning, Tewksbury, MA) was used for all experiments.

**In Vitro Incubations.** Reactions were conducted in a shaking water bath at 37°C. Incubations were carried out in 100 mM sodium phosphate ( $NaPO_4$ ) buffers adjusted to the pH of interest (6.0, 6.5, 7.0, 7.2, 7.4, 8.0, 8.5, 9.0) with phosphoric acid or sodium hydroxide as necessary. Linear conditions for metabolite formation with respect to time and protein at pH 6.0, pH 7.4, and pH 9.0 were determined for bufuralol and dextromethorphan, and are reflected in the final conditions described.

Substrates, buffer, and microsomes were premixed, and incubations were initiated by addition of the NADPH cofactor. In the case of reversible inhibition studies, inhibitor and cofactor were added at the initiation of the reaction simultaneously. Time-dependent inhibition studies were performed using the dilution method (Mohutsky and Hall, 2014). All incubations were carried out in 96-well plates in triplicate. Product formation (1'-hydroxybufuralol dextrorphan, 3-hydroxyquinidine) assays were performed on three separate occasions. Methanol (MeOH) was used as a solvent for all experiments at a final percent solvent percentage of less than 2% (v/v).

**1'-Hydroxybufuralol Formation.** Formation of 1'-hydroxybufuralol was determined using bufuralol (0.78–100  $\mu$ M) and HLM (0.125 mg/ml) in 100 mM  $NaPO_4$  buffer over a range of pH values between 6.0 and 9.0 (Crespi et al., 1998). The mixture was preincubated for 3 minutes at 37°C prior to reaction initiation through the addition of NADPH (1 mM, prepared in corresponding pH buffer), for a total volume of 150  $\mu$ l. The reaction was allowed to proceed for 20 minutes at 37°C, at which time a 50  $\mu$ l aliquot was added to 100  $\mu$ l of 90:10 (v/v) MeOH:H<sub>2</sub>O containing internal standard to stop the reaction. Plates were sealed with Easy Pierce 20  $\mu$ m foil (Thermo Fisher Scientific, Waltham, MA), vortexed for 20 seconds, centrifuged (3500g for 10 minutes), and analyzed by liquid

chromatography–tandem mass spectrometry (LC-MS/MS) (Supplemental Materials, Table S1). Reactions were performed in triplicate wells on three separate occasions. Metabolite formation was determined using a standard curve of 1'-hydroxybufuralol generated under identical conditions (0.5–1000 nM).

**Dextrorphan Formation.** Formation of dextrorphan from dextromethorphan (Schmider et al., 1997) was determined using the same procedure as described earlier for 1'-hydroxybufuralol with the following changes: dextromethorphan (0.39–50  $\mu$ M) and HLM (0.1 mg/ml) in 100 mM  $NaPO_4$  buffer at pH 6.0–9.0 were used; after preincubation and initiation, reactions proceed for 10 minutes at 37°C before being stopped. Metabolite formation was determined using a standard curve of dextrorphan generated under identical conditions (0.5–500 nM).

**3-Hydroxyquinidine Formation.** Formation of 3-hydroxyquinidine from quinidine was measured, as it is the major metabolite of quinidine metabolism and is only formed via CYP3A4 in vitro (Nielsen et al., 1999). Formation was determined at pH 7.0 and pH 7.4 as described for 1'-hydroxybufuralol formation, with the following changes: quinidine (1.95–250  $\mu$ M) and HLM (0.1 mg/ml) in 100 mM  $NaPO_4$  buffer at pH 7.0 or 7.4 were incubated at 37°C for 20 minutes after reaction initiation. Reaction aliquots (30  $\mu$ l) were added to 150  $\mu$ l of 90:10 (v/v) MeOH:H<sub>2</sub>O containing internal standard to stop the reaction. Metabolite formation was determined using a standard curve of 3-hydroxyquinidine generated under identical conditions (0.98–2000 nM).

**Reversible Inhibition ( $K_i$  Determination).** The equilibrium inhibition constant ( $K_i$ ) was determined at pH 7.0 and pH 7.4 for four reversible inhibitors (quinidine, amiodarone, desethylamiodarone, clozapine). Bufuralol or dextromethorphan (3.125, 6.25, 12.5, and 50  $\mu$ M) and HLM (0.125 and 0.1 mg/ml, respectively) in 100 mM  $NaPO_4$  buffer at pH 7.0 or 7.4 were prepared and kept on ice. After preincubation (3 minutes at 37°C), inhibitor [quinidine (0–0.2  $\mu$ M), amiodarone (0–200  $\mu$ M), desethylamiodarone (0–100  $\mu$ M), or clozapine (0–100  $\mu$ M)] was added with NADPH (1 mM prepared in corresponding buffer) (Fowler and Zhang, 2008). Reactions proceeded for 20 minutes for bufuralol and 10 minutes for dextromethorphan. Reaction (50  $\mu$ l) was stopped through the addition of 100  $\mu$ l of 90:10 (v/v) MeOH:H<sub>2</sub>O containing internal standard. Plates were sealed with Easy Pierce 20  $\mu$ m foil (Thermo Fisher Scientific), vortexed for 20 seconds, centrifuged (3500g for 10 minutes), and analyzed by LC-MS/MS (Supplemental Materials, Table S1).

**Time-Dependent Inhibition ( $K_I$  and  $k_{inact}$  Determination).** The maximum rate of enzyme inhibition ( $k_{inact}$ ) and inhibitor concentration at which half the maximal rate of inactivation occurs ( $K_I$ ) were determined for CYP2D6 using the dilution method (Mohutsky and Hall, 2014). In brief, perpetrator compounds [desethylamiodarone (0–50  $\mu$ M), paroxetine (0–5  $\mu$ M), metoclopramide (0–200  $\mu$ M)] were incubated at 37°C with pooled HLM (0.5 mg/ml) and NADPH (1 mM) in 100 mM  $NaPO_4$  buffer at pH 7.0 or 7.4 for 0, 2.5, 5, 15, and 30 minutes. After preincubation, a 10-fold dilution into a secondary incubation containing 50  $\mu$ M bufuralol or 50  $\mu$ M dextromethorphan with NADPH (1 mM) in corresponding buffer at pH 7.0 or 7.4 was performed. The secondary incubation was allowed to proceed for 10 minutes at 37°C, then an aliquot (50  $\mu$ l) was added to 100  $\mu$ l of 90:10 (v/v) MeOH:H<sub>2</sub>O containing internal standard to stop the reaction. Plates were sealed with Easy Pierce 20  $\mu$ m foil (Thermo Fisher Scientific), vortexed for 20 seconds, centrifuged (3500g for 10 minutes), and analyzed by LC-MS/MS (Supplemental Materials, Table S1).

**Fraction Unbound in Microsomes.** The fraction unbound in microsomes ( $f_{u,mic}$ ) was determined using a 96-well Micro-Equilibrium Dialysis Device HTD 96 (HTDialysis LLC, Gales Ferry, CT) per the manufacturer's instructions at HLM protein concentrations of 0.1 mg/ml for dextromethorphan, 0.5 mg/ml for metoclopramide and paroxetine, and 0.125 mg/ml for all other compounds. HLM were prepared in 100 mM  $NaPO_4$  buffer at pH 7.0 or 7.4 containing 1  $\mu$ M test drug and 100  $\mu$ l added to one side of the dialysis membrane. The corresponding buffer (pH 7.0 or pH 7.4; 100  $\mu$ l) was placed on the opposite side of the dialysis membrane. Samples ( $n = 6$  replicates per day, repeated on three separate runs) were incubated in a shaking incubator (400 rpm) at 37°C for 4 hours using regenerated cellulose dialysis membranes (molecular weight cutoff 6–8 K). After incubation, aliquots from microsomes and buffer sides were taken and quenched into 90:10 (v/v) MeOH:H<sub>2</sub>O containing internal standards. Plates were sealed with Easy Pierce 20  $\mu$ m foil (Thermo Fisher Scientific), vortexed for 20 seconds, centrifuged (3500g for 10 minutes), and analyzed by LC-MS/MS (Supplemental Materials, Table S1).

