

## METABOLISM OF PHENCYCLIDINE BY HUMAN LIVER MICROSOMES

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### ABSTRACT:

These studies examined *in vitro* metabolism of phencyclidine (PCP) in a series of human liver microsomes ( $N = 10$ ). Each sample was characterized for cytochrome P<sub>450</sub> (CYP) content and for CYP1A, CYP2A, CYP2C, CYP2D, CYP2E, CYP3A, CYP4A, and lauric acid 11-hydroxylation metabolic activities. At least five PCP metabolites (*c*-PPC, *t*-PPC, PCHP, an unknown metabolite, and an irreversibly bound metabolite) were formed by the various human liver microsomes. Nevertheless, there was a large degree of inter-individual variation in the metabolite formation. For example, the irreversibly bound metabolite was formed in detectable amounts in only four of the ten samples. *c*-PPC, *t*-PPC and the irreversibly bound PCP metabolite formation rates significantly correlated with CYP3A activity. The CYP3A inhibitor troleandomycin was used to

inhibit the formation of PCP metabolites. Troleandomycin inhibition was dose dependent with the highest dose producing complete inhibition of the formation of *c*-PPC, *t*-PPC, PCHP, and the irreversibly bound metabolite. In addition, PCP inhibited CYP3A-mediated testosterone 6 $\beta$ -hydroxylation by 50%. Furthermore, the relative intensity of CYP3A immunoreactive proteins significantly correlated with testosterone 6 $\beta$ -hydroxylation and with PCP metabolite formation (except for the unknown metabolite). PCHP formation also correlated with CYP1A activity, while the formation of the unknown PCP metabolite correlated with CYP2A activity. These studies suggest that several CYP isoforms contribute to PCP metabolism and that CYP3A plays a major role in PCP biotransformation in human liver microsomes.

Phencyclidine (PCP)<sup>2</sup> was originally developed by Parke-Davis in the mid-1950's for use as an anesthetic in humans but because of significant side effects it was never sold for human use. Nevertheless, in the 1960's and 1970's it became a popular drug of abuse. In addition to its anesthetic and analgesic effects in humans, PCP is known to produce a dose-dependent psychosis that resembles schizophrenia with behavior described as extremely agitated, bizarre, unpredictable, and paranoid (1–3). There is also a long-lasting PCP-induced psychosis that appears to be an idiosyncratic reaction to which only certain individuals are susceptible (1, 3). The cause of this PCP-induced psychosis is unknown, but changes in the affinity or density of PCP and dopamine receptors (4), autoimmune mechanisms (5, 6) and differences in PCP metabolism and/or PCP metabolite irreversible binding to critical neurological macromolecules (7, 8) are among the most often mentioned explanations.

Cook *et al.* have shown that the elimination  $t_{1/2}$  of PCP varies considerably in humans, ranging from 7 to 57 hr (9–11). The observed values in  $t_{1/2}$  show a bimodal distribution. Although the majority of individuals have an average elimination of  $t_{1/2} \sim 17$  hr, 2 of the 16

individuals in these studies had  $t_{1/2}$  values greater than 50 hr (11). These data suggest differences in PCP metabolism could help explain individual variations in PCP response and the reason for long-lasting effects in some individuals.

Oxidation by cytochrome P<sub>450</sub> (CYP) enzymes is an important determinant in the overall clearance of many drugs, and differences in the CYP metabolic capabilities of humans is well documented (12, 13). Indeed, deficiencies and/or increases in tissue concentrations of some CYP isoforms can lead to unexpected toxicities and/or altered pharmacological effects of various drugs and xenobiotics (14, 15).

PCP metabolism and irreversible binding of metabolites have been studied extensively in various tissues of rat and rabbit (*e.g.* 16, 17); however, relatively little is known about human PCP metabolism except for the pharmacokinetic studies by Cook *et al.* (9, 10). Since metabolism is the major mechanism for termination of the pharmacological effects of PCP in animals (18, 19) and large differences in the terminal elimination half-life of PCP in humans are known (9, 10), we investigated PCP human metabolism to help understand the reasons for the individual differences in PCP response and pharmacokinetics. In these studies we examined the metabolism of PCP using a series of human liver microsomal samples, identified some of the PCP metabolites formed, and identified potential CYP isoforms involved in PCP metabolism.

