ELETRIPTAN METABOLISM BY HUMAN HEPATIC CYP450 ENZYMES AND TRANSPORT BY HUMAN P-GLYCOPROTEIN

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ABSTRACT:

“Reaction phenotyping” studies were performed with eletriptan (ETT) to determine its propensity to interact with coadministered medications. Its ability to serve as a substrate for human P-glycoprotein (P-gp) was also investigated since a central mechanism of action has been proposed for this “triptan” class of drug. In studies with a characterized bank of human liver microsome preparations, a good correlation ($r^2 = 0.932$) was obtained between formation of N-desmethyl eletriptan (DETT) and CYP3A4-catalyzed testosterone 6β-hydroxylation. DETT was selected to be monitored in our studies since it represents a significant ETT metabolite in humans, circulating at concentrations 10 to 20% of those observed for parent drug. ETT was metabolized to DETT by recombinant CYP2D6 (rCYP2D6) and rCYP3A4, and to a lesser extent by rCYP2C9 and rCYP2C19. The metabolism of ETT to DETT in human liver microsomes was markedly inhibited by troleandomycin, erythromycin, miconazole, and an inhibitory antibody to CYP3A4, but not by inhibitors of other major P450 enzymes. ETT had little inhibitory effect on any of the P450 enzymes investigated. ETT was determined to be a good substrate for human P-gp in vitro. In biidirectional transport studies across LLC-MDR1 and LLC-Mdr1a cell monolayers, ETT had a BA/AB transport ratio in the range 9 to 11. This finding had significance in vivo since brain exposure to ETT was reduced 40-fold in Mdr1a−/− relative to Mdr1a+/+ mice. ETT metabolism to DETT is therefore catalyzed primarily by CYP3A4, and plasma concentrations are expected to be increased when coadministered with inhibitors of CYP3A4 and P-gp activity.

ELETRIPTAN [ETT$^1$; (R)-3-(1-methyl-2-pyrrolidinylmethyl)-5-[2-(phenylsulfonyl)ethyl]-1H-indole] (Fig. 1) is a selective agonist at 5-hydroxytryptamine (serotonin)$\text{1B/1D}$ receptors and, like the other drugs in this “triptan” class, has been shown to be clinically effective for the treatment of migraine (Jackson, 1996). The pharmacokinetics and metabolism of ETT have been investigated in the rat, dog, and human. In all three species, ETT was rapidly absorbed and extensively cleared by metabolism (Milton et al., 1997; Morgan et al., 2000). The pathways of ETT metabolism are similar in the rat, dog, and human, and principal routes include pyrrolidine N-demethylation to N-desmethyl eletriptan (DETT), together with N-oxidation, oxidation of the pyrrolidine ring, and formation of tetracyclic quaternary ammonium metabolites (Morgan et al., 2000).

Members of the cytochrome P450 (P450) superfamily are known to play a major role in the oxidative metabolism of both xenobiotics and certain endogenous compounds. Described herein are the first detailed studies to elucidate the P450 forms responsible for ETT metabolism to DETT in human liver. The metabolism of ETT to DETT was chosen to be monitored in our studies since DETT represents a significant metabolite observed to circulate in humans at levels 10 to 20% of those observed for ETT [Product Information for Eletriptan, Pfizer, Sandwich, UK (2001)]. Reaction phenotyping studies (Rodrigues, 1999) were performed by correlation analysis, the use of recombinant human P450 forms, chemical inhibition, and inhibitory antibodies. In addition, to evaluate the potential for drug-drug interactions, the effect of ETT on some selected P450 form enzyme activities was also investigated.

It was of interest also to determine whether ETT could serve as a substrate for P-glycoprotein (P-gp), an efflux transporter expressed on the apical side of gut epithelia and brain endothelia, which can limit oral absorption and brain penetration, respectively. The role of P-gp and P450 in the uptake and metabolism of ETT was investigated because these systems can work in concert to limit systemic exposure following oral dosing (Cummins et al., 2002), and they are also subject to inhibition and/or induction by a variety of xenobiotics (Wandel et al., 1999; Dresser et al., 2003). In addition, the role of P-gp in regulating the uptake of ETT into the brain was of interest because of the intense speculation about a central mechanism of action for the triptan class of antimigraine drugs (Goadsby and Hargreaves, 2000). In this regard, ETT was considered the ideal tool to investigate this
phenomenon, since it was the first lipophilic agent in this drug class that would be expected to have good intrinsic brain penetration. Our studies describe primarily the role of P-gp and P450 in the disposition of ETT from the perspective of its potential for drug-drug interactions. The role of P-gp in potentially modulating the dose required for antimigraine efficacy is also discussed in the context of a comparison to the other triptan drugs, naratriptan (NARA), rizatriptan (RIZA), sumatriptan (SUMA), and zolmitriptan (ZOLM).

