Investigation of the Inhibitory Effects of Various Drugs on the Hepatic Uptake of Fexofenadine in Humans

Soichiro Matsushima, Kazuya Maeda, Naoki Ishiguro, Takashi Igarashi, and Yuichi Sugiyama

Graduate School of Pharmaceutical Sciences, the University of Tokyo, Hongo, Bunkyo-ku, Tokyo, Japan (S.M., K.M., Y.S.); and Department of Pharmacokinetics and Non-Clinical Safety, Kawanishi Pharma Research Institute, Nippon Boehringer Ingelheim Co., Ltd., Yato, Kawanishi, Hyogo, Japan (N.I., T.I.)

Received July 25, 2007; accepted January 4, 2008

ABSTRACT:

Fexofenadine (FEX), an orally active nonsedating histamine H1-receptor antagonist, is eliminated from the liver mainly in an unchanged form. Our previous study suggested that organic anion-transporting polypeptide (OATP) 1B3 contributes mainly to the hepatic uptake of FEX. On the other hand, a clinical report demonstrated that a T521C mutation of OATP1B1 increased its plasma area under the plasma concentration-time curve. Several compounds are reported to have a drug interaction with FEX, and some of this may be caused by the inhibition of its hepatic uptake. We determined which transporters are involved in the hepatobiliary transport of FEX by using double transfectants and examined whether clinically reported drug interactions with FEX could be explained by the inhibition of its hepatic uptake. Vectorial basal-to-apical transport of FEX was observed in double transfectants expressing OATP1B1/multidrug resistance-associated protein 2 (MRP2) and OATP1B3/MDR2, suggesting that OATP1B1 as well as OATP1B3 is involved in the hepatic uptake of FEX and that MRP2 can recognize FEX as a substrate. The inhibitory effects of compounds on FEX uptake in OATP1B3-expressing HEK293 cells were investigated, and the maximal degree of increase in plasma AUC of FEX by drug interaction in clinical situations was estimated. As a result, cyclosporin A and rifampicin were found to have the potential to interact with OATP1B3-mediated uptake at clinical concentrations. From these results, most of the reported drug interaction cannot be explained by the inhibition of hepatic uptake of FEX, and different mechanisms such as the inhibition of intestinal efflux should be considered.

Fexofenadine (FEX) is an orally active nonsedating histamine H1-receptor antagonist for the treatment of allergic rhinitis and chronic idiopathic urticaria. After oral administration of [14C]FEX to healthy volunteers, 80% of the total dose was recovered in feces and 12% in urine in an unchanged form (Lippert et al., 1995). Because the absolute oral bioavailability of FEX was reported to be 33% (product information; Hoechst Marion, Roussel, Laval, QC, Canada), about two-thirds of bioavailable FEX is estimated to be excreted into bile. Accordingly, some drug transporters in the liver are major determinants for the clearance of FEX from systemic blood.

The first step in the process of elimination from the liver is hepatic uptake across the sinusoidal membrane. Accumulated evidence has supported the idea that organic anion-transporting polypeptide (OATP) 1B1 (OATP1B1) and OATP1B3 play major roles in the hepatic uptake of a wide variety of compounds including endogenous compounds and clinically important drugs such as HMG-CoA reductase inhibitors (statins) (Hagenbuch and Meier, 2004). Shimizu et al. (2005) have demonstrated that OATP1B3 contributes mainly to the hepatic uptake of FEX using transporter-expressing HEK293 cells. On the other hand, a recent clinical report has shown that the genetic polymorphism of OATP1B1 (T521C), which was reported to decrease the transport clearance, increased the plasma AUC of FEX (Niemi et al., 2005). These results suggested that OATP1B1 as well as OATP1B3 is involved in the uptake of FEX into human liver.

