Identification of Human Liver Cytochrome P450 Enzymes Involved in the Metabolism of SCH 530348 (Vorapaxar), a Potent Oral Thrombin Protease-Activated Receptor 1 Antagonist

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ABSTRACT:

Vorapaxar (SCH 530348), a potent oral thrombin protease-activated receptor 1 antagonist, is being developed as an antiplatelet agent for patients with established vascular disease. The objective of this study was to identify the human liver cytochrome P450 (P450) enzymes responsible for the metabolism of SCH 530348. Human liver microsomes metabolized SCH 530348 to M19, an amine metabolite formed via carbamate cleavage, and M20 (monohydroxy-SCH 530348). Recombinant human CYP3A4 exhibited the most activity (11.5% profiled radioactivity) for the formation of M19, followed by markedly less substrate conversion with CYP1A1 and CYP2C19. Trace levels of M19, a major excreted human metabolite, were detected with CYP1A2, CYP3A5, and CYP4F3A. Formation of M19 by human liver microsomes was inhibited 89% by ketoconazole, 75% by astemizole (a CYP2J2 inhibitor), and 43% by CYP3A4 monoclonal antibody. These results suggest that CYP3A4 and CYP2J2 are both involved in the formation of M20 metabolite.

Introduction

Vorapaxar (SCH 530348; [ethyl[(1R,3aR,4aR,6R,8aR,9S,9aS)-9-[(E)-2-[5-(3-fluorophenyl)-2-pyridinyl]ethenyl]-dodecahydro-1-methyl-3-oxonaphtho[2,3-c][furan-6-yl]carbamate]) (Fig. 1), an analog of the natural product himbacine, is a potent antagonist of protease-activated receptor 1 (PAR-1), the primary thrombin receptor on human platelets. Vorapaxar is under investigation for the treatment and prevention of acute coronary syndrome, including acute MI, and is a major contributor to the final underlying mechanism of atherothrombotic disease. Thrombosis caused by ruptured or eroded atherosclerotic plaque may result in partial or complete occlusion to coronary and other small arteries. This process is the final underlying mechanism of acute coronary syndrome, including acute MI, and is a major contributing process in ischemic stroke (Davies et al., 1976; Yeghiazarians et al., 2002). Thrombin is the most potent activator of human platelets, stimulating them primarily through the interaction with PAR-1 (Andersen et al., 1999; Anderluh and Dolenc, 2002). PAR-1 antagonists are expected to complement each other because they inhibit different molecular targets on the platelet. With the failure of the oral GpIIb/IIIa antagonists in clinical trials, the issue of interindividual variability in response and resistance to the effects of certain antiplatelet agents (e.g., aspirin), and evidence that generation of thrombin continues during long-term treatment with platelet inhibitors (Eikelboom et al., 2002), there exists a need for additional therapies for chronic use. Vorapaxar is being developed to address this need. The safety and tolerability of vorapaxar was recently demonstrated in patients who underwent non-urgent percutaneous coronary interventions or coronary angiographies with planned percutaneous coronary interventions (Becker et al., 2009).
the incubation mixture was preincubated for 2 min at 37°C. Reactions were initiated by the addition of drug or NADP<sup>+</sup>, allowed to proceed for 120 min at 37°C, and then terminated by the addition of 0.5 ml of methanol. The incubation mixtures were vortexed and centrifuged (10,000 g) at 4°C for 10 min, and the supernatants were analyzed by an HPLC-flow scintillation analyzer (LSA). Only samples from substrate concentrations of 10 and 50 μM were analyzed by LC-MS. Boiled human liver microsomes and incubations without NADPH served as negative controls. [<sup>14</sup>C]SCH 530348 (10 μM) was incubated with human liver S9 (1.6 mg protein/ml) using the procedures described above.

