INVOLVEMENT OF CYP3A IN THE METABOLISM OF EPLERENONE IN HUMANS AND DOGS: DIFFERENTIAL METABOLISM BY CYP3A4 AND CYP3A5

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ABSTRACT:
In vitro studies were conducted to identify the major metabolites of eplerenone (EP) and the cytochrome P450 (P450) isoforms involved in its primary oxidative metabolism in humans and dogs. The major in vitro metabolites were identified as 6β-hydroxy EP and 21-hydroxy EP in both humans and dogs. EP was metabolized by cDNA-expressed human CYP3A4 and dog CYP3A12 but only minimally by human CYP3A5. In human microsomes, inhibition of total metabolism by the CYP3A-selective inhibitors ketoconazole, trocleandomycin, and 6,7-dihydroxybergamottin, each at 10 μM concentration, was 83 to 95%, whereas inhibition with inhibitors selective for other P450 isoforms was minimal. In dog liver microsomes, the percentages of inhibition were 53 to 76% with the CYP3A-selective inhibitors. A monoclonal anti-CYP3A4 antibody inhibited EP metabolism by 84%, whereas other monoclonal antibodies had minimal effects. The formation of 6β-hydroxy and 21-

Activation of the renin-angiotensin-aldosterone system is linked to high blood pressure, cardiac hypertrophy, cardiac and vascular fibrosis, renal injury, magnesium loss, baroreceptor sensitivity, ventricular arrhythmias, and increased mortality in patients with heart failure (Struthers, 1996; Sun et al., 1997; Pitt et al., 1999). Traditionally, clinicians have tended to focus on the role of angiotensin II in these negative outcomes, but increasingly strong evidence indicates that aldosterone, the central mineralocorticoid hormone in salt and blood volume homeostasis, also plays a significant and important role. As an example, the Randomized Aldactone Evaluation Study showed that, in patients with heart failure, the addition of aldosterone antagonists to standard therapies, including angiotensin-converting enzyme (ACE) inhibitors and diuretics, decreased mortality rates by 30% (Pitt et al., 1999).

In part, the prior emphasis on angiotensin II has arisen from the erroneous assumption that ACE inhibitors and angiotensin II receptor blockers concomitantly inhibit aldosterone production. Although this assumption is true after initial treatment with these pharmacologic agents, several studies have shown that aldosterone levels rise to pretreatment levels or higher in the majority of patients who are treated chronically with ACE inhibitors or angiotensin II receptor blockers. This phenomenon has been dubbed “aldosterone escape” (MacFadyen et al., 1977; Staessen et al., 1981; Pitt et al., 1999). Aldosterone receptor blockers are therefore expected to play increasingly important roles in therapies for hypertension and heart failure in the future.

Eplerenone (EP) is the first highly selective aldosterone receptor blocker designed to effectively block aldosterone at receptor sites in tissues (de Gasparo et al., 1987; McMahon, 2001). The stable 9,11-epoxide group in the steroid molecule of EP (Fig. 1) reduces the pregestational and antiandrogenic actions associated with its nonselective predecessor, spironolactone, while maintaining its beneficial aldosterone-blocking properties (de Gasparo et al., 1987). Because of its selectivity, EP is expected to provide important clinical benefits not previously available with spironolactone. EP has been approved recently in the United States for the treatment of hypertension.

The present study was conducted to further define how EP is metabolized in humans and dogs, one of the animal species used in toxicity models. Specifically, the studies were designed to determine which P450 isoform(s) are responsible for the metabolism of EP, to identify the major in vitro metabolites formed by P450 isoforms and to determine whether EP could inhibit the major P450 isoforms in vitro.
Materials and Methods