Materials and Methods

**Materials.** ETT, NARA, RIZA, SUMA, ZOLM (Fig. 1), DETT, and L-844151 [internal standard for liquid chromatography/tandem mass spectrometry (LC/MS-MS)] were synthesized by Merck Sharp & Dohme (UK) with identity and purity confirmed by NMR, MS, HPLC, and elemental analysis. NADPH, Tris, diethyldithiocarbamate, erythromycin, miconazole, guanidine, sulfaphenazole, troleandomycin, (-)-4-hydroxytestosterone, and 6-7-ethoxyresorufin, resorufin, tolbutamide, debrisoquine, chlorzoxazone, testosterone, and 6-hydroxychlorzoxazone were obtained from Sigma-Aldrich Company Ltd. (Poole, Dorset, UK); and furafylline, diphenhydramine, droxidopa, atenolol, phenoxybenzamine, quinidine, and sulindac were obtained from Salford Ultrafine Materials. L-844151 [internal standard for liquid chromatography/tandem mass spectrometry (LC/MS-MS)] were synthesized by Merck Sharpe & Dohme (UK) Laboratories (Rahway, NJ) and stored at 30°C. CYP inhibitors, human NADPH-cytochrome P-450 reductase (OR) cDNA, and CYP2E1 cDNA were purchased from XenoTech LLC (Woburn, MA) were obtained from Cambridge Biosciences (Cambridge, UK). A reaction phenotyping kit (Product Number H0500, Version 5) containing 16 individual human P450 cDNAs was purchased from BD Gentest (Bracknell, Berkshire, UK) were used to introduce samples into a Micromass Fraction Collector (Manchester, UK). [Guanidine-14C]debrisoquine, S-[4-14C]mephenytoin, and [4-14C]testosterone (specific activities 53, 56, and 56 mCi/mmol, respectively) were purchased from Amersham Biosciences UK Ltd. (Little Chalfont, Buckinghamshire, UK).

**Human Liver Microsomes.** Washed microsomal fractions were prepared in 0.154 M KCl containing 50 mM Tris-HCl, pH 7.4, using standard methods. Two separate batches, designated pools I and II, of pooled human liver microsomes were prepared. Each batch was prepared by pooling liver samples from five subjects. Pool I comprised liver samples from males aged 2.5 and 58 years and females aged 14, 59, and 74 years, whereas pool II comprised liver samples from male subjects aged 44 and 50 years and female subjects aged 11, 31, and 55 years.

**Metabolism of ETT by Human Liver Microsomes.** The NADPH-dependent metabolism of ETT was studied in incubation mixtures containing 0.05 to 200 μM ETT (added in 0.25 ml of 0.1 M phosphate buffer, pH 7.4), 10 mM MgCl2, 2 mM EDTA, 85 mM phosphate buffer, pH 7.4, and 0.05 to 3 mg of microsomal protein in a final volume of 0.5 ml. After a 5-min preincubation at 37°C in a shaking water bath, the reaction was initiated by the addition of 1 mM NADPH. Incubations were performed in duplicate for 5 to 20 min at 37°C and were terminated by the addition of 0.5 ml of ice-cold acetonitrile containing the L-844151 internal standard for LC/MS-MS analysis (see below). Blank incubations contained all components except NADPH.

ETT metabolism to DETT was quantified by LC/MS-MS analysis. An HTS PAL autosampler (Presereach Ltd., Hitchin, Hertfordshire, UK) was attached to an HP1000 series high-performance liquid chromatograph (Hewlett Packard Ltd., Bracknell, Berkshire, UK) were used to introduce samples into a Micromass Quattro LC triple quadrupole mass spectrometer (Micromass UK Ltd., Altrincham, Cheshire, UK) using an Electrospray Z-spray source. All incubations were terminated by the addition of an equal volume of ice-cold acetonitrile containing 200 μM L-844151 internal standard. After vortex mixing, the tubes were centrifuged at 10,000g for 10 min at 4°C. Chromatography of 20-μl aliquots of the supernatant was performed with a 150 × 3.0 mm Kromasil C18 5-μm column (Thermo Hypersil-Keystone, Runcorn, Cheshire, UK) and isocratic elution with a mobile phase of 40% (v/v) acetonitrile, 6% (v/v) 250 mM ammonium formate, pH 3.0 and 54% (v/v) ultrapure water, at a flow rate of 0.4 ml/min and a column temperature of 35°C. The eluate was split volumetrically, with 20% passing directly into the triple quadrupole mass spectrometer operating in positive electrospray mode, with probe and source block temperatures of 400 and 100°C, respectively, using nitrogen for desolvation and nebulization, and a capillary voltage of 2.8 kV to initiate ionization. The compounds were selectively detected by multiple reaction monitoring using argon, collision energy 21 V; ETT m/z 383→84, DETT m/z 369→70, and L-844151 internal standard m/z 354→113.

**ETT Metabolism Correlation Analysis.** Incubation mixtures contained ETT (added in 0.25 ml of 0.1 M phosphate buffer, pH 7.4), 10 mM MgCl2, 2 mM EDTA, 85 mM phosphate buffer, pH 7.4, and 0.1 mg of microsomal protein in a final volume of 0.5 ml. After 5 min of preincubation at 37°C in a shaking water bath, the reaction was initiated by the addition of 1 mM (final concentration) NADPH. Incubations were conducted in triplicate with a single blank (no NADPH) for each of the 16 preparations of characterized human liver microsomes and were terminated after 5 min by the addition of 0.5 ml of 0.154 M KCl containing 50 mM Tris-HCl, pH 7.4, using standard methods.

![Fig. 1. Structures of 5-HT1B/1D agonists.](image-url)
ELETRiptan Interactions with CYP3A4 and P-Glycoprotein

ice-cold acetonitrile containing the L-844151 internal standard. Incubations were processed for LC/MS-MS analysis as described above.

