The Glucuronidation of R- and S-Lorazepam: Human Liver Microsomal Kinetics, UDP-Glucuronosyltransferase Enzyme Selectivity, and Inhibition by Drugs

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ABSTRACT

The widely used hypnotic-anxiolytic agent R,S-lorazepam is cleared predominantly by conjugation with glucuronic acid in humans, but the enantioselective glucuronidation of lorazepam has received little attention. The present study characterized the kinetics of the separate R and S enantiomers of lorazepam by human liver microsomes (HLMs) and by a panel of recombinant human UDP-glucuronosyltransferase (UGT) enzymes. Respective mean \( K_m \) and \( V_{max} \) values for R- and S-lorazepam glucuronidation by HLM were 29 ± 8.9 and 36 ± 10 \( \mu \)M, and 7.4 ± 1.9 and 10 ± 3.8 pmol/min ⋅ mg. Microsomal intrinsic clearances were not significantly different, suggesting the in vivo clearances of R- and S-lorazepam are likely to be similar. Both R- and S-lorazepam were glucuronidated by UGT2B4, 2B7, and 2B15, whereas R-lorazepam was additionally metabolized by the extrahepatic enzymes UGT1A7 and 1A10. Based on in vitro clearances and consideration of available in vivo and in vitro data, UGT2B15 is likely to play an important role in the glucuronidation of R- and S-lorazepam. However, the possible contribution of other enzymes and the low activities observed in vitro indicate that the lorazepam enantiomers are of limited use as substrate probes for UGT2B15. To identify potential drug-drug interactions, codeine, fluconazole, ketamine, ketoconazole, methadone, morphine, valproic acid, and zidovudine were screened as inhibitors of R- and S-lorazepam glucuronidation by HLM. In vitro–in vivo extrapolation suggested that, of these drugs, only ketoconazole had the potential to inhibit lorazepam clearance to a clinically significant extent.

Introduction

The UDP-glucuronosyltransferases (UGTs) comprise a superfamily of enzymes that catalyze the transfer of glucuronic acid from the cofactor UDP-glucuronic acid (UDPGA) to a nucleophilic acceptor on the substrate. Nineteen human UGTs that primarily use UDPGA as a cofactor have been identified, and these have been classified in three subfamilies, UGT1A, UGT2A, and UGT2B, based on amino acid sequence identity (Mackenzie et al., 2005). The individual UGT enzymes exhibit characteristic but not uncommonly overlapping substrate selectivities, especially in relation to low-molecular-weight phenols (Court, 2005; Kiang et al., 2005; Miners et al., 2006, 2010a). In addition, UGTs differ in terms of drug-drug interaction profile, and UGT enzyme activities are variably affected by age, dietary and environmental chemicals, disease states, epigenetic regulation, ethnicity, genetic polymorphism, and hormonal factors (Miners and Mackenzie, 1991; Miners et al., 2002, 2004; Guillemette, 2003; Court, 2010; Guillemette et al., 2010). The majority of UGT1 and UGT2 enzymes are expressed in the liver, although expression of UGT1A5, 1A7, 1A8, 1A10, 2B11, and 2B28 appears to be minor or negligible in this tissue (Ohno and Nakajin, 2009; Court, 2010). UGT1A5, 1A7, 1A8, and 1A10 are preferentially expressed in the gastrointestinal tract and may therefore contribute to the presystemic glucuronidation of xenobiotics.

UGTs metabolize a diverse range of compounds, including drugs from all therapeutic classes (Miners and Mackenzie, 1991; Kiang et al., 2005; Miners et al., 2010a). With respect to the hepatically expressed enzymes, UGT1A1, 1A3, 1A4, 1A6, 1A9, 2B7, and 2B15 appear to be of greatest significance in drug and xenobiotic metabolism and clearance, although there is also evidence demonstrating that UGT2B4, 2B10, and 2B17 may contribute to drug glucuronidation. Recognition of the importance of glucuronidation as a metabolic pathway for drugs and other xenobiotics has stimulated interest in the application of reaction phenotyping approaches to drug glucuronidation (Miners et al., 2006, 2010a). In particular, the availability of UGT enzyme–selective substrates allows investigation of relationships between the rates of glucuronidation of a “test” compound and enzyme-selective “probes” in a panel of human liver microsomes (HLMs) or hepatocytes, and provides a valuable experimental tool for investigating the UGT enzyme inhibition selectivity of the test drug. Furthermore, enzyme-selective substrates have been applied to...
investigation of the variability in the activities of UGTs in human liver and the mechanisms responsible for interindividual variability (Court, 2010). At present, highly selective substrates have been identified for UGT1A1, 1A4, 1A6, 1A9, and 2B7 (Miners et al., 2010a).

Lorazepam is used clinically as a hypnosedative-anxiolytic agent (including anticipatory nausea and vomiting during cancer chemotherapy and premedication for surgery) and for the treatment of status epilepticus. Lorazepam is a 3-hydroxy-1,4-benzodiazepine. Similar to the structurally related benzodiazepines oxazepam and temazepam, lorazepam is eliminated in humans primarily via glucuronidation of the 3-hydroxy group (Schwarz, 1979; Greenblatt, 1981). Approximately 75% of orally administered lorazepam is recovered in urine as the glucuronide (Greenblatt et al., 1976). Owing to the presence of the 3-hydroxy group, the carbon atom at position 3 is asymmetric, and hence lorazepam, oxazepam, and temazepam exist as pairs of enantiomers. Stereoselective glucuronidation of oxazepam has been reported; S-oxazepam is primarily glucuronidated by UGT2B15, whereas UGT1A9 and UGT2B7 glucuronidate R-oxazepam (Court et al., 2002). S-Lorazepam and S-oxazepam activities were shown to be highly correlated in a panel of HLMs (Court, 2005). S- and R-lorazepam were proposed as selective substrate probes for UGT2B15 and UGT1A3, respectively (Court, 2005), but apart from the activity correlation data referred to earlier, supporting data were not provided.

