Enzyme-transporter interplay in the formation and clearance of abundant metabolites of faldaprevir found in excreta but not in circulation

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B/P, blood to plasma ratio; CLh,B, Hepatic blood clearance; CLint, intrinsic clearance; CLint,passive, intrinsic clearance of passive diffusion; CLint,uptake, intrinsic clearance of sinusoidal uptake; Cmax, maximum plasma concentration; DDIs: Drug drug interactions; DMEs: drug metabolizing enzymes; Fa, fraction absorbed after oral administration; Fh, the fraction of drug escaping metabolism in the liver; Fg, the fraction of drug escaping metabolism in the intestine; fu,liver, free fraction of drug in liver; fu,p, free fraction of drug in plasma; HCV, hepatitis C virus; HBSS, Hanks’ balanced salt solution; HIM, human intestinal microsomes; HLC, human liver cytosol; HLM, human liver microsomes; IC50, concentration which achieves a 50% inhibitory effect; IVIVC, in vitro to in vivo correlation; ka, first order absorption rate constant; Km, Michaelis-Menten constant; LC-MS/MS, high performance liquid chromatography-tandem mass spectrometry; Peff, effective permeability in human; Qen, blood flow through enterocytes; Qh, hepatic blood flow; Qgut, hybrid term of the villous blood flow (Qvilli) and permeability clearance (CLperm); rCYP: recombinant human cytochrome P450; [S]h, unbound substrate concentrations in the liver; [S]g, unbound substrate concentrations in the intestine; Vmax, maximum reaction velocity
Abstract

Faldaprevir is an HCV protease inhibitor which effectively reduces viral load in patients. Since faldaprevir exhibits slow metabolism in vitro and low clearance in vivo, metabolism was expected to be a minor clearance pathway. The human [14C]ADME study revealed that two mono-hydroxylated metabolites (M2a and M2b) were the most abundant excretory metabolites in feces, constituting 41% of the total administered dose. In order to de-convolute formation and disposition of M2a and M2b in human and determine why the minor change in structure (addition of 16 amu) produced chemical entities that were excreted and not present in circulation, multiple in vitro test systems were employed. The results from these in vitro studies clarified the formation and clearance of M2a and M2b. Faldaprevir is metabolized primarily in liver by CYP3A4/5 to form M2a and M2b, which are also substrates of efflux transporters (P-gp and BCRP). The role of transporters is considered important for M2a and M2b as they demonstrate low permeability. It is proposed that both metabolites are efficiently excreted via bile into feces and do not enter the systemic circulation to an appreciable extent. If these metabolites permeate to blood, they can be readily taken up into hepatocytes from the circulation by uptake transporters (likely OATPs). These results highlight the critical role of drug metabolizing enzymes and multiple transporters in the process of the formation and clearance of faldaprevir metabolites. Faldaprevir metabolism also provides an interesting case study for metabolites which are exclusively excreted in feces, but are of clinical relevance.
Introduction

Chronic hepatitis C is a major clinical concern worldwide. It is one of the leading causes of liver transplantation (Gonzalez, 2010) and the second most common cause of hepatocellular cancer (Perz et al., 2006). Faldaprevir (BI 201335, FDV) (Fig. 1) is a potent and selective hepatitis C virus (HCV) NS3/4A protease inhibitor that has achieved high sustained viral response rates in treatment-naïve and treatment-experienced patients with chronic genotype 1 infection, when used in combination with pegylated interferon alfa-2a and ribavirin (Sulkowski et al., 2013a; Sulkowski et al., 2013b).

In the [14C]ADME study in human, faldaprevir was the predominant drug-related material in plasma, representing >97.9% of all drug-related material (Chen et al., 2013). Faldaprevir was almost exclusively excreted in bile with 98.7% of the radioactivity recovered from feces and negligible urinary excretion (0.11%). Unchanged faldaprevir comprised 52% of fecal radioactivity in human. The most abundant fecal metabolites were two mono-hydroxylated metabolites, M2a and M2b (Fig. 1), which represented 22% and 20% of fecal radioactivity (22% and 19% of the dose), respectively. There were 5 additional very minor phase I fecal metabolites.

Since faldaprevir exhibits slow metabolism in vitro and low clearance in vivo (Duan et al., 2012) and minimal metabolites were detected in human plasma, the substantial presence of two hydroxylated metabolites (M2a and M2b, combined 41% of the dose) in human feces was unexpected (Chen et al., 2013). Some phase II metabolites, such as glucuronides, are efficiently effluxed to GI tract after their formation in the gut or liver and are not detectable in plasma (Hjelle et al., 1984; Sfakianos et al., 1997; Zamek-Gliszczynski et al., 2006). However, this
phenomenon is unusual for phase I metabolites with one case reported recently for another developmental drug (Zamek-Gliszczynski et al., 2013). Why did a minor change in structure (addition of a mass of 16 to a molecular weight of 870 Da) produce chemical entities (M2a and M2b) that were excreted rather than being released into blood? In order to address this question, it was important to understand the role of drug metabolizing enzymes (DMEs) and transporters in the formation and clearance of M2a and M2b.

In order to de-convolute the formation and disposition of M2a and M2b in human, multiple in vitro test systems were employed. Reaction phenotyping studies revealed that both M2a and M2b were primarily formed via CYP3A4/5. A logical question to address was whether these metabolites are formed in liver and/or intestine. Liver and intestine are also the main organs involved in drug-drug interactions (DDIs) and so M2a and M2b may play a role in DDIs if formed in these organs. Also, as the liver is the target organ for HCV treatment, it was important to assess the anti-viral activity of M2a and M2b, and consider whether these metabolites could contribute toward efficacy. In addition, efflux and uptake transporter studies were performed in order to better define the role of transporters in the disposition of M2a and M2b. Slow in vitro metabolism of faldaprevir created unique challenges for describing the complete fate of M2a and M2b. An additional challenge in understanding faldaprevir disposition was that animals are not satisfactory surrogates to study faldaprevir metabolism in human, since formation of M2a and M2b is significantly lower in animals (Ramsden et al., 2013a). This finding necessitated in vitro investigations with human derived preparations.

These investigations are also in alignment with regulatory requirements to identify the clearance pathways and contributions of enzymes and transporters to drug disposition (FDA, 2012; EMA, 2012). Current regulatory guidances primarily focus on circulating metabolites
with little consideration for fecal metabolites. Faldaprevir metabolism provides an interesting case study for metabolites which are exclusively excreted in feces, but are of clinical relevance.
Materials and Methods

Chemicals, reagents and other materials. Faldaprevir, IN79158 (M2a) and IN79157 (M2b), $^{13}$C$_6$-faldaprevir and $[^{14}$C]faldaprevir were synthesized at Boehringer Ingelheim Pharmaceuticals, Inc (Ridgefield, CT). NADPH was purchased from Sigma-Aldrich (St. Louis, MO). Pooled heparinized human plasma was obtained from Biological Specialty Corp (Colmar, PA) and human serum albumin was obtained from Sigma Chemical Co. (St. Louis, MO). Fresh pooled heparinized blood was prepared at Boehringer Ingelheim Pharmaceuticals, Inc. Pooled male and female human liver microsomes (HLM), human liver cytosol (HLC), and human intestinal microsomes (HIM) were purchased from BD Biosciences/Gentest (Woburn, MA). Recombinant human cytochrome P450 (rCYP) (produced in baculovirus-infected insect cells) and control insect cell microsomes were also purchased from BD Biosciences/Gentest. Caco-2 cells were obtained from the American Type Culture Collection (ATCC, Rockville, MD). HCV genotype 1a (strain H77) and genotype 1b (strain HCV40) NS3/4A heterodimeric proteins were purified from baculovirus-infected Sf21 insect cells. The microsomes, cytosol, rCYPs and HCV proteins were stored at -80 °C until used. All other reagents and solvents were of analytical grade or higher purity and were obtained from commercial suppliers.

Protein binding and blood to plasma ratio. Teflon dialysis cells and dialysis membranes (Spectra/Por) with 12,000-14,000 molecular weight cut-off (Spectrum, Rancho Dominguez, CA) were used for equilibrium dialysis to determine binding of $[^{14}$C]faldaprevir in pooled human plasma, 4% human serum albumin, HLM (0.5 mg/ml) and HIM (0.5 mg/ml). Concentration ranges of $[^{14}$C]faldaprevir tested were 1.1-46 µM for plasma protein binding and 0.3-115 µM for albumin binding to cover therapeutic concentrations. $[^{14}$C]faldaprevir concentrations were 0.5-100 µM for microsomal binding to cover the concentrations used in the incubations with HLM.
and HIM described below. For each matrix and [¹⁴C]faldaprevir concentration tested, five individual dialysis cells were prepared and rotated at 20 rpm using a Spectrum dialysis cell rotator in a water bath maintained at 37°C for 4 hr. At the end of the incubation period, the contents of each side were transferred to scintillation vials and processed for liquid scintillation counting.