ETT Metabolism by Recombinant P450 Forms. Incubation mixtures contained 10 mM MgCl₂, 2 mM EDTA, 1 mM NADPH, and 90 mM phosphate buffer, pH 7.4, in a final volume of 0.25 ml. After a 5-min preincubation at 37°C in a shaking water bath, the reaction was initiated by adding 0.1 mg of B-lymphoblastoid cell microsomal protein with gentle mixing. The incubations were conducted in duplicate with duplicate blank (no microsomes) for each P450 form preparation. Reactions were terminated after either 5 or 30 min with 0.25 ml of ice-cold acetonitrile containing the L-844151 internal standard. Incubations were processed for LC/MS-MS analysis as described above.

ETT Metabolism Inhibition Studies. Apart from the studies with the CYP1A2 mechanism-based inhibitor furafylline (Newton et al., 1995), where dimethyl sulfoxide was used, methanol was used as the solvent for these investigations to minimize solvent effects on individual P450 forms.

For the mechanism-based inhibitors requiring preincubation with NADPH, incubation mixtures contained 10 mM MgCl₂, 2 mM EDTA, 1 mM NADPH, 84 mM phosphate buffer, pH 7.4, 0.1 mg of microsomal protein, and either 5 to 50 μM furafylline, 5 to 100 μM diethylthiocarbamate, 2 to 50 μM troleandomycin, or 2 to 50 μM erythromycin in a volume of 0.25 ml. The inhibitors were added in either methanol (5 μl/tube) or dimethyl sulfoxide (furafylline only, 5 μl/tube), and the concentrations refer to the final concentrations in a 0.5-ml incubation. Following a 30-min preincubation at 37°C in a shaking water bath, 60 μM ETT and 1 mM NADPH (final concentration 2 mM) were added in 0.25 ml of 0.1 M phosphate buffer, pH 7.4, at 37°C. Incubations were performed in duplicate for 5 min at 37°C and were terminated by the addition of 0.5 ml of ice-cold acetonitrile containing the L-844151 internal standard. Incubations were processed for LC/MS-MS analysis as described above.

For compounds not requiring extensive preincubation with NADPH, incubation mixtures contained 10 mM MgCl₂, 2 mM EDTA, 1 mM NADPH, 84 mM phosphate buffer, pH 7.4, 0.1 mg of microsomal protein, and either 2 to 50 μM sulfaphenazole, 2 to 20 μM quinidine, 50 to 500 μM S-mephenytoin, or 2 to 50 μM miconazole, in a volume of 0.25 ml. All the inhibitors were added in methanol (5 μl/tube), and the concentrations refer to the final concentrations in a 0.5-ml incubation. After a 10-min preincubation at 37°C in a shaking water bath, the reaction was initiated by the addition of 60 μM ETT (added in 0.25 ml of 0.1 M phosphate buffer, pH 7.4, at 37°C). Incubations were performed in duplicate for 5 min at 37°C and were terminated by the addition of 0.5 ml of ice-cold acetonitrile containing the L-844151 internal standard. Incubations were processed for LC/MS-MS analysis as described above.

For the effect of ETT on CYP450 Enzyme Activities. Individual enzyme activities were assessed using the L-844151 internal standard with the concentrations referred to the final concentration in a 0.5-ml incubation in a shaking water bath for 5 min in the presence of either no ETT (controls) or 0.2 to 100 μM ETT and an NADPH-generating system, prior to addition of the P450 substrate. The effect of ETT on the individual enzyme activities was determined as described for tolbutamide and debrisoquine metabolism, but with an ETT concentration range of 0.5 to 100 μM. For testosterone 6β-hydroxylase, the tubes were preincubated in duplicate at 37°C in a shaking water bath for 5 min in the presence of either no ETT (controls) or ETT (concentration range 0.2–100 μM or 1–100 μM) and 50 μM [4-14C]testosterone (0.5 μCi/tube), prior to the addition of 1 mM NADPH. To evaluate the effect of ETT as a mechanism-based inhibitor of testosterone 6β-hydroxylase activity, the tubes were preincubated at 37°C in a shaking water bath for 30 min in the presence of either no ETT (controls) or ETT (concentration range 0.5–50 μM or 0.2–100 μM) and 1 mM NADPH, prior to the addition of 50 μM [1-14C]testosterone (0.5 μCi/tube) and 1 mM NADPH (final concentration 2 mM). Chloroxazone 6-hydroxylation was determined in incubation mixtures containing 45 μM chloroxazone, 1 mM NADPH, 0.2 mg of microsomal protein, and 0.1 M phosphate buffer in a final volume of 1 ml. Incubations were terminated after 20 min with 0.2 ml of 30% (v/v) perchloric acid and the supernatant was analyzed by HPLC. Chromatography was performed as described previously for tolbutamide methylhydroxylase (Renwick et al., 2000), except that the mobile phase consisted of 23% (v/v) acetonitrile and 77% (v/v) 20 mM sodium perchlorate, pH 2.5, and the eluant was monitored at 287 nm. The metabolism of S-mephenytoin to both 4′-hydroxymephenytoin and N-desmethyl S-mephenytoin was determined in incubation mixtures containing 60 μM S-[4-14C]mephenytoin (0.5 μCi/tube), 1 mM NADPH, 7.5 mM N-isocitric acid, 2 mM isocitric dehydrogenase, 5 mM MgSO₄, 0.5 mg microsomal protein and 0.1 M phosphate buffer pH 7.4 in a final volume of 0.5 ml. Incubations were terminated after 30 min with 0.1 ml of 30% (v/v) perchloric acid and the supernatant analyzed by HPLC. Chromatography was performed as described previously for debrisoquine 4-hydroxylase (Renwick et al., 2000), except that the mobile phase consisted of 17% (v/v) acetonitrile and 83% (v/v) 20 mM sodium perchlorate, pH 2.5, with quantitation by liquid scintillation counting. The effect of 0.2 to 100 μM ETT on chloroxazone and S-mephenytoin metabolism was studied using a preincubation period of 5 min as described above for tolbutamide and debrisoquin. For all P450 form enzyme activities studied, plots were constructed of enzyme activity (percentage of control rate in the absence of added ETT) against ETT concentration (logarithmic scale). Where inhibition of enzyme activity was observed, IC₅₀ values (i.e., concentration of ETT to produce a 50% inhibition of enzyme activity) were calculated by linear regression analysis.