Materials. [14C]EP (lot numbers, GDS-8181–53A, GDS-8181–51A, GDS-8181–80B, and GDS-8181–28A, specific activity 16.5 or 125 μCi/mg, purity >95%), nonradiolabeled EP (lot numbers B900081 and 99K008-F3A) and 6β-hydroxyepilone were obtained from Pharmacia Corporation (Skokie, IL). Male and female dog liver microsomes were obtained from In Vitro Technologies (Baltimore, MD) and pooled equally for the appropriate experiments. Pooled human liver microsomes and the Reaction Phenotyping kit were obtained from Xenotech LLC (Kansas City, KS). Microsomes prepared from cDNA-transfected human B-lymphoblastoid cell lines that stably express CYP1A2, CYP2A6, CYP2B6, CYP2C8, CYP2C9, CYP2C19, CYP2D6, CYP2E1, CYP3A4, or CYP3A5, and several of their respective monoclonal or polyclonal antibodies, were obtained from BD Gentest Corporation (Woburn, MA). The specific CYP3A inhibitor, 6,7-dihydroxybergamottin was synthesized by Pharmacia Corporation using the method reported by Bellevue et al. (1997). Dog CYP2D15 and CYP3A12 were cloned by Pharmacia Corporation using methods reported previously (Paulson et al., 1999). The recombinant dog P450 enzymes were expressed in S. cerevisiae (Costa Mesa, CA), or Salford Ultrafine Chemicals (Manchester, UK), and were of the highest quality available.

Metabolism of EP Using Human and Dog Microsomes. [14C]EP, prepared by combining appropriate amounts of radiolabeled and nonradiolabeled compound in an aqueous solution of acetone (1% v/v final concentration), was incubated with human and dog liver microsomes and cDNA expressed P450 microsomes (human CYP1A2, CYP2A6, CYP2B6, CYP2C8, CYP2C9, CYP2C19, CYP2D6, CYP2E1, CYP3A4, and CYP3A5, and dog CYP2D15 and CYP3A12). The incubation mixtures consisted of microsomal protein, 0.1 mM EDTA, 0.1 M sodium phosphate buffer (pH 7.4), 5 mM MgCl2, 0.6 H2O, 4 mM glucose 6-phosphate, 1.25 mM NADP+, and 2 U/ml glucose-6-phosphate dehydrogenase (Sigma-Aldrich, type VII from baker’s yeast) in 1.5-ml capacity disposable polypropylene microcentrifuge tubes. The concentrations of human and dog microsomal proteins used ranged from 0.1 to 4.0 mg/ml, depending on the experiment. The final substrate concentration and incubation time also depended on the experiment, however, under the conditions used for kinetic experiments, metabolic rate of EP was linear with respect to substrate concentration and incubation time, as well as protein concentration. Also, preliminary experiments indicated the EP was stable in 37°C phosphate buffer for at least 2 h. Reaction mixtures were preincubated for 5 min in a 37°C shaking water bath. The reaction was initiated with the addition of [14C]EP and terminated with the addition of 200 μl of MeOH. Samples were centrifuged; the supernatants were transferred to borosilicate glass test tubes and evaporated to dryness under a stream of nitrogen (N2). The asterisk indicates the position of the labeled carbon atom.

Inhibition of EP Metabolism by Chemical Inhibitors. The effects of P450-selective chemical inhibitors on [14C]EP metabolism with liver microsomes were evaluated by determining the substrate metabolism rate in the absence (control) or presence of the following known isomform-selective inhibitors: furafylline (CYP1A2), tranylcypromine (CYP2A6/2C19), orphenadrine (CYP2B6), sulfaphenazole (CYP2C9), quinidine (CYP2D6), dihydrocapsaicin.
Inhibition of EP Metabolism by Human P450 Antibodies. Four P450-specific monoclonal antibodies (anti-CYP2A6, anti-CYP2B6, anti-CYP2E1, and anti-CYP3A4) and two polyclonal antibodies (anti-CYP1A1 and anti-CYP2C) were used to inhibit P450 isoforms in pooled human liver microsomes. Incubates were prepared and incubated (final [14C]EP concentration of 50 μM) as described previously, except that human liver microsomes and antibodies (1 mg of protein/ml) were preincubated for 15 min at 37°C before adding the substrate. Alternatively, control incubates contained an equivalent volume of 25 mM Tris buffer (pH of 7.4). Concentrations of [14C]EP and metabolites were determined using an HPLC procedure.