Faldaprevir blood to plasma ratio was determined by measuring the total radioactivity in plasma and whole blood after spiking [¹⁴C]faldaprevir at two clinically relevant concentrations (0.03 µM and 17 µM) to fresh human blood. All vials were incubated at 37°C with gentle agitation and samples were collected at 20, 40 and 60 min from each vial. The radioactivity in whole blood (after oxidizing) and plasma was analyzed by liquid scintillation counting. The experiment was run in duplicate.

**Stability of faldaprevir in fecal sample during storage and extraction.** Fresh human fecal sample (2.89 g) from a healthy male subject was weighed and homogenated with 3.2 ml of water. Faldaprevir stock solution was spiked to the fecal homogenate at a final concentration of 0.37 mM to mimic faldaprevir concentration in GI tract. Sample was vortexed and kept at room temperature for 4 hr and then stored at -20°C for 3 days. A fraction of the spiked fecal homogenate (1.40 g) was centrifuged at 13,000 rpm for 10 min. After the supernatant was separated, the pellet was extracted three times with 1.2 ml of 5% acetic acid in acetonitrile. The extracts were combined with the supernatant and then mixed with 1 ml of methanol containing 0.2% formic acid. After centrifugation, the supernatant was separated and evaporated to dryness under a stream of nitrogen gas at 35°C, and then reconstituted in 0.35 ml of methanol with 0.2% formic acid. After centrifugation at 13,000 rpm for 3 min, the supernatant was submitted for analysis by LC-MS/MS to monitor the formation of M2a and M2b.
Incubation with human gut content. Individual fecal samples from two healthy male subjects were collected and mixed with Dulbecco’s Phosphate Buffer Saline containing 20 mM glucose to reach a concentration of 0.1 g/ml. The mixture was then homogenized and centrifuged at 500 g for 5 min at 4°C to remove debris. The supernatant was transferred to each well and pre-incubated for 5 min at 37 °C. Reactions were initiated by the addition of faldaprevir (final concentration 50 µM) to each well and conducted under either aerobic or anaerobic conditions (Li et al., 2012) at 37 °C. Final organic solvent concentration in each reaction was 1%. At 0, 10, 20, 40 and 60 min, a 50 µL aliquot was transferred out and processed by protein precipitation with organic solvent. The samples were analyzed by LC-MS/MS to monitor the formation of M2a and M2b.

Incubation with human liver microsomes, human liver cytosol and recombinant CYPs. Faldaprevir (50 µM) was incubated with HLM, HLC, rCYP1A2, rCYP2B6, rCYP2C8, rCYP2C9, rCYP2C19, rCYP2D6, rCYP3A4 or rCYP3A5 at a protein concentration of 1 mg/ml in 50 mM potassium phosphate buffer (pH 7.4). All samples were pre-incubated for 5 min and reactions were initiated by the addition of NADPH (2 mM) for incubations with HLMs and rCYPs. For incubations with cytosol, faldaprevir was added to initiate the reaction and no NADPH was used. Final organic solvent concentration in each reaction was 1%. At different time points up to 60 min, a 50 µL aliquot was transferred out and processed by protein precipitation with organic solvent. The samples were analyzed by LC-MS/MS to monitor the formation of M2a and M2b.

Kinetic determination of the formation of M2a and M2b by HLM and HIM. Faldaprevir, at total concentrations ranging from 0.363 to 100 µM, was incubated with HLM and HIM at a protein concentration of 0.5 mg/ml. The reactions were initiated by the addition of NADPH at a final concentration of 2 mM. Organic solvent was kept at 1% in all incubations. At specified
time points up to 60 min, a 50 μL aliquot was transferred out and processed by protein precipitation with organic solvent. The samples were analyzed by LC-MS/MS to monitor the formation of M2a and M2b.

**Permeability of faldaprevir, M2a and M2b through Caco-2 cells and their interactions with efflux transporters as substrates.** Caco-2 cells were seeded to collagen-coated, 12-well, polycarbonate membranes in Costar Transwell plates (1.13 cm² insert area, 0.4 μm pore size; Corning Life Sciences, Corning, NY) at a density of 60,000 cells/cm². The plates were placed in a humidified incubator (37°C, 5% CO₂) and the culture medium was changed every other day until the monolayers reached confluence. To initiate the study, the donor compartment was rinsed with the incubation solution (Hanks’ balanced salt solution HBSS containing 10 mM HEPES, 15 mM D-glucose with individual test compound, i.e. M2a at 3 μM, M2b at 3 μM or faldaprevir at 1 μM), to minimize the non-specific binding of the test compound. After the rinse, 0.5 ml (apical) or 1.5 ml (basolateral) of another fresh incubation solution was added to the donor compartment, and 1.5 ml (or 0.5 ml) of HBSS (containing 10 mM HEPES, 15 mM D-glucose and 1% BSA) was added to the receiver compartment. The bidirectional permeability assessment of faldaprevir, M2a and M2b was performed in the incubator in triplicate in each apical-to-basolateral (AP-to-BL) and BL-to-AP direction in the absence and presence of inhibitors of efflux transporters (valspodar at 1 μM, Ko143 at 2 μM or MK-571 at 30 μM). For receiver samples, aliquots (300 μL) were taken at four time points up to 120 min, and the same volume of fresh HBSS containing 10 mM HEPES, 15 mM D-glucose and 1% BSA was added to replace the aliquot. For donor samples, aliquots (20 μL) were taken at the selected time points without replacement. Concentrations of faldaprevir, M2a, and M2b were determined by LC-MS/MS.
Liver uptake of M2a and M2b into human hepatocytes. The HepatoPac model from a female Caucasian donor was prepared by Hepregen Corporation™ as described previously (Khetani et al., 2008). Cryopreserved human hepatocytes were seeded with 5,000 cells per well and cultured for 9 days before being used. Reactions were initiated by adding M2a or M2b (0.01 µM-100 µM), in fresh HepatoPac incubation medium (65 µl) containing 5% bovine serum albumin, to HepatoPac and fibroblast only plates in the absence and presence of an inhibitor, rifamycin SV (100 µM). The plates were cultured in an incubator with 10% CO₂ and 99% relative humidity at 4°C or 37°C. At each time point (0, 2.5, 5, 15, 60, 120, 240, 480, 720, 1440 min), the entire medium was removed from each well, transferred to a 96-well glass fiber filter plate assembly which contained 130 µl of the reaction termination solution (40% acetonitrile, 0.25% formic acid and 0.1 µM internal standard d⁷-faldaprevir in water). These samples were designated as the medium samples. The wells with hepatocytes were quickly washed twice with ice-cold medium to remove residual compound. All wash medium was discarded. After the washes were complete, an equivalent volume of medium (65 µl) was added to each well and the cells were scraped from the bottom of the well using the sharp end of a pipette tip to aid in detachment. The cells were resuspended in the medium aliquot and then transferred to a 96-well glass fiber filter plate assembly containing 130 µl of the reaction termination solution. These samples were designated as the lysate samples. Removal of cell monolayers was confirmed microscopically. All samples were filtered by centrifugation (3000 rpm for 15 min at 4°C). The filtered samples were analyzed by LC-MS/MS to determine the levels of M2a and M2b.

A separate study with human HepatoPac was performed to evaluate the inhibition of M2a and M2b uptake into hepatocytes after their formation from faldaprevir. The study was initiated by adding faldaprevir at a final concentration of 0.3 µM [free concentration at 0.00306 µM, relevant
to free therapeutic concentrations (Ramsden et al., 2013b), in fresh HepatoPac incubation medium (65 µl) containing 5% bovine serum albumin, to HepatoPac plates in the absence and presence of an inhibitor, rifamycin SV (100 µM). At each time point (0, 0.5, 1, 2, 4, 8, 12, 24, 48, 72 and 96 hr), both medium and lysate samples were collected as described above and were analyzed by LC-MS/MS to determine the levels of faldaprevir, M2a and M2b.