To clarify the enantioselective glucuronidation of lorazepam, we characterized the kinetics of R- and S-lorazepam glucuronidation by HLM and by a panel of recombinant human UGT enzymes. Since altered lorazepam clearance may impact efficacy and safety, further studies were performed to investigate potential drug-drug interactions (DDIs) arising from inhibition of lorazepam glucuronidation. Inhibition of human liver microsomal S- and R-lorazepam glucuronidation by known substrates and/or inhibitors of UGT2B enzymes, including codeine, fluconazole, ketamine, ketocconazole, methadone, morphine, valproic acid, and zidovudine, was characterized, and in vitro–in vivo extrapolation (IVIVE) was used to assess the likely significance of DDIs.

**Materials and Methods**

**Materials**

Alamethicin (from *Trichoderma viride*), codeine, ketamine hydrochloride, R,S-lorazepam, UDPGA (trisodium salt), β-glucuronidase (from *Escherichia coli*), valproic acid, and zidovudine were purchased from Sigma-Aldrich (Sydney, NSW, Australia). Supremes expressing UGT2B4, 2B7, 2B15, and 2B17 were purchased from BD Biosciences (Wembly, WA, Australia). Fluconazole was obtained from Pfizer Australia (Sydney, NSW, Australia), ketoconazole from Janssen-Cilag Pty. Ltd. (Sydney, NSW, Australia), methadone hydrochloride from Professor A. A. Somogyi (University of Adelaide, SA, Australia), and morphine hydrochloride from GlaxoSmithKline (Melbourne, VIC, Australia). Solvents and other reagents were of analytical reagent grade.

**Enzyme Sources and Preparation**

Human livers (H7, H10, and H40—female donors; H12 and H13—male donors) were sourced from the human liver “bank” of the Department of Clinical Pharmacology of the Flinders University School of Medicine. Approval was obtained from the Flinders Medical Centre Research Ethics Committee for the use of human liver tissue in xenobiotic metabolism studies. HLMs were prepared by differential centrifugation, as described by Bowalgaha et al. (2005). HLMs were activated with the pore-forming peptide alamethicin (50 μg/mg microsomal protein) by preincubation on ice for 30 minutes according to Boase and Miners (2002). UGT1A cDNAs (viz. 1A1, 1A3, 1A4, 1A6, 1A7, 1A8, 1A9, and 1A10) were stably expressed in a human embryonic kidney cell line (HEK293), as described previously (Stone et al., 2003; Uchaipichat et al., 2004). After growth to at least 80% confluency, cells were harvested and washed twice in phosphate-buffered saline (0.1 M, pH 7.4). The harvested cells were lysed by sonication (Heat Systems Ultrasonics, Plainview, NY) set at a microtip limit of 4 and sonicated with 4 × 1–second “bursts,” each separated by 3 minutes of cooling on ice. lysed cells were then centrifuged at 12,000g for 1 minute at 4°C. The supernatant fraction was collected and kept at −80°C until use. Due to the relatively low activities of UGT2B4, 2B7, 2B15, and 2B17 expressed in HEK293 cells, UGT2B enzymes expressed in insect cells (Supersomes) were used in activity and inhibition studies.

The expression of UGT proteins was demonstrated by immunoblotting using a nonselective UGT antibody (raised against purified mouse Ugt; see Uchaipichat et al., 2004) or an antibody that recognizes UGT2B7 (Kerdipin et al., 2009). UGT1A1, 1A3, 1A6, 1A7, 1A8, 1A9, 1A10, 2B7, 2B15, and 2B17 activities were confirmed using the nonselective substrate 4-methylumbelliferyl (Uchaipichat et al., 2004; Lewis et al., 2007), whereas UGT1A4 and UGT2B4 activities were demonstrated by measurement of lamotrigine N2-glucuronidation and codeine 6-glucuronidation formation, respectively (Rowland et al., 2006; Kubota et al., 2007; Raungrut et al., 2010).

**Lorazepam Glucuronidation Assay**

Incubations, in a total volume of 0.2 ml, contained phosphate buffer (0.1 M, pH 7.4), MgCl2 (4 mM), UDP-glucuronic acid (5 mM), R,S-lorazepam (10–500 μM), and amethicin-activated HLM (1 mg/ml) or recombinant UGT protein (2 mg/ml). Reactions were initiated by the addition of UDP-glucuronic acid and performed at 37°C in a shaking water bath for 150 and 180 minutes for HLM and the recombinant UGTs, respectively. Reactions were terminated with 70% HClO4 (2 μl) and then centrifuged at 5000g for 10 minutes at 10°C. A 0.12-ml aliquot of the supernatant fraction was transferred to a 1.5-ml eppendorf tube containing 4 M KOH (2 μl), then mixed and centrifuged at 14,000g for 5 minutes. A 20-μl aliquot of the supernatant fraction was injected into the high-performance liquid chromatography (HPLC) column. Rates of R- and S-lorazepam glucuronidation formation were optimized for linearity with respect to incubation time and protein concentration.

