Species Differences in Hepatobiliary Disposition of Taurocholic Acid in Human and Rat Sandwich-Cultured Hepatocytes: Implications for Drug-Induced Liver Injury

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ABSTRACT

The bile salt export pump (BSEP) plays an important role in bile acid excretion. Impaired BSEP function may result in liver injury. Bile acids also undergo basolateral efflux, but the relative contributions of biliary (CL\textsubscript{Bile} versus basolateral efflux (CL\textsubscript{BL}) clearance to hepatocellular bile acid excretion have not been determined. In the present study, taurocholic acid (TCA; a model bile acid) disposition was characterized in human and rat sandwich-cultured hepatocytes (SCH) combined with pharmacokinetic modeling. In human SCH, biliary excretion of TCA predominated (CL\textsubscript{Bile} = 0.14 ± 0.04 ml/min per g liver; CL\textsubscript{BL} = 0.042 ± 0.019 ml/min per g liver), whereas CL\textsubscript{Bile} and CL\textsubscript{BL} contributed approximately equally to TCA hepatocellular excretion in rat SCH (CL\textsubscript{Bile} = 0.34 ± 0.07 ml/min per g liver; CL\textsubscript{BL} = 0.26 ± 0.07 ml/min per g liver). Troglitazone decreased TCA uptake, CL\textsubscript{Bile}, and CL\textsubscript{BL}: membrane vesicle assays revealed for the first time that the major metabolite, troglitazone sulfate, was a noncompetitive inhibitor of multidrug resistance–associated protein 4, a basolateral bile acid efflux transporter. Simulations revealed that decreased CL\textsubscript{Bile} led to a greater increase in hepatic TCA exposure in human than in rat SCH. A decrease in both excretory pathways (CL\textsubscript{Bile} and CL\textsubscript{BL}) exponentially increased hepatic TCA in both species, suggesting that 1) drugs that inhibit both pathways may have a greater risk for hepatotoxicity, and 2) impaired function of an alternate excretory pathway may predispose patients to hepatotoxicity when drugs that inhibit one pathway are administered. Simulations confirmed the protective role of uptake inhibition, suggesting that a drug’s inhibitory effects on bile acid uptake also should be considered when evaluating hepatotoxic potential. Overall, the current study precisely characterized basolateral efflux of TCA, revealed species differences in hepatocellular TCA efflux pathways, and provided insights about altered hepatic bile acid exposure when multiple transport pathways are impaired.

Introduction

Bile acids are important endogenous molecules that are involved in the digestion and absorption of fats and regulation of lipid and glucose homeostasis (Hofmann, 1999a; Nguyen and Bouscarel, 2008). However, bile acids can exert toxic effects at supraphysiologic concentrations through disruption of mitochondrial ATP synthesis, necrosis, and apoptosis (Perez and Briz, 2009; Maillette de Buy Wenniger and Beuers, 2010); thus, defects in excretion may lead to hepatic accumulation of bile acids and subsequent hepatotoxicity.

Hepatic transport proteins play important roles in vectorial transport of bile acids. Sodium-taurocholate cotransporting polypeptide (NTCP) and organic anion transporting polypeptides are responsible for sodium-dependent and -independent uptake of bile acids from sinusoidal blood into hepatocytes, respectively. Bile acids in hepatocytes are excreted into bile across the canalicular membrane, predominantly via the bile salt export pump (BSEP). Consistent with the important role of BSEP in bile acid excretion, impaired BSEP function due to genetic polymorphisms has been shown to induce liver injury (e.g., progressive familial intrahepatic cholestasis type II) (Jansen et al., 1999). Also, increasing evidence suggests that inhibition of BSEP by drugs is associated with cholestatic/mixed-type drug-induced liver injury (DILI) (Morgan et al., 2010, 2013; Dawson et al., 2012; Pedersen et al., 2013).

In addition to BSEP-mediated canalicular excretion, bile acids also are transported from the hepatocyte into sinusoidal...
inhibitors. This study also investigated the effects of TGZ and its inhibitors of canalicular excretion and/or basolateral efflux. This hepatobiliary TCA disposition in human and rat SCH due to species differences exist in cellular TCA efflux pathways in laboratories combined with pharmacokinetic modeling (Pfeifer et al., 2013). In brief, on day 4 (rat) or day 7 (human) of culture, the culture medium (the same feeding medium used for in vivo studies) was changed daily until experiments were performed on day 7.