**Activity assessment of M2a and M2b.** Inhibition potency of M2a and M2b, in comparison to faldaprevir, against the NS3/4A serine proteases of HCV genotypes 1a and 1b was determined using a fluorogenic assay performed with the NS3/4A heterodimer protease genotype 1a and 1b as described previously (White et al., 2010). Briefly, the reaction mixture comprised 0.5 nM NS3/4A serine proteases of HCV genotypes 1a or 1b, 5 µM fluorogenic depsipeptide substrate anthranilyl-DDIVPAbu[C(O)-O]AMY(3-NO2)TW-OH and inhibitor in a reaction buffer composed of 50 mM Tris-HCl (pH 8.0), 0.25 M sodium citrate, 0.01% n-dodecyl-β-D-maltoside, 1 mM tris(2-carboxyethyl)phosphine (TCEP) plus 5% dimethyl sulfoxide (DMSO). The reaction mixtures were incubated at 23°C for 60 min (genotype 1a NS3/4A protease) or 45 minutes (genotype 1b NS3/4A protease) and terminated by the addition of 1 M morpholineethanesulfonic acid (MES) (pH 5.8). Fluorescence of the N-terminal product anthranilyl-DDIVP-Abu was measured using a POLARStar Galaxy plate reader (BMG Labtech Inc., Cary, NC). Calculated percent inhibition at each inhibitor concentration was then used to determine the median 50% inhibition concentration (IC$_{50}$) (Assay Explorer v3.2; Symyx Technologies).

**LC-MS conditions.** The formation of M2a and M2b from faldaprevir during storage and sample extraction was monitored by an LC-MS/MS system under the same conditions as used for metabolite identification in the human [14C] ADME study. This system consisted of an Agilent 1200 high performance LC system (Palo Alto, CA) with a Thermo LTQ Orbitrap XL
mass spectrometer (Thermo Scientific, San Jose, CA) equipped with Advion TriVersa NanoMate ion source (Advion BioSystems, Ithaca, NY). Metabolite separation was achieved using a reverse-phase HPLC column (Phenomenex Gemini C18, 3 µm, 150 x 4.6 mm column; Torrance, CA). Mobile phase A consisted of 40 mM ammonium acetate in water, adjusted to pH 5.5 with formic acid and mobile phase B consisted of acetonitrile. The gradient conditions were: 100% A for 5 min, then to 15% B over 15 min, to 75% B over 40 min, to 100% B over 5 min, and held at 100% B for 5 min. The HPLC flow rate was 0.7 ml/min.

The levels of faldaprevir, M2a and M2b in other in vitro assays were quantitated by LC-MS/MS using a 4000 Qtrap (AB Sciex, Thornhill, Ontario, Canada) attached to either a CTC PAL autosampler (Leap Technologies, Carrboro, NC)-Agilent 1200 UPLC system or a Waters Acquity UPLC system (Milford, MA). Mobile phases included 5% acetonitrile in water as the aqueous phase and 95% acetonitrile in water as the organic phase. Each mobile phase contained 0.1% acetic acid. Columns used included Waters Acquity UPLC BEH C18 column (50 x 2.1 mm, 1.7 µm) or Thermo Hypersil GOLD column (50 x 2.1 mm, 1.9 µm) and were maintained at 50 or 45°C, respectively. The MRM transitions were 869→422 for faldaprevir, 885→422 for M2a and M2b, and 876→429 for d7-faldaprevir using positive ionization mode.

Data analysis.

Determination of CLint at estimated hepatic substrate concentrations. Km and Vmax values for the formation of M2a and M2b with HLM and HIM, using the 5-min incubation time point, were determined by fitting the data with nonlinear least squares regression using GraphPad Prism Version 5 (GraphPad Software Inc.; San Diego, CA). Intrinsic clearance (CLint) for formation of M2a or M2b was estimated with Equation 1. Substrate concentration [S] in
Equation 1 refers to the effective in vivo substrate concentration in respective organs ([S]_h for liver or [S]_g for gut). Multiple [S]_h values were estimated, including maximum unbound plasma concentration (Equation 2), maximum unbound hepatic inlet concentration (Equation 3) (Ito et al., 2002), or maximum unbound plasma concentration times a liver enrichment factor (Equation 4). The liver enrichment factors at clinically relevant doses of 120 mg QD and 240 mg QD were estimated to be 31.5 and 21.9, respectively, based on the concentration differences in culture medium and cell lystate determined in the human HepatoPac model (Ramsden et al., 2013b). [S]_g was estimated with Equation 5 (Rostami-Hodjegan et al., 2004).

\[
\text{Equation 1} \quad \text{CL}_{\text{ext}} = \frac{V_{\text{max}}}{K_m + [S]}
\]

\[
\text{Equation 2} \quad [S]_{h,A} = f_{u,p} \cdot C_{\text{max}}
\]

\[
\text{Equation 3} \quad [S]_{h,B} = f_{u,p} \cdot C_{\text{max}} + \left(\frac{f_{u,p}}{B/P}\right) \cdot k_a \cdot F_a \cdot \frac{\text{Dose} / Q_h}{K_v = 0.1 \text{ min}^{-1}}
\]

\[
\text{Equation 4} \quad [S]_{h,D} = f_{u,p} \cdot C_{\text{max}} \cdot \text{Liver enrichment factor}
\]

\[
\text{Equation 5} \quad [S]_g = k_a \cdot F_a \cdot \frac{\text{Dose} / Q_{en}}{}
\]

In Equations 2 to 5, f_{u,p} is the free fraction of faldaprevir in human plasma; B/P refers to faldaprevir blood to plasma ratio; F_a is the fraction of faldaprevir absorbed after oral administration (a value of 1 was used); k_a refers to first order absorption rate constant and either a default value of 0.1 min^{-1} or an estimated value based on clinical t_{max} and t_{1/2} was used (Gertz et al., 2011); C_{\text{max}} is the maximum faldaprevir plasma concentration; Q_h is hepatic blood flow (Q_h=...
1617 ml/min) (Yang et al., 2007a); and Q_{en} is blood flow through enterocytes (Q_{en}= 300 ml/min) (Yang et al., 2007b).

**Estimate of CL_{h,B} and F_{h}**  Hepatic clearance (CL_{h,B}) was calculated based on the *in vitro* clearance and whole blood drug concentration using three models: standard well-stirred model (Equation 6) (Yang et al., 2007a) and two modified well stirred models incorporating either binding differences in liver and plasma (Equation 7) (Poulin et al., 2012a) or liver uptake (Equation 8) (Webborn et al., 2007). F_{h} (the fraction of drug escaping metabolism through the formation of M2a and M2b in the liver) was calculated based on Equation 9.

**Equation 6**

\[
CL_{h,B,M \ 2a+M \ 2b} = \frac{Q_{h} \cdot \frac{f_{u,p}}{B/P} \cdot CL_{\text{int}, M \ 2a+M \ 2b}}{Q_{h} + \frac{f_{u,p}}{B/P} \cdot CL_{\text{int}, M \ 2a+M \ 2b}}
\]

**Equation 7**

\[
CL_{h,B,M \ 2a+M \ 2b} = \frac{Q_{h} \cdot \frac{f_{u,liver}}{B/P} \cdot CL_{\text{int}, M \ 2a+M \ 2b}}{Q_{h} + \frac{f_{u,liver}}{B/P} \cdot CL_{\text{int}, M \ 2a+M \ 2b}}
\]

**Equation 8**

\[
CL_{h,B,M \ 2a+M \ 2b} = \frac{Q_{h} \cdot \frac{f_{u,p}}{B/P} \cdot CL_{\text{int}, M \ 2a+M \ 2b} \cdot (CL_{\text{uptake, liver}} + CL_{\text{uptake, passive}})}{Q_{h} \cdot (CL_{\text{uptake, liver}} + CL_{\text{uptake, passive}}) + \frac{f_{u,p}}{B/P} \cdot CL_{\text{uptake, liver}} + \frac{f_{u,p}}{B/P} \cdot CL_{\text{uptake, passive}}}
\]

**Equation 9**

\[
F_{h,M \ 2a+M \ 2b} = 1 - \frac{CL_{h,B,M \ 2a+M \ 2b}}{Q_{h}}
\]

**Equation 10**

\[
f_{u,liver} = \frac{PLR \cdot f_{u,p} \cdot F_{I}}{1 + (PLR - 1) \cdot f_{u,p} \cdot F_{I}}
\]
Where $Q_h$ refers to hepatic blood flow (1617 ml/min), $f_{u,p}$ is the free fraction of faldaprevir in plasma, $B/P$ is the blood to plasma ratio, and $CL_{int,M2a+M2b}$ is the sum of intrinsic clearance values for the formation of M2a and M2b in the liver. The scaling factor of hepatic microsomal recovery was 40 mg/g of liver (Barter et al., 2007), and the total liver weight was 1800 g per 70 kg body weight (Davies et al., 1993). The $CL_{int,uptake}$ and $CL_{int,passive}$ in Equation 8 refer to the intrinsic clearance of sinusoidal uptake and passive diffusion, respectively. The input values for $CL_{int,uptake}$ were 41446 ml/min for 120 mg QD dosing and 32118 ml/min for 240 mg QD dosing, and the input value for $CL_{int,passive}$ was 13428 ml/min (Ramsden et al., 2013b).