As indicated in the Introduction, lorazepam exists as a pair of enantiomers: R- and S-lorazepam. The rate of lorazepam racemization at pH 7.4 and 37°C is relatively fast (Lu and Yang, 1990; Nishikawa et al., 1997). The half-life of lorazepam racemization under these conditions is ≤5 minutes, which is short relative to the incubation times (150–180 minutes) used here. Thus, it can be assumed that the concentration of each of R- and S-lorazepam is half of the total R,S-lorazepam concentration added to incubations. In the latter regard, substrate utilization was <5% in all experiments. It should be noted that substitution of the 3-hydroxy group of lorazepam to form an ester or ether (as occurs in glucuronidation) forms a derivative that is stable to racemization (Lu and Yang, 1990; Baldacci and Thormann, 2006).

**Quantification of R- and S-Lorazepam Glucuronides by HPLC**

The analytical conditions for measurement of the R- and S-lorazepam glucuronides were modified from the method of Franzelius and Besserer (1993). HPLC was performed using an Agilent 1100 series instrument (Agilent Technologies, Sydney, NSW, Australia) fitted with a Zorbax Eclipse XBD-C8 analytical column (4.6 × 150 mm, 5 μm; Agilent Technologies). Analytes were separated using a linear gradient with a mobile phase flow rate of 1 ml/min. Initial conditions were 10 mM sodium phosphate buffer (pH 7)-acetoni trile (87.5:12.5) held for 5 minutes. The proportion of acetonitrile was then increased to 30% over 20 minutes and then continued for 7 minutes. Column eluant was monitored by UV absorbance at 230 nm. Under these conditions, retention times of the lorazepam glucuronides, designated LZPG1 (R-lorazepam) and LZPG2 (S-lorazepam), and R,S-lorazepam were 12.3, 13.4, and 26.3 minutes, respectively (Fig. 1). LZPG1 and LZPG2 were quantified by comparison of peak areas to those of an R,S-lorazepam external standard curve prepared over the concentration range 0.5–5 μM, since authentic standards of the glucuronides were unavailable. Thus, values should be considered “apparent.” Within-day overall assay reproducibility was assessed by measuring LZPG1 and LZPG2 formation in nine separate incubations of the same batch of pooled HLM (from
human livers 7, 10, 12, 13 and 40). Coefficients of variation were less than 2% for added R,S-lorazepam concentrations of 25 and 400 \( \mu M \). The lower limit of quantification of the lorazepam glucuronides, defined as 5 times background noise, was 0.005 \( \mu M \), which translates to a rate of 0.015 pmol/min × mg.

### Identification of the R- and S-Lorazepam Glucuronides

The identity of the lorazepam glucuronides (LZPG1 and LZPG2) was confirmed by enzymatic hydrolysis. It has been reported that the glucuronides of the R diastereoisomers of benzodiazepines are more resistant to hydrolysis by \( \beta \)-glucuronidase from \( E. \ coli \) compared with the S diastereoisomers (Ruelius et al., 1979). Thus, identification of the R- and S-lorazepam glucuronides may be inferred from differences in the rates of enzymatic hydrolysis. An incubation of R,S-lorazepam and UDPGA with HLM as the enzyme source (as described earlier) was terminated with 70% HClO\(_4\) (2 \( \mu l \)) and centrifuged. The aqueous sample was decanted and mixed with 2.2 \( \mu l \) of 4 M KOH (to increase the pH to 6.5), and 25 units of \( \beta \)-glucuronidase (to provide a final concentration of 125 units/ml) from \( E. \ coli \) was added. A control reaction was performed in the same manner, except distilled water was added instead of \( \beta \)-glucuronidase. The sample was incubated at 37°C for 0, 2, 4, 10, and 120 minutes. After incubation, a 150-\( \mu l \) aliquot was separated and treated with 70% HClO\(_4\) (1.5 \( \mu l \)). Following centrifugation (5000 \( \times g \) for 10 minutes), 10 \( \mu l \) of the supernatant fraction from each reaction was injected into the HPLC column. The hydrolysis reaction resulted in a 50% reduction in the area of the peak.

**Fig. 1.** Chromatograms of R,S-lorazepam (A) and the lorazepam glucuronides LZPG1 and LZPG2 (B). R,S-lorazepam (400 \( \mu M \)) was incubated with pooled human liver microsomes (1 mg/ml) for 150 minutes in the absence (A) and presence (B) of UDPGA (5 mM).
corresponding to LZPG2 within 10 minutes, and this peak was undetectable after 2 hours. In contrast, the peak corresponding to LZPG1 was resistant to hydrolysis by \( \beta \)-glucuronidase (125 units/ml) from \( E. coli \). LZPG1 and LZPG2 peak areas were unchanged in the control incubations. Thus, the LZPG1 and LZPG2 peaks were assigned as R-lorazepam glucuronide and S-lorazepam glucuronide, respectively.