Materials and Methods

All chemicals were purchased from Sigma-Aldrich (St. Louis, MO) unless otherwise stated. TGZ [5-(4-[(6-hydroxy-2,5,7,8-tetramethylchroman-2-yl)methoxy]benzyl)thiazolidine-2,4-dione] was purchased from Cayman Chemical Company (Ann Arbor, MI). TS (5-[4-[(3,4-dihydro-2,5,7,8-tetramethyl-6-sulfoxy)-2H-1-benzopyran-2-yl]methoxyphenyl[methyl]-2-thiazolidinedione) was kindly provided by Daiichi-Sankyo Co., Ltd. (Tokyo, Japan). TS was also synthesized from TGZ in-house as described by Saha et al. (2010). [3H]TCA (5 Ci/mmol) and [3H]dehydroepiandrosterone sulfate (DHEAS; 79.5 Ci/mmol) were purchased from PerkinElmer (Waltham, MA). Dimethylsulfoxide was obtained from Fisher Scientific (Fairlawn, NJ). GIBCO brand fetal bovine serum, recombinant human insulin, and Dulbecco’s modified Eagle’s medium (DMEM) were purchased from Life Technologies (Carlsbad, CA). Insulin/transferrin/selenium culture supplement, BioCoat culture plates, and Matrigel extracellular matrix were purchased from BD Biosciences Discovery Labware (Bedford, MA).

Sandwich-Cultured Hepatocytes. Rat hepatocytes were isolated from male Wistar rats (234–245 g; Charles River Laboratories, Inc., Wilmington, MA) using a two-step collagenase perfusion method as previously described (LeCluyse et al., 1996). Animals had free access to water and food before surgery and were allowed to acclimate for at least 5 days. All animal procedures complied with the guidelines of the Institutional Animal Care and Use Committee (University of North Carolina, Chapel Hill, NC). Rat hepatocytes were seeded onto six-well BioCoat culture plates at a density of 1.75 × 10^6 cells/well in seeding medium (DMEM containing 5% fetal bovine serum, 10 μM insulin, 1 μM dexamethasone, 2 mM l-glutamine, 1% minimum essential medium nonessential amino acids, 100 units/ml of penicillin G sodium, and 100 μg/ml of streptomycin) as described previously (Swift et al., 2010). Hepatocytes were incubated for 2 hours at 37°C in a humidified incubator (95% O_2, 5% CO_2) and allowed to attach to the collagen substratum, after which time the medium was aspirated to remove unattached cells and replaced with fresh medium. The next day, cells were overlaid with BD Matrigel at a concentration of 0.25 mg/ml in ice-cold feeding medium (DMEM supplemented with 0.1 μM dexamethasone, 2 mM l-glutamine, 1% minimum essential medium nonessential amino acids, 100 units/ml of penicillin G sodium, 100 μg/ml of streptomycin, and 1% insulin/transferrin/selenium). The culture medium was changed daily until experiments were performed on day 4. Fresh human SCH, seeded onto 24-well BioCoat culture plates and overlaid with Matrigel, were purchased from Triangle Research Laboratories (Research Triangle Park, NC). Fresh human hepatocytes were obtained from two Caucasian females (31 years old, body mass index (BMI) 29.1 kg/m^2, 56 years old, BMI 22.3 kg/m^2) and one African American female (48 years old, BMI 24.9 kg/m^2). The culture medium (the same feeding medium used for rat SCH) was changed daily until experiments were performed on day 7.

Uptake and Efflux Studies in SCH. Uptake and efflux studies of TCA were performed in human and rat SCH as previously described (Pfeifer et al., 2013). In brief, on day 4 (rat) or day 7 (human) of culture, SCH were preincubated for 10 minutes in 1.5 ml/well (rat) or 0.3 ml/well (human) standard (Ca^2+-containing) or Ca^2+-free (Ca^2+/Mg^2+-free buffer containing EGTA) Hanks’ balanced salt solution (HBSS). Incubating SCH in Ca^2+-free HBSS disrupts the tight junctions that form the bile canicular networks (B-CLEAR technology; Quality Transporter Solutions, Research Triangle Park, NC). For uptake and efflux studies with TCA, SCH were treated with 1 μM [3H]TCA (400 nCi/ml) in 1.5 ml/well (rat) or 0.3 ml/well (human) standard HBSS for 20 minutes at 37°C.
After the 20-minute uptake phase, buffers containing TCA were removed, cells were washed twice with 1.5 ml/well (rat) or 0.3 ml/well (human) standard or Ca²⁺-free HBSS buffer at 37°C, and the third application of buffer was added to SCH for the 15-minute (rat) or 10-minute (human) efflux phase (Fig. 1). For determination of TGZ effects on TCA disposition, SCH were preincubated with 10 μM TGZ for 30 minutes in 1.5 ml/well (rat) or 0.3 ml/well (human) standard HBSS before 10-minute application of standard or Ca²⁺-free HBSS. The rest of the experiment (uptake and efflux) was performed as described earlier. Preincubation was selected to minimize the inhibitory effects of TGZ and its metabolites on TCA uptake, and to allow enough time for the formation of TS, a potent BSEP inhibitor. TCA accumulation in cells was quantified by liquid scintillation counting (Packard TriCarb; PerkinElmer).