**PBPK Simulations.** The population-based PBPK simulator Simcyp (V14; Certara, Princeton, NJ) was used to simulate exposure and DDI. Three separate

simulation scenarios were performed based on 1) baseline Simcyp compound file (Sim<sub>pH 7.4</sub>), 2) baseline Simcyp compound file with the incorporation of  $F_i$  correction (Sim<sub>pH 7.4, F<sub>i</sub></sub>), and 3) baseline Simcyp compound file corrected as described later using in vitro results from pH 7.0 and 7.4 in the current study to correct baseline compound file (Sim<sub>pH 7.0, F<sub>i</sub></sub>).

The ionization factor was calculated as described by Berezhkovskiy (2011) as the ratio of ionized drug fractions in plasma to intracellular hepatocyte space by eq. 1:

$$F_i = \frac{1 - f_p^i}{1 - f_h^i} \quad (1)$$

where  $f_p^i$  and  $f_h^i$  are the fraction of charged (ionized) drug in the plasma (p) and intracellular hepatocyte space (h), respectively. The fraction of ionized drug was determined using the Henderson-Hasselbalch equation for monoprotic bases (eq. 2)

$$f_{\text{base}}^i = \frac{1}{1 + 10^{\text{pH} - \text{pK}_a}} \quad (2)$$

and the diprotic bases (eq. 3) quinidine and metoclopramide

$$f_{\text{base}}^i = \frac{1}{1 + \left[ 10^{\text{pK}_{a1} - \text{pH}} + 10^{\text{pK}_{a2} - \text{pH}} + 10^{\text{pK}_{a1} + \text{pK}_{a2} - 2\text{pH}} \right]^{-1}} \quad (3)$$

The pH values were 7.4 for plasma and 7.0 for the intracellular hepatocyte space.

The pH-specific in vitro  $CL_{\text{int}}$  ( $CL_{\text{int in vitro pH}}$ ) was calculated as shown in eq. 4 using  $K_m$ ,  $f_{\text{mic}}$ , and  $V_{\text{max}}$  values determined at pH 7.0 or 7.4:

$$CL_{\text{int in vitro pH}} = \frac{V_{\text{max in vitro pH}}}{K_m \text{ in vitro pH} \times f_{\text{mic pH}}} \quad (4)$$

To account for the kinetic parameter changes ( $K_m$ ,  $V_{\text{max}}$ ) and  $f_{\text{mic}}$  at the specific pH, assuming that all bottom-up data in the Simcyp files were generated at pH 7.4, eq. 5 describes the calculations used for the intrinsic clearances of the victim drugs, dextromethorphan and bufuralol. For dextromethorphan, the CYP2D6 HLM  $CL_{\text{int}}$  ( $CL_{\text{int, Simcyp}}$ ) value provided in the elimination characteristics of the baseline Simcyp compound file and our own in vitro data were used to calculate an adjusted  $CL_{\text{int}}$  for the pH 7.0 simulations:

$$\text{Simulation } CL_{\text{int pH 7.0}} = \left( \frac{CL_{\text{int in vitro pH 7.0}}}{CL_{\text{int in vitro pH 7.4}}} \right) \times (CL_{\text{int Simcyp}}) \quad (5)$$

In the case of bufuralol, the baseline Simcyp bufuralol file was used as a starting point. Enzyme-specific pharmacokinetic (PK) parameters ( $V_{\text{max}}$  and  $K_m$ ), determined in a recombinant system, for the conversion of bufuralol to either the metabolite 1'-hydroxybufuralol or 6'-hydroxybufuralol are provided in the elimination characteristics of the compound file. These PK parameters were used to calculate a  $CL_{\text{int}}$  ( $V_{\text{max}}/K_m$ ) for each enzyme isoform and metabolite pathway combination (e.g., a separate  $CL_{\text{int}}$  for CYP2D6 conversion of bufuralol to 1'-hydroxybufuralol and 6'-hydroxybufuralol was determined). Since the contribution of the 6'-hydroxybufuralol metabolic pathway toward the total clearance is minor (~3%), the calculated  $CL_{\text{int}}$  values for the 1'-hydroxybufuralol and

6'-hydroxybufuralol for each isoform were combined to provide a total  $CL_{\text{int}}$  ( $CL_{\text{int total}}$ ) for each of the individual recombinant enzyme isoforms. Each enzyme isoform  $CL_{\text{int total}}$  was converted to an HLM  $CL_{\text{int total}}$  by using the relative abundance of the enzyme isoform per milligram of protein from the healthy volunteers population. This provided a fraction metabolized ( $f_m$ ) for CYP2D6 of 0.617, which is much lower than the literature-calculated  $f_m$  of 0.83 based on extensive metabolizer/poor metabolizer ratios (Dayer et al., 1985, 1986). To compensate, CYP2D6  $CL_{\text{int total}}$  was increased to achieve an  $f_m$  of 0.83, whereas CYP2C19  $CL_{\text{int total}}$  was decreased to maintain the same total clearance of all isoforms combined. This new value for CYP2D6  $CL_{\text{int total}}$  was used for the simulations, and eq. 5 was used to calculate changes with regard to pH 7.0 (Supplemental Material, Table S2 and Fig. S1).

Simcyp baseline files for clozapine and paroxetine were used, and only the inhibition parameters ( $K_i$ ,  $K_i$ ,  $k_{\text{inact}}$ , and  $f_{\text{mic}}$ ) determined in vitro at the different pH values were altered in these files. In the case of quinidine, the baseline Simcyp compound file was used and the changes in inhibition parameters made. Additionally, the elimination through the major pathway (formation of 3-hydroxyquinidine by CYP3A4) was altered, based on our in vitro findings at pH 7.0 and pH 7.4, in the same manner as described earlier for dextromethorphan.

Compound files for amiodarone and desethylamiodarone were built as described by Chen et al. (2015) with the following exceptions: amiodarone and desethylamiodarone were categorized as monoprotic bases with  $\text{pK}_a$  values of 8.47 and 9.4, respectively, and the fraction available from dosage form ( $f_a$ ) was increased from 0.6 to 0.8, as it provided a better fit to the clinical data from Andreasen et al. (1981) and Haffajee et al. (1983).

The ionization correction proposed by Berezhkovskiy (2011) was calculated based on the physicochemical properties of the compounds (acid/base;  $\text{pK}_a$ ) and the pH of the intracellular (7.0) and extracellular (7.4) compartments (Table 1). This  $F_i$  value was then incorporated into the elimination section of the compound file as an *active uptake into hepatocytes*. This value alters the intracellular concentration of the compound by changing the  $K_{\text{pu}}$  to compensate for the difference in pH between the extracellular and intracellular compartments.

Simulation dosing schedules were chosen to mimic clinical dosage and/or clinical DDI studies, if available; however, for bufuralol, a literature search did not identify any DDI studies, and therefore, the dextromethorphan DDI study design information was used for bufuralol. All simulations were performed using the Simcyp healthy volunteer population using a 10-by-10 subject trial setup (total population size 100; equal portion male/female, age range 20–50 year) in the fasted state.