Optimization and Kinetic Parameters using Human Liver Microsomes from a Donor with High CYP3A4 Activity. Initial incubations of [<sup>14</sup>C]-SCH 530348 with pooled human liver microsomes showed a low level of conversion to metabolites. Therefore, all subsequent incubations were performed using human liver microsomes from a single donor with high CYP3A4 activity. In vitro incubations of [<sup>14</sup>C]-SCH 530348 with human liver microsomes were performed using various P450 concentrations (0.25–1 nmol P450/ml) and 10 μM [<sup>14</sup>C]-SCH 530348 for 30, 60, 90, and 120 min. Substrate concentrations of 1 to 100 μM were used subsequently to optimize the concentration of the drug and to calculate K<sub>m</sub> and V<sub>max</sub>. Reactions were initiated and terminated as described above. The quantitation of M19 (confirmed by LC-MS) was based on radio metric detection and a standard curve (linear least-square fit) of seven concentrations (0.05, 0.1, 0.2, 0.5, 1, 2, and 5 μM).

**Materials and Methods**

**Chemicals.** Glucose-6-phosphate dehydrogenase, monosodium L-glutamic acid, NADP, magnesium chloride, Trizma base, ammonium acetate, and quinidine were purchased from Sigma-Aldrich (St. Louis, MO). Ketocazole was purchased from Oxford Biomedical Research (Oxford, MI). Acetonitrile acetic acid and methanol were high-performance liquid chromatography (HPLC) grade and purchased from Thermo Fisher Scientific (Waltham, MA); distilled water was prepared using a Milli-Q water purification system from Millipore Corporation (Billerica, MA); and Tris buffer was purchased from BD Biosciences (Woburn, MA). Unlabeled SCH 530348 and M20 were obtained from Schering-Plough (Kenilworth, NJ). Radiolabeled SCH 530348 (<sup>3</sup>H, radiochemical purity >97%, specific activity 126 μCi/mg) (Fig. 1) was prepared by the radiochemistry group at Schering-Plough Research Institute (Kenilworth, NJ). Single donor (H0029), pooled human liver microsomes (n = 10), intestine and lung microsomes, and a Reaction Phenotyping Kit were purchased from Xenotech, LLC (Lenexa, KS). P450 Supersomes and CYP3A4 monoclonal antibodies were purchased from BD Biosciences.

**Incubations with HLMs and S9.** Pooled HLMs (1 nmol P450/ml) were incubated with [<sup>3</sup>H]-SCH 530348 (1–50 μM) for 120 min in the presence of an NADPH-generating system as described previously (Ghosal et al., 2006, 2007). All incubation mixtures contained 3 mM magnesium chloride in 0.5 ml of 100 mM potassium phosphate buffer, pH 7.4. Before the addition of drug, the incubation mixture was preincubated for 2 min at 37°C. Reactions were initiated by the addition of drug or NADP<sup>+</sup>, allowed to proceed for 120 min at 37°C, and then terminated by the addition of 0.5 ml of methanol. The incubation mixtures were vortexed and centrifuged (10,000 g) at 4°C for 10 min, and the supernatants were analyzed by an HPLC-flow scintillation analyzer (LSA). Only samples from substrate concentrations of 10 and 50 μM were analyzed by LC-MS. Boiled human liver microsomes and incubations without NADPH served as negative controls. [<sup>14</sup>C]-SCH 530348 (10 μM) was incubated with human liver S9 (1.6 mg protein/ml) using the procedures described above.

**Screening of Human P450 Supersomes.** Screening of human P450 Supersomes (CYP1A1, CYP1A2, CYP2A6, CYP1B1, CYP2B6, CYP2C8, CYP2C9, CYP2C18, CYP2C19, CYP2D6, CYP2E1, CYP2J2, CYP3A4, CYP3A5, CYP4F2, CYP4A11, CYP4F3A, CYP4F3B, and CYP4F12) was initially conducted using a constant amount of P450 (0.2 nmol/ml) and 10 μM [<sup>14</sup>C]-SCH 530348 (10 μM) for 120 min. The screening was also performed under in vitro steady-state conditions of 25 μM [<sup>14</sup>C]-SCH 530348 (~K<sub>m</sub> concentration). All incubations were performed in 100 mM potassium phosphate buffer, pH 7.4, as described above. For CYP2C9 and CYP2A6 Supersomes, incubations were performed in 100 mM Tris buffer (pH 7.4) as recommended by the supplier. Insect microsomes without CDNA of human P450 were used as control. For LC-MS analysis, supernatants were concentrated under nitrogen at room temperature. Because the rate of M20 formation was low in human liver microsomes and below the detection limit in some cases, kinetic parameters were not determined for M20 formation.