**Pharmacokinetic Modeling.** Pharmacokinetic modeling was used to evaluate the hepatobiliary disposition of TCA (control), and to determine the effects of TGZ on TCA disposition (+TGZ) in human and rat SCH. A model scheme incorporating linear parameters governing TCA disposition (Fig. 1) was fit to mass versus time data from individual SCH experiments (Fig. 2). The model fitting was performed with Phoenix WinNonlin, version 6.1 (Certara, St. Louis, MO) using the stiff estimation method and a power model to account for residual error. The following differential equations, which were developed based on the model scheme depicted in Fig. 1, were fit simultaneously to data generated in SCH in the presence of intact and disrupted bile canaliculi for each condition (human and rat; control and +TGZ):

**Mass in standard HBSS buffer:**

\[
\frac{dX_{\text{buffer}}}{dt} = CL_{\text{bil}} \times C_{\text{cell}} + K_{\text{flux}} \times X_{\text{bile}} - CL_{\text{uptake}} \times C_{\text{buffer}} - K_{\text{wash}} \times X_{\text{buffer}} \quad X_{\text{buffer}} = X_{\text{dose}}
\]

**Mass in Ca²⁺-free HBSS buffer:**

\[
\frac{dX_{\text{buffer}}}{dt} = (CL_{\text{bil}} + CL_{\text{bile}}) \times C_{\text{cell}} - CL_{\text{uptake}} \times C_{\text{buffer}} - K_{\text{wash}} \times X_{\text{buffer}} \quad X_{\text{buffer}} = X_{\text{dose}}
\]
Mass in cells:
\[
d\frac{X_{\text{cells}}^+}{d} = CL_{\text{uptake}} \times C^+ - (CL_{\text{BL}} + CL_{\text{Bile}}) \times X_{\text{cells}}^+ - \frac{dX}{dt} = 0
\]

Mass in bile (standard HBSS):
\[
d\frac{X_{\text{Bile}}}{d} = CL_{\text{Bile}} \times C_{\text{cell}}^+ - K_{\text{flux}} \times X_{\text{Bile}}, \quad X_{\text{Bile}} = 0
\]

Mass in cells + bile (standard HBSS):
\[
d\frac{X_{\text{cells} + \text{Bile}}}{d} = d\frac{X_{\text{cells}}}{d} + d\frac{X_{\text{Bile}}}{d}, \quad X_{\text{cells} + \text{Bile}} = 0
\]

where \(CL_{\text{Bile}}\) is the biliary clearance, \(CL_{\text{BL}}\) is the basolateral efflux clearance, \(CL_{\text{Uptake}}\) is the uptake clearance, and variables and parameters are defined as in Fig. 1, and \(K_{\text{wash}}\) was activated for 1 minute at the end of the 20-minute uptake phase and fixed at \(1 \times 10^4\) min \(^{-1}\) based on simulations to eliminate the TCA dose from the buffer compartment and represent the wash step. \(C_{\text{cell}}\) represents the intracellular concentration, calculated as \(X_{\text{cell}}/V_{\text{cell}}\) was estimated based on the protein content of each preparation, using a value of 7.4 \(\mu\)g protein (Lee and Brouwer, 2010). \(C_{\text{Buffer}}\) represents the buffer concentration, calculated as \(X_{\text{buffer}}/V_{\text{buffer}}\), where the buffer volume \(V_{\text{buffer}}\) was constant \((1.5 \text{ ml}\) for rat SCH and \(0.3 \text{ ml}\) for human SCH). Initial parameter estimates were obtained from noncompartmental analysis of SCH data, where \(CL_{\text{Uptake}}\) was estimated from the initial \((2 \text{ minutes})\) uptake data as follows: \(CL_{\text{Uptake}} = (dX_{\text{cells} + \text{Bile}}/d)/C_{\text{buffer}} - CL_{\text{BL}}\) and \(CL_{\text{Bile}}\) were estimated from efflux phase data under \(Ca^{2+}\)-free conditions, where \((CL_{\text{BL}} + CL_{\text{Bile}}) = X_{\text{buffer}}/V_{\text{buffer}}/AUC_{\text{cells} + \text{Bile}}\) (area under the cellular TCA concentration versus time curve from 0 to 15 minutes, obtained using the linear trapezoidal rule). \(K_{\text{flux}}\), which represents the flux of substrate out of bile networks in standard HBSS conditions, was estimated initially from simulations using Berkeley-Madonna. The impact of impaired function of canalicul and/or basolateral efflux transporters on hepatic TCA exposure in human and rat SCH was simulated using the TCA model and parameter estimates (Fig. 1; Table 1); parameters representing transport-mediated efflux \((CL_{\text{BL}}\) and \(CL_{\text{Bile}}\)) were decreased by 10-fold in isolation, or in combination, in human and rat SCH; the resulting changes in predicted cellular TCA concentrations are plotted in Fig. 4. To determine the net effect of impaired function of uptake and/or efflux (basolateral and canalicul) transporters on hepatic TCA exposure in human SCH, simulations were performed by decreasing \(CL_{\text{uptake}}\) and \(CL_{\text{Bile}}\) (sum of biliary and basolateral efflux clearances; \(CL_{\text{BL}} + CL_{\text{Bile}}\)) gradually by 10- to 100-fold in combination; it was assumed that both efflux pathways \((CL_{\text{BL}}\) and \(CL_{\text{Bile}}\)) were impaired to the same extent. Simulated cellular TCA concentrations are presented in Fig. 5. All simulations were performed using Berkeley-Madonna version 8.3.11.