### Materials and Methods

**Materials.** Phencyclidine hydrochloride (PCP), *cis*-1-(1-phenyl-4-hydroxycyclohexyl)piperidine (*c*-PPC), *trans*-1-(1-phenyl-4-hydroxycyclohexyl)piperidine (*t*-PPC), 1-(1-phenylcyclohexyl)-4-hydroxypiperidine (PCHP), 5-[*N*-(1'-phenylcyclohexyl)amino]pentanoic acid (PCHAP) and 1-(1-[phenyl-3-<sup>3</sup>H(n)]cyclohexyl)piperidine ([<sup>3</sup>H]-PCP, 15.69 Ci/mmol labeled at a metabolically stable site) were obtained from the National Institute on Drug Abuse (Rockville, MD). All other chemicals were purchased from Fisher Scientific (Springfield, NJ) unless otherwise stated. Trichloroacetic acid (TCA, 10%) was purchased from Baxter Scientific Products (Grand Prairie, TX). Troleandomycin (TAO), D-glucose-6-phosphate, glucose-6-phosphate dehydrogenase,

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<sup>2</sup> Abbreviations used are: CYP, cytochrome P450; PCP, phencyclidine; [<sup>3</sup>H]-PCP, 1-(1-[phenyl-3-<sup>3</sup>H(n)]cyclohexyl)piperidine; PCHP, 1-(1-phenylcyclohexyl)-4-hydroxypiperidine; PCHAP, 5-(*N*-[1'-phenylcyclohexyl]amino)pentanoic acid; *c*-PPC, *cis*-1-(1-phenyl-4-hydroxycyclohexyl)piperidine; *t*-PPC, *trans*-1-(1-phenyl-4-hydroxycyclohexyl)piperidine; TAO, troleandomycin; TCA, trichloroacetic acid.

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TABLE 1

Donor information for human microsomal preparations

Sample	Gender	Age (yr)	Race	Smoker	Alcohol Use
H2	Female	53	Caucasian	yes	no
H3	Male	33	Caucasian	yes	yes
H5	Male	42	Caucasian	no	no
H6	Female	51	Caucasian	yes	yes
H7	Male	45	Caucasian	yes	yes
H9	Female	11 months	Caucasian	no	no
H10	Female	54	Hispanic	no	yes
H11	Male	54	African American	no	yes
H12	Female	36	Caucasian	?	yes
H13	Female	52	Caucasian	yes	yes

NADP<sup>+</sup>, EDTA, testosterone, 4-androstene-3,17-dione, 5 $\alpha$ -androstan-3 $\beta$ ,17 $\beta$ -diol and 5 $\alpha$ -androstan-17 $\beta$ -ol-3-one, bovine serum albumin, and goat anti-rabbit IgG (whole molecule) alkaline phosphatase conjugate were purchased from Sigma Chemical Company (St. Louis, MO). The testosterone metabolites 4-androsten-7 $\alpha$ ,17 $\beta$ -diol-3-one, 4-androsten-16 $\alpha$ ,17 $\beta$ -diol-3-one, 4-androsten-6 $\alpha$ ,17 $\beta$ -diol-3-one, 4-androsten-6 $\beta$ ,17 $\beta$ -diol-3-one, 4-androsten-2 $\beta$ ,17 $\beta$ -diol-3-one, and 4-androsten-2 $\alpha$ ,17 $\beta$ -diol-3-one were obtained from Steraloids Inc. (Wilton, NH). Trimethylamine was purchased from Aldrich Chemical Company (Milwaukee, WI). Ecoscint A scintillation cocktail was purchased from National Diagnostics Inc. (Manville, NJ). Polyacrylamide and N, N'-methylene-bis-acrylamide were purchased from U.S. Biochemical Corp. (Cleveland, OH). The GF/B filters and filtration device (Model M24R) for determination of PCP metabolite covalent binding were obtained from Brandel Laboratories (Gaithersburg, MD). C<sub>18</sub> preparative columns (3 ml, Bakerbond spe, high hydrophobic octadecyl) were purchased from J.T. Baker (Phillipsburg, NJ). The  $\mu$ Bondapak C<sub>18</sub> steel column (10  $\mu$ m, 3.9  $\times$  300 mm) was obtained from Waters (Milford, MA). Silica aluminum TLC sheets were purchased from EM Separations. The anti-rat CYP3A1/2 antiserum was purchased from Human Biologics, Inc. (Phoenix, AZ). Alkaline phosphatase color development reagents, 5-bromo-4-chloro-3-indoyl phosphate p-toluidine salt and p-nitro blue tetrazolium chloride, and molecular weight markers were purchased from Bio-Rad Laboratories (Hercules, CA).

**Human Liver Microsomes.** A HepatoScreen Test Kit was purchased from Human Biologics, Inc. Table 1 shows a summary of the human donor characteristics. The metabolic activities of these microsomes was characterized by Human Biologics, Inc. using the following selective substrates for CYP enzymes: 7-ethoxyresorufin O-dealkylation (CYP1A (20)), caffeine N3-demethylation (CYP1A (21)), coumarin 7-hydroxylation (CYP2A (22)), tolbutamide methyl-hydroxylation (CYP2C, (23)), S-mephenytoin 4'-hydroxylation (CYP2C (23)), dextromethorphan O-demethylation (CYP2D (24)), chlorzoxazone 6-hydroxylation (CYP2E (25)), testosterone 6 $\beta$ -hydroxylation (CYP3A (26)), lauric acid 12-hydroxylation (CYP4A (27)) and lauric acid 11-hydroxylation (unknown isozyme).