**Inhibition with Selective P450 Inhibitors and Inhibitory Antibodies.** Inhibition of SCH 530348 metabolism was initially evaluated using selective chemical inhibitors of cytochrome P450 enzymes (ketocazole for CYP3A4, quinidine for CYP2D6, sulfaphenazole for CYP2C9, omeprazole/ticlopidine/tranylcypromine for CYP2C19, orphenadrine/ticlopidine for CYP2B6, astemizole for CYP2J2, a-naphthoflavone for CYP1A1/CYP1A2, and inhibitory monoclonal antibodies against CYP2D6 and CYP3A4). Human liver microsomes (pooled or individual donor, 1 nmol/ml) were preincubated separately with each of the inhibitors for 15 min at room temperature followed by the addition of buffer, cofactor, and substrate (10 and 25 μM [<sup>14</sup>C]-SCH 530348) for 15 min at room temperature followed by the addition of buffer, cofactor, and substrate (10 and 25 μM [<sup>14</sup>C]-SCH 530348) for M19 formation. The inhibition of M20 formation was also studied with 25 μM unlabeled SCH 530348. All incubations were performed as described previously. Incubation volumes were 0.5 ml, and the final concentration of the organic solvents in the incubation system was less than 1% (v/v).

**Inhibition of [<sup>14</sup>C]-SCH 530348 metabolism to M19 was further evaluated using selective chemical inhibitors of cytochrome P450 enzymes (ketocazole for CYP3A4, ticlopidine for CYP2B6/CYP2C19, and tranylcypromine for CYP2C19). Human liver microsomes from donor H0029 (0.5 nmol/ml) were preincubated separately with each of the inhibitors for 15 min at room temperature followed by the addition of buffer, cofactor, and substrate (25 μM [<sup>14</sup>C]-SCH 530348). All incubations were performed as described above. The IC<sub>50</sub> of ketocazole (0.1–2 μM) for M19 formation was determined using human liver microsomes with high CYP3A4 activity under the conditions described previously.

**Correlation Analysis.** A reaction phenotyping kit consisting of 10 individual human liver microsomal preparations from individual donors was used for correlation analysis. The ability of human liver microsomes from each donor to metabolize SCH 530348 to its metabolite M19 was correlated with the
P450-specific enzyme activities for each sample. The assays were performed as described previously, with 25 μM substrate and an incubation period of 120 min. Because the rate of M20 formation was low in human liver microsomes and below the detection limit in some cases, correlation study was not performed for M20 formation.

**Detection and Identification of In Vitro Metabolites of SCH 530348.** Samples from the initial microsomal incubations were analyzed for the identification of metabolites using an LC-MS system comprising a TSK Quantum mass spectrometer (Thermo Fisher Scientific) operated in a positive electrospray ionization mode, an Alliance 2695 HPLC module (Waters, Milford, MA), and a model 525F00 FSA (PerkinElmer Life and Analytical Sciences, Waltham, MA). A Luna Phenyl-Hexyl 250 × 4.6 mm column (5-μm particle size; Phenomenex, Torrence, CA), which was connected to a Luna Phenyl-ProPyl 4.0 × 3.0 mm guard column (5-μm particle size), was used for metabolism-profiling analyses. The mobile phases, which consisted of 95% 20 mM ammonium acetate (pH adjusted to 6.0 by glacial acetic acid) and 5% acetonitrile (phase A), and 95% acetonitrile and 5% 20 mM ammonium acetate (pH adjusted to 6.0 by glacial acetic acid) (phase B), were maintained at a constant flow rate of 1 ml/min. The temperature of the column was kept at 40°C. Separation was achieved using programmed linear changes in mobile phase composition starting with 10% of phase B for 2 min, increasing to 50% from 2 to 25 min, increasing to 98% from 25 to 52 min, and then maintaining at 98% from 52 to 57 min. The HPLC column effluent was divided so that 18% (SCH 530348), 49.9% (SCH 530348), 0.2% (M19) and 30% (M20) of the flow was directed to waste for the first 1.5 min to reduce the contribution to the radioactive peak was determined.