**Membrane Vesicles.** Human MRP4 plasmid [pcDNA3.1(−)−MRP4] was provided by Dr. Dietrich Keppler (German Cancer Research Center, Heidelberg, Germany). Human embryonic kidney 293T cells stably transfected with pcDNA3.1(−)−MRP4 or an empty plasmid vector (control) were established as previously described (Köck et al., 2014). Membrane vesicles were prepared from these cell lines, and transport experiments were carried out by a rapid filtration assay as described previously (Gibellini et al., 2008). In brief, membrane vesicles (5 \(\mu\)g of protein) were incubated at 37°C in Tris-sucrose buffer (TSB; 50 mM Tris-HCl/250 mM sucrose) containing 10 mM MgCl\(_2\), 10 mM creatine phosphate, 100 \(\mu\)g/ml creatine kinase, 4 mM ATP or AMP, and [\(^3\)H]DHEAS (0.75 \(\mu\)Ci/ml) in the absence and presence of TS, in a volume of 50 \(\mu\)l. After incubation for 2 minutes, the reaction was stopped by the addition of 0.8 ml of ice-cold TSB and immediately applied to a glass fiber filter (type A/E; Pall Corp., Port Washington, NY) and washed twice with 2 ml of ice-cold TSB. Filters were mixed by vortexing in 5 ml of scintillation fluid, and radioactivity was quantified by liquid scintillation counting (Packard TriCarb). The ATP-dependent uptake of substrate was calculated by subtracting substrate uptake in the presence of AMP from substrate uptake in the presence of ATP. The MRP4-dependent uptake of substrate was calculated by subtracting ATP-dependent uptake in MRP4-overexpressing vesicles from that in control vesicles. Initially, the inhibitory effect of TS (10 \(\mu\)M) on MRP4-dependent transport of [\(^3\)H]DHEAS (2 \(\mu\)M) was evaluated in the presence or absence of 3 mM glutathione (GSH). Further studies were performed using concentration ranges of [\(^3\)H]DHEAS (0.5–20 \(\mu\)M) and TS (5–50 \(\mu\)M) in the absence of GSH to determine the inhibition constant \((K_i)\). Initial estimates of \(K_i\) values and the type of inhibition were derived from Dixon plots of TS concentrations versus 1/velocity data. Then the kinetic parameters \((V_{\max}, V_{\max}, S, K_i)\) and type of inhibition were determined by fitting competitive, noncompetitive, and uncompetitive models to the transformed data by nonlinear regression analysis using Phoenix WinNonlin, version 6.1. Equations used for each inhibition model are as follows:

**Competitive :** \(v = \frac{V_{\max} \times S}{K_m + \left(1 + \frac{S}{K_i}\right)} + S\)

**Noncompetitive :** \(v = \frac{V_{\max} \times S}{K_m + \left(1 + \frac{S}{K_i}\right)} + S\)

**Uncompetitive :** \(v = \frac{V_{\max} \times S}{K_m + \left(1 + \frac{S}{K_i}\right)} + S\)

where \(S\) represents the concentration of [\(^3\)H]DHEAS, \(I\) represents the concentration of TS, and \(V\) denotes the rate of [\(^3\)H]DHEAS transport. The best-fit model was assessed from visual inspection of the observed versus predicted data and Akaike Information Criterion (AIC). Representative data from \(n = 2\) independent experiments in triplicate are presented in Fig. 3.

**Data Analysis.** TCA accumulation was corrected for nonspecific binding to the BioCoat plate without cells, and normalized to protein concentration measured by the BCA protein assay (Pierce Chemical, Rockford, IL). The intracellular concentration of TCA was obtained by dividing TCA accumulation (picomoles per milligram protein) by the previously reported hepatocyte volume (7.4 \(\mu\)g/mg protein) (Lee and Brouwer, 2010). Apparent \((CL_{\text{Bile,app}})\) and intrinsic \((CL_{\text{Bile,int}})\) biliary clearance values were calculated using B-CLEAR technology (Quaylet Transporter Solvers) based on the following equations:

\(CL_{\text{Bile,app}} = \frac{\text{Accumulation}_{\text{cells + Bile}} - \text{Accumulation}_{\text{Cells}}}{\text{AUC}_{\text{Buffer}} 0 - t}\)