The free fraction of drug in liver ($f_{u,liver}$) in Equation 7 was estimated using Equation 10, which considered the difference in drug ionization and binding proteins in plasma and in liver. The $F_I$ in Equation 10 corresponds to the ratio of fraction of unionized drugs in extracellular plasma (pH 7.4) to intracellular tissue water (pH 7.0). Faldaprevir is an ampholyte, with acidic pKa of 5.7 and basic pKa of 3.1 (data on file, Boehringer Ingelheim Pharm. Inc.). At pH 7.4 and 7.0, the basic ionization group is mostly unionized. $F_I$ value was therefore calculated to be 0.410 based on the fraction of unionized species of the acidic ionization group at pH 7.4 to pH 7.0. The PLR in Equation 10 refers to the ratio of binding protein concentration in the plasma to the whole liver. Faldaprevir extensively binds to serum albumin (see result section). Thus a value of 13.3 was used according to Poulin et al. (Poulin et al., 2012b).

**Estimate of gut metabolism.** $Q_{gut}$ model was used to scale the *in vitro* clearance to intestinal clearance using Equations 11 and 12 (Yang et al., 2007b).

Equation 11

$$Q_{gut} = \frac{Q_{villi} \cdot CL_{perm}}{Q_{villi} + CL_{perm}}$$
In this model, \( f_{u, \text{gut}} \) is the free fraction of faldaprevir in gut and was assumed to be equal to 1 (Yang et al., 2007b) and \( F_{g, M2a+M2b} \) is the fraction of drug escaping metabolism through the formation of M2a and M2b in the intestine. The \( Q_{\text{gut}} \) in Equation 12 is a hybrid term of the villous blood flow (\( Q_{\text{villi}} \)) and permeability clearance (\( CL_{\text{perm}} \)) (Equation 11). The input value for \( Q_{\text{villi}} \) was 300 ml/min. The \( CL_{\text{perm}} \) is calculated as the net cylindrical surface area of the small intestine (\( A \)) times the effective permeability in human (\( P_{\text{eff}} \)). The input value for \( A \) was 0.66 m\(^2\). \( CL_{\text{int}, M2a+M2b} \) in Equation 12 is the sum of intrinsic clearance values for the formation of M2a and M2b in gut. The \( CL_{\text{int}, M2a+M2b} \) in gut was scaled by two methods: 1) based on average CYP3A abundance (50 pmol/mg of protein) (Gertz et al., 2010) and total intestinal CYP3A content (70.5 nmol) (Paine et al., 1997); and 2) based on intestinal microsomal recovery (3 mg/g of intestine and the total intestine weight of 2100 g per 70 kg human) (Soars et al., 2002).
**Results**

**Stability of faldaprevir in human feces.** Faldaprevir was spiked into fresh human fecal samples, followed by storage and sample extraction, which mimicked the conditions used for the processing of fecal samples in the [14C] human ADME studies. No M2a and M2b were found in these samples.

**Formation of M2a and M2b in various enzyme systems.** Faldaprevir was incubated with fresh human feces under aerobic and anaerobic conditions. Neither M2a nor M2b was detected after the incubations. Similarly, M2a and M2b were not found after incubation with HLC. M2a and M2b were detected in the human liver microsomal incubation samples.

Formation rates of M2a and M2b by rCYP isoforms (rCYP1A2, rCYP2B6, rCYP2C8, rCYP2C9, rCYP2C19, rCYP2D6, and rCYP3A4) were determined. The contribution of each CYP to the formation of M2a and M2b was determined based on rates of metabolite formation after normalization by relative liver content of each CYP. The normalized contributions by rCYP3A4 were 94% and 97%, respectively, for M2a and M2b. Minimal contribution was observed in incubations with CYP2C8 and no formation of M2a and M2b was observed with other CYP isoforms (Fig. 2).

The relative contribution of CYP3A4 and CYP3A5 to the formation of M2a and M2b was assessed using recombinant enzymes (208 pmol/ml) in a separate study. rCYP3A4 and rCYP3A5 formed M2a at comparable rates, while the formation rate of M2b was 27-fold higher in incubations with rCYP3A4 compared to rCYP3A5 (Table 1). Based on the relative content of CYP3A4 and CYP3A5 in subjects with different CYP3A5 genotypes (Lin et al., 2002), the expected relative contributions of CYP3A4 and CYP3A5 to the formation of M2a and M2b and
the relative ratio of the formation of M2a and M2b were calculated specifically for each CYP3A5 genotypes (Table 1). CYP3A5 has minimal contribution to the formation of M2b, and its contribution to the formation of M2a varies based on CYP3A5 genotype.

Considering the slow in vitro metabolism of faldaprevir, a high faldaprevir concentration (50 µM) and high protein concentrations were used in these in vitro systems in order to ensure sufficient turnover to form the metabolites. This faldaprevir concentration is 10-fold higher than steady-state plasma C_{max} of faldaprevir (4.18 µM in Phase II trial 1220.5, Data on file, Boehringer Ingelheim Pharmaceuticals, Inc.) after oral dosing of faldaprevir at 120 mg QD in patients but was still relevant to therapeutic concentrations at the higher dose since there is non-linearity in PK (steady-state plasma C_{max} of faldaprevir was 23.9 µM after oral dosing of faldaprevir at 240 mg QD in patients in Phase II trial 1220.5; Data on file, Boehringer Ingelheim Pharmaceuticals, Inc.). As for the CYP phenotyping study, since there was almost no turnover with recombinant CYPs other than rCYP3A4/5 at a faldaprevir concentration of 50 µM, significant turnover with CYPs other than CYP3A4/5 at lower substrate concentrations would not be expected.

**Kinetics of the formation of M2a and M2b.** Faldaprevir was incubated with HLM or HIM at 0.5 mg/ml protein concentration and the formation of M2a and M2b over time was measured. Fraction of unbound faldaprevir (f_u) in the HLM and HIM incubations were measured by equilibrium dialysis at the same protein concentration (0.5 mg/ml). The average f_u of faldaprevir was determined to be 0.275 and 0.127 for HIM and HLM, respectively, and the f_u values in each matrix were consistent over a wide range of faldaprevir concentrations (0.5 µM to 100 µM). Unbound substrate concentrations ([S]_u) in incubations were calculated after correcting the total concentrations with microsomal binding. The kinetic profiles for M2a and
M2b formation by HLM and HIM are presented in concentration-velocity plots (Fig. 3A-3D).

Although the kinetic profiles for M2a and M2b formation resemble a typical substrate inhibition kinetic profile, the empirical substrate inhibition model did not accurately describe the kinetic data, suggesting that the decrease in velocity at high substrate concentrations may be due to other mechanism(s). A time and faldaprevir concentration-dependant loss of CYP3A4 enzyme activity was observed in a separate study, which is related to weak to moderate inactivation of CYP3A4 by faldaprevir (Data on file, Boehringer Ingelheim Pharmaceuticals, Inc.).

Based on these findings, the kinetic analysis for parameter estimation was then performed with the 5-min incubation data sets as these were the least affected by time-dependent inhibition of CYP3A4. Data points which displayed substrate-inhibition (decreasing velocity with increasing substrate concentration) were also eliminated from further kinetic analysis since these points were likely affected by faldaprevir-mediated CYP3A4 inactivation. Fig. 4A and Fig. 4B show the kinetic plots for M2a and M2b formation by HLM and HIM, respectively, using only the 5-min incubation data and after removing free concentrations above 8 µM to minimize the impact of CYP3A4 inactivation. The kinetic data fitted the Michaelis-Menten equation and the kinetic parameters generated are shown in Table 2. Intrinsic clearance, organ clearance (CL_{h,B} and CL_{g}), and the fraction of drug escaping metabolism (F_{h} and F_{g}) were estimated using multiple estimated hepatic/intestinal concentrations and multiple in vitro to in vivo correlation (IVIVC) models. The results are shown in the supplemental data (Table S-1 to S-3) and are summarized in Table 3. The unbound fraction of faldaprevir in plasma (f_u,p) was determined to be 0.002 by equilibrium dialysis using pooled human plasma and remained constant over a range of faldaprevir concentrations (1.1 µM-46 µM). Binding of faldaprevir to human serum albumin was high with f_u determined to be 0.003 to 0.008 over a wide range of faldaprevir concentrations.
(0.3-115 µM). Blood to plasma ratio (B/P) of faldaprevir was determined in vitro by measuring the total radioactivity in human plasma and whole blood. Blood cell partitioning was not dependent on faldaprevir concentration, with an average B/P ratio of 0.613. The other parameters used in the calculations of intrinsic clearance, organ clearance, and the fraction of drug escaping metabolism in liver and intestine are listed in the method section and contained in the supplemental data.