Inhibition of Human P450 Isozyme Activities by EP. Inhibition of P450 enzymes was measured with model substrates for cDNA-derived enzymes (BD Gentest Corporation) in microsomes prepared from human lymphoblastoid cell lines (CYP1A2, CYP2C9, CYP2D6, and CYP3A4) or from baculovirus-infected insect cells (CYP2C19). A single concentration (approximately 2 times apparent K_{m}) of each model substrate was used, and their metabolic rates were determined by the measurement of an appropriate metabolite. Each enzyme assay included multiple EP concentrations separated by approximately 1/2 log (0, 0.01, 0.03, 0.1, 0.3, 1, 3, 10, 30, 100, and 300 μM) and two concentrations of a positive control inhibitor specific to the enzyme in question. Acetonitrile (final concentration 1%) was used as the substrate and inhibitor cosolvent. For this experiment, each enzyme assay required distinct incubation methods. These conditions were provided by BD Gentest Corporation and used with minor modifications. Briefly, the incubation conditions used for each enzyme assay were as follows:

1. All assays were performed in a final volume of 25 ml containing 3.3 mM MgCl_{2}, 6.7 mM n-glucose-6-phosphate, 1.3 mM NADP+, and 0.4 U/ml n-glucose-6-phosphate dehydrogenase (Sigma-Aldrich, type VII from baker's yeast), and incubated at 37°C in a shaking water bath for 30 min.

CYP1A2 catalytic activity was measured by the dehydroxylation of phenacetin (50 μM) in incubates containing 0.4 mg/ml CYP1A2 enzyme protein and 0.1 M potassium phosphate, pH 7.4. Reactions were stopped by adding 50 μl of acetonitrile. The positive control inhibitor sulfinpyrazone was included at concentrations of 0.1 and 1 μM.

HPLC. An aliquot (200 μl) of sample was injected into an HPLC system comprised of a Hewlett Packard series 1050 autosampler and pump (Hewlett Packard Analytical Direct, Wilmington, DE), equipped with an Alltech Altima C18 guard column (5 μ, 7.5 × 4.6 mm) and an Alltech Altima C18 HPLC column (5 μ, 150 × 4.6 mm) (Alltech Associates, Deerfield, IL). The linear gradient system was used consisting of acetonitrile and water, from 10:90 by volume to 50:50 over 40 min, at a flow rate of 1.0 ml/min. The column was re-equilibrated with mobile phase A for 15 min between injections. A Radiomatic Flow-One/beta series A-500 radiochemical detector (PerkinElmer Life Sciences, Boston, MA), pumping Packard Flo-Scint III at 3 ml/min, detected the radiocromatographic profiles. Assay sensitivity of the system allowed for the detection of any radioactive metabolic peak areas greater than 1% of the total sample radioactivity.

LC-MS. Identification of the hydroxy metabolites of EP was performed on a Finnigan TSQ-700 triple quadrupole LC-MS system (Thermo Finnigan, San Jose, CA) equipped with an atmospheric pressure chemical ionization unit. The corona current was set to 5 μA, the vaporizer temperature to 500°C, the capillary temperature to 200°C, the sheath gas to 80 psi, and the auxiliary gas to 10 ml/min. Samples were scanned at a mass range of 70 to 750 amu every 2 s. Samples were injected onto a 3.5 μ, 3 × 150 mm Zorbax SB-C18, LC column (MAC-MOD Analytical Inc., Chadds Ford, PA) at 50°C. The mobile phase gradient consisted of a 40-min ramp from 100% mobile phase A (95% H_{2}O, 5% MeOH, 12.5 mM ammonium acetate, pH 4.5) to 100% mobile phase B (5% H_{2}O, 95% MeOH, 12.5 mM ammonium acetate, pH 4.5).