\(CL_{\text{Bile,int}} = \frac{\text{Accumulation}_{\text{cells + Bile}} - \text{Accumulation}_{\text{Cells}}}{\text{AUC}_{\text{Cells}} 0 - t}\)

where \(\text{AUC}_{\text{Buffer}} 0 - t\) is the area under the TCA buffer concentration versus time curve, which is the product of the initial TCA buffer concentration (1 \(\mu\)M) and the incubation time \((t)\), assuming that sink conditions of TCA in the buffer are maintained (concentration changes <10% during the uptake phase). \(\text{AUC}_{\text{Cells}} 0 - t\) is the area under the TCA cellular concentration versus time curve, which was obtained using the linear trapezoidal rule. Clearance units (milliliters per minute per milligram protein) were converted to milliliters per minute per gram liver based on the protein content in liver tissue (90 and 112 mg protein/g liver for human and rat, respectively) (Sohlenius-Sternbeck, 2006). The paired Student’s \(t\) test was used to compare parameters in the presence or absence of TGZ preincubation. In all cases, \(P < 0.05\) was considered statistically significant. All
statistical analyses were performed using SigmaStat 3.5 (Systat Software, San Jose, CA).

Results

TCA Disposition in Human and Rat SCH with and without TGZ Preincubation. TCA uptake and efflux studies were conducted as described in Fig. 1. The mass-time profiles of TCA in cells + bile and cells (during the uptake and efflux phases) and buffer (during the efflux phase) in human and rat SCH in the absence (control) and presence (+TGZ) of TGZ preincubation are presented in Fig. 2. Under all conditions, TCA accumulation in cells + bile and cells increased during the uptake phase and decreased during the efflux phase. Appearance of TCA in the standard and Ca²⁺-free HBSS buffer increased during the efflux phase. TGZ preincubation decreased TCA accumulation in cells + bile, cells, and the efflux into buffers in both human and rat SCH. CL_Bile,app of TCA during the uptake phase was also significantly decreased after preincubation with TGZ compared with the control group, indicating that TGZ decreased uptake and/or biliary excretion of TCA; in human SCH, CL_Bile,app values after 10-minute uptake (standard B-CLEAR method) in control and +TGZ groups were 1.1 ± 0.3 and 0.10 ± 0.02 ml/min per g liver, respectively (P = 0.035). The corresponding values in rat SCH were 0.48 ± 0.08 and 0.07 ± 0.01 ml/min per g liver, respectively (P = 0.008). TCA CL_Bile,int also was significantly decreased after TGZ preincubation, suggesting that TGZ decreased TCA biliary excretion; in human SCH, CL_Bile,int values after 10-minute uptake in control and +TGZ groups were 0.31 ± 0.07 and 0.15 ± 0.09 ml/min per g liver, respectively (P = 0.004). The corresponding values in rat SCH were 0.62 ± 0.11 and 0.22 ± 0.08 ml/min per g liver, respectively (P = 0.049).

Parameter estimates recovered from fitting differential equations (see Materials and Methods) based on the model scheme in Fig. 1 to TCA accumulation data from independent SCH preparations are presented in Table 1. In the absence of TGZ preincubation (control), human SCH showed greater CL_Uptake, slightly lower CL_Bile, and notably lower CL_BL relative to rat SCH. This is consistent with greater cellular accumulation of TCA observed in human SCH (Fig. 2). Interestingly, CL_Bile was about 3.3-fold greater than CL_BL in human SCH, whereas CL_Bile and CL_BL showed a similar contribution to the total cellular efflux of TCA in rat SCH in the absence of TGZ. In human SCH, TGZ preincubation significantly decreased CL_Uptake (P = 0.017); there were trends toward decreased CL_BL and CL_Bile after TGZ preincubation compared with the control groups. In rat SCH, CL_Bile was significantly decreased after TGZ preincubation (P = 0.017); there were trends toward decreased CL_Uptake and CL_BL after TGZ preincubation compared with the control groups. However, these differences failed to reach statistical significance due to large variability in mean differences.

Inhibitory Effects of TS on MRP4-Mediated [3H]DHEAS Transport in Membrane Vesicles. The inhibitory effects of TS on MRP4, a basolateral bile acid efflux transporter, were evaluated using membrane vesicles prepared from human embryonic kidney 293T cells overexpressing MPR4 or control cells. TS (10 μM) inhibited MRP4-mediated transport of [3H]DHEAS (2 μM) by 78 and 72% in the absence and presence of GSH, respectively (Fig. 3A). Inhibition of MRP4-mediated [3H]DHEAS transport by TS was determined in two independent membrane vesicle studies over a range of substrate concentrations (DHEAS, 0.5–20 μM) and inhibitor concentrations (TS, 5–50 μM). In both studies, the noncompetitive inhibition model best described the inhibition data visually and generated the lowest AIC value; AIC values for competitive, noncompetitive, and uncompetitive inhibition models were
TABLE 1
Summary of recovered parameter estimates based on the model scheme depicted in Fig. 1 describing TCA disposition in human and rat SCH without (control) or with 10 µM troglitazone (+TGZ) preincubation.