The free steady state C\text{max} ([S]_{h,A}) was 0.00836 and 0.0478 µM using f_o of 0.002 after dosing with faldaprevir 120 mg QD and 240 mg QD, respectively, in Phase II trials (Table S-1 in the supplemental data). Other estimated liver concentrations ([S]_{h, B-D}) ranged from 0.0127 µM to 1.05 µM (Table S-1in the supplemental data). These concentrations were all below 8 µM (the highest in vitro free concentration in Fig. 4), supporting the removal of higher concentrations in generating kinetics. The concentration of faldaprevir in enterocytes ([S]_{g}) was estimated to be 7.22 to 92.0 µM after 120 mg and 240 mg QD dosing (Table S-1in the supplemental data), which are at the high end of the curve or greater than the concentration range used to generate kinetics for the formation of M2a and M2b in HIM. Therefore, the decrease of velocity at the higher concentrations in the HIM incubations may not be captured in the calculation of CL_{int, M2a+M2b} in the gut, resulting in an overestimation of CL_{g, M2a+M2b}. However, even with this overestimation, the calculated CL_{g, M2a+M2b} was still very low comparing to intestinal blood flow. Therefore, the overestimation is not expected to impact the conclusion.

**Permeability and interaction with efflux transporters of M2a and M2b and comparison with faldaprevir.** The absorptive permeability (apical to basolateral) and efflux transport (basolateral to apical) of M2a, M2b and faldaprevir were evaluated using Caco-2 cell monolayers and are shown in Fig. 5. The absorptive permeability values for M2a and M2b were similar at
approximately 0.14 x 10^{-6} \text{ cm/sec} \text{ and } 0.16 x 10^{-6} \text{ cm/sec} and were lower than the efflux permeability values of approximately 5.8 x 10^{-6} \text{ cm/sec} \text{ and } 4.2 x 10^{-6} \text{ cm/sec}, \text{ respectively}. These permeability values were considerably lower than for faldaprevir which were approximately 11 x 10^{-6} \text{ cm/sec} \text{ and } 61 x 10^{-6} \text{ cm/sec} for absorptive and efflux permeability, respectively.

The impact of specific inhibitors of transport was evaluated. Valspodar, Ko143, and MK571 were used as specific inhibitors of P-gp, BCRP, and MRP2, respectively. The efflux ratios of both metabolites were significantly reduced by inhibitors of P-gp (valspodar) and BCRP (Ko143), indicating both metabolites are substrates of P-gp and BCRP. Consequently, the efflux ratios of both metabolites were further reduced by a mixture of valsopodar and Ko143. MK571, an MRP2 inhibitor, together with valsopodar and Ko143, had no to minimal impact on the efflux ratios of M2a and M2b, suggesting they are not substrates of MRP2.

Faldaprevir is subject to efflux by P-gp since valsopodar partially reduced the efflux transport of faldaprevir. The addition of Ko143 and MK571 on top of valsopodar had limited impact on the efflux of faldaprevir. However, the efflux ratios did not normalize to ~1 even in the presence of inhibitors of all three efflux transporters, suggesting possible involvement of other efflux transporters.

**Active uptake of M2a and M2b in hepatocytes.** The active uptake of M2a and M2b was determined using the human HepatoPac model in the presence and absence of rifamycin SV (100 \mu M) and at 37\textdegree C \text{ vs. } 4\textdegree C by measuring intracellular levels of the test compounds over 60 min (Fig. 6, A and B). The passive permeability was minimal for M2a and M2b at all time points as determined at 4\textdegree C (with or without rifamycin SV). Significant active uptake was observed for
M2a and M2b at 37°C compared to 4°C and the uptake of M2a and M2b was markedly inhibited by rifamycin SV at 37°C by 15- and 17-fold, respectively.

In a separate study, the impact of rifamycin SV inhibition on the formation of M2a and M2b from faldaprevir was also evaluated (Fig. 7). In the absence of rifamycin SV, both M2a and M2b were detected in the medium and lysate, with M2b levels slightly higher than M2a. In the presence of rifamycin SV, the total amounts of M2a and M2b formed decreased on average by ~60% over 24 hr and neither of the metabolites were detected in the lysate. In the same study, faldaprevir uptake was inhibited to a similar extent (~60%) on average over the experimental time-course (through 24 hr).

**Activity of M2a and M2b against NS3/4A protease.** M2a and M2b were tested in the genotype 1a and 1b protease assays using the same method described previously (White et al., 2010). The activity of faldaprevir was also measured in parallel for comparison. Both metabolites were more potent inhibitors of genotype 1 NS3/4A proteases than faldaprevir. M2a had IC\textsubscript{50} values of 1.5 and 1.7 nM and M2b had IC\textsubscript{50} values of 3.6 and 2.2 nM for genotype 1a and 1b enzymes, respectively (Table 4).
Discussion

Human $^{14}$C ADME studies can provide a thorough assessment of the metabolism and excretion of compounds in Drug Development. Recent technological advances provide confidence in metabolite profiling via non-radiolabelled methods, generally applied to plasma and urine samples (Nedderman et al., 2011; Obach et al., 2012). These approaches have meant that there should be few surprises from human $^{14}$C ADME studies. The human $^{14}$C ADME study for faldaprevir revealed the unexpected presence of two abundant hydroxylated metabolites in feces that were not detected in the systemic circulation (Chen et al, 2013). It was therefore important to identify the enzymes and tissues responsible for the metabolism of faldaprevir in order to understand the formation and distribution of these metabolites.

Using recombinant CYPs, CYP3A4 was shown to be almost exclusively responsible for the formation of M2a and M2b, with a very minor contribution from CYP2C8 (Fig. 2). Both CYP3A4 and CYP2C8 have an expansive active site (Yano et al., 2004; Scott et al., 2005, Schoch et al., 2008) capable of accommodating large molecules such as faldaprevir (870 Da). Formation of M2a and M2b by additional mechanisms, e.g. faldaprevir degradation in feces or metabolism by gut bacteria, although unlikely, was evaluated and excluded.

CYP3A4 and CYP3A5 have overlapping substrate specificities (Lamba et al., 2002) and both enzymes can produce M2a and M2b (Table 1). CYP3A5 expression is highly variable in humans, with readily detectable levels in 25 to 30% of the population and very low or undetectable levels in the remainder (Wrighton et al., 1990; Paine et al., 1997; Wrighton et al., 2000). Normalizing the formation of M2a and M2b by the relative content of CYP3A4 and CYP3A5 in subjects with different CYP3A5 genotypes (Lin et al., 2002) indicated that M2a is formed primarily by CYP3A4 with substantial contribution by CYP3A5 only in subjects with the
CYP3A5 genotype *1*1 (~1.7% of population) (Table 1). M2b was mostly formed by CYP3A4 with negligible contribution from CYP3A5. Interestingly, in the most abundant CYP3A5 genotype (*3/*3), the formation of M2b is slightly higher than M2a (1.5-fold; Table 1). Overall, CYP3A5 polymorphisms are not expected to significantly impact the variability of faldaprevir exposure.

Since CYP3A4 and CYP3A5 are extensively expressed in liver and intestine, it was important to determine whether M2a and M2b are formed in the intestine, then excreted directly into feces, or are formed in the liver. The intestine is an important site for CYP3A-dependant first pass metabolism (Paine et al., 1997). For example, extraction ratios for the prototypical CYP3A substrate, midazolam, are comparable in liver and intestine (Paine et al., 1996; Thummel et al., 1996). The *in vitro* kinetics of faldaprevir metabolism did not fit to a substrate inhibition model (Fig. 3) and was complicated by the fact that faldaprevir is a weak to moderate inactivator of CYP3A4. Using the shortest incubation time (5 min) and lower unbound substrate concentrations to minimize the impact of CYP3A4 inactivation, the formation of M2a and M2b fitted to Michaelis-Menten kinetics with similar apparent $K_m$ values (Table 2). The CYP3A4 activity of the pooled HLM and HIM lots used in our studies was average for humans (testosterone-6β-hydroxylation, 5300 and 1260 pmol/min/mg, respectively). By comparison, the $V_{max}$ values for M2a and M2b were much lower (<34 pmol/min/mg for HLM and <7 pmol/min/mg for HIM). Intrinsic clearances for formation of M2a and M2b in liver and intestine were calculated, after incorporation of estimated hepatic and intestinal concentrations of faldaprevir (Table 3).