**In vitro Metabolic Incubations.** Before determination of *in vitro* PCP metabolite formation by human liver microsomes, experiments were performed to determine the effect of microsomal protein concentration and reaction time. The incubation mixtures (final volume 0.5 ml) consisted of microsomal protein (0.1–2 mg/ml) and a NADPH regenerating system consisting 8 mM glucose-6-phosphate, 1 unit/ml glucose-6-phosphate dehydrogenase, 4 mM MgCl<sub>2</sub> with the presence or absence (for the controls) of 5 mM NADP<sup>+</sup>. This mixture was pre-incubated at 37°C for 5 min. The reaction was initiated by the addition of PCP (1  $\mu$ M) and [<sup>3</sup>H]-PCP as a tracer. Incubation times ranged from 5 to 120 min.

The 1  $\mu$ M concentration of PCP was chosen based on the average serum concentrations of 216 patients who were diagnosed with acute PCP intoxication after admission to an emergency room (28). These data showed that the majority of the patients had serum PCP concentrations ranging from 0.10–0.62  $\mu$ M (or 25–150 ng/ml), but some individuals had >2.1  $\mu$ M (or >500 ng/ml). Although no data is available for human PCP tissue to serum ratios, these data are available in the rat (29). In rats administered a dose of 1 mg/kg of PCP, a representative serum concentration at 15 min after dosing is 0.74  $\mu$ M (or 180 ng/ml). At this same time, liver concentrations are nearly 9 times higher (*i.e.*

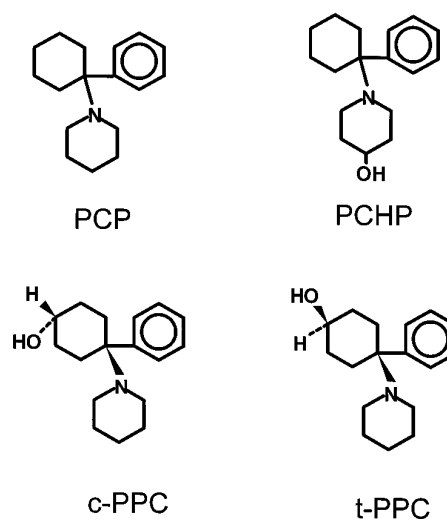


FIG. 1. Structure of PCP and three phase I metabolites in this study which were identified and quantitated by HPLC analysis.

6.7  $\mu$ M). Therefore, assuming similar liver tissue to serum ratios in humans, when serum concentrations are 0.1–0.62  $\mu$ M in humans, the liver concentrations should be about 0.9–5.6  $\mu$ M.

**HPLC Analysis of PCP and Metabolites.** Following the metabolic incubations, the PCP metabolites were immediately extracted from the incubation mixture. A 350  $\mu$ l aliquot of the mixture, along with the internal standards of PCP and metabolites, was passed over a solvent-conditioned 3 ml C<sub>18</sub> column. Prior to adding the metabolic incubation mixture, the extraction column was conditioned with 2.5 ml of 5% CH<sub>3</sub>CN containing 0.1% trifluoroacetic acid and 1% (CH<sub>3</sub>)<sub>3</sub>N. After adding the samples, the column was washed twice with 2.5 ml of conditioning buffer. PCP and the metabolic products formed were then eluted with two 2.5-ml washes of 100% CH<sub>3</sub>CN containing 0.1% trifluoroacetic acid and 1% (CH<sub>3</sub>)<sub>3</sub>N. The eluted PCP and metabolites were taken to dryness by vacuum centrifugation and were resuspended in 120  $\mu$ l of 15% CH<sub>3</sub>CN:H<sub>2</sub>O containing 0.1% trifluoroacetic acid and 0.1% (CH<sub>3</sub>)<sub>3</sub>N. PCP and metabolites (100  $\mu$ l per injection) were separated by HPLC using a  $\mu$ Bondapak C<sub>18</sub> steel column. A linear gradient from 15–20% CH<sub>3</sub>CN:H<sub>2</sub>O containing 0.1% trifluoroacetic acid and 0.1% (CH<sub>3</sub>)<sub>3</sub>N was held for 3 min, followed by a 20–35% gradient for the next 4 min, and isocratic conditions of 35% for the next 8 min. The flow rate was 2 ml/min. The Waters HPLC system consisted of Millennium chromatography software, a model 600E multisolvent delivery system, a model 717 autoinjector, and a model 486 tunable absorbance detector. Twenty *sec*-fractions were collected and analyzed for radioactive PCP and metabolites by liquid scintillation spectrometry. Analytical recoveries and identity of the metabolic products were determined by comparison with an exact amount of authentic external standards injected at the start of each analytical run. The elution of external and internal standards was monitored at 254 nm. This procedure could separate PCP and six known PCP metabolites. Since we did not detect two of these metabolites in preliminary experiments, they were not included in the analysis. These two minor dihydroxylated metabolites were: *cis*-4-(4'-hydroxypiperidino)-4-phenylcyclohexanol and *trans*-4-(4'-hydroxypiperidino)-4-phenylcyclohexanol. The four major metabolites used in this study and their HPLC retention times were *c*-PPC at 3.9 min, *t*-PPC at 6.05 min, PCHP at 7.4 min, PCHAP at 8.6 min, and PCP at 9.5 min (see fig. 1). Because of the apparent covalent type bond of the irreversibly bound PCP metabolite, it had to be detected by trapping microsomal proteins on glass fiber filters after TCA precipitation of the proteins (see next section).