**Optimization and Kinetic Parameters using Human Liver Microsomes and S9.** The metabolic conversion of [14C]SCH 530348 to metabolites was low (3–6%) after incubation of the drug (1, 10, and 50 μM) with human liver microsomes and S9 (data for 1 and 50 μM are not shown). LC-MS analysis demonstrated that SCH 530348 was converted primarily to an amine metabolite (M19) by carbamate cleavage (Table 1). The structure of M19 was confirmed by LC-MS analysis. The syringe was washed immediately after sample injection with 500 μl of strong wash solvent (0.1:95:5 formic acid/acetoniitrile/water) and 500 μl of weak wash solvent (25:75 methanol/water).

**Results**

**Incubation with Pooled Human Liver Microsomes and S9.** The kinetic parameters for the formation of M19 following incubation of [14C]SCH 530348 with human liver microsomes and P450 Supersomes are presented in Table 2. The kinetic parameters for the formation of M19 following incubation of [14C]SCH 530348 with human liver microsomes and human CYP3A4 Supersomes are also presented in Table 2.

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**Table 1**

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<th>Metabolite Label</th>
<th>Name</th>
<th>m/z</th>
<th>HLM</th>
<th>S9</th>
<th>CYP1A1</th>
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<th>CYP2B6</th>
<th>CYP2C9</th>
<th>CYP2C19</th>
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**Table 2**

**Kinetic parameters for the formation of M19 following incubation of [14C]SCH 530348 with human liver microsomes and CYP3A4 Supersomes.**

**Human liver microsomes with high CYP3A4 activity.**

<table>
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<tr>
<th>Kinetic Parameters</th>
<th>Human Liver Microsomes</th>
<th>CYP3A4</th>
</tr>
</thead>
<tbody>
<tr>
<td>$K_m$ (μM)</td>
<td>23.5 ± 1.91b</td>
<td>22.9 ± 1.84a</td>
</tr>
<tr>
<td>$V_{max}$ (pmol/nmol P450/min)</td>
<td>57.9 ± 1.75b</td>
<td>166 ± 4.92a</td>
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<td>$V_{max}/K_m$ (μmol P450/min)</td>
<td>2.46</td>
<td>7.25</td>
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*a* Kinetic parameters were determined by the GraFit 5.00.1 program.

*b* ± S.E.

*C* Intrinsic clearance.
parameters, are shown in Table 2. The $K_m$ for formation of M19 was 23.5 μM, and its $V_{max}$ was 57.9 pmol/nmol P450/min (Table 2). A substrate concentration of 25 μM was chosen for further experiments with human liver microsomes considering the linearity, percentage of conversion, and detection sensitivity for M19. Representative radiometric profiles of metabolites from incubation of SCH 530348 (25 μM) with human liver microsomes are presented in Fig. 2. Metabolite M20 formation was below the detection limit of the radiometric detector. Therefore, a more sensitive LC-MS/MS system was used for quantitation of M20. In the absence of the NADPH-generating system, no metabolite formation was observed (data not shown). The total recovery of injected radioactivity from the HPLC column was 92%.

**Incubation of SCH 530348 with Microsomes from Human Liver, Intestine, and Lung Tissues.** Incubation of unlabeled SCH 530348 with microsomes from human liver, intestine, and lung tissues showed that M20 was generated in all microsomal fractions, and its formation is highest in the liver > intestine > pulmonary tissues (trace level) (Fig. 3). After incubation of SCH 530348 (25 μM) with human liver microsomes, the rate of M19 formation (~30 pmol/nmol P450/min; data not shown) was much higher compared to the rate of M20 formation (~0.4 pmol/nmol P450/min) (Fig. 4, A and B). Experimental variability for the incubations was 2 to 6%.