Inhibition by quinidine followed the study design from Abdul Manap et al. (1999), whereby a single dose of quinidine (50 mg) was given 1 hour prior to administration of bufuralol (60 mg) or dextromethorphan (30 mg) and followed for 96 hours. For clozapine, a single dose (12.5, 400, or 900 mg to represent possible dosing range) was given simultaneously with bufuralol (60 mg) or dextromethorphan (30 mg) and simulated for a 24-hour period (Perry et al., 1991). Interaction with amiodarone followed the study by Funck-Brentano et al. (1991), where a 1000 mg loading dose was given every day (QD) for 10 days followed by a 400 mg maintenance dose QD for 10 days. On day 20, a single dose of bufuralol (60 mg) or dextromethorphan (40 mg) was given, and the simulation proceeded for 24 hours after victim drug dosing. Paroxetine interaction followed the study format of Liston et al. (2002), where paroxetine (20 mg) was given QD for 10 days

TABLE 1  
Physicochemical properties of the CYP2D6 substrates and inhibitors

Compound	$\text{pK}_a$ /p $\text{K}_a2$	Ionization Factor	Designation
Bufuralol	8.97 <sup>a</sup>	2.472	Substrate
Dextromethorphan	8.3 <sup>a</sup>	2.343	Substrate
Quinidine	4.2/8.8 <sup>a</sup>	2.456	Reversible inhibitor
Amiodarone	8.47 <sup>b</sup>	2.393	Reversible inhibitor
Desethylamiodarone	9.4 <sup>b</sup>	2.497	Reversible inhibitor; time-dependent inhibitor
Clozapine	7.75 <sup>a</sup>	2.045	Reversible inhibitor
Paroxetine	9.66 <sup>a</sup>	2.504	Reversible inhibitor; time-dependent inhibitor
Metoclopramide	0.6/9.3 <sup>c</sup>	2.493	Reversible inhibitor; time-dependent inhibitor

<sup>a</sup>Source: Simcyp.

<sup>b</sup>Source: The Human Metabolome Database (<http://www.hmdb.ca>).

<sup>c</sup>Foye et al. (2013).

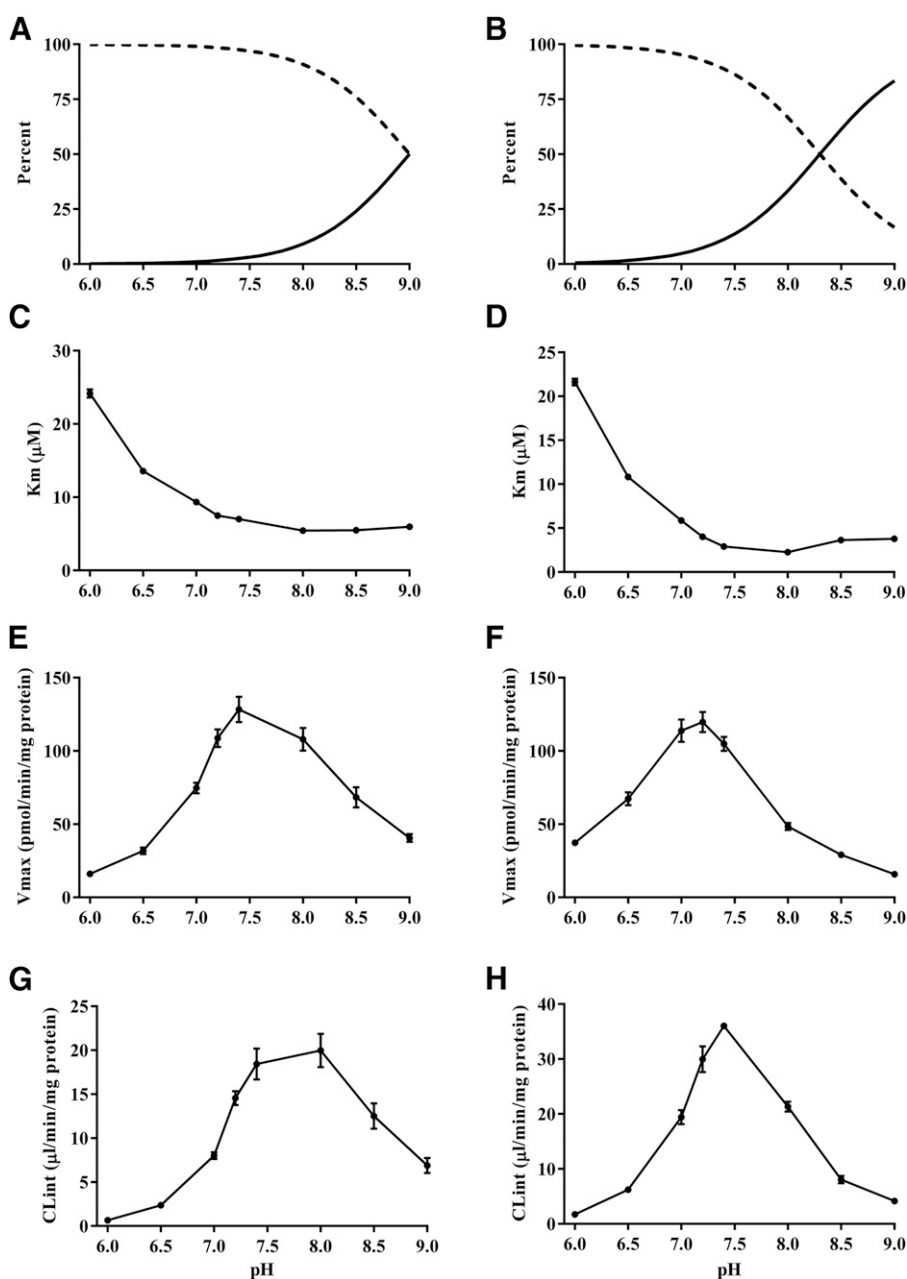
followed by dextromethorphan (30 mg) or bufuralol (60 mg) on day 10 and followed for 24 hours.

**Statistical Analysis.** The HLM enzyme kinetic parameters ( $V_{max}$ ,  $K_m$ , and  $CL_{int}$ ) for bufuralol, dextromethorphan, and quinidine, as well as  $f_{u,mic}$  values for all drugs, represent the mean of triplicate runs. Mean values of the replicates for pH 7.0 and 7.4 were analyzed for statistical differences with an unpaired, two-tailed  $t$  test using GraphPad Prism version 6.05 (GraphPad Software, San Diego, CA) using  $\alpha = 0.05$ . The ratio of the values obtained at pH 7.0 to values obtained at pH 7.4 is represented in the text of the results section as  $Ratio_{7.0:7.4}$ .

## Results

**Impact of pH on CYP2D6 Enzyme Kinetics.** Enzyme kinetic parameters  $K_m$ ,  $V_{max}$ , and  $CL_{int}$  varied with incubation pH, but the changes did not correlate with an increased abundance of ionized or un-ionized bufuralol and dextromethorphan (Fig. 1). The greatest

affinity (lowest  $K_m$ ) was observed at pH 8.0 for both substrates (Fig. 1, C and D), whereas  $V_{max}$  peaked at pH 7.4 and pH 7.2 for bufuralol and dextromethorphan, respectively (Fig. 1, E and F). This resulted in  $CL_{int}$  being highest at pH 8.0 for bufuralol and pH 7.4 for dextromethorphan (Fig. 1, G and H). Comparing pH values 7.0 and 7.4, represented as the ratio of the values obtained at pH 7.0 to values obtained at pH 7.4 ( $Ratio_{7.0:7.4}$ ),  $K_m$  was increased (lower affinity) at pH 7.0 compared with pH 7.4, with a  $Ratio_{7.0:7.4}$  of 1.3 and 2 for bufuralol and dextromethorphan, respectively. Conversely, the  $V_{max}$  was decreased at pH 7.0 compared with pH 7.4 for bufuralol ( $Ratio_{7.0:7.4} = 0.6$ ) but remained relatively unchanged for dextromethorphan ( $Ratio_{7.0:7.4} = 1.1$ ). The calculated  $CL_{int}$  was lower at pH 7.0 compared with pH 7.4 for both substrates, with a  $Ratio_{7.0:7.4}$  of 0.4 and 0.5 for bufuralol and dextromethorphan, respectively. This decrease in  $CL_{int}$  was statistically significant between the two pH values for both bufuralol ( $P = 0.004$ ) and dextromethorphan ( $P < 0.001$ ).