**Binding of R,S-Lorazepam to Human Liver Microsomes**

The binding of R,S-lorazepam to HLM was characterized by equilibrium dialysis as described by McLure et al. (2000). One side of the dialysis cell contained R,S-lorazepam (10, 50, 100, 300, or 500 \( \mu \)M) in phosphate buffer (0.1 M, pH 7.4), and the other side contained a suspension of pooled HLM (1 mg/ml). The dialysis cell assembly was immersed in a water bath at 37°C and rotated at 12 rpm for 4 hours. Control experiments were performed with phosphate buffer or HLM on both sides of the cell, at low and high R,S-lorazepam concentrations, to ensure that equilibrium was attained. A 200-\( \mu \)l aliquot was collected from each cell and treated with 200 \( \mu \)l of ice-cold methanol containing 4% glacial acid. Samples were chilled on ice for 20 minutes and subsequently centrifuged at 5000g for 10 minutes at 10°C. A 10-\( \mu \)l aliquot of the supernatant fraction was analyzed by HPLC. The HPLC system and conditions were essentially as described previously for the measurement of the R- and S-lorazepam glucuronides, except that the mobile phase (60% phosphate buffer/acetonitrile) was delivered isocratically at a flow rate of 1 ml/min. Under these conditions, R,S-lorazepam eluted at 4.5 minutes. R,S-lorazepam standards in the concentration range of 1-250 \( \mu \)M were prepared in phosphate buffer (100 mM, pH 7.4), alone or in a suspension of pooled HLM in phosphate buffer, and treated in the same manner as the dialysis samples. The R,S-lorazepam concentrations of dialysis samples were determined by comparison of peak areas with those of a standard curve. The fraction unbound of R,S-lorazepam in incubations of HLM (\( f_{\text{inc}} \)) was determined by dividing the drug concentration in the buffer compartment by the drug concentration in the protein compartment.

**Inhibition of R- and S-Lorazepam Glucuronidation**

Inhibition of R- and S-lorazepam glucuronidation was investigated using pooled HLM, prepared by mixing equal protein amounts of microsomes from the five livers used in the lorazepam glucuronidation kinetic study. Inhibition screening studies were performed using an R,S-lorazepam concentration of 100 \( \mu \)M (i.e., 50 \( \mu \)M of each of separate enantiomers), which corresponds to the approximate apparent \( K_m \) (viz. 37 \( \mu \)M) for both R- and S-lorazepam glucuronidation by pooled HLM (see Results). Concentrations of codeine, fluconazole, ketamine, ketoconazole, methadone, morphine, and zidovudine added to incubations (i.e., total drug concentration) in the inhibition screening studies were in the range of 10-1000 \( \mu \)M, which was considered sufficient to detect potentially clinically significant inhibition. The concentration range of valproic acid was 100-7500 \( \mu \)M, which spanned the expected \( IC_{50} \) (determined in preliminary inhibition experiments). All inhibitors were dissolved in distilled water, except for ketoconazole and valproic acid, which were dissolved in methanol such that the final concentration of solvent in the incubation mixture was 1% v/v. It has been shown that 1% methanol (v/v) has a negligible effect on UGT enzyme activities (Uchaipichat et al., 2004). Further experiments to determine the inhibitor constants (\( K_i \)) for ketoconazole and valproic acid included four inhibitor concentrations at each of three R,S-lorazepam concentrations (50, 100, and 200 \( \mu \)M).

**Kinetic Analysis of In Vitro Glucuronidation Activity Data**

Kinetic constants for R- and S-lorazepam glucuronidation by HLM or recombinant human UGTs were derived by fitting equations for empirical kinetic models (viz. Michaelis-Menten, substrate inhibition and Hill equations; see Uchaipichat et al., 2004 for expressions) to untransformed experimental data using EnzFitter (Biosoft, Cambridge, UK). Intrinsic clearance (\( CL_{\text{in}} \)) was calculated as \( V_{\text{max}}/K_m \) and maximal clearance (\( CL_{\text{max}} \); Uchaipichat et al., 2004) as:

\[
\frac{V_{\text{max}}}{S_{50}} \times \frac{(n-1)}{n(n-1)^{1/2}}
\]  

where \( S_{50} \) is the substrate concentration corresponding to half \( V_{\text{max}} \) and \( n \) is the Hill coefficient (from fitting with the Hill equation). Inhibitor constants (\( K_i \)) values were estimated by fitting the expressions for competitive, uncompetitive, noncompetitive, and mixed inhibition models to untransformed data using EnzFitter (Biosoft). Goodness of fit to kinetic and inhibition models was assessed from the \( F \) statistic, \( r^2 \) values, parameter standard error estimates, and 95% confidence intervals. Kinetic constants are reported as the value \( \pm \) standard error of the parameter estimate.

**Results**

**Non Specific Binding of R,S-Lorazepam to Human Liver Microsomes**

The average binding of R,S-lorazepam to HLM, which was concentration independent over the range investigated, was 28% (\( f_{\text{inc}} = 0.72 \pm 0.01 \)). The non specific binding of the putative inhibitors investigated here has been determined previously in this laboratory. Ketoconazole and methadone bind to HLM with mean \( f_{\text{inc}} \) values of 0.27 \( \pm \) 0.005 and 0.72 \( \pm \) 0.039, respectively, whereas the binding of codeine and valproic acid to HLM is negligible (Raungrut et al., 2010). The binding of fluconazole, ketamine, morphine, and zidovudine to HLM is also minor (Uchaipichat et al., 2006, 2011). Where binding was observed, \( f_{\text{inc}} \) was accounted for in the calculation of kinetic parameters (\( K_m, IC_{50}, \) and \( K_i \) values).