**Determination of PCP Metabolite Irreversible Binding.** The method for determination of *in vitro* metabolite irreversible binding was as previously described (30, 32). Briefly, duplicate 50  $\mu$ l aliquots were removed from the incubation mixtures and the microsomal proteins were precipitated by addition of 2 ml ice cold 10% TCA and incubation on ice for 1 hr. The precipitated aliquots were then passed over GF/B filters and extensively washed with additional volumes of 10% TCA and 40% ethanol until no more radioactivity

could be removed. The filters were air dried and the amount of metabolite irreversible binding was determined by liquid scintillation spectrometry analysis of the filters.

**In Vitro CYP Inhibition Experiments.** For substrate inhibition experiments, TAO, a selective human CYP3A inhibitor (31, 33), was used. The TAO was dissolved in methanol (final concentration of methanol in the incubation mixture was <0.05%). Varying concentrations of TAO were added just prior to addition of the components of the NADPH regenerating system and the mixtures were incubated at 37°C for 5 min. PCP was added and the reaction mixtures were incubated at 37°C for 20 min.

A method similar to the procedure used by Waxman *et al.* (34) was used for the testosterone metabolism experiments. Testosterone was dissolved in methanol and aliquoted into tubes, and the methanol was allowed to evaporate. The amount of testosterone added to the tubes equaled a concentration of 100  $\mu$ M (440,000 DPM) in the final reaction volume. In separate tubes, varying amounts of PCP were combined with human liver microsomal protein (1 mg/ml) and the NADPH regenerating system (final volume 80  $\mu$ l). This mixture was preincubated at 37°C for 5 min. The mixture was then transferred to the tubes containing testosterone and the reaction was carried out at 37°C for 10 min. The reactions were terminated by pipeting 5  $\mu$ l of each mixture onto separate lanes of a silica gel TLC plate. The plates were allowed to dry and unlabeled testosterone and testosterone metabolite standards were then added to the lanes. The TLC solvent system consisted of 80% methylene chloride and 20% acetone. The plates were subjected to two consecutive TLC solvent separation steps to enhance the separation of the metabolites. The radioactivity on the plates was then analyzed by autoradiography. Areas on the plate corresponding to authentic testosterone and the 6 $\beta$ -hydroxylated testosterone metabolite were cut out and analyzed by liquid scintillation spectrometry.

**Western Blot Analysis of CYP3A.** Duplicate samples (10  $\mu$ g/lane) of human liver microsomes were subjected to sodium dodecyl sulfate polyacrylamide gel electrophoresis on a standard size 8% polyacrylamide gel for 5 hr at ~35 mAmp. The proteins were transferred to nitrocellulose filters at 12 V overnight at 4°C using prechilled 25 mM Tris, 192 mM glycine, 20% v/v methanol (pH 8.3) transfer buffer. The nitrocellulose filter was incubated for 2 hr in BSA blocking buffer (3% w/v BSA in TBS containing 0.05% v/v Tween-20) to reduce nonspecific binding and then washed twice for 5 min in TBS containing 0.05% Tween-20. Anti-rat CYP3A1/2 was diluted in antibody buffer (1% w/v gelatin in TBS containing 0.05% v/v Tween-20) and added to the filters at a final titer of 1:4,000. Characterization of this antibody is published elsewhere (35, 36). The filters were incubated overnight at room temperature with gentle mixing. Filters were washed as previously described and a goat anti-rabbit IgG alkaline phosphatase conjugate (1:20,000) was added. After incubation at room temperature for about 2 hr, the filter was washed and protein bands were detected with Bio-Rad color development reagents following the manufacturer's directions. The relative amount of anti-CYP3A reactive protein was measured using a Bio-Rad GS-670 imaging densitometer. As part of the validation of this assay, we first established there was a linear relationship between amount of rat liver microsomal protein (range of 0.25 to 20  $\mu$ g/lane) applied to the gel and the relative band intensities. The correlation coefficient for this relationship was 0.987 ( $p < 0.05$ ).