**Fig. 1.** Effect of pH on CYP2D6 enzyme kinetic parameters. (A) Calculated percentage of bufuralol (base,  $pK_a = 9.0$ ) ionized and un-ionized species. (B) Calculated percentage of dextromethorphan (base,  $pK_a = 8.3$ ) ionized and un-ionized species. (C)  $K_m$  of 1'-hydroxybufuralol formation from bufuralol. (D)  $K_m$  of dextrophan formation from dextromethorphan. (E)  $V_{max}$  of 1'-hydroxybufuralol formation from bufuralol. (F)  $V_{max}$  of dextrophan formation from dextromethorphan. (G)  $CL_{int}$  of 1'-hydroxybufuralol formation from bufuralol. (H)  $CL_{int}$  of dextrophan formation from dextromethorphan. Dashed line represents the percentage ionized of the substrate; solid line represents the percentage un-ionized of the substrate. Symbols represent the mean of triplicate determinations, with vertical bars representing S.E.M.

TABLE 2

Reversible CYP2D6 inhibition kinetic parameters at pH 7.0 and pH 7.4.

Ratio between pH 7.0 and pH 7.4 results are given.

Substrate/Inhibitor	$f_{u,mic}$ pH 7	$K_{i,u}$ pH 7	$f_{u,mic}$ pH 7.4	$K_{i,u}$ pH 7.4	$K_{i,u}$ Ratio
	$\mu M$		$\mu M$		
<b>Bufuralol</b>					
Quinidine	0.934	0.090	0.939	0.041	2.21
Amiodarone	0.0020	0.096	0.0016	0.112	0.86
Desethylamiodarone	0.0046	0.078	0.0043	0.087	0.89
Clozapine	0.843	28.6	0.830	28.4	1.01
Paroxetine	0.493 <sup>a</sup>	0.46	0.410 <sup>a</sup>	0.33	1.39
<b>Dextromethorphan</b>					
Quinidine	0.946 <sup>a</sup>	0.051	0.951 <sup>a</sup>	0.026	1.95
Amiodarone	0.0026 <sup>a</sup>	0.083	0.0020 <sup>a</sup>	0.134	0.62
Desethylamiodarone	0.0057 <sup>a</sup>	0.043	0.0054 <sup>a</sup>	0.034	1.27
Clozapine	0.870 <sup>a</sup>	14.9	0.859 <sup>a</sup>	15.6	0.96
Paroxetine	0.549 <sup>a</sup>	0.32	0.465 <sup>a</sup>	0.28	1.14

<sup>a</sup> $f_{u,mic}$  for inhibitor under in vitro assay conditions calculated from Austin et al. (2002).

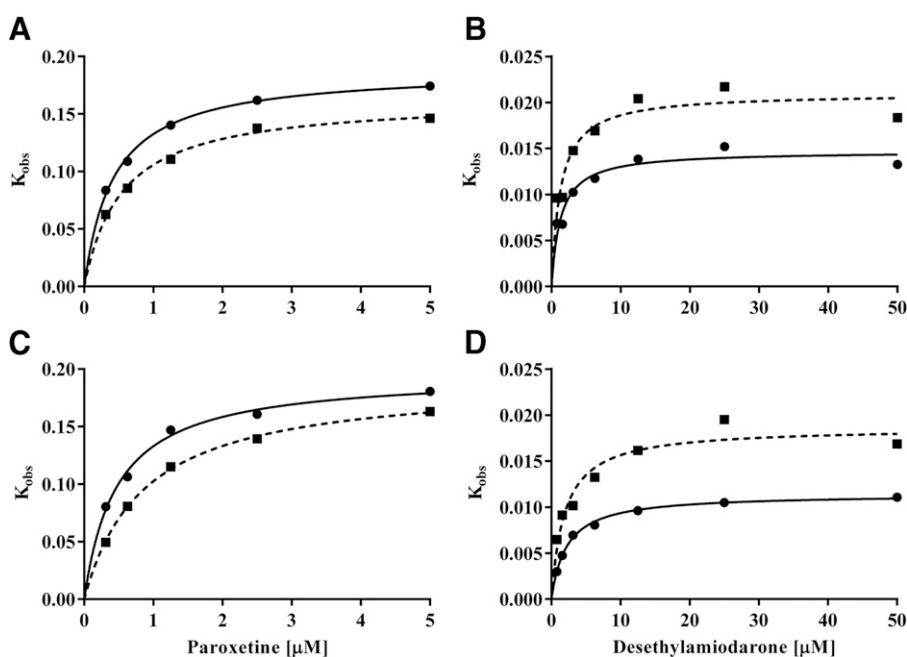
Although  $f_{u,mic}$  differed between pH values, no statistical significance was reached in the fraction unbound between pH 7.0 and pH 7.4 for bufuralol, dextromethorphan, clozapine, quinidine, desethylamiodarone, and metoclopramide. A statistically significantly higher  $f_{u,mic}$  was determined for pH 7.0 compared with pH 7.4 for amiodarone (Ratio<sub>7.0:7.4</sub> = 1.3;  $P = 0.001$ ) and paroxetine (Ratio<sub>7.0:7.4</sub> = 1.3;  $P = 0.003$ ). When pH 7.0 and pH 7.4 results were corrected for fraction unbound in microsomes, the previously described ratios were unaffected, with the exception of the Ratio<sub>7.0:7.4</sub> for the  $K_m$  for bufuralol, which increased from 1.3 to 1.4.

**Impact of pH on Quinidine Metabolism.** The enzyme kinetic parameters for quinidine metabolism were significantly different ( $P < 0.001$  for  $K_m$  and  $V_{max}$ , respectively) between pH 7.0 ( $K_m = 398.8 \mu M$ ;  $V_{max} = 671.8$  pmol/min/mg protein) and pH 7.4 ( $K_m = 72.3 \mu M$ ;  $V_{max} = 1094.0$  pmol/min/mg protein). This resulted in a statistically significant decrease ( $P < 0.001$ ) in the  $CL_{int}$  at pH 7.0 (1.7  $\mu l$ /min/mg protein) compared with  $CL_{int}$  at pH 7.4 (15.3  $\mu l$ /min/mg protein) with a Ratio<sub>7.0:7.4</sub> of 0.1.

**Impact of pH on CYP2D6 Inhibition.** Reversible inhibition, described by unbound corrected  $K_i$  ( $K_{i,u} = K_i \cdot f_{u,mic}$ ), did not appear to be significantly affected by the change in pH for the victim compound bufuralol with perpetrators amiodarone, desethylamiodarone, and clozapine, or dextromethorphan with clozapine (Table 2). A slight increase in inhibitor potency at pH 7.0 was observed for the perpetrator/victim combination of amiodarone/dextromethorphan (Ratio<sub>7.0:7.4</sub> = 0.6), whereas a slight decrease in inhibitor potency at pH 7.0 was determined for desethylamiodarone/dextromethorphan (Ratio<sub>7.0:7.4</sub> = 1.3). However, the  $K_{i,u}$  for quinidine was approximately 2-fold higher (weaker inhibition) at pH 7.0 compared with pH 7.4 for both bufuralol (Ratio<sub>7.0:7.4</sub> = 2.2) and dextromethorphan (Ratio<sub>7.0:7.4</sub> = 2.0).