**Screening with cDNA-Expressed Human P450 Supersomes.** In vitro screening of [14C]SCH 530348 (10 μM) with recombinant human P450 Supersomes showed that only CYP1A1, CYP1A2, CYP2C19, CYP3A4, and CYP3A5 yielded metabolites (mainly M19), suggesting the possible involvement of these enzymes in the metabolism of SCH 530348. CYP3A4 exhibited the most activity (109.8 pmol/nmol P450/min), followed by markedly less substrate conversion with CYP2C19, CYP3A4, and CYP3A5 (Fig. 4A, insert). The screening was repeated under steady-state condition (25 μM), and the results confirmed that CYP1A1, CYP2C19, CYP3A4, and CYP3A5 yielded M19 (Fig. 4A). As expected, CYP3A4 exhibited the most activity (11.5% profiled radioactivity), followed by markedly less substrate conversion by CYP1A1, CYP2C19, and CYP3A5 (Fig. 4A).
4A). Trace levels of M19 were also detected after incubation of 
\[^{14}\text{C}]\text{SCH 530348}\) with CYP1A2 and CYP4F3A. The formation of 
radioactive metabolites with recombinant CYP1A1, CYP1A2, CYP2C19, 
CYP3A4, CYP3A5, and CYP4F3A suggested involvement of these en-
zymes in the metabolism of SCH 530348.

The metabolite profiles obtained in various incubations are pro-
vided in Table 1. For most of the analyzed samples, the conversion 
(1–6%) was represented by various amounts of amine (M19, \(m/z = 421\)) and mono-oxy (M20a, \(m/z = 509\)) metabolites. CYP3A4 showed 
significantly higher conversion (27.5%), \(~22.1\%\) of which is repre-
sented by M19. Therefore, M19 represents 80.4% of all metabolites 
catalyzed by CYP3A4. Low amounts (\(~1\%\)) of three other oxidative 
metabolites M20a (M22, \(m/z = 509\)) and a mono-oxy-M19 (M18, 
\(m/z = 437\)) were also detected. Trace levels of two additional mono-
 oxy-SCH 530348 metabolites (M23 and M24, \(m/z = 509\)) were 
detected by LC-MS/MS in selected incubations.

Optimization with human CYP3A4 Supersomes was performed 
with 25 \(\mu\text{M}\) \[^{14}\text{C}]\text{SCH 530348}\) at various concentrations of cyto-
chrome P450 (0.1–0.3 \(\text{nmol/ml}\)) and for various time periods (30–120 
min). A P450 concentration of 0.2 \(\text{nmol/ml}\) and incubation time of 
120 min was found to be optimal for the assay (data not shown). \(K_m\) 
for the formation of M19 from CYP3A4 Supersomes was 22.9 \(\mu\text{M}\),
whereas its $V_{\text{max}}$ was 166 pmol/nmol P450/min (Table 2). Similar $K_{\text{m}}$ values for M19 formation determined from incubation with human liver microsomes (23.5 μM) and CYP3A4 (22.9 μM) strongly suggest the involvement of CYP3A4 in its formation from SCH 530348. A representative radiometric profile of metabolites from incubation of $[^{14}\text{C}]$SCH 530348 (25 μM) with CYP3A4 Supersomes is presented in Fig. 2.

The accumulation of M20, an active metabolite in human plasma, was established only after chronic administration of vorapaxar. The amount of circulating M20 formed was too low for detection by flow scintillation analysis after a single radioactive dose of vorapaxar to humans. Therefore, the in vitro enzymology of M20 was investigated separately with unlabeled compound using a highly sensitive LC-MS/MS method. Screening of unlabeled SCH 530348 with human P450 Supersomes showed that CYP2J2 is the major enzyme generating M20 followed by CYP3A4 (Fig. 4B). Other P450s generated M20 in trace levels. However, the rate of M19 formation (109.8 pmol/nmol P450/min) mediated by CYP3A4 was much higher compared to the rate of M20 formation (0.7 pmol/nmol P450/min) mediated by CYP3A4. The rate of M20 formation by CYP2J2 was 30.6 pmol/nmol P450/min.