<table>
<thead>
<tr>
<th>Conditions</th>
<th>CL_{Uptake}</th>
<th>CL_{Bile}</th>
<th>CL_{BL}</th>
<th>K_{i}</th>
</tr>
</thead>
<tbody>
<tr>
<td>Human SCH</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Control</td>
<td>2.2 ± 0.4</td>
<td>0.14 ± 0.04</td>
<td>0.042 ± 0.019</td>
<td>0.043 ± 0.015</td>
</tr>
<tr>
<td>+TGZ</td>
<td>0.23 ± 0.04*</td>
<td>0.084 ± 0.069</td>
<td>0.022 ± 0.018</td>
<td>0.070 ± 0.036</td>
</tr>
<tr>
<td>Rat SCH</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Control</td>
<td>1.2 ± 0.5</td>
<td>0.34 ± 0.07</td>
<td>0.26 ± 0.07</td>
<td>0.053 ± 0.015</td>
</tr>
<tr>
<td>+TGZ</td>
<td>0.20 ± 0.04</td>
<td>0.18 ± 0.05*</td>
<td>0.22 ± 0.06</td>
<td>0.077 ± 0.038</td>
</tr>
</tbody>
</table>

*Significantly different from control (P < 0.05).

Impact of Impaired Function of Canalicular versus Basolateral Efflux Transporters on Hepatic TCA Exposure.

The altered hepatobiliary disposition of TCA due to impaired function of bile acid efflux transporters was simulated based on the TCA model described in this report (Fig. 1; Table 1). Simulated hepatic TCA concentrations, uptake clearance remained unchanged over time in human SCH (Liu et al., 1998; Kotani et al., 2011; Tchaparian et al., 2011). To account for decreased Ntcp function over days of culture, simulations were also performed with a 5-fold higher CL_{Uptake} in rat SCH (Fig. 4C). TCA C_{H,ss} was higher in human SCH (11.1 µM) compared with rat SCH (1.9 µM) (Fig. 4, A and B); this is consistent with the observed higher cellular TCA accumulation during uptake and efflux studies compared with rat SCH (Fig. 2). However, TCA C_{H,ss} in rat SCH with 5-fold greater CL_{Uptake} (9.1 µM) is comparable to that in human SCH (Fig. 4, A and C). Simulations revealed that in human SCH, a 10-fold decrease in CL_{Bile} increased TCA C_{H,ss} by 2.9-fold compared with control, whereas a 1.3-fold increase in TCA C_{H,ss} occurred relative to control when CL_{BL} was decreased by 10-fold (Fig. 4A). Interestingly, a 10-fold decrease in both CL_{Bile} and CL_{BL} increased TCA C_{H,ss} by 7.0-fold compared with control, which is a greater than proportional increase compared with inhibiting either pathway in isolation. Simulations in rat SCH revealed that TCA C_{H,ss} was increased by 2.0- and 1.6-fold when CL_{Bile} and CL_{BL} were decreased by 10-fold, respectively, relative to control (Fig. 4B). TCA C_{H,ss} increased by 9.3-fold relative to control when both CL_{Bile} and CL_{BL} were decreased by 10-fold; similar to human SCH simulations, the increase in C_{H,ss} is greater than proportional compared with conditions in which either pathway is impaired in isolation. The same trends were observed in rat SCH when 5-fold greater CL_{Uptake} was simulated (Fig. 4C); the fold increase in TCA C_{H,ss} was 1.9, 1.6, and 7.3 relative to control when CL_{Bile}, CL_{BL}, and both CL_{Bile} and CL_{BL} were decreased 10-fold, respectively.

Impact of Impaired Function of Uptake versus Efflux Transporters on Hepatic TCA Exposure in Human SCH.

Hepatic bile acid concentrations are determined by both hepatic uptake and efflux processes; drugs that inhibit efflux transporters often also inhibit uptake transporters. To understand the net effects of impaired function of uptake and efflux transporters on hepatic TCA exposure, TCA C_{H,ss} in human SCH was simulated based on various values of

632.4, 628.9, and 664.6, respectively, in the first study, and were 740.0, 738.3, and 786.0, respectively, in the second study. K_i values based on a noncompetitive inhibition model were 8.0 ± 0.70 and 8.5 ± 1.2 µM in the first and the second studies, respectively. A representative fit of the noncompetitive inhibition model to the data is presented in Fig. 3B.
but the fold change in TCA was unchanged (for example, fractional inhibition of CL was 1). If the fractional inhibition of CL_{Uptake} was greater than the fractional inhibition of CL_{Efflux} then TCA C_{H,ss} was decreased (fold change < 1). If the fractional inhibition of CL_{Uptake} was less than the fractional inhibition of CL_{Efflux} then the fold change in TCA C_{H,ss} was greater than 1; TCA C_{H,ss} increased exponentially with increasing fractional inhibition of CL_{Efflux}, but the fold change in TCA C_{H,ss} decreased with increasing fractional inhibition of CL_{Uptake}. Notably, a greater than 10-fold increase in TCA C_{H,ss} was observed only when the fractional inhibition of CL_{Uptake} was less than 0.6.