Despite reports of metoclopramide as a time-dependent inhibitor (TDI) (Desta et al., 2002; Berry and Zhao, 2008), in our hands, no evidence of time-dependent inhibition of CYP2D6 was observed. The unbound  $K_i$  ( $K_{i,u} = K_i \cdot f_{u,mic}$ ) of paroxetine was higher (decreased potency) at pH 7.0 compared with pH 7.4 (Ratio<sub>7.0:7.4</sub> of 1.7 and 2.4 for bufuralol and dextromethorphan, respectively, as the victim drug), whereas  $k_{inact}$  was unaffected for bufuralol (Ratio<sub>7.0:7.4</sub> = 0.9) and dextromethorphan (Ratio<sub>7.0:7.4</sub> = 1.0) as the victim drug (Fig. 2; Table 3). This trend was reversed with the TDI perpetrator desethylamiodarone, where  $K_{i,u}$  was unaffected (Ratio<sub>7.0:7.4</sub> of 1.1 and 0.9 for bufuralol and dextromethorphan, respectively), but  $k_{inact}$  was higher (greater rate of enzyme inactivation) at pH 7.0 for both bufuralol (Ratio<sub>7.0:7.4</sub> = 1.4) and dextromethorphan (Ratio<sub>7.0:7.4</sub> = 1.7) (Fig. 2; Table 3). No reversible inhibition at time zero for the secondary incubation was observed for desethylamiodarone or metoclopramide TDI experiments. However, some reversible inhibition was observed for the two highest concentrations of paroxetine (5 and 2.5  $\mu M$ , with activity inhibited by 45 and 30%, respectively, compared with controls). This was expected due to final concentrations of paroxetine in the secondary incubation being close to  $K_i$  after dilution.

**PBPK Simulations Using In Vitro Parameters.** The simulations including the  $F_I$  correction alone for bufuralol and dextromethorphan predicted a 2-fold lower exposure of drug given by the area under the concentration-time profile curve (AUC). A 0.4- and 0.5-fold difference between Sim<sub>pH 7.4, FI</sub> and Sim<sub>pH 7.4</sub>, respectively, was observed when the



**Fig. 2.** Pseudo first-order inhibition rate constants for loss of CYP2D6 activity versus inhibitor concentration performed at pH 7.0 (dashed line with square symbols) and pH 7.4 (solid line with circle symbols). (A) Paroxetine inhibition of 1'-hydroxybufuralol formation from bufuralol. (B) Desethylamiodarone inhibition of 1'-hydroxybufuralol formation from bufuralol. (C) Paroxetine inhibition of dextromethorphan formation from dextromethorphan. (D) Desethylamiodarone inhibition of dextromethorphan formation from dextromethorphan. Symbols represent mean of triplicates.

TABLE 3  
Time-dependent CYP2D6 inhibition kinetic parameters at pH 7.0 and pH 7.4

Results for the ratio between pH 7.0 and pH 7.4 are given.

Substrate/Inhibitor	$f_{u,mic}$ pH 7	$K_{L,u}$ pH 7	$k_{inact}$ pH 7	$f_{u,mic}$ pH 7.4	$K_{L,u}$ pH 7.4	$k_{inact}$ pH 7.4	$K_{L,u}$	$K_{inact}$
		<i>nM</i>	<i>min<sup>-1</sup></i>		<i>nM</i>	<i>min<sup>-1</sup></i>	<i>Ratio</i>	<i>Ratio</i>
Bufuralol								
Paroxetine	0.196	106.43	0.163	0.148	62.60	0.189	1.70	0.86
Desethylamiodarone	0.0011 <sup>a</sup>	1.47	0.021	0.0011 <sup>a</sup>	1.41	0.015	1.05	1.40
Dextromethorphan								
Paroxetine	0.196	167.38	0.190	0.148	70.30	0.196	2.38	0.97
Desethylamiodarone	0.0011 <sup>a</sup>	2.19	0.019	0.0011 <sup>a</sup>	2.38	0.011	0.92	1.73

<sup>a</sup> $f_{u,mic}$  for inhibitor under in vitro assay conditions prior to dilution (0.5 mg/mL) was calculated from Austin et al. (2002).

ionization correction was used, as a result of an increase in the rate of elimination due to a greater intracellular unbound concentration available in the hepatocyte (Fig. 3; Table 4). When pH 7.0 in vitro data were combined with the ionization correction, the calculated exposure for  $Sim_{pH\ 7.0, F_1}$  was within 20% of the  $Sim_{pH\ 7.4}$  with an AUC fold difference of 0.8 for both bufuralol and dextromethorphan (Fig. 3; Table 4). The increase in intracellular unbound concentration due to the ionization correction was offset by the decrease in  $CL_{int}$  determined at pH 7.0.

The AUC ratios (AUC in the presence of inhibitor to absence of inhibitor) for the victim-perpetrator combinations are listed in Table 5. No significant change in AUC ratio was observed for clozapine, regardless of dosage (single dose of 12.5, 400, or 900 mg). Under the  $Sim_{pH\ 7.4, F_1}$  conditions, interaction studies showed a slight increase in AUC ratio for both bufuralol and dextromethorphan compared with  $Sim_{pH\ 7.4}$  (Ratio<sub>7.0:7.4</sub> ranging from 1.2 to 1.5) for the amiodarone (including desethylamiodarone metabolite), quinidine, and paroxetine perpetrators. However, when  $Sim_{pH\ 7.0, F_1}$  conditions were used, the AUC ratio returned to the  $Sim_{pH\ 7.4}$  observations for all perpetrators, with the exception of quinidine, which maintained the higher AUC ratio with dextromethorphan, and paroxetine, where a lower AUC ratio was determined for both bufuralol and dextromethorphan.

The lack of clinically observed DDI observations makes it difficult to assess the predictability of the models. The only clinical observations reported for dextromethorphan dosed alone as the victim are with quinidine as the perpetrator. Two studies which followed the same dosing design described in *Materials and Methods* (single 30 mg dose of dextromethorphan with single 50 mg dose of quinidine) observed a dextromethorphan AUC ratio of 16.2 (Abdul Manap et al., 1999) and 43 for extensive metabolizers (Capon et al., 1996). These interactions are significantly higher than the current model predictions, which range from 3.3 to 4.5 (Table 5). Additional clinical studies of various designs were modeled and resulted in an underprediction of the quinidine

interaction (Supplemental Material, Table S3). The underprediction of quinidine suggests that other factors may influence the level of inhibition observed in vivo and highlights the importance of understanding all pharmacokinetic attributes of the victim and perpetrator compounds.

## Discussion

Intracellular pH is consistently reported in the range of 6.8–7.2, depending on the cell and tissue type, with hepatocytes having an intracellular pH 7.0 in humans and animal species (Waddell and Bates, 1969; Park et al., 1979; Roos and Boron, 1981; Pollock, 1984; Bonventre and Cheung, 1985; Andersson et al., 1987; Fitz et al., 1992; Durand et al., 1993; Strazzabosco et al., 1995; Gerweck and Seetharaman, 1996; Vidal et al., 1998; Schmitt, 2008; Sanchez and Lopez-Zapata, 2015). Since plasma pH is 7.4, this results in a pH differential between plasma and the intracellular environment that theoretically would lead to a  $pK_a$ -dependent change in the ratio of intracellular unbound concentration to the unbound plasma concentration, or  $K_{p,u}$ . In vitro evidence has been presented demonstrating the differential accumulation of diverse acid, base, and neutral compounds in support of the pH partitioning theory (Shore et al., 1957; Mateus et al., 2013). Since the liver is the major route of drug elimination, and given the phenomenon of  $K_{p,u}$  changing based on the physicochemical properties of the drug and the pH of plasma and the hepatocyte, hepatic models for clearance can be modified to account for changes in intracellular concentration through an  $F_1$  correction (Berezhkovskiy, 2011).