**Identification of the R- and S-Lorazepam Glucuronides**

The separate R- and S-lorazepam glucuronides were identified on the basis of the known relative sensitivity of the diastereoisomeric benzodiazepine glucuronides to hydrolysis by \( \beta \)-glucuronidase (Ruelius et al., 1979). The peak in the high-performance liquid chromatogram eluting with a retention time of 12.3 minutes (designated LZPG1; Fig. 1) was resistant to hydrolysis, whereas the peak eluting at 13.4 minutes was readily hydrolyzed by \( \beta \)-glucuronidase. Thus, LZPG1 and LZPG2 were assigned as the glucuronides of R- and S-lorazepam, respectively. Liquid chromatography-mass spectroemetry analysis of each peak gave \( m/z \) values of 497 and 495 in positive and negative ion modes, respectively, which correspond to the molecular mass of lorazepam glucuronide. It is further known that, in general, the R-glucuronides of benzodiazepines elute before the S-glucuronides when separated by reversed-phase HPLC (Ruelius et al., 1979; Franzelius et al., 2000).
and Besserer, 1993). As indicated in Materials and Methods, substitution of the 3-hydroxy group of lorazepam to form an ester or ether (including lorazepam glucuronide) forms a derivative that is stable to racemization (Lu and Yang, 1990; Baldacci and Thormann, 2006).

**Kinetics of R- and S-Lorazepam Glucuronide Formation by Human Liver Microsomes**

Representative kinetic plots and derived kinetic parameters for R- and S-lorazepam glucuronidation by nongenotyped HLM are shown in Fig. 2 and Table 1, respectively. R- and S-lorazepam glucuronidation by microsomes from all five livers exhibited weak substrate inhibition ($K_{si} > K_m$). Mean $K_m$, $V_{max}$, and $CL_{int}$ values were similar for each enantiomer, although the $K_m$ value for S-lorazepam was significantly higher (by 24%; $P < 0.05$). R- and S-lorazepam glucuronidation by pooled HLM, prepared by mixing equal protein amounts of microsomes from the five separate livers, also exhibited substrate inhibition kinetics. Mean kinetic constants for R- and S-lorazepam glucuronidation by the HLM pool were comparable to the mean data obtained using microsomes from the separate livers (Table 1). Thus, subsequent experiments investigating the magnitude of the interaction between lorazepam and putative inhibitors used pooled HLM as the enzyme source.

**Lorazepam Glucuronidation by Recombinant UGT Enzymes**

Twelve recombinant UGTs were screened for R- and S-lorazepam glucuronidation activity at three R,S-lorazepam concentrations, 20, 100, and 500 μM, which correspond to separate R- and S-lorazepam concentrations of 10, 50, and 250 μM. Results are shown in Fig. 3. UGT2B4, 2B7, and 2B15 were the only hepatically expressed enzymes that catalyzed R-lorazepam glucuronidation, with rates >0.1 pmol/min/mg. UGT2B4, 2B7, and 2B15 also catalyzed S-lorazepam glucuronidation. The highest activity was associated with UGT2B15. At S-lorazepam concentrations of 50 and 250 μM, UGT2B15 activity was approximately 4- to 6-fold higher than the activities observed with UGT2B4 and UGT2B7. Notably, UGT1A7 and 1A10, which are

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**Fig. 2.** Representative rate versus substrate concentration (A and C) and Eadie-Hofstee (B and D) plots for R- and S-lorazepam glucuronidation by human liver microsomes. Points are experimentally determined values (mean of duplicate estimates), whereas the solid lines are the computer-generated curves of best fit.
expressed only in the gastrointestinal tract, also glucuronidated R-lorazepam.

The kinetics of both R- and S-lorazepam glucuronidation by UGT2B4, 2B7, and 2B15 and R-lorazepam glucuronidation by UGT1A7 and 1A10 were further investigated. R-lorazepam glucuronidation by UGT2B4, UGT2B7, and UGT2B15 followed sigmoidal (autoactivation), Michaelis-Menten, and substrate inhibition kinetics, respectively (Fig. 4; Table 2). In contrast, sigmoidal kinetics were observed for S-lorazepam glucuronidation by UGT2B4, UGT2B7, and UGT2B15 (Fig. 5; Table 3). Derived $K_m$ or $S_{50}$ values for UGT2B4-, 2B7-, and 2B15-catalyzed R-lorazepam glucuronidation ranged from 13 to 44 $\mu$M, and the $S_{50}$ values for S-lorazepam glucuronidation spanned a similar range (17–46 $\mu$M). The kinetics of UGT1A7- and UGT1A10-catalyzed R-lorazepam glucuronidation were well modeled by the Michaelis-Menten and substrate inhibition equations, respectively. The $K_m$ for R-lorazepam glucuronidation by UGT1A10 was approximately an order of magnitude higher than that for UGT1A7, and the $K_m$ values for both R- and S-glucuronidation by UGT2B4, 2B7, and 2B15.

### Inhibition of R- and S-Lorazepam Glucuronidation

The inhibition of R- and S-lorazepam glucuronidation by codeine, fluconazole, ketamine, ketoconazole, methadone, morphine, valproic acid, and zidovudine was investigated using pooled HLM as the enzyme source. Four concentrations of each inhibitor (see Materials and Methods) were screened at an R,S-lorazepam concentration of 100 $\mu$M, which provides separate enantiomer concentrations close to the $K_m$ (37 $\mu$M) for R- and S-lorazepam glucuronide formation by pooled HLM. Nonspecific binding of inhibitors was taken into account in the estimation of IC$_{50}$ values. Each compound generally inhibited both R- and S-lorazepam glucuronidation to a similar extent (Table 4). Ketoconazole was the only compound with an IC$_{50} < 100$ $\mu$M.