Many clinical reports have indicated the interaction between FEX and several drugs. Among them, itraconazole (Shon et al., 2005; Shimizu et al., 2006a,b; Uno et al., 2006), ketoconazole [Common Technical Document for the Registration of Pharmaceuticals for Human Use, http://www.jpec.or.jp/contents/c01/link.html (in Japanese)], azithromycin (Gupta et al., 2001), erythromycin (Common Technical Document), ritonavir, lopinavir (van Heeswijk et al., 2006), verapamil, and probenecid (Yasui-Furukori et al., 2005) increased the plasma AUC of FEX, whereas rifampicin (Hamman et al., 2001) decreased it. One of the possible mechanisms for the increase of its AUC is the inhibition of multidrug resistance 1 (MDR1/ABCB1) in the small intestine by the concomitantly administered compounds. Vectorial transport was reported to be observed in MDR1-expressing LLC-PK1 cells but not in parent cells (Cvetkovic et al., 1999). Furthermore, after oral administration of FEX, the plasma AUC in Mdr1a/1b−/− mice was approximately 6 times greater than that in FVB mice, whereas
after i.v. administration of FEX, there was no difference in the pharmacokinetics of FEX between FVB and Mdr1a/1b−/− mice, suggesting that Mdr1a/1b in the small intestine limits the absorption of FEX (Tahara et al., 2005). Because most of the compounds that clinically increase the AUC of FEX have the ability to inhibit MDR1 function, these are likely to increase the intestinal absorption of FEX by the inhibition of MDR1 in the small intestine.

However, considering that the main elimination pathway of FEX is biliary excretion of the unchanged form (Lippert et al., 1995), it is also possible that drug interaction with FEX is caused by the inhibition of its hepatic uptake. Hirano et al. (2006) performed detailed investigations to see whether the inhibitory effects of various compounds on OATP1B1-mediated uptake of pitavastatin were clinically relevant. However, the inhibition potencies of several compounds for OATP1B3-mediated uptake have not yet been clarified.

Therefore, the purpose of this study was to determine which transporters are involved in the hepatobiliary transport of FEX and explore which instances can be explained by the inhibition of its hepatic uptake among clinically reported drug interactions. We identified the transporters that can transport FEX by using double transfectants expressing OATP1B1/multidrug resistance-associated protein (MRP) 2 and OATP1B3/MRP2 (Matsushima et al., 2005; Ishiguro et al., 2008). It has often been found that the transcellular transport assay using double transfectants is more sensitive in detecting transporter-mediated transport than the uptake assay in single transporter-expressing cells. Thus, we analyzed the inhibitory effects of several compounds that are reported to interact with FEX in clinical situations on FEX uptake in OATP1B3-expressing HEK293 cells and compared the in vitro inhibition constant (Ki) for OATP1B1 with that for OATP1B1 obtained from a previous study (Hirano et al., 2006). After that, to determine whether the inhibition of FEX uptake by several compounds is clinically relevant, we also estimated the maximal degree of increase in the plasma AUC of FEX by considering the maximal unbound concentration of inhibitors at the inlet to the liver estimated by an established method for this calculation (Ito et al., 1998).

Materials and Methods

Materials. [3H]Estradiol-17β-β-glucuronide (EG) (1.6 TBq/mmol) was purchased from PerkinElmer Life and Analytical Sciences (Boston, MA). FEX hydrochloride was purchased from Toronto Research Chemicals (North York, ON, Canada). All other chemicals and reagents were of analytical grade and commercially available.

Cell Culture. MDCKII cells expressing OATP1B1/MRP2, OATP1B3/ MRP2 and vector-transfected control MDCKII cells have been described previously (Matsushima et al., 2005; Ishiguro et al., 2008). OATP1B3-expressing HEK293 cells and vector-transfected control cells were also constructed previously (Hirano et al., 2004). Transporter-expressing or vector-transfected MDCKII and HEK293 cells were grown in Dulbecco’s modified Eagle’s medium (low glucose) (Invitrogen, Carlsbad, CA) supplemented with 10% fetal bovine serum (Sigma-Aldrich, St. Louis, MO) and 1% antibiotic-antimycotic solution (Sigma-Aldrich) at 37°C under 5% CO2 and 95% humidity.