Use of the  $F_1$  correction assumes that metabolism of a drug is driven by the sum of the ionized and un-ionized forms, and that the rate of reaction is not driven solely by a single species. This is not the case for the monoamine oxidase B enzyme that has been shown to predominantly metabolize the protonated (ionized) form of  $\beta$ -phenylethylamine (Jones et al., 2007). However, in our current study, a wide range of pH values

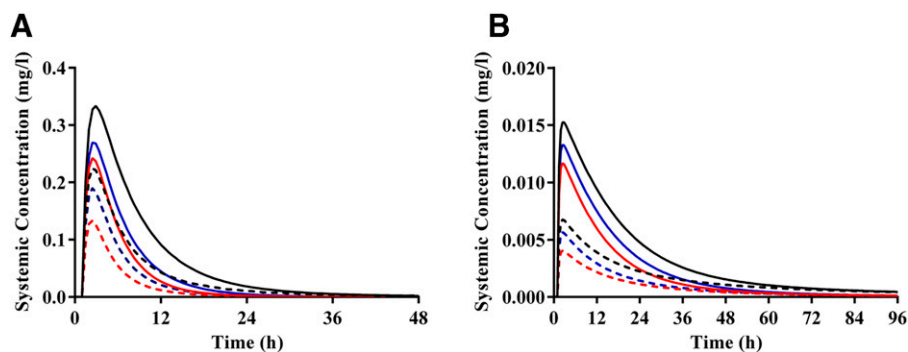


Fig. 3. Simulated plasma concentration time curves of bufuralol (A) and dextromethorphan (B) in the absence and presence of quinidine. Black lines represent baseline Simcyp compound file with pH 7.4 in vitro findings and the incorporation of  $F_1$  correction; red lines represent baseline Simcyp compound file with pH 7.4 in vitro findings only; blue lines represent baseline Simcyp compound file with pH 7.0 in vitro correction and the incorporation of  $F_1$  correction (see *Materials and Methods* for details). Dashed lines represent substrate concentration in the absence of quinidine; solid lines represent substrate concentration in the presence of quinidine.

TABLE 4

Simulated PK parameters for bupropion and dextromethorphan

Dose of bupropion (60 mg) or dextromethorphan (30 mg) simulation for 24 h. Geometric means reported with fold difference between simulation and traditional  $Sim_{pH7.4}$  given in parentheses.

Simulation	Bupropion				Dextromethorphan			
	$CL_{int,u}$	CL	$C_{max}$	AUC	$CL_{int,u}$	CL	$C_{max}$	AUC
	$\mu l/min/mg$ protein	$l/h$	$\mu g/l$	$\mu g/l \cdot h$	$\mu l/min/mg$ protein	$l/h$	$\mu g/l$	$\mu g/l \cdot h$
$Sim_{pH7.4}$	20.0	49.02	209.02	1223.91	36.0	500.47	5.16	59.94
$Sim_{pH7.4, FI}$	20.0 (1.0)	118.70 (2.4)	116.84 (0.6)	505.47 (0.4)	36.0 (1.0)	1085.39 (2.2)	2.61 (0.5)	27.64 (0.5)
$Sim_{pH7, FI}$	8.3 (0.4)	64.72 (1.3)	180.45 (0.9)	927.01 (0.8)	19.4 (0.5)	630.14 (1.3)	4.28 (0.8)	47.61 (0.8)
Observed	—	66.96	164 <sup>a</sup>	896 <sup>a</sup>	—	845.1	3.49 <sup>b</sup>	35.5 <sup>b</sup>

CL, clearance calculated as dose/AUC;  $CL_{int,u}$ , in vitro intrinsic clearance corrected for fraction unbound in microsomes.<sup>a</sup>Dayer et al. (1982).<sup>b</sup>Chi et al. (2013).

(6.0–9.0) were used to investigate metabolism through CYP2D6. This range included considerable changes in the ratio of ionized and un-ionized forms of bupropion and dextromethorphan. Evidence to suggest that a single species of either substrate was responsible for the metabolism was not observed. Therefore, the assumption was made that the total concentration of drug, the sum of the ionized and un-ionized species, drives the reaction, and the total concentration of intracellular drug can be used in the adjusted models for predictions.

An important caveat of studying the influence of pH is that both the charged state of the compound and the enzyme can be altered, which can result in differences in interactions. Enzyme activity changes with respect to pH have been demonstrated in the literature for P450 enzymes and vary between isoforms and substrates investigated. For example, 7-ethoxycoumarin *O*-deethylase activity peaks at pH 7.4 over the pH range of 7.0–8.5 in mice liver fractions (Greenlee and Poland, 1978), and whereas  $6\beta$ -hydroxytestosterone formation in HLM is higher at pH 7.4 compared with pH 7.1, different oxidative pathways for testosterone metabolism peak at different pH values between 6.8 and 8.0 (Gemzik et al., 1990; Fisher et al., 2000). Our findings show that pH significantly impacts CYP2D6 as evidenced through changes in affinity and the rate of reaction, given by  $K_m$  and  $V_{max}$ , toward the substrates with respect to pH. These observations represent the net effect of the changes in the enzyme as well as changes in the substrate ionization ratio in the reaction. Therefore, regardless of which species (ionized or un-ionized) is metabolized or the state of the enzyme, if the in vitro measurements mimic the in vivo physiology, then these changes are accounted for and the results can be scaled without correcting for an in vitro bias, as they provide a more physiologically accurate measure of  $CL_{int}$ . Additionally, the buffering capacity, ionic strength, and buffer constituents can all influence the activity of enzymes differently (Gemzik et al., 1990; Maenpaa et al., 1998), and further investigations are needed to understand the influence of different buffer conditions in conjunction with changing pH.

This is in contrast to the work done by Berezhkovskiy et al. (2012), who investigated the difference in protein binding and intrinsic clearance at pH 7.0 and pH 7.4 for a set of seven proprietary compounds. Although changes were detected between the different pH values, Berezhkovskiy et al. concluded the results to be within assay variability, and the novel equations using  $F_I$  could be applied to in vitro values determined at pH 7.4. However, work presented here illustrates that significant changes in the measured in vitro parameters at pH 7.0 compared with pH 7.4 are reproducible and outside of assay variability. Changes appear to be on a case-by-case basis, and therefore, no general conclusion for all clearance pathways and drugs can be made. Further implementation of  $F_I$  with in vitro hepatocyte data improved in vivo predictions and led the author to question whether the intracellular pH of hepatocytes in vitro is maintained (Berezhkovskiy, 2011). The author hypothesized that a disproportionately large ratio of incubation buffer to hepatocyte cell surface area would destroy the pH gradient, resulting in an intracellular pH equivalent to the extracellular environment. Metabolic stability of six commercial drugs in hepatocytes incubated in buffer at pH 7.0 compared with pH 7.4 was not different. Berezhkovskiy et al. (2013) argued that depletion would theoretically be altered if hepatocytes were able to maintain an intracellular pH 7.0 with a higher external pH due to an increase or decrease in intracellular concentration, and lack of difference between the two incubation conditions indicated that intracellular pH of the hepatocytes reflected the extracellular pH. However, this conclusion is based on the assumption that the rate of metabolism is identical at each pH since the drug concentration would theoretically be the same in the intracellular and extracellular compartments if buffer pH matched intracellular pH. Our current results indicate that intrinsic clearance can be altered between the two pH values. Therefore, Berezhkovskiy's conclusion can only be supported by determining whether the intrinsic clearance of the compounds investigated is unaltered between the two pH values. Further work in our laboratory has indicated that one of the compounds investigated, diclofenac, has a metabolism sensitive to pH in

TABLE 5

Ratio of AUC in the presence and absence of inhibitor from simulations. Ratio between simulation and traditional  $Sim_{pH7.4}$  given in parentheses.

Simulation	Bupropion				Dextromethorphan			
	Clozapine <sup>a</sup>	Amiodarone	Quinidine	Paroxetine	Clozapine <sup>a</sup>	Amiodarone	Quinidine	Paroxetine
$Sim_{pH7.4}$	1.04	4.43	2.04	4.19	1.14	6.42	3.34	6.93
$Sim_{pH7.4, FI}$	1.06 (1.0)	5.50 (1.2)	2.40 (1.2)	5.00 (1.2)	1.21 (1.1)	9.61 (1.5)	4.47 (1.3)	10.21 (1.5)
$Sim_{pH7, FI}$	1.04 (1.0)	3.33 (0.8)	1.93 (1.0)	2.69 (0.6)	1.17 (1.0)	7.32 (1.1)	3.92 (1.2)	4.81 (0.7)

<sup>a</sup>AUC ratios for 900 mg of clozapine dose given.