**Data Analysis.** Linear regression analysis was used for determining the relationship between PCP metabolism and CYP metabolic activity. It was also used for determining the relationship between PCP metabolism and relative intensity of CYP3A immunoreactivity on Western blots. An ANOVA followed by Dunnett's multiple range test were used for comparing control and treatment groups. All statistical analyses were performed using SigmaStat for Windows (Jandel Scientific Software, San Rafael, CA). Statistical significance was defined at a level of  $p < 0.05$ .

## Results

**In Vitro Formation of PCP Metabolites by Human Liver Microsomes.** Formation of PCP metabolites was dependent on the presence of NADP<sup>+</sup>, protein concentration, and was linear for at least 40 min (data not shown). Based on these experiments, a protein concentration of 1 mg/ml and an incubation time of 20 min were chosen as optimal. At least five PCP metabolites (*c*-PPC, *t*-PPC, PCHP, an unknown PCP metabolite, and an irreversibly bound PCP metabolite)

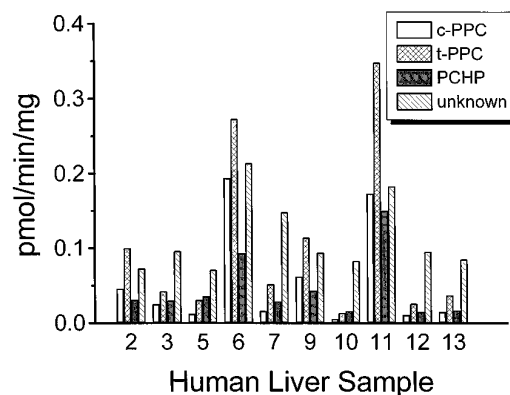


FIG. 2. Inter-individual variability in the ability of human liver microsomes to form PCP metabolites.

PCP (1  $\mu$ M and a tracer dose of [<sup>3</sup>H]-PCP) were incubated with human liver microsomal protein (1 mg/ml) for 20 min at 37°C in the presence of a complete NADPH regenerating system. Metabolites were extracted from metabolic incubation mixtures and separated as described in experimental procedures. All values were corrected for control incubations without NADP<sup>+</sup>. See table 1 for individual human donor characteristics. The unknown metabolite eluted from the HPLC column just after PCHP.

were formed at significant levels by the human liver microsomal samples, depending on the human liver sample (figs. 2 and 3). The identity of *c*-PPC, *t*-PPC and PCHP was based on co-elution with external standards. The PCHAP metabolite was not detected. An additional radioactive peak eluted from the HPLC column just after the PCHP external standard but before PCHAP. Since it did not co-elute with any of known metabolite standards and since the radiolabel on the [<sup>3</sup>H]-PCP was at a metabolically stable site, we assumed it was a PCP metabolite. No attempt was made to determine its identity. There was a large degree of inter-individual variation in the ability of the human liver microsomal samples to form some of the PCP metabolites (figs. 2 and 3). There was no evident correlation between the variation in PCP metabolism and the age, gender, or drug history of the donors. The formation rate of *c*-PPC varied 36-fold between individuals. The variation in *t*-PPC and PCHP formation rates were 20- and 10-fold, respectively. There was only a 3-fold variation in the ability to form the unknown metabolite. The irreversibly bound PCP metabolite was formed at appreciable amounts only in human liver samples 2, 6, 9, and 11 (fig. 3).

**Correlation of PCP Metabolite Formation with CYP Isoform Activity.** The formation rates of each of the PCP metabolites were correlated with each of the characterized CYP activities listed in the experimental procedures. The PCP metabolite formation rates that significantly correlated with the CYP activities are shown in table 2. PCHP formation also correlated with CYP1A activity, while CYP2A activity correlated with the formation of the unknown PCP metabolite. In addition, formation of *c*-PPC, *t*-PPC and the irreversibly bound PCP metabolite correlated with CYP3A-mediated metabolism.

**In Vitro Inhibition of PCP Metabolite Formation by TAO.** Because CYP3A appeared to play a major role in PCP metabolism, we tested the ability of TAO to inhibit the formation of PCP metabolites. Although TAO is a selective inhibitor of the CYP3A family, it is not specific for a single CYP3A isozyme (31, 33). Because human liver microsomal samples 2, 6, and 11 had intermediate to high CYP3A activities (fig. 4) and intermediate to high PCP metabolite formation rates, these three microsomal samples were chosen for further analysis. Although human liver sample 9 also had an intermediate rate of PCP metabolism, this sample was not included in this particular experiment because the microsomes were obtained from an infant. We

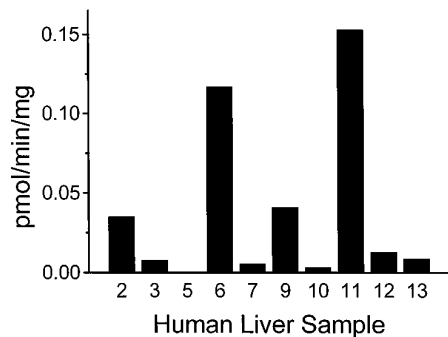


FIG. 3. Inter-individual variation in the ability of human liver microsomes to form irreversibly bound PCP metabolite(s).