Transcellular Transport Study. The transcellular transport study was performed as reported previously (Matsushima et al., 2005). Briefly, MDCKII cells were grown on Transwell membrane inserts (6.5 mm diameter, 0.4 μm pore size; Corning Coster, Bodenheim, Germany) at confluence for 7 days, and the medium was replaced with Dulbecco’s modified Eagle’s medium supplemented with 5 mM sodium butyrate 2 days before the transport study to induce the expression of exogenous transporter. In the transport assay, cells were first washed with Krebs-Henseleit buffer (118 mM NaCl, 23.8 mM NaHCO3, 4.83 mM KCl, 0.96 mM KH2PO4, 1.20 mM MgSO4. 12.5 mM HEPES, 5.0 mM glucose, and 1.53 mM CaCl2, adjusted to pH 7.4) at 37°C and preincubated with Krebs-Henseleit buffer for 10 min. Subsequently, substrates were added in Krebs-Henseleit buffer either to the apical compartment (250 μl) or to the basolateral compartment (1 ml). After a designated period, 50 or 100 μl of medium was taken from the opposite side to the added substrate. Using FEX as a substrate, 50-μl aliquots were used for LC/MS quantification as described below. At the end of the experiments, cells were washed with ice-cold Krebs-Henseleit buffer and solubilized in 500 μl of 0.2 N NaOH. After addition of 100 μl of 1 N HCl, 50-μl aliquots were used to determine protein concentrations by the method of Lowry et al. (1951) with bovine serum albumin as a standard.

Uptake Study Using OATP1B3-Expressing HEK293 Cells. Cells were seeded in 12-well plates coated with poly-l-lysine/poly-l-ornithine (Sigma-Aldrich) at a density of 1.5 × 105 cells/well. After 2 days, the cell culture medium was replaced with culture medium supplemented with 5 mM sodium butyrate 24 h before the transport assay to induce the expression of exogenous transporters. The transport study was carried out as described previously (Sugiyama et al., 2001). Uptake was initiated by adding Krebs-Henseleit buffer containing FEX. All of the procedures were performed at 37°C. The uptake was terminated at a designated time by adding ice-cold Krebs-Henseleit buffer after removal of the incubation buffer. Then, cells were washed twice with 1 ml of ice-cold buffer, solubilized in 500 μl of 0.2 N NaOH, and kept overnight at room temperature. Using EG as a substrate, aliquots (300 μl) were transferred to vials after addition of 100 μl of 1 N HCl. Using FEX as a substrate, aliquots (240 μl) were used for LC/MS quantification as described below. The remaining 50 μl of the aliquots of cell lysate were used to determine the protein concentration by the method of Lowry et al. (1951) with bovine serum albumin as a standard.

Internalization of FEX by LC/MS. The aliquots (50 μl) obtained from the transcellular transport study were precipitated with 200 μl of methanol containing 10 nM midazolam as an internal standard, whereas the aliquots (240 μl) obtained from the uptake study were precipitated with 480 μl of methanol containing 50 nM midazolam as an internal standard. After centrifugation (15,000g for 10 min at 4°C) of the mixture, 50 μl of 0.05% formic acid was added to 50 μl of supernatant. The samples obtained were subjected to LC/MS analysis to determine the concentration of FEX. An LC-MS/MS system equipped with a Prominence LC system (Shimadzu, Kyoto, Japan) was used for the analysis. The samples were separated on a CARBOCEL PAC18 MG column (3 μm, 4.6 mm i.d., 75 mm; Shiseido, Tokyo, Japan) in binary gradient mode. For the mobile phase, 0.05% formic acid and methanol were used. The methanol concentration was initially 48%, which was then linearly increased up to 61.5% over 4.5 min. Finally, the column was reequilibrated in a methanol concentration of 48% for 3 min. The total run time was 7.5 min. By using this method, FEX was eluted at 4.1 min and midazolam at 2.8 min. In the mass analysis, FEX and midazolam were detected at mass-to-charge ratios of 502.3 and 326.1 under positive ionization conditions. The interface voltage was 3.5 kV, and the nebulizer gas (N2) flow was 1.5 liters/min. The heat block and curved desolvation line temperatures were 200 and 150°C, respectively.