Brain Penetration of the 5-HT₉R Agonists in Mdr1a⁻/⁻ and Mdr1a⁺/⁺ CF-1 Mice. The effect of the drug efflux pump, P-gp (Umbenhauer et al., 1997) on the brain entry of the triptan drugs was investigated in vivo using male CF-1 mice. ETT was formulated in 25% polyethylene glycol 300/water at 0.5 mg free base equivalents/ml, and NARA, RIZA, ZOLM, and SUMA were formulated as aqueous solutions at the same concentration. All drugs were dosed at 1 mg free base equivalents/kg as a bolus injection into the tail vein (dose volume 2 ml/kg) to 24 male CF-1 mice (12 Mdr1a⁻/⁻, 12 Mdr1a⁺/⁺), approximate weight 35 g. Blood (by cardiac puncture into heparinized containers) and brain samples were taken at either 0.5, 2, 4, or 6 h after dosing (n = 3 per time point per genotype). Samples were stored frozen (-80°C) until analysis.

To blood (0.1 ml) was added internal standard (10 μl of a 10 ng/μl solution), 1 mM sodium hydroxide (0.05 ml), water (1 ml), and ethyl acetate (4 ml). Samples were vortex mixed and centrifuged. Supernatant was removed and evaporated to dryness (70°C, under nitrogen), and the residue was dissolved in mobile phase (0.1 ml) and transferred to a HPLC vial. Calibration standards covering appropriate ranges were prepared by spiking solutions of analyte at appropriate concentrations into control blood (0.1 ml).

To weighed samples of brain cortex were added internal standard (10 μl of a 10 ng/μl solution) and water (2 ml). After homogenization with an ultrasonic probe, 1 M sodium hydroxide (0.2 ml) and ethyl acetate (4 ml). Samples were vortex mixed and centrifuged. Supernatant was removed and evaporated to dryness (70°C, under nitrogen), and the residue was dissolved in mobile phase (0.15 ml) and transferred to a HPLC vial. Calibration standards covering appropriate ranges were prepared by spiking solutions of analyte at appropriate concentrations into control brain cortex.

Typically 25-μl injections were made onto a KR100-5C8 HPLC column (150 × 3.2 mm i.d., Hichrom Ltd., Reading, UK) with a mobile phase consisting of acetonitrile (A) and 25 mM ammonium formate, adjusted to pH 3 with formic acid, at a flow rate of 0.4 ml/min, with the following time program: 0 min, 20% A; 2 min, 20% A; 6 min, 50% A; 7 min, 20% A; 10 min, 20% A. Detection was for appropriate fragmentation transitions as determined by infusion of 1 ng/μl solutions at 10 ml/h into the mass spectrometer (Micromass Quattro).

Since three animals per time point were used to construct blood and brain concentration versus time profiles, Bailer’s method for determining area under
the curve (AUC) confidence intervals during sparse sampling was applied (Bailer, 1988; Nedelman et al., 1995). Standard error of the mean (S.E.M.) for the brain/blood ratio was determined using the following equation: S.E.M. = (Brain AUC S.E.M.²/Blood AUC²) + (Brain AUC² - Blood AUC S.E.M.²/Blood AUC²). An unpaired two-tailed test was performed to determine the significance of the difference between brain/blood AUC in Mdr1a⁻/⁻ and Mdr1a⁺/⁺ mice.