Typically, the well stirred model is used for estimation of hepatic clearance (Houston, 1994). The Poulin method showed better accuracy (Poulin et al., 2012a), compared to other *in vitro-in*
*vivo* extrapolation methods for hepatic clearance estimation, especially for low clearance compounds highly bound to albumin. Faldaprevir fits this profile. This method incorporates a correction factor for higher fraction of unbound drug in the liver, resulting in higher metabolic CL. Because faldaprevir is a substrate of uptake transporters, a modification of the well-stirred model, incorporating active uptake, was also used (Webborn et al., 2007). These modified models were preferred because they incorporated important properties of faldaprevir (high protein binding and liver uptake), and resulted in higher hepatic clearance compared to the standard well stirred model (Table 3).

F_{g} was estimated with a “Q_{gut}” model (Table 3), which retains the form of the well-stirred model, but the flow term (Q_{gut}) is a hybrid of both permeability through the enterocyte membrane and villous blood flow, which captures the fact that lower permeability would increase the compound’s first-pass exposure to DMEs in gut. The Q_{gut} model showed significantly improved predictive accuracy for F_{g} over the well-stirred model (Yang et al., 2007b).

Formation of M2a and M2b is expected to be very slow in both liver and intestine based on low CL_{h,B} and CL_{g} (<< hepatic and intestinal blood flow) and high fraction of drug escaping hepatic and intestinal metabolism (Table 3). This is also consistent with low oral clearance of faldaprevir in humans (oral blood clearance at steady state, CL_{B}/F_{ss}, from the Phase II study 1220.5 was approximately 67.4 ml/min after 120 mg QD dosing and 19.7 ml/min after 240 mg QD dosing, data on file, Boehringer Ingelheim Pharmaceuticals, Inc.). Using the modified well stirred models, CL_{h,B} was estimated to be significantly higher than CL_{g}. In addition, faldaprevir has a long half life in human (>20 hr), taking 7 days to excrete 85% of the dose (Chen et al,
Therefore, faldaprevir is expected to be slowly metabolized in the liver to form M2a and M2b over several days and as such first pass intestinal metabolism is minimal.

Accumulation of faldaprevir in liver (Ramsden et al., 2013a; 2013b) raises questions about possible contributions of uptake and efflux transporters (Shitara et al., 2005; Shitara et al., 2006). Compared to faldaprevir, M2a and M2b demonstrated considerably lower (10-fold) absorptive and efflux transport in Caco-2 cells (Fig. 5). M2a and M2b are good substrates of P-gp and BCRP with efflux ratios greater than 26 (Fig. 5A and 5B). The passive permeability of M2a and M2b into hepatocytes was also negligible (Fig. 6). The active uptake of M2a and M2b into hepatocytes was largely inhibited by rifamycin SV, suggesting that they are substrates of OATPs (Vavricka et al., 2002). Rifamycin SV has also been shown to inhibit NTCP (Mita et al., 2006). Therefore, the possibility that M2a and M2b are substrates of NTCP cannot be excluded.

Incubation of faldaprevir with human HepatoPac resulted in very high intracellular levels of M2a and M2b (Fig. 7). This enrichment is likely an artifact because the metabolites are initially formed in cells. After that, they are excreted (passively or actively) into medium at low levels and are then more efficiently taken back into hepatocytes by uptake transporters, resulting in artificially high hepatocyte enrichment values. Consistent with this hypothesis, in the presence of rifamycin SV, the levels of M2a and M2b in incubations decreased and the metabolites were no longer detectable in hepatocytes (Fig. 7). Faldaprevir uptake was inhibited by ~60% in the same study, contributing to the lower formation of M2a and M2b. The absence of M2a and M2b in cell lysate, in the presence of rifamycin SV, is likely a combination of inhibition of re-uptake of M2a and M2b and lower formation. By contrast, in vivo, M2a and M2b, once formed in liver, would be efficiently removed from the cells via bile and excreted. Therefore the levels of M2a
and M2b in the liver *in vivo* are expected to be low. This is also consistent with the lack of circulating levels of M2a and M2b in blood.

M2a and M2b are pharmacologically active (2- to 4-fold more potent than faldaprevir in HCV Genotype 1a and 1b NS3/4A protease inhibition assays; Table 4). However, the contribution of M2a and M2b to the clinical efficacy should be limited considering their expected low exposure in liver due to slow formation and efficient efflux into bile.

Since faldaprevir is predominantly metabolized by CYP3A in the liver, its exposure may be affected by concomitant medications that inhibit or induce hepatic CYP3A. Based on our findings, inhibition of CYP3A in the gut is unlikely to change faldaprevir exposure. Administration of faldaprevir with an inducer (efavirenz) (Kiser et al., 2013) or an inhibitor (itraconazole, data unpublished) of CYP3A produced moderate DDIs. Thus, although faldaprevir has a very low metabolic clearance, metabolism is still an important clearance pathway.

In summary, faldaprevir is metabolized primarily in liver by CYP3A4/5 to form two abundant metabolites, M2a and M2b. With low permeability, M2a and M2b are not expected to diffuse freely from the liver. Efflux transporters (P-gp and BCRP) facilitate excretion of M2a and M2b into bile. If low levels of metabolites permeate to blood, they can be readily taken back up into hepatocytes by uptake transporters (likely OATPs). In addition, as a result of the low permeability, the absorption of M2a and M2b from the intestine is expected to be limited. The combination of these processes explains the absence of these metabolites in the systemic circulation. Overall, understanding the fate of M2a and M2b has been helpful to explain/predict clinical DDIs with faldaprevir as a victim drug and qualify their possible contribution to the overall anti-viral activity. Fecal metabolites are generally overlooked due to a lack of clinical
impact. Our studies demonstrate that some fecal metabolites could be of clinical relevance and may warrant further evaluation.
Acknowledgments:

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Authorship Contributions:

Participated in research design: Li, Zhou, Ramsden, Taub, and Tweedie.

Conducted experiments: Zhou, Ramsden, O'Brien, and Xu.

Contributed new reagents or analytic tools: Busacca and Gonnella.

Performed data analysis: Li, Zhou, Ramsden, O'Brien, Xu, and Taub.

Wrote or contributed to the writing of the manuscript: Li, Ramsden, and Tweedie
References


Ramsden D, Tweedie DJ, St George R, Chen LZ, and Li Y (2013a) Generating an IVIVC for metabolism and liver enrichment of an HCV drug, faldaprevir, using a rat hepatocyte model (HepatoPac™). *Drug Metab Dispos*, submitted.


Pharmacokinetics, metabolism, and excretion of the glycogen synthase kinase-3 inhibitor LY2090314 in rats, dogs, and humans: a case study in rapid clearance by extensive metabolism with low circulating metabolite exposure. *Drug Metab Dispos* 41:714-726.
Footnote:

This research was funded by Boehringer Ingelheim Pharmaceuticals, Inc.
Figure legends:

Fig. 1. Chemical structures of faldaprevir, M2a and M2b

Fig. 2. Relative contribution (%) of major 7 CYPs to the formation of M2a and M2b using rCYPs

Fig. 3. Concentration-velocity plots for the formation of M2a (A) and M2b (B) in HLM and the formation of M2a (C) and M2b (D) in HIM. Experiments were conducted on two separate occasions.

Fig. 4. Kinetic plots for the formation M2a and M2b in HLM (A) and HIM (B) with 5-min incubation. Data points which have lower velocity at a higher substrate concentration were eliminated. The solid lines in the concentration-velocity plots were generated by fitting Michaelis-Menten model to data.

Fig. 5. Transport of M2a (A), M2b (B) and faldaprevir (C) in the absence and presence of inhibitors. Val: valspodar; Ko: Ko143; MK: MK571; ER: efflux ratio. (n=3)

Fig. 6. Uptake of M2a (A) and M2b (B) into human hepatocytes. RIFsv represents rifamycin SV; Data points with 37°C, -RIFsv represent the sum of uptake and passive permeability of test compounds; Data points with 4°C, -RIFsv represent passive permeability of test compounds; the inhibitory effects of rifamycin SV were evaluated at 37°C, +RIFsv and 4°C, +RIFsv by comparing to the data points obtained at 37°C, -RIFsv and 4°C, -RIFsv, respectively. (n=3)

Fig. 7. Concentrations of M2a and M2b in medium (white bar □) and lysate (black bar ■) after incubating faldaprevir (0.3 µM) with human HepatoPac for 24 hr without rifamycin SV (-RIFsv) or with rifamycin SV (100 µM) (+RIFsv). (n=3)
TABLE 1: Comparison of the contribution of CYP3A4 vs. CYP3A5 to the formation of M2a and M2b