#### Table 1

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<th>$K_m$</th>
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<th>$K_{si}$</th>
<th>$CL_{int}^a$</th>
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<td>367 ± 62</td>
<td>0.26 ± 0.08</td>
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$^a$ CL$_{int}$ calculated as $V_{max}/K_m$. $^*$ P < 0.05.

Fig. 3. Formation of R-lorazepam (A) and S-lorazepam (B) glucuronides by recombinant human UGT enzymes at R- and S-lorazepam concentrations of 10, 50, and 250 $\mu$M. Results represent the mean of duplicate measurements (<10% variance).

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TABLE 1

Derived kinetic parameters of R- and S-lorazepam glucuronidation by human liver microsomes

Data are modeled using the substrate inhibition equation.

**A R-lorazepam**

- 2B17
- 2B15
- 2B7
- 2B4
- 1A10
- 1A9
- 1A8
- 1A7
- 1A6
- 1A4
- 1A3
- 1A1

**B S-lorazepam**

- 2B17
- 2B15
- 2B7
- 2B4
- 1A10
- 1A9
- 1A8
- 1A7
- 1A6
- 1A4
- 1A3
- 1A1
TABLE 2
Derived kinetic constants for R-lorazepam glucuronidation by recombinant human UDP-glucuronosyltransferase enzymes

<table>
<thead>
<tr>
<th>UGT Enzyme</th>
<th>Kinetics</th>
<th>$K_m$ or $S_0$</th>
<th>$V_{max}$</th>
<th>$CL_{int}^a$ or $CL_{max}^b$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>µM</td>
<td>pmoles/min·mg</td>
<td>µM/min·mg</td>
<td></td>
</tr>
<tr>
<td>1A7*</td>
<td>Michaelis-Menten</td>
<td>25 ± 1</td>
<td>0.44 ± 0.01</td>
<td>0.0176</td>
</tr>
<tr>
<td>1A10f</td>
<td>Substrate inhibition</td>
<td>236 ± 19</td>
<td>2.8 ± 0.5</td>
<td>0.0119</td>
</tr>
<tr>
<td>2B4f</td>
<td>Hill equation</td>
<td>43 ± 4.2</td>
<td>0.29 ± 0.02</td>
<td>0.0034</td>
</tr>
<tr>
<td>2B7</td>
<td>Michaelis-Menten</td>
<td>13 ± 0.05</td>
<td>0.52 ± 0.01</td>
<td>0.0000</td>
</tr>
<tr>
<td>2B15*</td>
<td>Substrate inhibition</td>
<td>44 ± 6.5</td>
<td>0.5 ± 0.07</td>
<td>0.0114</td>
</tr>
</tbody>
</table>

a $CL_{int}$ calculated as $V_{max}/K_m$.

b $CL_{max}$ calculated as $V_{max} \times (n-1)/(n\alpha-1)\gamma$

= $K_m$ = 350 ± 121 from substrate inhibition equation.

= $n = 1.7 ± 0.2$ from Hill equation.

$\delta = 65 ± 15$ from substrate inhibition equation.

TABLE 3
Derived kinetic constants for S-lorazepam glucuronidation by recombinant human UDP-glucuronosyltransferase enzymes

<table>
<thead>
<tr>
<th>UGT</th>
<th>$S_0$</th>
<th>$n$</th>
<th>$V_{max}$</th>
<th>$CL_{int}^a$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>µM</td>
<td></td>
<td>µM/min·mg</td>
<td></td>
</tr>
<tr>
<td>2B4</td>
<td>46 ± 8</td>
<td>1.6</td>
<td>0.13 ± 0.01</td>
<td>0.0015</td>
</tr>
<tr>
<td>2B7</td>
<td>17 ± 0.7</td>
<td>1.5</td>
<td>0.20 ± 0.01</td>
<td>0.0062</td>
</tr>
<tr>
<td>2B15</td>
<td>23 ± 0.8</td>
<td>1.4</td>
<td>0.83 ± 0.01</td>
<td>0.0198</td>
</tr>
</tbody>
</table>

a $CL_{int}$ calculated as $V_{max}/S_0 \times (n-1)/(n\alpha-1)\gamma$.

Discussion

The human liver microsomal glucuronidation kinetics and UGT enzyme selectivity of the lorazepam enantiomers have been characterized here for the first time. R- and S-oxazepam glucuronidation by HLM exhibited substrate inhibition kinetics, and the derived mean kinetic parameters for each enantiomer were close in value. $CL_{int}$ values varied 2.3- and 4.9-fold for R- and S-lorazepam glucuronidation, respectively. The lack of enantioselectivity observed here for lorazepam glucuronidation by HLM suggests that the in vivo clearances of R- and S-lorazepam are likely to be similar. Studies with recombinant human UGTs demonstrated that both enantiomers were glucuronidated by UGT2B4, UGT2B7, and UGT2B15, although R-lorazepam was additionally metabolized by the extrahepatic enzymes UGT1A7 and UGT1A10. The UGT protein content of the recombinant enzyme systems is unknown, and hence it is not possible to unequivocally determine the relative contributions of UGT2B4, UGT2B7, and UGT2B15 to R- and S-lorazepam glucuronidation by HLM. However, the $CL_{int}$ value for S-lorazepam glucuronidation by UGT2B15 was an order of magnitude higher than those by UGT2B4 and UGT2B15, whereas the $CL_{int}$ values for R-lorazepam glucuronidation by UGT2B7 and UGT2B15 were an order of magnitude higher than that by UGT2B4.