Human MDR1 and Mouse Mdr1a P-Glycoprotein Bidirectional Transport Assay. The extent of P-gp-mediated transport of ETT, NARA, RIZA, ZOLM, and SUMA was also evaluated in LLC-PK1 wild-type, LLC-MDR1 (human), and LLC-Mdr1a (mouse) cell lines (kindly provided by Dr. A. H. Schinkel, The Netherlands Cancer Institute, Amsterdam, The Netherlands). Cells were cultured in 199 medium as described. For transport experiments, cells were cultured in 24-well Transwell plates (Falcon) at a density of 1.5 × 10⁶ cells/well with 0.3 ml of medium in the upper compartment and 35 ml of medium in the lower nonsubdivided compartment. After culturing for 5 days, the transport wells were transferred to a 24-well plate. The incubation and sampling procedure during the transport experiment was performed on a Tecan Genesis Workstation 150 Robot (Tecan, Zürich, Switzerland). Cells were washed three times with Hank’s balanced salt solution containing Hepes (10 mM). Subsequently, analyte in Hank’s balanced salt solution containing Hepes (500 µM) was added either to the apical or basolateral compartment. Analyte concentrations used were: 10 µM ETT, NARA, RIZA, ZOLM, and SUMA, 10 µM dexamethasone, 5 µM ritonavir, and 0.5 µM verapamil. After incubating for 4 h at 37°C, samples (100 µl) were taken from both the apical and basolateral compartment and transferred to a 96-well microtiter plate. Samples were analyzed by positive ion single ion monitoring atmospheric pressure chemical ionization on a SCIEX API 2000 triple quadrupole mass spectrometer (PerkinElmerSciex, Concord, ON, Canada). The HPLC system used was a PerkinElmer Series 200 system with 2 Micro pumps (PerkinElmer Instruments, Shelton, CT) and a Leap HTS PAL autosampler (LEAP Technologies, Carrboro, NC). Samples were chromatographed using an Aquasil C18, 2 × 20 mm, 5-µm HPLC column (Thermo Hypersil, Keystone Scientific Operations, Bellefonte, PA). The mobile phase used was 0.1% acetic acid in water (A) or in acetonitrile (B) at 2.0 ml/min with a 4:1 split. The HPLC run time was 2 min/sample. Standard curves were prepared by a 2-fold serial dilution in water/methanol (60:40, v/v) of a standard prepared at 2 times the dosing solution concentration for an 11-point standard curve. Percentage of transport was calculated by dividing the concentration of the compound appearing in the receiver compartment by the sum of the compound concentrations measured in the receiver and donor compartment (× 100%). The BA/AB ratio was calculated by dividing the concentration of compound measured in the apical compartment (resulting from introduction of compound in the basolateral well) by the concentration of compound measured in the basolateral compartment (resulting from introduction of the compound in the apical well).

Lipophilicity Measurements. Octanol-pH 7.4 buffer partition coefficients (logD₇.₄) were determined by the shake flask method with HPLC-UV analysis of the aqueous and organic phases after equilibration (Hansch and Leo, 1979). Results were derived from the mean of two partition coefficient determinations performed at overall concentrations of 0.5 and 0.25 mg/ml in 1:1 pH 7.4 buffer/octanol mixtures.

Results

Metabolism of ETT by Human Liver Microsomes. Studies were performed with two pools, namely pool I and pool II, of human liver microsomes. The total P450 content of the pool I and II microsomal preparations was determined to be 0.72 and 0.51 nmol/mg protein, respectively. The linearity of 50 µM ETT metabolism with respect to both incubation time and protein concentration was investigated initially. ETT metabolism to DETT was found to be linear with respect to incubation time (up to at least 6 min) and protein concentration (up to at least 0.2 mg of protein/incubation).

Kinetics of ETT Metabolism in Human Liver Microsomes. The kinetics of the NADPH-dependent metabolism of 0.05 to 200 µM ETT to DETT was examined with both the pool I and pool II human
liver microsomal preparations. Pooled, rather than individual, liver microsomal preparations were used for these studies since the aim was to identify average $K_m$ (i.e., the concentration of substrate giving half-maximal velocity) values to select a suitable substrate concentration for the reaction phenotyping studies. With both liver microsome pools, DETT formation was detected at all ETT substrate concentrations examined.

The kinetics of ETT metabolism to DETT was examined with Michaelis-Menten and Eadie-Hofstee plots. Kinetic analysis of data for both liver microsome pools revealed mean $K_m$ and $V_{max}$ (i.e., the maximal velocity) values of 27.1 μM (pool I and pool II individual values were 24.3 and 29.9 μM, respectively) and 78 pmol/min/mg protein (pool I and pool II individual values were 105.4 and 50.5 pmol/min/mg protein, respectively). The mean intrinsic clearance ($CL_{int}$; i.e., $V_{max} / K_m$) value was 3.02 l/min/mg protein (pool I and pool II individual values were 4.34 and 1.69 l/min/mg protein).

An ETT substrate concentration of 60 μM was selected for the reaction phenotyping studies described below. This substrate concentration was approximately 2 times the $K_m$ value for DETT formation.

ETT Metabolism Correlation Analysis. The metabolism of 60 μM ETT to DETT was examined with a characterized panel of 16 human liver microsomal preparations. ETT was metabolized to DETT by all 16 human liver microsomal preparations examined. Microsomal ETT metabolism varied from 58 to 635 pmol/min/mg protein, with most of the individual human liver microsomal preparations being more active than the two pooled human liver microsomal preparations.

The rates of ETT metabolism to DETT were correlated with data for total P450 content and a range of P450 form enzyme activities. A good correlation ($r^2 = 0.932$) was observed between ETT metabolism to DETT and CYP3A4-catalyzed testosterone 6β-hydroxylation. Although some correlation ($r^2 = 0.541$) was observed between ETT metabolism to DETT and total P450 content, only low correlations were observed ($r^2 = 0.000$–0.361) with P450 form enzymatic markers for CYP1A2, CYP2A6, CYP2B6, CYP2C8, CYP2C9, CYP2C19, CYP2D6, CYP2E1, and CYP4A9/11. These enzyme activities (with $r^2$ values in parentheses) comprised 7-ethoxyresorufin O-deethylase (0.023, CYP1A2), coumarin 7-hydroxylase (0.022, CYP2A6), S-mephenytoin N-demethylase (0.310, CYP2B6), paclitaxel 6β-hydroxylase (0.361, CYP2C8), diclofenac 4′-hydroxylase (0.104, CYP2C9), S-mephenytoin 4′-hydroxylase (0.145, CYP2C19), dextromethorphan O-demethylase (0.098, CYP2D6), chlorzoxazone 6-hydroxylase (0.004, CYP2E1), and lauric acid 12-hydroxylase (0.000, CYP4A9/11).