Further screening of M20 (25 μM) with human liver microsomes and 19 P450s after 120-min incubation showed that M20 was further metabolized by CYP3A4 and CYP2J2 to downstream metabolites M16 ($m/z$ 523) and M19 ($m/z$ 421) (data not shown). Proposed P450-mediated in vitro biotransformation pathways for SCH 530348 is provided in Fig. 8.

**Inhibition of M19 with Selective P450 Inhibitors.** The results of chemical inhibition studies using pooled human liver microsomes with selective chemical inhibitors showed that ketoconazole (a CYP3A4 inhibitor) at 2 μM inhibited the formation of M19/M20a by 74% (Fig. 5A). Tranylcypromine (50 μM) and orphenadrine (300 μM) inhibited M19/M20a formation by 16 and 41%, respectively. In contrast, sulfaphenazole (3 μM), quinidine (5 μM), omeprazole (10 μM), and α-naphthoflavone (10 μM) showed no inhibition. Because orphenadrine, a reported CYP2B6 inhibitor, showed 41% inhibition, CYP2B6-specific antibody was used to explore the contribution of CYP2B6 in the metabolism of SCH 530348. CYP3A4-specific inhibitory monoclonal antibody inhibited M19 by 89%, whereas the CYP2B6-specific inhibitory antibody had no effect (Fig. 5A). Experimental variability was 2 to 7%. These study results indicate that the effect of orphenadrine may be due to inhibition of CYP3A4. Guo et
al. (1997) have reported that orphenadrine inhibits multiple P450 enzymes, including CYP3A4, in human liver microsomes. Our studies also suggest that CYP3A4 is inhibited by orphenadrine, whereas CYP2B6 has minimal effects on vorapaxar metabolism.

The results of the inhibition studies using human liver microsomes expressing high CYP3A4 activity showed that ketoconazole (2 µM) inhibited the formation of M19 by 89% (Fig. 5A). The IC50 value of ketoconazole was 0.73 µM (Fig. 6). These inhibition studies suggest that CYP3A4 is primarily responsible for the metabolism of SCH 530348. Tranylcypromine at a higher concentration of 100 µM and ticlopidine at 20 µM inhibited M19 formation by 34 and 5%, respectively (Fig. 5A). Ticlopidine is an inhibitor of CYP2B6 and CYP2C19 (Turpeinen et al., 2004). The very low level of inhibition by ticlopidine and no metabolite formation by CYP2B6 Supersomes again suggests no involvement of CYP2B6 in the metabolism of SCH 530348. However, moderate inhibition by tranylcypromine suggests the minor involvement of CYP2C19.

**Inhibition of M20 with Selective P450 Inhibitors.** Investigation of the effect of ketoconazole and astemizole on the formation of M20 from CYP3A4, CYP2J2 Supersomes, and human liver microsomes showed that ketoconazole inhibited M20 formation in human liver microsomes and CYP3A4 by ~90% and in CYP2J2 by ~51% (Fig. 5B). The present study with recombinant CYP3A4 and recombinant CYP2J2 demonstrated that ketoconazole is a potent inhibitor of CYP3A4 and a moderate inhibitor of CYP2J2 (Fig. 7). Astemizole inhibited M20 formation in human liver microsomes and CYP3A4 by ~76% and in CYP2J2 by ~87%. Hence, astemizole is an inhibitor of both CYP2J2 and CYP3A4 (Fig. 7). These data suggested that both CYP3A4 and CYP2J2 were involved in the formation of M20. In human intestine, ketoconazole and astemizole inhibit M20 by 80 and 77%, respectively, suggesting its potential formation via intestinal P450s (CYP3A4 and CYP2J2).

In human liver microsomes, CYP3A4 monoclonal antibody inhibited M20 by ~43%, suggesting the involvement of CYP3A4 (Fig. 5B). These data also suggest that ~43% of M20 formation is catalyzed by CYP3A4.

**Correlation Analysis.** The formation rate of M19 from [14C]SCH 530348 was measured in each of the 10 human liver microsomal sample provided in the reaction phenotyping kit. These values were then correlated with the biochemical activity data provided with the kit. Because the biochemical activities are mediated by specific P450 enzymes, a high correlation would suggest that similar enzymes were involved in the formation of metabolite(s) from SCH 530348.