Kinetic Analyses. Ligand uptake in transporter-expressing cells was expressed as the uptake volume (microliters per milligram of protein), given as the amount associated with the cells divided by its initial concentration in the incubation medium. Transporter-specific uptake was obtained by subtracting the uptake into vector-transfected cells from that into transporter-expressing cells. Inhibition constants (Ki) of a series of compounds could be calculated by the following equation, if the substrate concentration was low enough compared with its Km value:

$$CL_{\text{I} \text{t}} = \frac{CL}{1 + EK_i}$$

where CL represents the uptake clearance in the absence of inhibitor, CLI reflects the uptake clearance in the presence of inhibitor, and I represents the inhibition constant. When the data were fitted to determine the Ki value, the input data were weighted as the reciprocal of the observed values. The Damping Gauss-Newton method algorithm was used with a MULTI software program (Yamaoka et al., 1981) to fit the data.

Prediction of Clinical Drug-Drug Interactions between FEX and Various Compounds. The degree of inhibition of uptake via OATP1B1 and OATP1B3 in humans was estimated by calculating the following R value, which represents the ratio of the uptake clearance in the absence of inhibitor to that in its presence,
blood flow rate in humans (1610 ml/min) (Ito et al., 1998). To estimate the 
translated-to-apical transcellular transport of EG in vector-transfected con-
mponents (Fig. 1H), whereas we could not see any 
time higher than that in the opposite direction in OATP1B1/MRP2 double transfectants (Fig. 2, A–C). As a positive control, the basal-to-apical transport of 
EG was approximately 2.9 times higher than that in the opposite direction in OATP1B3/MPR2 double transfectants (Fig. 2D), whereas the difference in each direc-
tional transport of EG was less than 2 times that in vector-transfected 
control cells and single transfectants expressing OATP1B1 or MRP2 (Fig. 2, B and C). The basal-to-apical transport of FEX was approximately 2.9 
time higher than that in the opposite direction in OATP1B3/MPR2 double transfectants (Fig. 2D), whereas the difference in each direc-
tional transport of EG was less than 2 times that in vector-transfected control cells and single transfectants expressing OATP1B3 or MRP2 (Fig. 2D). We also obtained the protein unbound fraction in blood (f_u) from the 
literature and calculated the estimated maximal concentration at the 
inlet to the liver (I_{max}) of the inhibitors. K_i values of various 
compounds for OATP1B3 obtained in the present study and the ratio of the 
uptake clearance in the absence of inhibitor to that in its 
presence (R value) are summarized in Table 1. Among several drugs 
that we tested, only the 
values of clarithromycin and ritonavir for OATP1B1-mediated uptake 
were more than 5-fold less compared with that for 
OATP1B3-mediated uptake of FEX.

\begin{equation}
R = 1 + \frac{f_u \cdot I_{max}}{K_i}
\end{equation}

where \( f_u \) represents the protein unbound fraction of the inhibitor in blood and 
\( I_{max} \) represents the estimated maximal blood concentration of the inhibitor at the 
inlet to the liver. The \( K_i \) value for OATP1B3 was obtained from the present 
in vitro study using OATP1B3-expressing HEK293 cells described above, and the 
\( K_i \) value for OATP1B1 is quoted from the previous reports in which 
pitavastatin was used as a substrate of OATP1B1 (Hirano et al., 2006). For 
estimation of the \( R \) value, \( I_{max} \) was calculated by the method of Ito et al. 
(1998) as shown by