Metabolism of ETT by Recombinant P450 Forms. The metabolism of 60 μM ETT to DETT was examined with rCYP1A2, rCYP2A6, rCYP2B6, rCYP2C8, rCYP2C9, rCYP2C19, rCYP2D6, rCYP2E1, and rCYP3A4, together with microsomes from control cells (which contain native CYP1A1) was studied. Incubations were performed for 5 and 30 min. Only trace amounts of DETT were observed in incubations with the control cell microsomes (data not shown) and with rCYP2A6, rCYP2B6, and rCYP2E1 preparations (Fig. 2). Low rates of DETT formation were observed with the rCYP1A2 and rCYP2C8 forms.
preparations, with higher rates being observed with rCYP2C9 and rCYP2C19 preparations. The highest rates of ETT metabolism to DETT were observed with the rCYP2D6 and rCYP3A4 preparations (Fig. 2).

Inhibition of ETT Metabolism. The effect of some human P450 form inhibitors and one P450 form substrate (S-mephenytoin) on the metabolism of ETT to DETT in human liver microsomes was studied. For the mechanism-based inhibitors (Newton et al., 1995) furafylline (CYP1A2), diethylthiocarbamate (CYP2E1), erythromycin (CYP3A4), and troleandomycin (CYP3A4), the compounds were preincubated for 30 min at 37°C with liver microsomes and NADPH prior to the addition of ETT and another aliquot of NADPH. In the studies with the inhibitors sulfaphenazole (CYP2C9) and quinidine (CYP2D6), and the substrate S-mephenytoin (CYP2C19), the compounds were preincubated with liver microsomes for 10 min at 37°C prior to the addition of NADPH and ETT.

ETT metabolism to DETT was not markedly affected by 5 to 50 μM furafylline, 2 to 50 μM sulfaphenazole, 50 to 500 μM S-mephenytoin, and 2 to 20 μM quinidine (Fig. 3, A and B). Whereas 100 μM diethylthiocarbamate produced some inhibition of ETT metabolism, little effect was observed with lower concentrations of this inhibitor (Fig. 3A).

The effect of erythromycin, miconazole, and troleandomycin on ETT metabolism to DETT was studied with both pools of human liver microsomes. ETT metabolism to DETT was markedly inhibited to 3 to 13% of control (mean of both liver microsome pools) by 2 to 50 μM miconazole and to 20 to 35% of control by 2 to 50 μM troleandomycin (Fig. 4). Erythromycin also produced a concentration-dependent inhibition of ETT metabolism, with enzyme activity being reduced to 23% of control by 50 μM erythromycin.

The effect of inhibitory antibodies to CYP2C8/9, CYP2D6 and CYP3A4 on ETT metabolism to DETT in human liver microsomes was studied. With both pools of human liver microsomes treatment with 0.05-5 μM/ml incubation of either the CYP2C8/9 or the CYP2D6 antibodies had little effect on ETT metabolism (Fig. 5A and B). In contrast, the CYP3A4 antibody produced a marked inhibition of the metabolism of ETT to DETT in human liver microsomes.

Effect of ETT on P450 Form Enzyme Activities. The effect of addition of ETT at concentrations of up to 100 μM on some P450 form enzyme activities in human liver microsomes was studied. ETT produced a weak inhibition of CYP2D6-dependent debrisoquine 4-hydroxylation activity, with a calculated IC50 value (i.e., concentration of ETT to produce a 50% inhibition of enzyme activity) of 84 μM (Table 1). The addition of ETT had no effect (IC50 values all >100 μM) on 7-ethoxyresorufin O-deethylation (CYP1A2), S-mephenytoin N-deethylase (CYP2B6), tolbutamide methylhydroxylase (CYP2C9), S-mephenytoin 4′-hydroxylation (CYP2C19), and chlorozoxazone 6-hydroxylation (CYP2E1) activities. ETT produced a weak inhibition of CYP3A4-dependent testosterone 6β-hydroxylation activity, with a calculated IC50 value (mean of two liver microsomes) of 95 μM (Table 1). When ETT was evaluated as a mechanism-based inhibitor of testosterone 6β-hydroxylation activity, an observed IC50 value (mean of two microsomes) of 40 μM was obtained. Using a 30-min preincubation period with NADPH, 20 μM troleandomycin (positive control) inhibited testosterone 6β-hydroxylation activity to 18% of control levels.

Brain Penetration of the 5-HT1B/1D Agonists in Mdr1a−/− and Mdr1a+/+ CF-1 mice. The brain penetration of ETT, NARA, RIZA, SUMA, and ZOLM was investigated in Mdr1a−/− and Mdr1a+/+ mice (Umbenhauer et al., 1997). Of the 5-HT1B/1D agonists investigated, ETT was shown to be the best substrate for P-gp; the brain/blood AUC ratio was 13 in Mdr1a−/− mice, which lack the brain endothelial Mdr1a P-gp efflux pump, and 0.3 in Mdr1a+/+ mice, which express Mdr1a P-gp. The mouse P-gp efflux pump therefore has the effect of reducing brain exposure to ETT by approximately 40-fold (Fig. 6A). The effect for all the other triptan molecules, NARA, RIZA, SUMA, and ZOLM, was smaller and less than 5-fold. The brain/blood AUC ratio for inulin, a poorly brain-permeant reference compound, was approximately 0.16 in both mutant and wild-type CF-1 mice, indicating that the integrity of the blood-brain barrier was not compromised by the absence of P-gp. The brain penetration of 5-HT1B/1D agonists in Mdr1a−/− mice appeared to be in line with their lipophilicity (Fig. 6B).