A significant contribution of UGT2B15 to lorazepam glucuronidation is supported by the observation that the systemic clearance of lorazepam was 42% lower in subjects homozygous for the UGT2B15*2 allele compared with subjects who were homozygous for wild-type UGT2B15*1 (Chung et al., 2005). Indeed, in the absence of interacting drugs, the UGT2B15 genotype was estimated to account for 61% of the interindividual variability in lorazepam clearance (Chung et al., 2005). Further, Court (2005) reported a high correlation between S-lorazepam and S-oxazepam glucuronidation in a panel of HLMS; available evidence indicates that S-oxazepam is glucuronidated largely by UGT2B15 (see later discussion). In the same review, Court (2005) presented data showing lower rates of S-lorazepam glucuronidation by HLM from donors carrying the UGT2B15*2 allele, consistent with the in vivo study by Chung et al. (2005). It should be noted, however, that experimental details were not provided by Court (2005). In an investigation of the influence of UGT2B7 polymorphism on lorazepam disposition, lorazepam clearance was not significantly different between subjects with the UGT2B7*1 and *2 genotypes (Chung et al., 2008). However, the latter polymorphism appears to minimally affect the glucuronidation of UGT2B7 substrates, and hence little can be inferred regarding the role of UGT2B7 in lorazepam glucuronidation in vivo from this observation (Bhasker et al., 2000).
serum albumin sequesters the inhibitory fatty acids released from membranes during the course of an incubation, resulting in a reduction in $K_m$ to a value which presumably reflects true substrate binding affinity. More recently, 0.1% BSA was shown to reduce the $K_m$ values for UGT2B15-catalyzed 17α-estradiol and 4-methylumbelliferone glucuronidation by 45 and 77%, respectively, with variable effects on $V_{max}$ (Manevski et al., 2013). Since lorazepam binds extensively to albumin, addition of BSA to incubations was not feasible in the present study. However, based on the data of Manevski et al. (2013), the $K_m$ values for R- and S-lorazepam reported here may be higher than the “true” parameter.

Despite the structural similarity of lorazepam and oxazepam, marked differences occur in glucuronidation kinetics and enantioselectivity. Court et al. (2002) reported that $K_m$ values for S-oxazepam glucuronidation by three livers were lower than those of R-oxazepam (54 versus 277 μM) and $V_{max}$ values were higher (303 versus 101 pmol/min·mg), resulting in an approximately 10-fold higher $CL_{int}$ for S-oxazepam. Although Patel et al. (1995a) observed similar $K_m$ values for R- and S-oxazepam glucuronidation (250 versus 219 μM) for “typical” livers in a larger sample of HLM ($n = 33$), the mean $V_{max}$ was 3.6-fold higher for S-oxazepam (249 versus 70 pmol/min·mg). Despite the differences between the two reports, the higher $CL_{int}$ for S-oxazepam glucuronidation by HLM determined by Court et al. (2002) and Patel et al. (1995a) is consistent with the preferential glucuronidation of S-oxazepam in vivo; the ratios of S-oxazepam to R-oxazepam glucuronide observed in plasma and urine are 3.5 and 3.9, respectively (Patel et al., 1995a). The $K_m$ values for R- and S-lorazepam found in the present study are similar to those reported by...
Court et al. (2002) for S-oxazepam, but the $V_{\text{max}}$ values are considerably lower than those for both R- and S-oxazepam. Comparative data for S-lorazepam and S-oxazepam glucuronidation activities in a panel of HLMs reported by Court (2005) are also consistent with an approximate 10-fold lower rate of S-lorazepam glucuronidation.

In comparison with lorazepam, Court et al. (2002) further reported marked differences in the UGT enzyme selectivity of the oxazepam enantiomers. Whereas S-oxazepam was glucuronidated almost exclusively by UGT2B15 (with minor contributions from UGT1A1, 1A6, and 2B7), R-oxazepam was glucuronidated by UGT1A9 and UGT2B7. Moreover, recombinant UGT2B15*2 exhibited very low activity with S-oxazepam. UGT1A7, which was observed here to glucuronidate R-lorazepam, also metabolized R-oxazepam. Court et al. (2004) and He et al. (2009) subsequently showed that S-lorazepam, but not R-lorazepam, glucuronidation activity was reduced in HLM from donors expressing UGT2B15*2, and the apparent oral clearance of oxazepam was reduced in subjects homozygous for UGT2B15*2. Overall, the UGT2B15*2 allele was estimated to account for 34% of the interindividual variability in oxazepam clearance (He et al., 2009). The differential effects of inhibitors on R- and S-oxazepam glucuronidation by HLM further support the involvement of different UGT enzymes in the glucuronidation of the oxazepam enantiomers (Patel et al., 1995b). In contrast to lorazepam and oxazepam, there appear to be no studies that have investigated the UGT enzymes involved in the glucuronidation of temazepam.

In addition to characterizing the kinetics and UGT enzyme selectivity of lorazepam glucuronidation, this study also aimed to investigate consistent with an approximate 10-fold lower rate of S-lorazepam glucuronidation.