PCP (1  $\mu$ M and a tracer dose of [ $^3$ H]-PCP) were incubated with human liver microsomal protein (1 mg/ml) for 20 min at 37°C in the presence of a complete NADPH regenerating system. PCP metabolite irreversible binding was determined as described in experimental procedures. All values were corrected for control incubations without NADP<sup>+</sup>.

TABLE 2

Correlation of PCP metabolite formation with CYP isoform activities in human liver microsomal samples<sup>a,b</sup>

PCP Metabolite	CYP isoform that Correlates with PCP Metabolite Formation	Correlation Coefficient (r)	p value
<i>c</i> -PPC	CYP3A	0.76	0.011
<i>t</i> -PPC	CYP3A	0.70	0.025
PCHP	CYP1A	0.74	0.012
Unknown Metabolite	CYP2A	0.66	0.039
Irreversibly bound PCP Metabolite	CYP3A	0.68	0.029

<sup>a</sup> N = 10 per group.

<sup>b</sup> CYP activities that did not show a significant correlation were CYP2C, CYP2D, CYP2E, CYP4A, and lauric acid 11-hydroxylation.

were concerned that the differential expression of CYP3A isozymes by fetal livers (37) could have added an unknown variable to the interpretation of these results. TAO inhibited the formation of *c*-PPC, *t*-PPC, PCHP and the unknown PCP metabolite in a dose-dependent fashion in these microsomes (fig. 5). The formation of all PCP metabolites was completely inhibited by TAO except for the unknown metabolite, which was inhibited to ~75% of the control value. In addition, TAO completely inhibited the formation of the irreversibly bound metabolite in human liver samples 6 and 11 (fig. 6). Human liver samples 2 and 9 were not included in this analysis because of their lower ability to form the irreversibly bound metabolite (see fig. 3).

#### In Vitro Inhibition of Testosterone 6 $\beta$ -hydroxylation by PCP.

Since testosterone 6 $\beta$ -hydroxylation is considered to be a CYP3A specific reaction, the ability of PCP to inhibit this reaction was tested. PCP inhibited the 6 $\beta$ -hydroxylation of testosterone in a dose-dependent fashion, however the highest dose of PCP (1 mM) only produced a 50% inhibition in each of the samples (fig. 7).

**Correlation of PCP Metabolite Formation with CYP3A Protein Levels.** To provide further evidence that CYP3A plays a role in PCP metabolism, PCP metabolite formation rates were correlated with the relative CYP3A content of each of the human liver microsomal samples using linear regression analysis. Prior to this analysis, we also used linear regression to determine if testosterone 6 $\beta$ -hydroxylase activities (see fig. 4) correlated with CYP3A protein levels in the human liver microsomal samples. This analysis showed that the

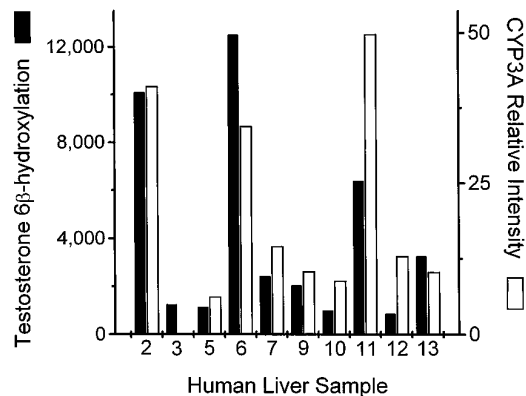


FIG. 4. CYP3A testosterone 6 $\beta$ -hydroxylase activity and CYP3A protein content of human liver microsomes.

The values for CYP3A-mediated testosterone 6 $\beta$ -hydroxylation (left axis, solid bars, in pmol/mg protein/min) were obtained from the HepatoScreen test kit instructions (see *Materials and Methods*). The values for the CYP3A protein content (right axis, open bars) were determined by Western blot analysis of the human microsomes. The relative intensity of anti-CYP3A protein was measured by densitometry. A relative intensity value for sample 3 is not shown because the relative intensity of the protein band on the Western blot gel was below the accurate detection limit of the densitometer. Nevertheless, a band could be seen on the gel.

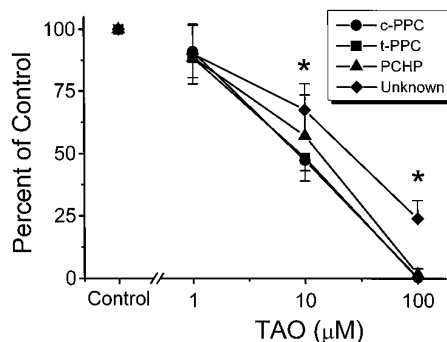


FIG. 5. Effect of TAO on the formation of PCP metabolites by human liver microsomal protein.