Human MDR1 and Mouse Mdr1a P-Glycoprotein Bidirectional Transport Assay. The transport of NARA, RIZA, SUMA, and ZOLM across LLC-PK1 parent cell monolayers was poor, with <5% of each drug being transported in either the B to A or A to B direction over a 4-h period. This diffusion rate was too low to reliably test whether these compounds were substrates for P-gp. In contrast, the transport of ETT was >10% in this parent cell line, a value consistent with the extent of transport observed for the positive control compounds used: dexamethasone, ritonavir, and verapamil (Table 2). In transport experiments across LLC-MDR1 and LLC-Mdr1a cell monolayers, the BA/AB ratio for ETT was in the range 9 to 11, highlighting it to be a good substrate of human and mouse P-gp in vitro, and similar to the positive control compounds studied.

Discussion
The role of CYP3A and human P-gp in the metabolism and transport of ETT in vitro has been investigated. These studies were performed to understand the potential for ETT to be involved in drug-drug interactions with other drugs that inhibit or induce these
In our studies, the potential for ETT to produce drug-drug interactions as a consequence of inhibiting P450-mediated reactions was also evaluated. Overall, ETT at concentrations of up to 40 μM had little effect on the enzymatic markers of CYP1A2, CYP2B6, CYP2C9, inhibitors troleanandomycin and erythromycin, together with miconazole, produced a marked concentration-dependent inhibition of ETT metabolism to DETT in human liver microsomes (Fig. 4). Previous studies have demonstrated that troleanandomycin is a specific inhibitor of human hepatic CYP3A4 (Newton et al., 1995). In addition, both erythromycin and miconazole are also known to inhibit CYP3A4-catalyzed reactions in human liver microsomes (Thummel and Wilkinson, 1998).

The NADPH-dependent metabolism of 60 μM ETT to DETT by recombinant P450 4A1 and by pooled human liver microsomes was studied. The highest rates of DETT formation were observed with rCYP2D6 and rCYP3A4 preparations (Fig. 2). Although ETT was also metabolized to DETT by rCYP2C9 and rCYP2C19 preparations, rates of DETT formation were much lower, or essentially undetectable with the rCYP1A2, rCYP2A6, rCYP2B6, rCYP2C8, and rCYP2E1 preparations.

The observation that ETT is extensively metabolized to DETT by rCYP3A4 is in agreement with the results of the correlation analysis, chemical inhibition, and inhibitory antibody studies. The finding that ETT is also extensively metabolized by rCYP2D6 appears to have little significance when other competing enzymes are present. This finding is borne out by the correlation analysis study, and the lack of effect of quinidine and the CYP2D6-inhibitory antibody on DETT formation in liver microsomes. This result is probably attributable to the relatively higher levels of CYP3A4 compared with those of CYP2D6 in human liver. Levels of CYP3A4/CYP3A4 in human liver microsomes have been reported to range from 44 to 250 pmol/mg protein, whereas those for CYP2D6 have been reported to range from only 5 to 25 pmol/mg protein (Shimada et al., 1994; Rodrigues, 1999).

Many examples of drug-drug interactions in human subjects have been described, and these may be due to either the induction or inhibition of P450-dependent and other xenobiotic metabolizing enzyme activities (Lin and Lu, 1998). The implication of our in vitro data that ETT dependence on CYP3A4 for metabolic clearances and its potential for drug interactions when coadministered with CYP3A4 inhibitors or inducers, is that plasma concentrations of ETT in patients would be expected to either increase or decrease, respectively.

With regard to coadministration of ETT (Relpax) with CYP3A4 inhibitors, this is borne out in the Product Information for Eletriptan [Pfizer, Sandwich, UK (2001)]. In clinical studies with erythromycin (1000 mg) and ketoconazole (400 mg), which are both strong inhibitors of CYP3A4, significant increases in ETT concentrations were observed following such a dosing regimen.

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In our studies, the potential for ETT to produce drug-drug interactions as a consequence of inhibiting P450-mediated reactions was also evaluated. Overall, ETT at concentrations of up to 40 μM had little effect on the enzymatic markers of CYP1A2, CYP2B6, CYP2C9,
CYP2C19, CYP2D6, CYP2E1, and CYP3A4 studied (Table 1). These data suggest that ETT is unlikely to produce any significant inhibitory interactions in vivo with other drugs that are metabolized by these P450 forms.

P-gp plays a role in modulating oral exposure and brain penetration. Unlike the other triptans investigated, ETT was an excellent substrate for human and mouse P-gp in vitro, with BA/AB ratios in bidirectional transport studies across LLC-MDR1 and LLC-Mdr1a cell monolayers in the range 9 to 11 (Table 2). This finding has significance clinically since it was reported recently that administration of the powerful vasodilator calcitonin gene-related peptide. The third mechanism, for brain-penetrant compounds, is antinociceptive activity within the brain stem sensory trigeminal nuclei; anatomical studies having shown a high concentration of 5-HT1B/1D receptors in the trigeminal ganglion of animals and humans. It might be that each of these mechanisms operates in a complementary manner to reduce the intense central trigeminal input that occurs during a migraine headache (Goadsby and Hargreaves, 2000). If the central site is important for antimigraine efficacy, then P-gp might be expected to limit the accessibility of ETT to central sites of action. An analysis of the available pharmacokinetic data for lead triptans indeed indicates that higher free drug levels of ETT, the most potent of all the triptans at 5HT1B/1D receptors in the trigeminal ganglion of animals and humans.