\begin{equation}
I_{max} = I_{max} + F_u \cdot \frac{Q_o}{k_i}
\end{equation}

where \( I_{max} \) represents the reported value for the maximal blood concentration 
of the inhibitor in the systemic circulation in clinical situations, \( F_u \) represents the fraction absorbed from the intestine of the inhibitor, \( k_i \) is the 
absorption rate constant in the intestine, and \( Q_o \) represents the hepatic 
blood flow rate in humans (1610 ml/min) (Ito et al., 1998). To estimate the 
maximal \( I_{max} \), \( F_u \) was set at 1, \( k_i \) was set at 0.1 ml \cdot 1^{-1} \cdot [	ext{minimum gastric emptying time (10 min)}], 
and the blood-to-plasma concentration ratio was 
assumed to be 1.

**Results**

**Transcellular Transport of FEX and EG across the MDCKII**

**Cell Monolayer.** The transcellular transport of 5 \( \mu \)M FEX and 0.1 
\( \mu \)M EG across the MDCKII monolayer was determined. The basal-
to-apical transport of FEX was approximately 3.6 times higher than 
that in the opposite direction in OATP1B1/MPR2 double transfectants (Fig. 1D), whereas no difference in basal-to-apical transcellular transport of 
EG was less than 2 times that in vector-transfected control cells and single transfectants expressing OATP1B1 or MRP2 (Fig. 1, A–C). On the other hand, 
the basa-to-apical transport of EG was approximately 22 times higher than that in the opposite direction in OATP1B1/ 
MPR2 double transfectants (Fig. 1H), whereas we could not see any 
basal-to-apical transcellular transport of EG in vector-transfected con-
Fig. 2. Time profiles for the transcellular transport of FEX and EG across MDCKII cell monolayers expressing OATP1B3 and/or MRP2. The transcellular transport of 5 µM FEX (A–D) and 0.1 µM EG (E–H) across MDCKII cell monolayers expressing OATP1B3 (B and F), MRP2 (C and G), and both OATP1B3 and MRP2 (D and H) was compared with that across the control MDCKII cell monolayer (A and E). ○, transcellular transport in the apical-to-basal direction; ●, transcellular transport in the basal-to-apical directions, respectively. These data were obtained from three independent experiments, and each experiment was performed in triplicate. Each point with vertical bar represents the mean and S.D. Where a vertical bar is not shown, the S.D. was contained within the limits of the symbol.

Fig. 3. Inhibitory effects of various drugs on the OATP1B3-mediated uptake of FEX. The OATP1B3-mediated uptake of FEX (10 µM) was determined in the absence or presence of inhibitors cyclosporin A (A), rifampicin (B), fluconazole (C), itraconazole (D), ketoconazole (E), clarithromycin (F), erythromycin (G), azithromycin (H), ritonavir (I), lopinavir (J), diltiazem (K), verapamil (L), omeprazole (M), and cimetidine (N) using OATP1B3-expressing HEK293 cells. These data were obtained from three independent experiments, and each experiment was performed in triplicate. Each point with vertical bar represents the mean and S.D. Where a vertical bar is not shown, the S.D. was contained within the limits of the symbol. Each solid line represents the fitting curve obtained by nonlinear regression analysis.
Discussion

To determine which transporters are involved in the hepatobiliary transport of FEX, we investigated the transcellular transport of FEX using OATP1B1/MRP2 and OATP1B3/MRP2 double-transfected cells. Furthermore, to investigate whether the inhibition of hepatic uptake of FEX by several drugs is clinically relevant, the inhibition constants of several drugs for OATP1B3-mediated FEX uptake obtained from in vitro analyses were determined, and the maximal degrees of increase in the plasma AUC through drug interactions were calculated using estimated maximal protein unbound concentrations of inhibitors at the inlet to the liver.