The highest correlation \( r \) between the reaction phenotyping kit assay data \( (n = 10) \) and the formation of M19 was noted for midazolam 1’-hydroxylation \( (r = 0.75) \) and testosterone 6β-hydroxylation \( (r = 0.92) \) (Table 3), which are catalyzed by CYP3A4 and CYP3A4/CYP3A5, respectively. There was poor correlation between the formation of M19 and phenacetin O-deethylation mediated by CYP1A2 \( (r = 0.22) \) and S-mephenytoin 4’-hydroxylation mediated by CYP2C19 \( (r = 0.22) \), suggesting that CYP1A2 and CYP2C19 have minor involvement. Results of correlation analysis between the enzyme activities and M19 formation confirmed that SCH 530348 is metabolized to M19 primarily by CYP3A4 in human liver microsomes.

**Discussion**

Clinical studies have shown that vorapaxar is extensively metabolized in humans. The major route of elimination of the drug is via an
amino metabolite (M19) formed by carbamate cleavage. However, after multiple dose administrations, metabolite M20 becomes a major (>10% total) circulating metabolite when steady state for the parent is achieved. Minor amounts of mono- and dihydroxy metabolites are also formed. To better predict the potential for possible drug-drug interactions after coadministration of SCH 530348 with other drugs, this study was undertaken to characterize the P450 enzymes responsible for the metabolism of vorapaxar. Characterization of the P450 enzyme(s) responsible for the metabolism of SCH 530348 was accomplished by "reaction phenotyping," including correlation analysis with a panel of characterized microsomal preparations, chemical inhibition, and the use of cDNA-expressed human P450 enzymes.

Initially, \(^{14}C\)-labeled SCH 530348 was incubated with pooled human liver microsomes and S9 in the presence of an NADPH-generating system to identify in vitro metabolites of SCH 530348. These in vitro incubations demonstrated that SCH 530348 was metabolized primarily to M19 and trace amounts of several other oxidative metabolites. The conversion to M19 was relatively low (<6%), and the level of M20 was below the detection limit. Preliminary identification of the CYP450 enzymes involved in the metabolism of SCH 530348 using a screen of 17 recombinant human P450 Supersomes suggested the possible involvement of CYP1A1, CYP1A2, CYP3A4, CYP3A5, and CYP2C19 in the metabolism of SCH 530348, with M19 being the major metabolite formed under the in vitro conditions used. CYP3A4 exhibited the highest activity, followed by markedly less substrate conversion with CYP2C19, CYP3A5, and CYP1A1.

Reaction conditions were subsequently optimized using human liver microsomes from a single donor expressing high CYP3A4 activity. However, the level of M20 was still near or below the detection limit (flow scintillation analyzer). Optimal conditions were determined to be a P450 concentration of 0.5 nmol and an incubation time of 120 min. Further screening of 19 recombinant human P450 Supersomes showed that CYP1A1, CYP1A2, CYP2C19, CYP3A4, CYP3A5, and CYP4F3A yielded M19. As with the initial screening, CYP3A4 exhibited the most activity (11.5% profiled radioactivity), followed by markedly less substrate conversion by CYP1A1 and CYP2C19. The \(K_{in}\) for the formation of M19 from human liver microsomes was 23.5 \(\mu\)M and from CYP3A4 Supersomes was 22.9 \(\mu\)M. The comparable \(K_{in}\) values for M19 formation using human liver microsomes (23.5 \(\mu\)M) and CYP3A4 (22.9 \(\mu\)M) strongly suggest the involvement of CYP3A4 in its formation (Table 2).