Determination of P450 Marker Substrates. Methodologies for determination of P450 marker substrate metabolites were provided by BD Gentest Corporation and used with minor modifications. Briefly, sample aliquots were injected into an HPLC system using a Waters model 510 pump and a Waters model 717 plus autosampler (Waters, Milford, MA). Separation occurred at 45°C and 1 ml/min on a Supelco 4.6 × 250 mm Nucleosil C_{18}, 5 μ HPLC column (Bellefonte, PA), with linear mobile phase gradients. Differing mobile phases, gradients of water and methanol, or water, acetonitrile, and perchloric acid were used, depending on the analyte. A Waters model 486 tunable absorbance detector monitored for the metabolites acetaminophen (absorbance at 244 nm), 4'-hydroxy-diclofenac (absorbance at 280 nm), and 6β-hydroxytestosterone (absorbance at 254 nm). A Packard model 150TR Radiomatic Flow-One flow scintillation analyzer (PerkinElmer Life Sciences) was used to detect [14C]hydroxyphenytoin. A Fobi System 3 scanning spectrotuflurometer (Optical Technology Devices, Inc., Elmsford, NY) monitored for 1'-hydroxybufuralol (excitation at 252 nm and emission at 302 nm). When using absorbance or fluorescence methods, analytes were quantified by comparison to a appropriate standard curve.

Results

Metabolism of EP In Liver Microsomes and cDNA-Expressed P450 Isozymes. Metabolic profiles of [14C]EP after incubation with human and dog liver microsomes are shown in Fig. 2, A and B. The metabolites peaks eluting at the HPLC retention time of 22 to 22.5 min and 23 to 23.5 min were identified as 6β-hydroxy EP and 21-hydroxy EP, respectively, as described below. The major metabolite of [14C]EP produced with human microsomes was 6β-hydroxy EP, and a relatively small amount of 21-hydroxy EP was also found. With dog microsomes, the major metabolites were also 6β-hydroxy and 21-hydroxy EP.

Following a 1-h incubation in various cDNA-expressed isozymes, extensive metabolism of [14C]EP was observed with CYP3A4 (approximately 35% in Fig. 2C). Minimal metabolism (<1%) was observed in CYP3A5 (data not shown) whereas 50 μM [14C]testosterone, a positive control, showed extensive metabolism (>30%) with both CYP3A4 and CYP3A5 after a 10-min incubation. Finally, there was no apparent metabolism with CYP1A2, CYP2A6, CYP2B6, CYP2C8, CYP2C9, CYP2C19, CYP2D6, or CYP2E1 (metabolic
Metabolic profiles from CYP3A4 incubates were similar to that in human liver microsomes. The major in vitro metabolites with human liver microsomes or CYP3A4 were 6β-hydroxy and 21-hydroxy EP, which accounted for greater than 90% of the total metabolism in incubates.

From the large-scale CYP3A4 incubation, the metabolite peaks eluting at the HPLC retention time of 22 to 22.5 min and 23 to 23.5 min were identified as 6β-hydroxy EP and 21-hydroxy EP by an LC-MS procedure comparing their HPLC retention times and MS fragmentation pattern with those of human in vivo metabolites previously identified by both NMR and LC-MS/MS. The atmospheric pressure chemical ionization LC-MS scans (Fig. 3) for the metabolites at retention times 22 to 22.5 min and 23 to 23.5 min were the same as those of the reference compounds 6β-hydroxy and 21-hydroxy EP, respectively. With dog P450 isozymes, the major metabolites were identified by HPLC retention time comparison. Substantial formation of 6β-hydroxy and 21-hydroxy EP was observed with CYP3A12 (Fig. 2D). However, there was no apparent metabolism with CYP2D15 (metabolic profile not shown). The metabolic profile from CYP3A12 incubates was similar to that in dog liver microsomes, although quantitative differences among the metabolite peaks were observed.