Each value is calculated as the mean percentage of control ( $\pm$  SD) of human liver samples 2, 6, and 11. Each human sample served as its own control due to inter-individual differences in the ability to form PCP metabolites. The asterisks indicate a significant decrease in formation of all PCP metabolites. Error bars for the PCP metabolite control values are not shown for clarity, but ranged from 3–8% of control values.

CYP3A protein relative intensity on Western blots was a good indicator of testosterone 6 $\beta$ -hydroxylase activity ( $r = 0.80$ ,  $y = 213x - 28$ ,  $p < 0.05$ ). The formation rates of *c*-PPC, *t*-PPC and PCHP were significantly correlated with CYP3A protein expression in the human liver samples (table 3). The formation rate of the unknown PCP metabolite did not significantly correlate with CYP3A content.

#### Discussion

These studies examined the *in vitro* metabolism of PCP by human liver microsomal samples. Depending on the human liver microsomal sample, up to five PCP metabolites were formed (*c*-PPC, *t*-PPC, PCHP, an unknown PCP metabolite, and an irreversibly bound PCP metabolite). The formation of each of the PCP metabolites appeared to be mediated to some extent by members of the CYP3A family. Thus, PCP can be added to the increasing list of commonly used drugs

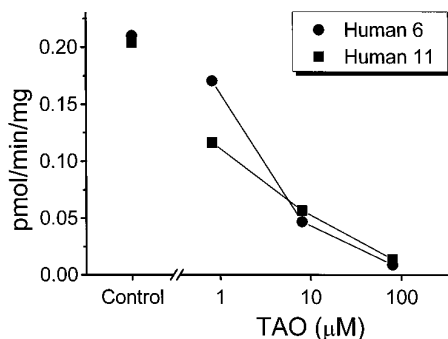


FIG. 6. Effect of TAO on the formation of the irreversibly bound PCP metabolite(s) by human liver microsomes.

Irreversible binding of PCP metabolite(s) was determined as described in *experimental procedures*. Human liver samples 6 and 11 were used in this analysis because they formed the largest amounts of the irreversibly bound metabolite (see fig. 3).

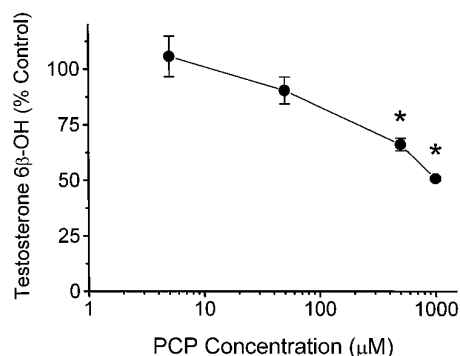


FIG. 7. Effect of PCP on testosterone 6β-hydroxylase activity in human liver microsomes.

Experiments were performed as described in *experimental procedures*. Asterisks indicate values significantly different ( $p < 0.05$ ) from controls. Human liver samples 2, 6, and 11 were used for this analysis because of their high levels of testosterone 6β-hydroxylase activity.

TABLE 3

Results from the correlation of PCP metabolite formation rates with relative intensity of CYP3A immunoreactivity protein in human liver microsomal samples<sup>a</sup>

PCP Metabolite	Correlation Coefficient (r)	P Value
<i>c</i> -PPC	0.77	0.015
<i>t</i> -PPC	0.83	0.005
PCHP	0.77	0.015
Unknown	0.58	0.10

<sup>a</sup>  $N = 10$  per group. Determined by Western blot analysis.

that are metabolized by the CYP3A isoforms (38).

In humans, the CYP3A family accounts for a major portion (~30%) of the total CYP content in liver (13). Three known functional isoforms (CYP3A4, CYP3A5, and CYP3A7) comprise the CYP3A family in humans (39). Of these forms, CYP3A4 appears to be the most abundant in adult human liver, while CYP3A7 appears to be the major fetal CYP (37). CYP3A5 is polymorphically expressed in humans, with only 30% of human livers expressing detectable levels (40, 41). In addition, although there was a large variation in the CYP3A content between individual subjects (as measured by CYP3A-mediated testosterone 6β-hydroxylase activity, fig. 4), these data correlated well with the amount of CYP3A immunoreactive protein in

the microsomes (as measured by Western blot analysis). Indeed, linear regression analysis of the CYP3A catalytic activity vs. CYP3A protein content showed a significant correlation ( $r = 0.80$ ). A large variation in CYP3A content between subjects has been reported by other investigators (13).