In the transcellular transport study using double-transfected cells, we observed the basal-to-apical vectorial transport of FEX not only in OATP1B3/MRP2 but also in OATP1B1/MRP2 double-transfected cells (Figs. 1 and 2). Our previous report indicated that OATP1B3 contributes mainly to the hepatic uptake of FEX in humans and that OATP1B1-mediated uptake was not statistically significant although the uptake in OATP1B1-expressing cells was slightly larger than that in control cells (Shimizu et al., 2005). The involvement of OATP1B1 in FEX uptake in humans was also supported by the recent clinical report demonstrating that the genetic polymorphism of OATP1B1 (T521C) increased the plasma concentration of FEX (Niemi et al., 2005). The apparently conflicting results obtained from the present study showed that ketoconazole and verapamil did not have a significant effect on the in vivo intestinal absorption of FEX when coadministered or given as a pretreatment despite increasing the plasma AUC in the previous clinical studies. Data for dosages, \( I_{\text{max}} \), and \( f_u \) are from product information of each drug except for the data with footnotes. \( R \) and \( I_{\text{max}} \) values are calculated according to eq. 2 and eq. 3, respectively (see Materials and Methods).

\[
\begin{array}{cccccc}
\text{Inhibitor} & \text{Dosage} & \mu\text{M} & \mu\text{M} & K_i & K_i^a \mu\text{M} & R \mu\text{M} \\
\text{Cyclosporin A} & 100 & 15.9 & 1.02 & 1.26 & 0.029 & 3.55 \\
\text{Rifampicin} & 100 & 47.6 & 2.01 & 0.030 & 13.3 \\
\text{Fluconazole} & 100 & 18.5 & 1.01 & 0.026 & 3.29 \\
\text{Itraconazole} & 100 & 38.3 & 1.08 & 0.016 & 1.25 \\
\text{Ketoconazole} & 200 & 18.4 & 1.04 & 0.531 & 3.49 \\
\text{Clarithromycin} & 400 & 28.5 & 1.39 & 0.781 & N.D. \\
\text{Azithromycin} & 1200 & 47.1 & 1.52 & 0.048 & 1.14 \\
\text{Ritonavir} & 800 & 15.9 & 1.37 & 76.2 & 1.64 \\
\text{Lopinavir} & 400 & 15.9 & 1.02 & 0.54 & 3.29 \\
\text{Omeprazole} & 20 & 53.9 & 1.00 & 5.96 & 8.88 \\
\text{Cimetidine} & 200 & 52.0 & 1.02 & 15.0 & 0.01 \\
\end{array}
\]

\( K_i \), not determined.

<table>
<thead>
<tr>
<th>Inhibitor</th>
<th>Dosage</th>
<th>( I_{\text{max}} )</th>
<th>( I_{\text{max}} )</th>
<th>( f_u )</th>
<th>( K_i )</th>
<th>( R )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cyclosporin A</td>
<td>100</td>
<td>0.596</td>
<td>5.76</td>
<td>0.10</td>
<td>0.573</td>
<td>2.01</td>
</tr>
<tr>
<td>Rifampicin</td>
<td>600</td>
<td>7.90</td>
<td>53.2</td>
<td>0.11</td>
<td>1.45</td>
<td>7.03</td>
</tr>
<tr>
<td>Fluconazole</td>
<td>100</td>
<td>8.62</td>
<td>28.9</td>
<td>0.89</td>
<td>&gt;100</td>
<td>&lt;1.26</td>
</tr>
<tr>
<td>Itraconazole</td>
<td>100</td>
<td>0.0792</td>
<td>8.88</td>
<td>0.002</td>
<td>&gt;30</td>
<td>1.00</td>
</tr>
<tr>
<td>Ketoconazole</td>
<td>200</td>
<td>3.20</td>
<td>26.6</td>
<td>0.01</td>
<td>18.5</td>
<td>3.0</td>
</tr>
<tr>
<td>Clarithromycin</td>
<td>400</td>
<td>1.86</td>
<td>35.1</td>
<td>0.54</td>
<td>53.6</td>
<td>15.9</td>
</tr>
<tr>
<td>Erythromycin</td>
<td>200</td>
<td>1.12</td>
<td>18.0</td>
<td>0.16</td>
<td>38.3</td>
<td>7.7</td>
</tr>
<tr>
<td>Azithromycin</td>
<td>1200</td>
<td>0.881</td>
<td>100</td>
<td>0.34</td>
<td>161</td>
<td>7.7</td>
</tr>
<tr>
<td>Ritonavir</td>
<td>800</td>
<td>28.5</td>
<td>97.4</td>
<td>0.02</td>
<td>5.64</td>
<td>1.39</td>
</tr>
<tr>
<td>Lopinavir</td>
<td>400</td>
<td>15.2</td>
<td>54.8</td>
<td>0.015</td>
<td>18.4</td>
<td>7.2</td>
</tr>
<tr>
<td>Omeprazole</td>
<td>20</td>
<td>53.9</td>
<td>14.3</td>
<td>1.00</td>
<td>51.6</td>
<td>15.9</td>
</tr>
<tr>
<td>Cimetidine</td>
<td>200</td>
<td>2.75</td>
<td>52.0</td>
<td>0.81</td>
<td>&gt;100</td>
<td>&lt;1.42</td>
</tr>
</tbody>
</table>