**Kinetics of EP Metabolism.** The \( V_{\text{max}} \) and \( K_{\text{m}} \) (±S.E.) measured from 6β-hydroxylation and 21-hydroxylation were 0.973 ± 0.132 nmol/min/mg and 217 ± 56.0 \( \mu \)M, and 0.143 ± 0.035 nmol/min/mg and 211 ± 101 \( \mu \)M, respectively (Fig. 4). The corresponding values, as measured from the disappearance of EP (total metabolism), were 1.76 ± 0.24 nmol/min/mg and 303 ± 70.0 \( \mu \)M. Even though enough curvature was present in the data to obtain estimated \( V_{\text{max}} \) and \( K_{\text{m}} \) values using WinNonlin, solubility of EP was the major limitation in determining metabolic rates at concentrations higher than 300 \( \mu \)M, thereby causing a relatively large standard error in their estimation. The \( CL_{\text{int}} \) for 6β-hydroxylation, 21-hydroxylation, and total metabolism of EP were 5.24, 0.79, and 6.78 ml/min/kg, respectively, when calculated from the \( V_{\text{max}} \) and \( K_{\text{m}} \) values. Using \( CL_{\text{int}} \) and hepatic blood flow, the estimated \( CL_{H} \) of EP due to 6β-hydroxylation, 21-hydroxylation, and total metabolism were 1.84, 0.31, and 2.30 ml/min/kg. In this respect, \( CL_{H} \) measured from 6β-hydroxy and 21-hydroxy metabolites alone accounted for 93.4% of total EP \( CL_{H} \) as estimated using human liver microsomes.

**Correlation with P450 Isozyme Activities.** The metabolic rate of \( [14C] \)EP was correlated with specific P450 isozyme activities from human liver microsomes in the Reaction Phenotyping kit (Table 1). The total rate of \( [14C] \)EP metabolism was best correlated with the dextromethorphan N-demethylation (CYP3A) and testosterone 6β-hydroxylation (CYP3A) rates compared with rates of other marker metabolic reactions. When metabolism of EP to the two major metabolites was compared with P450 isozyme activities, the formation rates of both 6β-hydroxy and 21-hydroxy EP were best correlated with CYP3A activity. In this experiment, \( [14C] \)EP also seemed to correlate moderately (an \( r \) value of approximately 0.5) with coumarin 7-hydroxylation (CYP2A6), 7-ethoxy-4-trifluoromethylcoumarin O-dealkylation (CYP2B6) and paclitaxel 6β-hydroxylation (CYP2C8). To verify whether these isoforms play a minor role in EP metabolism and whether the correlation improves by inhibition of CYP3A activities, the phenotyping experiment was repeated in the presence of ketoconazole. With ketoconazole, 10 \( \mu \)M EP metabolism was com-

**Fig. 2.** Representative HPLC profile of \([14C] \)EP (48 \( \mu \)M, 1 h incubation) metabolism by human liver microsomes (A), dog liver microsomes (B), human cDNA-expressed CYP3A4 (C), and dog cDNA-expressed CYP3A12 (D).

M1, 6β-hydroxy EP; M2, 21-hydroxy EP.
pletely inhibited, and metabolites were not measurable in any of the microsomal preparations. Therefore, correlation values could not be determined. Using the modified conditions described earlier (i.e., using 50 μM EP, 1 mg protein/ml and 30-min incubation), moderate metabolism was observed in the presence of ketoconazole. In this case, the metabolic rates tended to be reduced by 90% when normalized for initial substrate concentration, and both 6β-hydroxy and 21-hydroxy metabolites were observed. However, the correlation values calculated for 6β-hydroxylation, 21-hydroxylation and total metabolism remained the same as in the experiment without ketoconazole. That is, correlations with CYP3A activity remained greater than 0.9, whereas correlations with CYP2A6, CYP2B6, and CYP2C8 activities remained approximately 0.5.