Discussion

The present study determined the hepatobiliary disposition of TCA in human and rat SCH using a novel uptake and efflux protocol recently developed in our laboratory combined with pharmacokinetic modeling (Pfeifer et al., 2013). The results demonstrated that species differences exist in the hepatocellular excretion of TCA; in human SCH, biliary excretion predominated, whereas biliary excretion and basolateral efflux contributed approximately equally to hepatocellular TCA excretion in rat SCH (Table 1). Jemmitz et al. (2010) reported that basolateral and biliary excretion contribute equally to TCA efflux in human SCH, whereas basolateral efflux was the dominant cellular efflux pathway of TCA in rat SCH. The likely reason for these discrepancies is that these investigators did not account for the TCA “flux” from the canalicular spaces into the buffer, which results from regular “pulsing” of the bile canaliculi in SCH (K_{Flux} in Fig. 1) (Pfeifer et al., 2014). Regular, ordered contraction of bile canaliculi has been reported previously in isolated couplets and cultured hepatocytes (Oshio and Phillips, 1981; Phillips et al., 1982), and has been shown to facilitate bile flow in vivo in rat liver (Watanabe et al., 1991). In the study by Jemmitz et al. (2010), basolateral efflux was evaluated by measuring TCA in standard buffer during the efflux phase. However, the amount of TCA that appeared in the buffer during the efflux phase was actually the sum of basolateral efflux and flux from the bile canalicular spaces, which led to an overestimation of basolateral efflux.

Troglitazone, a known hepatotoxic compound, was selected in the current study because disposition of TGZ and its derived metabolites was well characterized in human and rat SCH (Lee et al., 2010). After preincubation with TGZ, CL_{Bile} was significantly decreased (rat) or tended to decrease (human) compared with control (Table 1), consistent with reported inhibitory effects of TGZ and TS on BSEP (Funk et al., 2001; Dawson et al., 2012). Interestingly, CL_{BL} tended to decrease after TGZ preincubation compared with control.
suggesting that TGZ and/or TS also might inhibit basolateral efflux of TCA. TGZ has been reported to inhibit the basolateral efflux transporters MRP3 and MRP4 (Morgan et al., 2013), but hepatic TGZ concentrations are minimal, whereas TS accumulates in hepatocytes due to extensive hepatic metabolism of TGZ (Funk et al., 2001; Lee et al., 2010). Thus, inhibitory effects of TS on MRP4-mediated transport were investigated. MRP4 was selected because TCA is transported by human MRP4, but not by human MRP3 (Akita et al., 2002; Rius et al., 2006). Since GSH is cotransported with bile acids by MRP4 (Rius et al., 2006), the inhibitory effect of TS at 10 μM was tested initially in the absence and presence of GSH. TS inhibited MRP4-mediated transport of \(^{3}H\)DHEAS to a similar extent regardless of GSH, suggesting that the inhibitory effects of TS on MRP4 are independent of GSH (Fig. 3A). Further studies were performed in the absence of GSH, and revealed that TS inhibited MRP4-mediated \(^{3}H\)DHEAS transport by noncompetitive inhibition, with a \(K_M\) value of 8 μM (Fig. 3B).

In addition to inhibition of efflux, \(CL_{Uptake}\) of TCA was significantly decreased (human) or showed trends toward a decrease (rat) compared with control after TGZ preincubation (Table 1). Although TGZ is a potent inhibitor of NTCP/NTcp-mediated bile acid uptake (Marion et al., 2007), TGZ concentrations in the buffer were minimal during the uptake phase because TGZ-containing buffer was removed and replaced with TGZ-free buffer during the 10-minute preincubation (standard or Ca\(^{2+}\)-free buffers) as well as the 20-minute uptake phase. These data suggest that TGZ might inhibit NTCP/NTcp by mechanisms other than direct inhibition; further studies are needed to characterize the precise mechanism(s) of inhibition.

Preclinical animals often are less sensitive to bile acid–mediated DILI compared with humans, and thus, do not reliably predict human hepatotoxicity. Potential reasons include species differences in toxic bile acid composition, substrate and/or inhibitor specificity of bile acid transporters, and metabolism/detoxification pathways of drugs as well as bile acids (Setchell et al., 1997; Hofmann, 2004; Leslie et al., 2007; Chiang, 2009). In addition, differential inhibition of hepatocellular excretion pathways, as demonstrated in the current study, may contribute to species differences in bile acid–mediated hepatotoxicity. Simulations revealed that impaired function of canaliculc and/or basolateral efflux transporters led to differential hepatobiliary disposition of TCA in human and rat SCH. In human SCH, hepatic TCA concentrations, which are relevant to hepatotoxicity, were increased 2.9-fold relative to control when canaliculc transporter function was impaired, whereas impaired function of basolateral efflux transporters minimally increased hepatic TCA concentration (1.3-fold) (Fig. 4A). This was expected due to the predominant role of biliary excretion and the minor contribution of basolateral efflux to the overall hepatocellular excretion of TCA in human SCH. Interestingly, impaired function of both canaliculc and basolateral efflux transporters further increased hepatic TCA concentrations by 7-fold compared with control (Fig. 4A), suggesting that basolateral efflux, despite serving as a minor route of hepatic excretion under normal conditions, plays an important role as a compensatory efflux pathway when canaliculc excretion is impaired in human hepatocytes.