<table>
<thead>
<tr>
<th>CYP3A5 allelic variants</th>
<th>Frequency (Lin et al., 2002)</th>
<th>Contribution of CYP3A4:CYP3A5, normalized by relative content of CYP3A4 and CYP3A5 in subjects with different CYP3A5 allelic variants</th>
<th>Ratio of formation rates for M2a vs. M2b, normalized by relative content of CYP3A4 and CYP3A5 in subjects with different CYP3A5 allelic variants</th>
</tr>
</thead>
<tbody>
<tr>
<td>*1/*1</td>
<td>1.7%</td>
<td>M2a: 30 : 70, M2b: 89 : 11</td>
<td>M2a:M2b: 1:0.51</td>
</tr>
<tr>
<td>*1/*3</td>
<td>22%</td>
<td>M2a: 58 : 42, M2b: 96 : 4</td>
<td>M2a:M2b: 1:0.92</td>
</tr>
<tr>
<td>*3/*3</td>
<td>77%</td>
<td>M2a: 97 : 3, M2b: 99.8 : 0.2</td>
<td>M2a:M2b: 1:1.5</td>
</tr>
</tbody>
</table>

Metabolite formation rate in rCYP3A4 : Metabolite formation rate in rCYP3A5
(at the same CYP content, 208 pmol/ml)

<table>
<thead>
<tr>
<th>Metabolite formation rate</th>
<th>M2a</th>
<th>M2b</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1.4 : 1</td>
<td>27 : 1</td>
</tr>
</tbody>
</table>

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TABLE 2. Kinetic parameters of the formation M2a and M2b in HLM and HIM (n=2 for each experiment)

<table>
<thead>
<tr>
<th></th>
<th>HLM</th>
<th>M2a</th>
<th>M2b</th>
<th>HIM</th>
<th>M2a</th>
<th>M2b</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Km (μM)</td>
<td>V&lt;sub&gt;max&lt;/sub&gt; (pmol/min/mg of protein)</td>
<td>Km (μM)</td>
<td>V&lt;sub&gt;max&lt;/sub&gt; (pmol/min/mg of protein)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Experiment 1</td>
<td>4.30</td>
<td>(0.274)&lt;sup&gt;a&lt;/sup&gt;</td>
<td>25.1</td>
<td>(0.823)</td>
<td>4.27</td>
<td>(0.334)</td>
</tr>
<tr>
<td>Experiment 2</td>
<td>3.70</td>
<td>(0.172)</td>
<td>23.8</td>
<td>(0.538)</td>
<td>3.78</td>
<td>(0.212)</td>
</tr>
<tr>
<td>Average</td>
<td>4.00</td>
<td></td>
<td>24.5</td>
<td></td>
<td>4.02</td>
<td></td>
</tr>
<tr>
<td>Experiment 1</td>
<td>4.74</td>
<td>(0.528)</td>
<td>4.59</td>
<td>(0.299)</td>
<td>4.56</td>
<td>(0.455)</td>
</tr>
<tr>
<td>Experiment 2</td>
<td>4.62</td>
<td>(0.701)</td>
<td>4.27</td>
<td>(0.345)</td>
<td>3.94</td>
<td>(0.532)</td>
</tr>
<tr>
<td>Average</td>
<td>4.68</td>
<td></td>
<td>4.43</td>
<td></td>
<td>4.25</td>
<td></td>
</tr>
</tbody>
</table>

<sup>a</sup> Numbers in parentheses are SEs of estimates.
TABLE 3. Summary of CL_{int}, organ clearance, and the fraction of drug escaping metabolism through the formation of M2a and M2b in liver and intestine

<table>
<thead>
<tr>
<th>Organ</th>
<th>Clinical dose</th>
<th>( \text{CL}_{\text{int}, \text{M2a}} ) (µl/min/mg of protein)</th>
<th>( \text{CL}_{\text{int}, \text{M2b}} ) (µl/min/mg of protein)</th>
<th>( \text{CL}_{\text{int}, \text{M2a+M2b}} ) (µl/min/mg of protein)</th>
<th>( \text{CL}_{\text{h,B,M2a+M2b}} ) (ml/min/liver)</th>
<th>( F_{h, \text{M2a+M2b}} )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Liver</td>
<td>120 mg QD</td>
<td>5.75-6.11</td>
<td>8.01-8.52</td>
<td>13.8-14.6</td>
<td>3.94-4.24 (well stirred model)</td>
<td>0.986-0.998</td>
</tr>
<tr>
<td></td>
<td>240 mg QD</td>
<td>4.85-6.05</td>
<td>6.77-8.43</td>
<td>11.6-14.5</td>
<td>3.25-4.19 (well stirred model)</td>
<td>0.986-0.998</td>
</tr>
<tr>
<td>Intestine</td>
<td>Clinical dose</td>
<td>( \text{CL}_{\text{int}, \text{M2a}} ) (µl/min/mg of protein)</td>
<td>( \text{CL}_{\text{int}, \text{M2b}} ) (µl/min/mg of protein)</td>
<td>( \text{CL}_{\text{int}, \text{M2a+M2b}} ) (µl/min/mg of protein)</td>
<td>( \text{CL}_{\text{g,M2a+M2b}} ) (ml/min/intestine)</td>
<td>( F_{g, \text{M2a+M2b}} )</td>
</tr>
<tr>
<td></td>
<td>120 mg QD</td>
<td>0.0874-0.372</td>
<td>0.133-0.582</td>
<td>0.220-0.954</td>
<td>0.307-4.94</td>
<td>0.823-0.989</td>
</tr>
<tr>
<td></td>
<td>240 mg QD</td>
<td>0.0458-0.205</td>
<td>0.0693-0.315</td>
<td>0.115-0.520</td>
<td>0.167-2.93</td>
<td>0.895-0.994</td>
</tr>
</tbody>
</table>

\( ^a \) Estimates are shown as a range for each dose because four estimated hepatic concentrations were used to estimate intrinsic clearance and three IVIVC models were applied to estimate organ clearance. The detailed calculations are included in Table S-1 and S-2 in the Supplemental data.

\( ^b \) Estimates are shown as a range for each dose because intrinsic clearance in intestine was scaled using two estimated intestinal concentrations and two methods. The detailed calculations are included in Table S-1 and S-3 in the Supplemental data.
TABLE 4 Summary of activity of M2a and M2b against NS3/4A protease genotype 1a and 1b and comparison with faldaprevir (n=3)

<table>
<thead>
<tr>
<th>Compound</th>
<th>NS3 protease genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1a</td>
</tr>
<tr>
<td>M2a</td>
<td>1.5±0.3</td>
</tr>
<tr>
<td>M2b</td>
<td>3.6±1.4</td>
</tr>
<tr>
<td>Faldaprevir</td>
<td>6.1(^a)</td>
</tr>
</tbody>
</table>

\(^a\)Average of two determinations (7.7 and 4.4 nM), no standard deviation calculated
Figure 1
Figure 2
Figure 3
**Figure 4**

(A) Graph showing formation velocity (pmol/mg/min) vs. [Unbound faldaprevir] (µM) for M2a and M2b.

(B) Graph showing formation velocity (pmol/mg/min) vs. [Unbound faldaprevir] (µM) for M2a and M2b.
Figure 5
Figure 6
Figure 7
Supplemental data

Enzyme-transporter interplay in the formation and clearance of abundant metabolites of faldaprevir found in excreta but not in circulation

Yongmei Li, Jin Zhou, Diane Ramsden, Mitchell E. Taub, Drané O’Brien, Jun Xu, Carl A. Busacca, Nina Gonnella, and Donald J. Tweedie

*Drug Metabolism and Disposition*

Estimation of the formation of M2a and M2b in intestine and liver

**Estimate of hepatic and intestinal CL\textsubscript{int} for the formation of M2a and M2b.** The intrinsic clearances for the formation of M2a and M2b in liver and gut were estimated using Equation 1. Substrate concentrations \([S]\textsubscript{h}\) used in Equation 1 for hepatic metabolism were estimated using different conditions: unbound \(C\textsubscript{max}\), unbound hepatic inlet \(C\textsubscript{max}\) with \(K\textsubscript{a}\) at a default value of 0.1 \text{min}\(^{-1}\) or estimated based on clinical \(t\textsubscript{max}\) and \(t\textsubscript{1/2}\), and unbound \(C\textsubscript{max}\) times liver enrichment factor (Equation 2-4). Substrate concentrations \([S]\textsubscript{g}\) used in Equation 1 for intestinal metabolism were estimated based on Equation 5 with \(K\textsubscript{a}\) at a default value of 0.1 \text{min}\(^{-1}\) or estimated based on clinical \(t\textsubscript{max}\) and \(t\textsubscript{1/2}\). The results are presented in Table S-1.
Table S-1. Estimation of hepatic and intestinal CLₘᵢₜ for the formation of M2a and M2b