Chemical Inhibition. Inhibition of metabolism of [14C]EP in human liver microsomes was examined in the presence of various chemical inhibitors at a concentration of 10 μM. Total metabolism was markedly reduced with CYP3A inhibitors ketoconazole (95%), troleandomycin (83%), and 6′,7′-dihydroxybergamottin (86%). When formation of 6β-hydroxy EP and 21-hydroxy EP was measured individually, metabolism of [14C]EP to these metabolites was significantly inhibited by ketoconazole, troleandomycin, and 6′,7′-dihydroxybergamottin (Fig. 5, A and B). Formation of 6β-hydroxy EP was also significantly reduced by dihydrocapsaicin (31%) compared with control.

Inhibition of [14C]EP metabolism in dog liver microsomes was also examined in the presence of the various chemical inhibitors. With the dog microsomes, total metabolism of [14C]EP was markedly reduced only with CYP3A-selective inhibitors ketoconazole (66%), troleandomycin (76%), and 6′,7′-dihydroxybergamottin (53%). When formation of 6β-hydroxy and 21-hydroxy EP was measured individually, metabolism of [14C]EP to these two metabolites was also significantly inhibited only by ketoconazole, troleandomycin, and 6′,7′-dihydroxybergamottin (Fig. 5, C and D).

Immunoinhibition of 6β- and 21-Hydroxy EP Formation. Inhibition of [14C]EP metabolism in human microsomes was examined with human P450 antibodies. The total metabolism of [14C]EP was

![Fig. 3. MS of 6β-hydroxy EP (A) and 21-hydroxy EP (B) isolated from cDNA-expressed CYP3A4 incubates.](image1)

![Fig. 4. Rate of 6β-hydroxylation, 21-hydroxylation, and total metabolism in a pool of human liver microsomes.](image2)

Error bars indicate standard error of the mean for an n of 3.
inhibited by 84% with a monoclonal anti-CYP3A4 antibody. Inhibition of total metabolism of EP was minimal when human liver microsomes were incubated with other antibodies. When formation of 6β-hydroxy and 21-hydroxy EP was measured individually, metabolism of [14C]EP to these two metabolites was also significantly inhibited only by anti-CYP3A4 (Fig. 6).

**Inhibition of P450 Isozyme Activities by EP.** As indicated by metabolism of the marker substrates, EP at concentrations up to 300 μM did not remarkably reduce (<20% reduction) the activities of CYP1A2, CYP2C9, CYP2C19, or CYP2D6 (Fig. 7). Positive control inhibitors for these enzymes, however, did markedly reduce metabolism of marker substrates, indicating proper function of the assay. On the other hand, EP inhibited CYP3A4 catalytic activity by approximately 34% at 100 μM and approximately 45% at 300 μM. The IC50

### Table 1

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<th>Marker Reaction</th>
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<td></td>
<td>Total Metabolism</td>
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<tr>
<td>CYP1A2</td>
<td>7-Ethoxyresorufin O-dealkylation</td>
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<td>Coumarin 7-hydroxylation</td>
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<td>7-EFC* O-dealkylation</td>
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<td>Paclitaxel (Taxol) 6β-hydroxylation</td>
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*7-Ethoxy-4-trifluoromethylcoumarin.

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**Fig. 5.** Inhibition of 6β-hydroxy EP (A) and 21-hydroxy EP (B) formation in human liver microsomes and 6β-hydroxy EP (C) and 21-hydroxy EP (D) formation in dog liver microsomes by P450 chemical inhibitors at 10 μM.
for this interaction was not calculated because all inhibition values were below 50%. CYP3A activity was inhibited more than 75% by 0.1 \( \mu \text{M} \) and nearly 95% by 1.0 \( \mu \text{M} \) ketoconazole, the positive control inhibitor.