HLM (data publication in process), which would explain the difference observed for this compound (Berezhkovskiy et al., 2013).

Enzyme inhibition can also show a similar dependence on pH. Whereas differences in reversible inhibition between pH values were observed, these were mostly eliminated when correcting for fraction unbound at the specific pH with the exception of quinidine, which retained a 2-fold weaker inhibition at pH 7.0 compared with pH 7.4 for both bufuralol and dextromethorphan. Application of the  $F_1$  correction increased the intracellular concentration of quinidine, and this in isolation increased its inhibition potential. However, it was realized that the clearance of the inhibitor via CYP3A could also be affected at the different pH. Upon implementation of the change in metabolism and inhibition potential of quinidine, the change in metabolism of the victim drugs, and the ionization correction for both the victim and the perpetrator into the model, we found that the changes in intracellular concentration put forth by  $F_1$  were offset by the changes in PK and inhibition parameters at the intracellular pH 7.0. Furthermore, changes in TDI parameters varied inversely between the perpetrators investigated. Combined with the lack of change in the inhibition potential of some inhibitors, these findings reinforce that differences with respect to pH are not consistent and preclude generic conclusions toward inhibition in general.

Finally, PBPK models represent a convenient tool to incorporate the in vitro parameters necessary to make in vivo clearance and DDI predictions. Implementation of the  $F_1$  correction into these models resulted in a higher predicted intracellular concentration and hence an increase in the predicted rate of elimination, as well as a decreased plasma exposure and inhibition AUC ratio when using in vitro values determined at pH 7.4. Conversely, when using values determined at pH 7.0, the  $F_1$  increase in intracellular concentration was offset by the decrease in in vitro parameters measured at the lower pH and resulted in a plasma exposure and inhibition AUC ratio closer to that predicted without accounting for intracellular trapping or in vitro intrinsic clearance. This demonstrates that the assumption that in vitro intrinsic clearance is not affected by pH is inaccurate, at least for these enzyme and substrate combinations. Therefore, the implementation of a  $pK_a$ -dependent  $K_{pu}$  correction to account for a change in the rate of elimination of an ionizable drug must be applied to in vitro data generated at the correct hepatic intracellular pH 7.0. In the case of inhibitors, such as quinidine, in which in vitro assays tend to under-predict inhibition potency, the reasons remain unclear. We have demonstrated that the  $F_1$  correction cannot completely explain these in vitro to in vivo correlation disparities when combined with changes in the parameters measured at pH 7.0. This reveals the importance of using an integrated system that takes into account all of the different in vitro factors involved in making predictions (clearance of the compound, clearance of the inhibitor, fraction unbound, and inhibition potential) at the correct intracellular pH to make predictions based on physiologically accurate characteristics. It is recommended that in vitro parameters in drug discovery be determined at the physiologically appropriate intracellular pH 7.0, combined with an ionization correction, to provide a correct starting point from which to further explore other potential reasons for disparities between in vitro and in vivo outcomes.

#### Authorship Contributions

Participated in research design: Rougée, Mohutsky, Hall.

Conducted experiments: Rougée, Mohutsky, Bedwell, Ruterbories.

Contributed new reagents or analytic tools: Rougée, Mohutsky, Bedwell, Ruterbories.

Performed data analysis: Rougée, Mohutsky, Bedwell, Ruterbories, Hall.

Wrote or contributed to the writing of the manuscript: Rougée, Mohutsky, Bedwell, Ruterbories, Hall.

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## Supplemental Data

### **The Impact of the Hepatocyte-to-Plasma pH Gradient on the Prediction of Hepatic Clearance and Drug-Drug Interactions for CYP2D6 Substrates**

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Drug Metabolism and Disposition

**Analytical instrumentation and general aspects of bioanalysis.** Study samples were analyzed by LC-MS/MS using a Sciex API 6500 triple quadrupole mass spectrometer (Applied Biosystems/MDS; Foster City, CA) equipped with a TurboIonSpray interface, and operated in positive ion mode. The pumps were Shimadzu LC-10AD units with a SCL-10A controller (Kyoto, Japan), and a CTC PAL liquid handler (Zwingen, Switzerland) was used as the autosampler. Chromatography was performed at ambient temperature. All compounds were chromatographically separated using a Thermo Betasil Javelin C18 2x20 mm 5 micron HPLC column (Thermo Fisher Scientific; Waltham, MA), except for 3-hydroxyquinidine that utilized an Echelon Sprite C18 2.1x20mm, HPLC column (Analytical Sales and Services; Pompton Plains, NJ). Analytical details for mobile phase A, mobile phase B, Q1/Q3 transition, and collision energy are summarized in Table S1.

Table S1. Bioanalytical analysis details.

<i>Compound</i>	<i>Mobile Phase A (v:v)</i>	<i>Mobile Phase B</i>	<i>Q1</i>	<i>Q3</i>	<i>CE</i>
Bufuralol	Water:Formic acid (1000:1)	Methanol	262.1	188.1	23
1'-hydroxybufuralol	Water:Formic acid (1000:10)	Methanol	278.0	186.0	30
Dextromethorphan	Water:Formic acid (1000:1)	Methanol	272.2	215.0	35
Dextrorphan	Water:Formic acid (1000:1)	Methanol	258.1	201.1	30
Quinidine	Water:2M NH <sub>4</sub> CO <sub>3</sub> (1000:25)	Acetonitrile	325.2	160.1	40
3-hydroxyquinidine	Trifluoroacetic acid:2M NH <sub>4</sub> CO <sub>3</sub> (1000:4:0.5)	Acetonitrile	341.1	160.1	45
Amiodarone	Water:Formic acid (1000:1)	Methanol	646.1	588.0	65
Desethylamiodarone	Water:Formic acid (1000:1)	Methanol	618.1	547.1	26
Clozapine	Water:2M NH <sub>4</sub> CO <sub>3</sub> (1000:25)	Acetonitrile	327.2	270.0	33
Paroxetine	Water:2M NH <sub>4</sub> CO <sub>3</sub> (1000:25)	Acetonitrile	330.1	192.1	20

Table S2. Parameters used for PBPK modeling.

<i>Physical/Chemical Properties</i>	<i>Absorption &amp; Distribution</i>	<i>Elimination</i>	<i>Interactions</i>
<b>Bufuralol</b>			
MW: 261.36	ka: 1.32	Enzyme kinetics: HLM	
Log P <sub>o:w</sub> : 3.5	Model: Minimal PBPK	CL <sub>int, CYP1A2</sub> : 6.3	
Type: MB	V <sub>ss</sub> : 1.38	CL <sub>int, CYP2B6</sub> : 0.0207	
pKa 1: 8.97		CL <sub>int, CYP2C19</sub> : 3.9	
B:P: 0.68		CL <sub>int, CYP2D6</sub> : 63.6 <sup>a</sup> ; 26.4 <sup>b</sup>	
fu <sub>p</sub> : 0.19		CL <sub>int, CYP3A4</sub> : 2.7	
<b>Dextromethorphan</b>			
MW: 271.4	ka: 2.6	Enzyme kinetics: HLM	
Log P <sub>o:w</sub> : 3.8	Model: Minimal PBPK	CL <sub>int, CYP2B6</sub> : 4.7	
Type: MB	V <sub>ss</sub> : 14.3	CL <sub>int, CYP2C9</sub> : 0.9	
pKa 1: 8.3		CL <sub>int, CYP2C18</sub> : 0.052	
B:P: 1.32		CL <sub>int, CYP2C19</sub> : 0.117	
fu <sub>p</sub> : 0.5		CL <sub>int, CYP2D6</sub> : 253 <sup>a</sup> ; 136.3 <sup>b</sup>	
		CL <sub>int, CYP3A4</sub> : 4.3	
<b>Quinidine</b>			
MW: 324.4	ka: 3	Enzyme kinetics: HLM	
Log P <sub>o:w</sub> : 2.88	Model: Minimal PBPK	CL <sub>int, CYP2C9 (N-oxide)</sub> : 0.4	CYP2D6 K <sub>i</sub> : 0.0436 <sup>a</sup> ; 0.0966 <sup>b</sup>
Type: DB	V <sub>ss</sub> : Predicted using Method 1	CL <sub>int, CYP2E1 (N-oxide)</sub> : 0.52	CYP2D6 fu <sub>mic</sub> : 0.857 <sup>a</sup> ; 0.846 <sup>b</sup>
pKa 1: 4.2		CL <sub>int, CYP3A4 (N-oxide)</sub> : 2.6	CYP3A4 K <sub>i</sub> : 40