The formation of *c*-PPC, *t*-PPC, and the irreversibly bound PCP metabolite significantly correlated with testosterone 6β-hydroxylation, a reaction that is catalyzed primarily by CYP3A4 in humans (34, 41). To further investigate the role of CYP3A isoforms in PCP metabolism, substrate inhibition studies were conducted. For these studies, human liver samples 2, 6, and 11 were chosen because they had intermediate to high CYP3A (testosterone 6β-hydroxylase) activity and intermediate to high PCP metabolism rates (figs. 4 and 2, respectively). Despite the higher CYP3A activity in these three samples, only one donor had been treated with a prototypic phenobarbital-type CYP3A inducer (*i.e.* pentobarbital) (40, 42).

The selective CYP3A isozyme inhibitor, TAO (31, 33), completely inhibited the formation of *c*-PPC, *t*-PPC, PCHP, and the irreversibly bound PCP metabolite at 100 µM TAO (figs. 5 and 6). TAO inhibition of CYP3A catalyzed testosterone 6β-hydroxylation is reported to be specific even at concentrations of TAO much higher than used in this study (*i.e.* up to 400 µM TAO (31)). The complete inhibition of PCHP formation by TAO was somewhat surprising since PCHP formation rates did not significantly correlate with testosterone 6β-hydroxylation (a metabolic product of CYP3A). The cause of this discrepancy is not known. Nevertheless, the inhibition of PCHP formation by TAO is suggestive of CYP3A isozyme involvement in the formation of this metabolite.

The relative CYP3A content of each of the human liver samples (as determined by immunoblot) significantly correlated with the formation rates of *c*-PPC, *t*-PPC, and PCHP (table 3). The partial inhibition of testosterone 6β-hydroxylation by PCP also suggested that PCP could interact with a CYP3A isoform (fig. 7). These data provide strong evidence that one or more member(s) of the CYP3A isozyme family mediate the formation of *c*-PPC, *t*-PPC, PCHP, and the irreversibly bound PCP metabolites. Furthermore, since these studies show CYP3A is a major metabolic pathway for PCP liver elimination and there are large *in vivo* variations in CYP3A liver expression and activity (as found in this study), this could be a reason for the large variations in the PCP elimination half-life (ranging from 7 to 57 hr) found in humans (9–11). However, it is also worth noting that phase II metabolism of PCP (primarily sulfation and glucuronidation (16)) could also contribute to the variation in PCP half-life. Indeed, human liver sulfotransferase(s) are polymorphically expressed (43).

As previously mentioned, an unknown PCP metabolite was formed by the human liver microsomes. This metabolite did not co-elute with any of the authentic PCP metabolite standards. We did not attempt to determine the identity of this metabolite. Although the metabolite standards used in these studies were chosen because they are known to be major metabolites in several species (16), there are many other PCP metabolites which could be formed. For instance, 1-(1-phenyl-3-hydroxycyclohexyl)piperidine is formed by liver microsomes and has been detected in the urine of mice, monkeys, and humans (16, 44, 45). An authentic standard for this metabolite was unavailable.

While formation of the unknown PCP metabolite significantly correlated with CYP2A activity, it did not correlate with testosterone 6β-hydroxylation activity or with the relative CYP3A content of the human liver microsomal samples. However, formation of the unknown PCP metabolite was inhibited up to 80% by TAO (fig. 5). We do not have a good explanation for this seemingly conflicting result.

The PCP metabolites formed by human liver microsomes in this

study are consistent with previous reports (16, 17) with the exception of the irreversibly bound PCP metabolite. To our knowledge, our studies are the first to demonstrate the formation of the irreversibly bound PCP metabolite in human liver microsomes. Irreversibly bound PCP metabolites are known to be formed by rat liver microsomes (7, 46, 47), as well as by rabbit lung and liver microsomes (48, 49, 50). Shelnett *et al.* (32) have recently shown that the formation of this metabolite in normal rats is found only in the males and that the male-specific CYP2C11 isoform is responsible for (or at least involved in) its formation. The toxicological or pharmacological consequences of PCP metabolite irreversible binding are not known, and there are no reports of liver toxicity as a result of PCP use. Since CYP3A appears to play a role in the formation of the irreversibly bound PCP metabolite and CYP3A mRNA has been detected in human brain tissue (51), it is interesting to speculate that the formation of an irreversibly bound metabolite in the brain could play a role in the idiosyncratic psychotic reactions associated with PCP use. Future studies are needed to determine if this irreversibly bound PCP metabolite is formed in the human brain.

In conclusion, this study demonstrated that there are large inter-individual differences in the ability of human liver microsomes to metabolize PCP. In addition, members of the CYP3A family appeared to play a major role in the biotransformation of PCP. Since CYP3A isoforms are known to be variably and polymorphically expressed (13, 40), variability in human microsomal metabolism of PCP should be expected. Differences in pharmacological and/or toxicological response to drugs and other xenobiotics as a result of differences in CYP expression are well known (15). While there appears to be a large degree of variability in the ability of humans to metabolize PCP, the precise role of metabolism by CYP enzymes in mediating protective or toxic effects of PCP remains to be determined.

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