**Discussion**

The present study demonstrated that 6\( \beta \)- and 21-hydroxy EP are the major in vitro metabolites in both human and dog and that the metabolism to these hydroxy compounds was primarily mediated by CYP3A4 in humans and CYP3A12 in dogs. The involvement of CYP3A4 in the metabolism of EP in humans is well supported by the following findings: 1) metabolism of \([^{14} \text{C}]\text{EP}\) to 6\( \beta \)- and 21-hydroxy EP was best correlated with dextromethorphan N-demethylation and testosterone 6\( \beta \)-hydroxylation activities, which are typical markers for CYP3A activity; 2) correlation with other P450 marker reactions did not improve in the presence of CYP3A-selective inhibitor ketoconazole; 3) metabolism to both 6\( \beta \)- and 21-hydroxy EP was significantly inhibited by only CYP3A-selective inhibitors ketoconazole, troleandomycin, and 6\( ,7\)-dihydroxybergamottin; 4) metabolic activity was extensively inhibited by human anti-CYP3A4 antibody, but not by other antibodies; 5) EP was extensively metabolized to 6\( \beta \)- and 21-hydroxy \([^{14} \text{C}]\text{EP}\) by human cDNA-expressed CYP3A4 and only minimally by CYP3A5, but not by other CYP isozymes. With dog liver microsomes, metabolism of \([^{14} \text{C}]\text{EP}\) to both 6\( \beta \)- and 21-hydroxy EP, was inhibited by CYP3A-specific inhibitors, ketoconazole, troleandomycin, and 6\( ,7\)-dihydroxybergamottin, whereas the metabolism was not inhibited by the inhibitors for other P450 isoforms. Furthermore, metabolism of \([^{14} \text{C}]\text{EP}\) was observed with dog cDNA-expressed CYP3A12, and there was no notable metabolism with dog CYP2D15. These results indicate that formation of 6\( \beta \)- and 21-hydroxy \([^{14} \text{C}]\text{EP}\) in the dog was also primarily mediated by CYP3A.

The chemical inhibitors used in this study were chosen based on a review of literature that ascertained their potency and selectivity. Nevertheless, in P450-selective chemical inhibition experiments with human liver microsomes, dihydrocapsaicin, a selective CYP2E1 inhibitor, reduced metabolism of \([^{14} \text{C}]\text{EP}\) significantly at a concentration of 10 \( \mu \text{M} \) (Fig. 5). However, there was no apparent metabolism with cDNA-expressed CYP2E1, EP metabolism (alone or in the presence of ketoconazole) was not well correlated with CYP2E1 activities (Table 1), nor was EP metabolism inhibited by anti-CYP2E1 (Fig. 3). Therefore, the minor reduction of EP metabolism by dihydrocapsaicin may be nonselective at the concentrations studied.

Examining EP metabolism using the Reaction Phenotyping kit of human microsomes revealed some moderate correlations with CYP2A6, CYP2B6, and CYP2C8 activities (\( r \) values of approximately 0.5), in addition to higher correlations with CYP3A activities. These correlations were not improved in the presence of ketoconazole. Thus, these P450 isozymes were not involved in EP metabolism in vitro. Instead, these correlations appear to be artifacts of the microsomal samples chosen by XenoTech for this particular version of the Reaction Phenotyping kit. Using the marker reaction data alone, XenoTech determined that a selective CYP3A4/5 substrate reaction such as testosterone 6\( \beta \)-hydroxylation would have an apparent correlation of 0.46, 0.55 to 0.58, and 0.57 to marker reactions for CYP2A6, CYP2B6, and CYP2C8 activities, respectively (data provided by Xenotech). If EP were a substrate of one of these isoforms, a correlation value of significantly higher than 0.5 to 0.6 is expected, particularly in the presence of ketoconazole. This demonstrates the importance of in vitro inhibition experiments with cDNA-expressed P450 isoforms to evaluate isoform-specific metabolism in humans and dogs.
portance of evaluating the correlations between the marker metabolic reactions prior to final interpretation of the results from this type of phenotyping experiment.