Chemical inhibition studies also suggested the involvement of CYP3A4 in the formation of M19. Inhibition studies done with pooled human liver microsomes demonstrated that ketoconazole (2 \(\mu\)M), a selective CYP3A4 inhibitor, inhibited the formation of M19/M20a by 74%. The results of additional inhibition studies using human liver microsomes with high CYP3A4 activity showed that ketoconazole (2 \(\mu\)M) inhibited the formation of M19 by 89%. The IC\(_{50}\) value of ketoconazole was determined to be 0.73 \(\mu\)M. These inhibition studies suggest that CYP3A4 is primarily responsible for the metabolism of SCH 530348. Orphenadrine, a reported inhibitor of CYP2B6 and CYP3A4 (Guo et al., 1997), inhibited M19/M20a formation 41%. However, further studies using monoclonal antibodies demonstrated that whereas CYP3A4-specific inhibitory monoclonal antibodies inhibited M19 by 89%, CYP2B6-specific inhibitory antibodies showed no inhibition. These results suggested that CYP3A4 is primarily responsible for the metabolism of SCH 530348 to M19 and that CYP2B6 has no contribution.

![FIG. 8. Proposed P450-mediated in vitro biotransformation pathways for SCH 530348.](image-url)
Tranylcypromine (100 \mu M), a CYP2C19 inhibitor, and ticlopidine (20 \mu M), an inhibitor of CYP2B6 and CYP2C19 (Turpeinen et al., 2004), inhibited M19 formation by 34 and 5\%, respectively. The very low level of inhibition by ticlopidine again suggested the lack of involvement of CYP2B6 in the metabolism of SCH 530348. However, moderate inhibition by tranylcypromine suggested minor involvement of CYP2C19.

The results of correlation analysis between the enzyme activities and M19 formation confirmed that SCH 530348 is metabolized to M19 primarily by CYP3A4 in human liver microsomes. The highest correlation with the formation of M19 was noted for midazolam 1'-hydroxylation (r = 0.75) and testosterone 6\beta-hydroxylation (r = 0.92) catalyzed by CYP3A4 and CYP3A4/CYP3A5, respectively. There was no correlation between the formation of M19 and phenacetin O-deethylation mediated by CYP1A2 (r = 0.22) and S-mephenytoin 4'-hydroxylation mediated by CYP2C19 (r = 0.22). The poor correlation suggests that CYP1A2 and CYP2C19 may have only minor involvement in the formation of M19. The proposed biotransformation pathway of SCH 530348 to M19 (Fig. 8) involves oxidation primarily via CYP3A4 of the secondary carbon of the ethyl group, followed by loss of C\textsubscript{2}H\textsubscript{4}O and then CO\textsubscript{2}. Compared to CYP3A4, the contributions of CYP1A1, CYP1A2, CYP2C19, and CYP3A5 to the biotransformation of SCH 530348 in human liver microsomes are minor.

Screening of SCH 530348 with recombinant human P450 Super- somes showed that CYP2J2 is the major enzyme generated 20\%, followed by CYP3A4. Other P450s generated M20 in trace levels. In the chemical inhibition study using human liver microsomes (expressing high CYP3A4 activity), formation of M20 was inhibited \approx 89\% by ketoconazole and \approx 75\% by astemizole. Based on the literature and our study, ketoconazole and astemizole are both capable of inhibiting CYP3A4 and CYP2J2 (Matsumoto et al., 2003). Other P450 inhibitors showed little or negligible inhibition, suggesting that their role is minor. In human liver microsomes, CYP3A4-monoclonal antibody inhibited M20 by \approx 43\%, suggesting the involvement of CYP3A4. These data also suggest that \approx 43\% of M20 formation is catalyzed by CYP3A4 and the rest is catalyzed by CYP2J2 and other P450s. CYP2J2 antibody is not commercially available to distinguish contribution of CYP3A4 and CYP2J2. These data suggest that both CYP3A4 and CYP2J2 are involved in the formation of M20. Further screening of M20 (25 \mu M) with recombinant human P450s showed that M20 was further metabolized by CYP3A4 and CYP2J2 to downstream metabolites M16 and M19.

The overall role of CYP2J2 in drug metabolism has not been determined to date. Several antihistamine drugs, including terfenadine, ebastine, and astemizole, have been identified as good substrates and inhibitors. The role of CYP2J2 in drug metabolism has not been fully explored. The involvement of CYP2J2 in the metabolism of SCH 530348 has been proposed in the literature.