\( K_i \), not determined.

\( K_i^a \), calculated according to eq. 2 and eq. 3, respectively.

\( R \), calculated according to eq. 2.

\( K_i^a \), calculated according to eq. 3.

\( f_u \), calculated according to eq. 3.

\( I_{\text{max}} \), calculated according to eq. 2.

\( K_i \), calculated according to eq. 2.

\( I_{\text{max}} \), calculated according to eq. 3.

\( f_u \), calculated according to eq. 3.

\( K_i^a \), calculated according to eq. 3.

\( R \), calculated according to eq. 2.

\( K_i^a \), calculated according to eq. 3.

\( R \), calculated according to eq. 2.
of other mechanisms in addition to the inhibition of MDR1 has been suspected. One of the candidate mechanisms is considered to reduce the hepatic uptake clearance because the major route of FEX elimination is biliary excretion of the unchanged form. Because FEX is barely metabolized, the apparent intrinsic hepatic clearance is described as follows:

\[ CL_{int, h} = \frac{CL_{uptake} \cdot CL_{excretion}}{CL_{efflux} + CL_{excretion}} \]  

(4)

where \( CL_{int, h} \) represents the apparent intrinsic hepatic clearance, \( CL_{uptake} \) represents the hepatic uptake clearance, \( CL_{excretion} \) represents the biliary excretion clearance, and \( CL_{efflux} \) represents the backflux clearance from liver to blood. According to eq. 4, the change in the hepatic uptake clearance always directly affects the overall intrinsic hepatic clearance. The present study indicates that both OATP1B1 and OATP1B3 contribute to the hepatic uptake of FEX. Previously we reported the inhibitory effects of various drugs on OATP1B1-mediated uptake and their clinical relevance to drug-drug interaction (Hirano et al., 2006). However, this kind of systematic investigation for OATP1B3 has not been conducted. Therefore, the inhibitory effects of various drugs on OATP1B3-mediated uptake were determined. Among several compounds we tested, the \( R \) values of cyclosporin A and rifampicin for OATP1B3 as well as for OATP1B1 exceeded 2.0 (Table 1). To date, we have not been able to find a published report regarding a drug-drug interaction between FEX and cyclosporin A. Many clinical reports have indicated that cyclosporin A increases the AUC of a variety of substrates of OATP transporters, particularly HMG-CoA reductase inhibitors (Shitara et al., 2005). Although cyclosporin A is known as a clinically relevant potent OATP1B1 inhibitor (Shitara et al., 2003), we showed that cyclosporin A can also potently inhibit OATP1B3-mediated uptake. Accordingly, it is necessary to pay attention to not only the OATP1B1- but also the OATP1B3-mediated drug-drug interaction between FEX and cyclosporin A in clinical situations. Repetitive administration of rifampicin reduced the plasma AUC of FEX in a previous clinical study (Hamanman et al., 2001). This report Apparently conflicts with the present results in which rifampicin inhibited the OATP1B3-mediated uptake. However, rifampicin is a well known pregnancy X receptor-mediated inducer and increases the expression level of MDR1 in the small intestine (Schuetz et al., 1996). Therefore, in this case, repeated dosing of rifampicin increased the expression level of MDR1 in the small intestine, which masked its inhibitory effects on the OATP1B3-mediated uptake of FEX. This concept is supported by the recent report from Lam et al. (2006) indicating that drugs should be administered 1 day after the final dose of rifampicin to minimize potential inhibitory effects of OATP transporters in the induction study (Lam et al., 2006).