### Table 2

**Bidirectional transport of 5-HT1B/1D agonists across LLC-PK1, LLC-MDR1, and LLC-Mdr1a cell monolayers**

<table>
<thead>
<tr>
<th>Analyte</th>
<th>LLC-PK1</th>
<th>MDR1</th>
<th>Mdr1a</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>BA/AB Ratio</td>
<td>% Transport at r = 4 h</td>
<td>BA/AB Ratio</td>
</tr>
<tr>
<td>Eteleptan</td>
<td>1.5</td>
<td>13</td>
<td>23</td>
</tr>
<tr>
<td>Naratriptan</td>
<td>1.3</td>
<td>3.1</td>
<td>3.8</td>
</tr>
<tr>
<td>Rizatriptan</td>
<td>1.1</td>
<td>4.9</td>
<td>4.9</td>
</tr>
<tr>
<td>Sumatriptan</td>
<td>1.5</td>
<td>1.6</td>
<td>3.0</td>
</tr>
<tr>
<td>Zolmitriptan</td>
<td>1.0</td>
<td>2.2</td>
<td>2.5</td>
</tr>
<tr>
<td>Dexamethasone</td>
<td>1.3</td>
<td>14</td>
<td>18</td>
</tr>
<tr>
<td>Ritonavir</td>
<td>1.3</td>
<td>18</td>
<td>24</td>
</tr>
<tr>
<td>Verapamil</td>
<td>1.4</td>
<td>18</td>
<td>24</td>
</tr>
</tbody>
</table>

**Notes:**
- Substrate concentrations were 10 μM for ETT, NARA, RIZA, and ZOLM, and 0.5 μM for verapamil, and 5 μM for ritonavir and dexamethasone.
- Analyses were performed in triplicate and mean data are expressed to two significant figures (percentage CVs were <10% for ETT and <30% for NARA, RIZA, SUMA, and ZOLM).

### Table 3

**Physicochemical, pharmacological, and pharmacokinetic properties of selected 5-HT1B/1D agonists**

<table>
<thead>
<tr>
<th>Compound</th>
<th>Dose (mg/ml)</th>
<th>f4</th>
<th>5-HT1B Potency</th>
<th>5-HT1D Potency</th>
<th>Human Pharmacokinetic Parameters</th>
</tr>
</thead>
<tbody>
<tr>
<td>ETT80</td>
<td>382</td>
<td>0.24</td>
<td>7.7 ± 0.02</td>
<td>9.2 ± 0.02</td>
<td>226</td>
</tr>
<tr>
<td>ZOLM5</td>
<td>287</td>
<td>0.75</td>
<td>7.6 ± 0.05</td>
<td>8.9 ± 0.06</td>
<td>7.3–9.1</td>
</tr>
<tr>
<td>RIZA10</td>
<td>269</td>
<td>0.86</td>
<td>7.1 ± 0.04</td>
<td>8.4 ± 0.05</td>
<td>19.8</td>
</tr>
<tr>
<td>ETT40</td>
<td>382</td>
<td>0.24</td>
<td>7.7 ± 0.02</td>
<td>9.2 ± 0.02</td>
<td>113</td>
</tr>
</tbody>
</table>

**Notes:**
- All data are expressed as mean ± SD.
- Doses that provide superior efficacy to SUMA100.
- Doses that provide equivalent efficacy to SUMA100.
- Physicochemical data were abstracted from Palmer and Spencer (1997) for ZOLM, Sciberras et al. (1997) for RIZA, and Perry and Markham (1998) for SUMA. Pharmacokinetic data for ETT40 and ETT80 were approximated by pro-rataing data from an oral dose ranging study that used 15, 20, 30, 60, 90, and 120 mg of ETT (Milton et al., 2002).
- ETT AUC = 18.577·h.
- ETT AUC = 0.96.
- ETT AUC = 9.1.
- ETT AUC = 0.06.
- ETT AUC = 19.8.
- ETT AUC = 63.
- ETT AUC = 49.6.
- ETT AUC = 113.
- ETT AUC = 71.
- ETT AUC = 743.

### Table 4

**Bidirectional transport of 5-HT1B/1D agonists across LLC-PK1, LLC-MDR1, and LLC-Mdr1a cell monolayers**

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- Analyses were performed in triplicate and mean data are expressed to two significant figures (percentage CVs were <10% for ETT and <30% for NARA, RIZA, SUMA, and ZOLM).
penetration is, however, a poor guide to central activity, especially with potent agonist drugs such as the triptans, since they, in contrast to most other CNS agents that are antagonists, will require only low fractional receptor occupancy to exert central effects. Further studies are warranted to relate plasma and brain concentrations of the triptans to their occupancy of central antimigraine 5-HT1B/1D receptors in vivo to evaluate the potential contribution of central sites to their mechanism of action.

In summary, the results of this study demonstrate that ETT can be metabolized to DETT by human liver microsomal preparations, and this biotransformation is primarily catalyzed by CYP3A4. ETT was shown to be a substrate of human P-glycoprotein; although this of human P-glycoprotein, the importance of this in the context of a central mechanism of action remains inconclusive.

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References