A \( CL_{H1} \) value of 2.3 ml/min/kg was obtained from the total rate of EP metabolism using the well stirred model. The plasma clearance of EP after oral administration (CL/F) to humans was 2.7 ml/min/kg (C. S. Cook, L. M. Berry, A. Karim, J. Qian, M. Lonien, J. Hribar, R. Bible, unpublished data). Since \( F \) (fraction bioavailable) is expected to be greater than 0.7, and EP is extensively metabolized in humans, the in vivo hepatic clearance will be between 1.9 and 2.7 ml/kg/min. Thus, despite the solubility limitations in determining \( V_{max} \) and \( K_{m} \), the \( CL_{H1} \) predicted by the in vitro values is in close agreement with in vivo data.

Steroid molecules such as testosterone and progesterone are metabolized to 6β-hydroxy metabolites by CYP3A (Yamazaki and Shima, 1997), and it is not surprising to find that 6β-hydroxylation of EP is also catalyzed by CYP3A4. However, 6β-hydroxylation of testosterone and progesterone was also mediated by CYP2C9 and 2C19 although the rates of metabolism by these isozymes were much lower than those by CYP3A. Unlike these steroid molecules, there was no evidence that 6β-hydroxy EP was formed by these isozymes at the assay sensitivity level of 0.08 pmol/min/mg of protein. Moreover, EP was not substantially metabolized in the presence of cDNA-expressed CYP3A5, demonstrating that EP metabolism is highly selective to CYP3A4. Some steroid molecules, such as testosterone and estradiol, are good substrates of both CYP3A5 and CYP3A4, although the rates of metabolism of these compounds tended to be lower with CYP3A5 (Williams et al., 2002). In addition to 6β-hydroxylation, EP was also metabolized to 21-hydroxy EP, which has a hydroxyl group on the α-lactone ring. To our knowledge, EP is the first example that demonstrates involvement of CYP3A4 in the hydroxylation of a α-lactone ring. Hydroxylation of a α-lactone ring has been shown for carbenron (Karim, 1978) and the naphthalenic lignan lactone 5-lipoxygenase inhibitor, 1,702539 (Chauret et al., 1995). However, the P450 isozyme responsible for this type of metabolism has not been reported.

Even though the in vitro metabolites, 6β-hydroxy EP and 21-hydroxy EP, were formed by CYP3A subfamily enzymes in dogs, as observed in humans, the proportion of these two metabolites in dogs was substantially different from that in human. The major in vitro metabolite of EP formed in human liver microsomes was 6β-hydroxy EP, whereas only a small amount of 21-hydroxy was formed. In dog liver microsomes, on the other hand, there was relatively more 21-hydroxy EP formed than 6β-hydroxy EP. These results are in agreement with in vivo findings in which 6β-hydroxy EP is the major metabolite in humans (C. S. Cook, L. M. Berry, A. Karim, J. Qian, M. Lonien, J. Hribar, R. Bible, unpublished data), whereas in dogs, 21-hydroxy EP is the major metabolite (Cook et al., 2000). CYP3A4 and CYP3A12 share 79% amino acid sequence similarity. However, potential CYP3A inhibitors like ketoconazole, 6β,7-dihydroxybergamottin, and troleandomycin significantly reduced EP metabolism. Therefore, it is anticipated that other potent CYP3A4 inhibitors (e.g., erythromycin, flucloxacillin, cyclosporin, saquinavir) will also reduce the metabolism of EP, thereby potentially increasing in vivo exposure to EP.

In summary, the results of the present study indicate that EP was primarily metabolized to 6β- and 21-hydroxy metabolites by CYP3A4 in humans and by CYP3A12 in dogs. Additionally, it is highly unlikely that EP will reduce the metabolism of other drugs, whereas only very potent CYP3A inhibitors are expected to substantially reduce the metabolism of EP in vivo.

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**References**