When we compared \( K_i \) values for OATP1B1 with those for OATP1B3, \( K_i \) values for OATP1B1 and OATP1B3 were within the range of a 5-fold difference, except for clarithromycin and ritonavir, suggesting that the inhibitory potency of compounds for OATP1B1-mediated transport can be considered similar to that for OATP1B3-mediated transport. A specific inhibitor for each individual transporter is very useful for determining the contribution of each transporter to the overall membrane transport. Although EG and estrone-3-sulfate are recognized as selective inhibitors for OATP1B1/OATP1B3 and OATP1B1/OATP2B1, respectively (Hirano et al., 2006), unfortunately, specific inhibitors for OATP1B3 have not yet been identified. Because of the high homology and overlapping substrate specificities between OATP1B1 and OATP1B3, the use of in silico screening with a ligand-based drug design approach may be necessary to search for the selective inhibitors for OATP1B3 (Hirano et al., 2004).

Hirano et al. (2006) have indicated that cyclosporin A, rifampicin, clarithromycin, and ritonavir (\( R \) value for OATP1B1 > 2.0) have a potential to interact with OATP1B1-mediated transport of pitavastatin in clinical situations (Hirano et al., 2006). Although the \( K_i \) values for OATP1B1-mediated uptake were determined by using pitavastatin as a substrate because of no significant uptake of FEX into OATP1B1-expressing HEK293 cells, if we consider the possible contribution of OATP1B1 and OATP1B3 to the hepatic uptake of FEX, these drugs may also affect the hepatic clearance of FEX. To avoid false-negative predictions of drug-drug interactions, the maximal plasma unbound concentration of inhibitors at the inlet to the liver was calculated using eq. 3, which can overestimate these concentrations (Ito et al., 1998). Therefore, in most cases, a drug-drug interaction caused by inhibition of hepatic uptake of FEX might not occur in clinical situations.

In conclusion, both OATP1B1 and OATP1B3 are involved in the hepatic uptake of FEX, and MRP2 can recognize FEX as a substrate. Among the compounds we tested, cyclosporin A and rifampicin have the potential to inhibit the OATP1B1- and OATP1B3-mediated hepatic uptake of FEX at clinically relevant concentrations. However, most of the reported clinical drug-drug interactions cannot be explained simply by the inhibition of hepatic uptake of FEX, and other mechanisms should be taken into account (e.g., inhibition of MDR1-mediated efflux in small intestine).

Acknowledgments. We thank Dr. Junko Iida and Futoshi Kurotobi (Shimadzu Corporation, Kyoto, Japan) for technical support involving the LC/MS system. We also thank Atsushi Ose for providing valuable comments on the LC/MS system.

References


Tahara H, Kusuhara H, Fuse E, and Sugiyama Y (2005) P-glycoprotein plays a major role in the efflux of fexofenadine in the small intestine and blood-brain barrier, but only a limited role in its biliary excretion. Drug Metab Dispos 33:963–968.


Address correspondence to: Dr. Yuichi Sugiyama, Department of Molecular Pharmacokinetics, Graduate School of Pharmaceutical Sciences, The University of Tokyo, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan. E-mail: sugiyama@mol.f.u-tokyo.ac.jp