Table 4

<table>
<thead>
<tr>
<th>Inhibitor</th>
<th>IC$_{50}$ (R-Lorazepam)</th>
<th>IC$_{50}$ (S-Lorazepam)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Codeine (10–1000 μM)</td>
<td>809 ± 0.4</td>
<td>2562 ± 277</td>
</tr>
<tr>
<td>Fluconazole (10–1000 μM)</td>
<td>4599 ± 315</td>
<td>4245 ± 19</td>
</tr>
<tr>
<td>Ketamine (10–1000 μM)</td>
<td>205 ± 2</td>
<td>118 ± 0.1</td>
</tr>
<tr>
<td>Ketoconazole (2.7–270 μM)*</td>
<td>22 ± 0.1*</td>
<td>18 ± 0.1*</td>
</tr>
<tr>
<td>Methadone (7.2–720 μM)*</td>
<td>166 ± 4*</td>
<td>138 ± 1*</td>
</tr>
<tr>
<td>Morphine (10–1000 μM)</td>
<td>6259 ± 103</td>
<td>10629 ± 887</td>
</tr>
<tr>
<td>Valproic acid (100–7500 μM)</td>
<td>3575 ± 32</td>
<td>3200 ± 19</td>
</tr>
<tr>
<td>Zidovudine (10–1000 μM)</td>
<td>6471 ± 39</td>
<td>12818 ± 25</td>
</tr>
</tbody>
</table>

* IC$_{50}$ value is the unbound concentration (corrected for nonspecific binding to HLM).
potential DDIs that might arise from inhibition of lorazepam glucuronidation. Inhibition of lorazepam glucuronidation would be expected to prolong the hypnosedative effects of this drug, with potential effects on safety (Lee et al., 2002). Several studies have shown that valproic acid, which appears to be glucuronidated primarily by UGT2B7 (Jin et al., 1993; Argikar and Remmel, 2009), decreases the plasma clearance of lorazepam by approximately 20–40% for doses ranging from 500 to 1000 mg/day (Anderson et al., 1994b; Samara et al., 1997; Chung et al., 2005, 2008). Furthermore, several drugs have been shown to inhibit UGT2B4 and/or UGT2B7 in vitro and/or in vivo, including codeine, fluconazole, ketamine, ketoconazole, methadone, morphine, and zidovudine (Yong et al., 2005; Takeda et al., 2006; Uchaipichat et al., 2006, 2011; Raungrut et al., 2010).

Of the drugs screened for inhibition, ketoconazole was the only compound with an IC₅₀ <100 µM (Table 4). The Kᵢ values generated for ketoconazole inhibition of R- and S-lorazepam glucuronidation predicted AUC increases of 35 and 99%, respectively, based on total inhibitor concentration in blood, whereas no interaction was predicted when unbound inhibitor (ketoconazole) concentration was used for IVIVE. The magnitude of DDIs involving glucuronidated drugs appears to be predicted more accurately when total rather than unbound inhibitor concentration is used for IVIVE (Miners et al., 2010a,b). Likewise, the magnitude of the lorazepam–valproic acid interaction was more accurately predicted (15–18% increase in R-/S-lorazepam AUC) using total valproic acid concentration in blood. Differences were observed in the IC₅₀ values for inhibition of the glucuronidation of the separate lorazepam enantiomers by a number of drugs (Table 4), and Kᵢ values and mechanisms of inhibition for ketoconazole differed between R- and S-lorazepam. These observations may arise from differences in the effects of inhibitors of the various enzymes that contribute to R- and S-lorazepam. For example, codeine, morphine, and zidovudine are known substrates of UGT2B7 (and possibly UGT2B4), and might therefore be expected to inhibit UGT2B7 to a greater extent than UGT2B15 (Court et al., 2003; Stone et al., 2003; Raungrut et al., 2010).

In summary, kinetic parameters determined here for R- and S-lorazepam glucuronidation by HLM were similar in value, indicating a lack of stereoselectivity in lorazepam glucuronidation. Multiple UGT enzymes, including UGT2B4, 2B7, and 2B15, contribute to the hepatic glucuronidation of R- and S-lorazepam, although UGT2B15 appears to be the major form responsible for S-lorazepam glucuronidation. However, S-lorazepam is not recommended as a substrate “probe” for UGT2B15 given the potential involvement of other UGT enzymes in S-lorazepam glucuronidation and the low activities for this.

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**Fig. 6.** Dixon plots for the inhibition of R- and S-lorazepam by ketoconazole (A and B) and valproic acid (C and D). Points are experimentally determined values (mean of duplicate estimates), whereas the solid lines are the computer-generated curves of best fit.

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pathway in HLM. Inhibition studies in vitro suggest that coadministration of ketocazone, a commonly used antifungal agent, may result in inhibition of lorazepam clearance.

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Authorship Contributions

Participated in research design: Uchaipichat, Miners, Suthisangsi.

Conducted experiments: Uchaipichat.

Performed data analysis: Uchaipichat, Miners.

Wrote or contributed to the writing of the manuscript: Uchaipichat, Miners.

References


Argioli UA and Remmel RP (2009) Effect of aging on glucuronidation of amino acid in human liver microsomes and the role of UDG-glucuronosyltransferase UGT1A1, UGT1A9, and UGT1A10. Drug Metab Dispos 37:229–236.


Manevski N, Morello PS, Yli-Kauhaluoma J, and Finkel M (2011) Bovine serum albumin decreases the terminal values of the human UGT1A9, 1A10, and 1A27 and increases Vmax values of UGT1A9. Drug Metab Dispos 39:2117–2129.


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