<table>
<thead>
<tr>
<th>Dose (mg QD)</th>
<th>Estimated faldaprevir conc. (µM)</th>
<th>CLₘᵢₜ (µl/min/mg of protein)</th>
<th>Liver</th>
<th>Gut</th>
</tr>
</thead>
<tbody>
<tr>
<td>120</td>
<td>0.00836</td>
<td>M2a</td>
<td>6.11</td>
<td>0.0874</td>
</tr>
<tr>
<td></td>
<td></td>
<td>M2b</td>
<td>8.52</td>
<td>0.133</td>
</tr>
<tr>
<td></td>
<td></td>
<td>M₂a+M₂b</td>
<td>14.6</td>
<td>0.220</td>
</tr>
<tr>
<td>240</td>
<td>0.0478</td>
<td>M₂a</td>
<td>6.05</td>
<td>0.0458</td>
</tr>
<tr>
<td></td>
<td></td>
<td>M₂b</td>
<td>8.43</td>
<td>0.0693</td>
</tr>
<tr>
<td></td>
<td></td>
<td>M₂a+M₂b</td>
<td>14.5</td>
<td>0.115</td>
</tr>
</tbody>
</table>

\[\text{[S]_{h,A}} \text{= unbound C}_{\text{max}} = \text{f}_{\text{u,p}} \times \text{C}_{\text{max}}; \hline \text{[S]_{h,B}} = \text{unbound hepatic inlet C}_{\text{max}} \text{ assuming } \text{k}_a = 0.1 \text{ min}^{-1}; \hline \text{[S]_{h,C}} = \text{unbound hepatic inlet C}_{\text{max}} \text{ with estimated } \text{k}_a \text{ values; } \hline \text{[S]_{h,D}} = \text{unbound C}_{\text{max}} \times \text{liver enrichment factor}; \hline \text{f}_{\text{u,p}} \text{ is the free fraction of faldaprevir in human plasma and was determined in vitro as 0.002 by equilibrium dialysis; total steady-state plasma C}_{\text{max}} \text{ of faldaprevir was 3640 ng/ml (4.18 µM) after oral dosing of faldaprevir at 120 mg QD in patients and 20800 ng/ml (23.9 µM) after oral dosing of faldaprevir at 240 mg QD in patients from Phase II trial 1220.5 (Data on file, Boehringer Ingelheim Pharmaceuticals, Inc.); B/P refers to faldaprevir blood to plasma ratio and was determined as 0.613 for human; F_a is the fraction of faldaprevir absorbed after oral administration (a value of 1 was used); liver enrichment factors at 120 mg QD and 240 mg QD dosing were estimated to be 31.5 and 21.9, respectively.}

\[\text{Based on clinical } \text{t}_{\text{max}} \text{ and } \text{t}_{1/2} \text{ from Phase II trial 1220.5 of faldaprevir (Data on file, Boehringer Ingelheim Pharmaceuticals, Inc.), the } \text{k}_a \text{ was estimated to be 0.0157 min}^{-1} \text{ and 0.0184 min}^{-1} \text{ for 120 mg QD and 240 mg QD dosing, respectively, using the below equation:}

\[\ln \text{k}_{a,FDV} - \ln \text{t}_{1/2,ss} = \frac{0.693}{\text{t}_{\text{max,ss}}}\]

\[\text{[S]_{g,A}} = \text{F}_a \times \text{k}_a \times \text{Dose/QD}; \hline \text{Fa is the fraction of faldaprevir absorbed after oral administration (a value of 1 was used); } \hline \text{[S]_{g,B}} \text{ was calculated assuming } \text{k}_a \text{ was 0.1; } \hline \text{[S]_{g,B}} \text{ was calculated using estimated } \text{k}_a \text{ values.}

\[\text{CL}_{\text{int}} = \frac{\text{V}_{\text{max}}}{\text{K}_{\text{m}} + \text{[S]}}\]
Estimate of hepatic blood clearance and $F_h$ for the formation of M2a and M2b. The total hepatic metabolic clearance was estimated with the well-stirred model (Equation 6) and two modified well-stirred model with incorporation of binding difference in liver and plasma or active liver uptake (Equation 7 and 8). The results are presented in Table S-2.

Table S-2. Hepatic blood clearance and $F_h$ for the formation of M2a and M2b

<table>
<thead>
<tr>
<th>Faldaprevir dose</th>
<th>Equation used to calculate $CL_{h,B,M2a+M2b}$</th>
<th>$CL_{h,B,M2a+M2b}$ (ml/min/liver)</th>
<th>$F_{h,M2a+M2b}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>120 mg QD</td>
<td>Equation 6</td>
<td>4.24 4.20 4.23 3.94</td>
<td>0.997-0.998</td>
</tr>
<tr>
<td></td>
<td>Equation 7</td>
<td>22.6 22.4 22.6 21.1</td>
<td>0.986-0.987</td>
</tr>
<tr>
<td></td>
<td>Equation 8</td>
<td>15.7 15.6 15.7 Not calculatedb</td>
<td>0.990</td>
</tr>
<tr>
<td>240 mg QD</td>
<td>Equation 6</td>
<td>4.19 4.12 4.18 3.25</td>
<td>0.997-0.998</td>
</tr>
<tr>
<td></td>
<td>Equation 7</td>
<td>22.4 22.0 22.3 17.4</td>
<td>0.986-0.989</td>
</tr>
<tr>
<td></td>
<td>Equation 8</td>
<td>12.9 12.7 12.9 Not calculatedb</td>
<td>0.992</td>
</tr>
</tbody>
</table>

a See footnote a in Table S-1
b The substrate concentration was estimated as the free plasma $C_{max}$ x liver enrichment factor. Since liver enrichment is likely due to active uptake, the substrate concentration is not suitable for Equation 8, which is a modification of well-stirred model incorporating active uptake.
Estimation of \( Q_{\text{gut}} \), \( CL_g \), and fraction escaping gut metabolism \( (F_g) \). Intestinal metabolism was estimated based on the \( Q_{\text{gut}} \) model (Equation 11 and 12). The permeability clearance \( (CL_{\text{perm}}) \), estimated as the net cylindrical surface area of the small intestine \((0.66 \text{ m}^2)\) times the effective permeability of faldaprevir in human \( (P_{\text{eff}}=77.8 \times 10^{-6} \text{ cm/sec determined using MDCK cells and normalized with reference compounds, data on file, Boehringer Ingelheim Pharmaceuticals, Inc.}) \), was 30.8 ml/min. Thus, the \( Q_{\text{gut}} \) with Equation 11 was estimated to be 27.9 ml/min. Two methods were used to scale up the total \( CL_{\text{int}} \) generated from \textit{in vitro} HIM incubations to total gut \( CL_{\text{int}} \) based on either CYP3A abundance or microsomal protein recovery, but the results were similar. The fraction escaping gut metabolism \( (F_g) \) and clearance in the intestine are presented in Table S-3.

Table S-3. Estimation of \( F_{g,M2a+M2b} \) and \( CL_{g,M2a+M2b} \)

<table>
<thead>
<tr>
<th>Faldaprevir QD dose (mg)</th>
<th>( [S]_{g,A}^a )</th>
<th>( CL_{\text{int}} ) scaled based on CYP3A abundance</th>
<th>( CL_{\text{int}} ) scaled based on microsomal protein recovery</th>
<th>( [S]_{g,B}^a )</th>
<th>( CL_{\text{int}} ) scaled based on CYP3A abundance</th>
<th>( CL_{\text{int}} ) scaled based on microsomal protein recovery</th>
</tr>
</thead>
<tbody>
<tr>
<td>120</td>
<td>240</td>
<td>120</td>
<td>240</td>
<td>120</td>
<td>240</td>
<td>120</td>
</tr>
<tr>
<td>240</td>
<td>120</td>
<td>240</td>
<td>120</td>
<td>240</td>
<td>120</td>
<td>240</td>
</tr>
<tr>
<td>( F_{g,M2a+M2b} )</td>
<td>0.989</td>
<td>0.994</td>
<td>0.953</td>
<td>0.975</td>
<td>0.954</td>
<td>0.975</td>
</tr>
<tr>
<td>( CL_{g,M2a+M2b} )</td>
<td>0.307</td>
<td>0.167</td>
<td>1.31</td>
<td>0.698</td>
<td>1.28</td>
<td>0.698</td>
</tr>
</tbody>
</table>

\( ^a \) \( [S]_g=F_a \times k_a \times \text{Dose/}Q_{\text{en}}; F_a \) is the fraction of faldaprevir absorbed after oral administration (a value of 1 was used); \( [S]_{g,A} \) was estimated assuming \( k_a \) was 0.1; \( [S]_{g,B} \) was estimated using estimated \( k_a \) values

\( ^b \) \( CL_{g,M2a+M2b}=(1-F_{g,M2a+M2b}) \times Q_{\text{gut}} \)