pKa 2: 8.8

B:P: 0.88

fu<sub>p</sub>: 0.203

CL<sub>int, CYP3A4 (3-OH)</sub>: 20.65<sup>a</sup>; 7.9<sup>b</sup> CYP3A4 fu<sub>mic</sub>: 0.58

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<sup>a</sup>value determined at pH 7.4 value; <sup>b</sup>value determined at pH 7.0

B:P, blood-to-plasma ratio; CL<sub>int</sub>, intrinsic clearance (μl/min/mg protein); DB, diprotic base; fu<sub>mic</sub>, fraction unbound in microsomes; fu<sub>p</sub>, fraction unbound in plasma; HLM, human liver microsomes; ka, first-order absorption rate constant (h<sup>-1</sup>); K<sub>i</sub>, inhibitory constant for reversible inhibition (μM); Log P<sub>o:w</sub>, neutral species octanol: buffer partition coefficient; MB, monoprotic base; MW, molecular weight (g/mol); pKa, acid dissociation constant; V<sub>ss</sub>, volume of distribution at steady state (l/kg). Method 1 is based after Poulin P, Theil FP (2002) Prediction of pharmacokinetics prior to in vivo studies 1. Mechanism-based prediction of volume of distribution. Journal of Pharmaceutical Sciences 91(1):129-156. For all compounds, a First-Order Absorption Model was used with Lag time (h) of 0, a fraction available from dosage (fa) of 1, and an unbound fraction of drug in enterocytes (fu<sub>gut</sub>) of 1.

Table S3. Comparison of the AUC ratio predicted by the quinidine model under different dosing simulations to clinical interaction studies.

<i>Simulation</i>	<i>Literature Reference</i>					
	<i>Bosilkovska et al.</i>	<i>Bosilkovska et al.</i>	<i>Zawertailo et al.</i>	<i>Pope et al.</i>	<i>Pope et al.</i>	<i>Pope et al.</i>
	(2014) <sup>a</sup>	(2014) <sup>a</sup>	(2010) <sup>b</sup>	(2004) <sup>c</sup>	(2004) <sup>d</sup>	(2004) <sup>e</sup>
	<i>CYP2D6 EM</i>	<i>CYP2D6 IM</i>				
Sim <sub>pH 7.4</sub>	5.4	1.0	2.7	6.6	6.0	6.0
Sim <sub>pH 7.4, FI</sub>	7.4	1.0	2.3	8.2	7.6	7.6
Sim <sub>pH 7, FI</sub>	5.9	1.0	3.7	7.2	6.7	6.7
Observed	19.2	2.7	10	47.8	45.8	43.3

All simulations were performed using the Simcyp Healthy Volunteer Population using a 10 by 10 subject trial set up (total population size 100; equal portion male/female, age range 20-50 yr) in the fasted state.

<sup>a</sup>Dextromethorphan 10 mg single dose given alone or 2 hr after 200 mg of quinidine in extensive metabolizers only.

<sup>b</sup>Dextromethorphan 210 mg (3 mg/kg dose; calculated for 70 kg average adult) single dose given alone or after 100 mg of quinidine dosed QID for three days before in intermediate metabolizers only.

<sup>c</sup>Dextromethorphan 30 mg given BID alone or in combination with 75 mg of quinidine for 7 days.

<sup>d</sup>Dextromethorphan 45 mg given BID alone or in combination with 60 mg of quinidine for 7 days.

<sup>e</sup>Dextromethorphan 60 mg given BID alone or in combination with 60 mg of quinidine for 7 days.

Figure S1

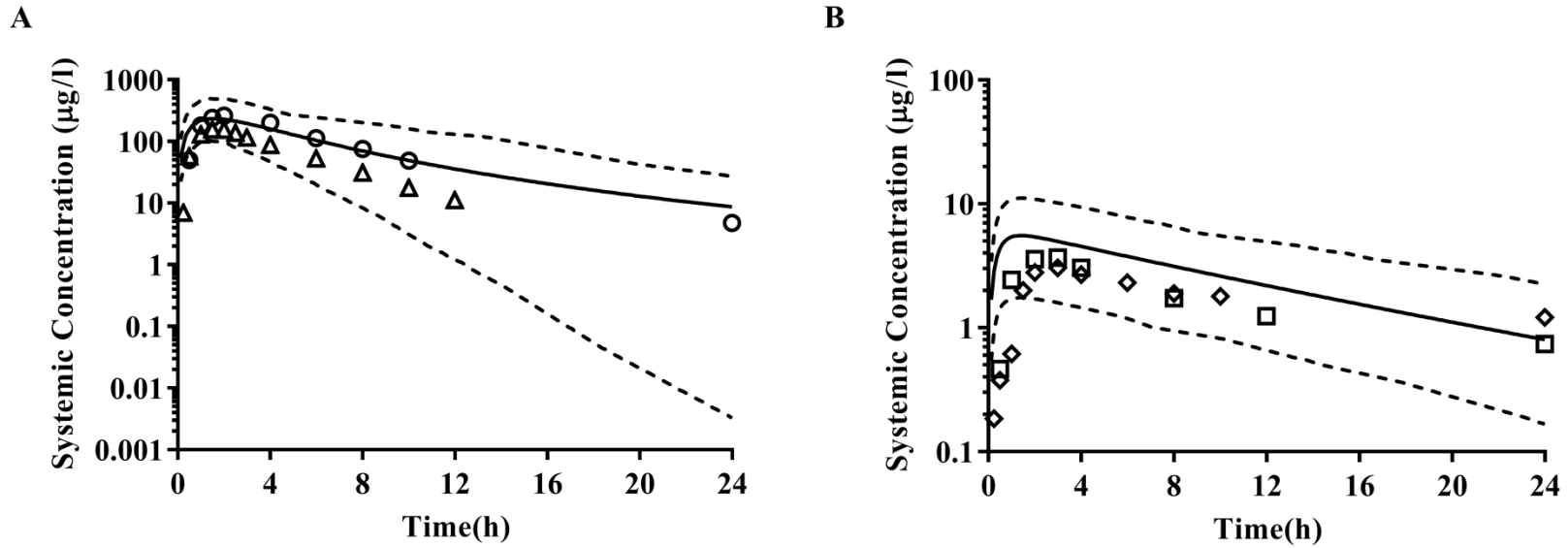


Figure S1. Predicted and observed plasma concentration-time profiles of A) bufuralol (60 mg) and B) dextromethorphan (30 mg). Solid and dashed lines represents the simulation average and 95 and 5% confidence interval respectively. Mean observed data from Pringle et al. (1986),(open circles) ; Dayer et al. (1985),(open triangles) ; Abdul Manap et al. (1999),(open squares) ; (Chi et al., 2013), (open diamonds).

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