Expression and/or function of NTcp has been reported to decrease over days of culture in rat SCH, whereas NTCP expression remains constant in human SCH; in rat SCH, TCA uptake clearance was decreased 5-fold on day 4 compared with day 0 (Liu et al., 1998; Kotani et al., 2011; Tchaparian et al., 2011). Thus, the \(CL_{Uptake}\) of TCA is likely underestimated in rat SCH, but not in human SCH. To account for the decreased function of Ntcp in day 4 rat SCH, simulations were performed in rat SCH with an \(CL_{Uptake}\) estimate obtained in day 4 rat SCH (1×\(CL_{Uptake}\)) as well as a 5-fold greater \(CL_{Uptake}\) estimate (5×\(CL_{Uptake}\)). Although robust functional or quantitative proteomics data for BSEP, MRP3, and MRP4 in SCH over time do not exist, available data suggest that Bsep protein expression in rat SCH and MRP3/Mrp3 and MRP4/Mrp4 in rat and human SCH remain relatively unchanged over days of culture under our culture conditions (Swift et al., 2010; Tchaparian et al., 2011).

In both human and rat SCH, an exponential increase in hepatic TCA concentrations was only observed when the function of both efflux pathways was decreased (Fig. 5). These results are consistent with the mathematical relationship that governs fold change in cellular exposure: 1/(1 – fe), where fe is the total fraction excreted by all pathways (biliary or basolateral) (Zamek-Gliszczynski et al., 2009). Zamek-Gliszczynski et al. demonstrated that, if multiple excretion pathways exist, minor changes in exposure (~2-fold) are expected when a transport pathway that contributes to no more than 50% of total excretion is impaired, as noted when biliary excretion (rat) or basolateral efflux (human and rat) pathways alone are decreased in the current study. However, hepatic exposure increases exponentially in response to loss of function of transport pathways that contribute to >50% of total excretion, as noted in the current study when both biliary excretion and basolateral efflux transporters are impaired.

Bile acids undergo efficient enterohepatic recirculation; only ~5% of the bile acid pool is synthesized in hepatocytes, whereas the remaining 95% is reabsorbed from the intestinal lumen after biliary excretion and taken up into hepatocytes (Hofmann, 1999b). Therefore, in addition to canaliculc and basolateral efflux transporters, hepatic bile acid exposure is also regulated by hepatic uptake transporters. Inhibition of bile acid efflux transporters by drugs is reported to be associated with cholestatic/mixed-type DILI, but often, these drugs also inhibit uptake transporters, which may exert protective effects (Leslie et al., 2007); the net effect will be determined by the relative extent (potency) of uptake inhibition versus efflux inhibition. As might be expected, simulations suggest that hepatic TCA exposure increases only when the extent of efflux inhibition exceeds that of uptake inhibition (Fig. 5). Notably, fractional inhibition of \(CL_{Uptake}\) > 0.6 prevents hepatic TCA exposure from increasing by more than 10-fold, thereby confirming the protective effects of uptake inhibition. Simulations in the current study were performed using a constant fractional inhibition of uptake and efflux transporters throughout the simulation, assuming steady-state drug (inhibitor) concentrations in the medium and in the cell. In reality, drug concentrations change over time. Thus, dynamic changes in inhibitor concentrations should be considered by incorporating drug disposition into the model to more accurately predict altered bile acid disposition by drugs.

In the current study, species differences in hepatic excretion of TCA in human and rat SCH were identified. In human SCH, biliary excretion predominated, whereas biliary excretion and basolateral efflux contributed approximately equally to TCA
efflux in rat SCH. As a result, the hepatic accumulation of TCA in rat SCH due to inhibition of BSEP alone might not be as extensive as that observed in human SCH. In human and rat SCH, inhibition of both excretion pathways led to exponential increases in hepatic TCA exposure, suggesting that inhibition of both excretion pathways might increase DILI liability. Alternatively, administration of a drug that inhibits one excretion pathway may predispose individuals with impaired transport function (due to disease or genetic polymorphisms) in the alternate pathway to hepatic bile acid accumulation and subsequent DILI. Simulations confirmed that uptake inhibition plays a protective role by helping minimize hepatic bile acid accumulation. This work emphasizes that the inhibitory effects of a drug on bile acid transporters mediating uptake as well as multiple efflux pathways should be considered when evaluating the hepatotoxic potential of drugs.

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Authorship Contributions
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Conducted experiments: Yang, Pfeifer, Köck.
Performed data analysis: Yang, Pfeifer, Köck.
Wrote or contributed to the writing of the manuscript: Yang, Pfeifer, Köck, Brouwer.

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