Human Placental Lactogen Induces CYP2E1 Expression via PI3-Kinase Pathway in Female Human Hepatocytes

Jin Kyung Lee, Hye Jin Chung, Liam Fischer, James Fischer, Frank J. Gonzalez, and Hyunyoung Jeong

**Department of Pharmacy Practice, College of Pharmacy, University of Illinois at Chicago, Chicago, Illinois (J.K.L., H.J.C., L.F., J.F., H.J.); College of Pharmacy, Gyeongsang National University, Jinju, South Korea (H.J.C.); Laboratory of Metabolism, National Cancer Institute, National Institutes of Health, Bethesda, Maryland (F.J.G.); and Department of Biopharmaceutical Sciences, College of Pharmacy, University of Illinois at Chicago, Chicago, Illinois (H.J.)**

Received October 11, 2013; accepted January 8, 2014

**Abstract**

The state of pregnancy is known to alter hepatic drug metabolism. Hormones that rise during pregnancy are potentially responsible for the changes. Here we report the effects of prolactin (PRL), placental lactogen (PL), and growth hormone variant (GH-v) on expression of major hepatic cytochromes P450 and a potential molecular mechanism underlying CYP2E1 induction by PL. In female human hepatocytes, PRL and GH-v showed either no effect or small and variable effects on mRNA expression of CYP1A2, 2A6, 2B6, 2C9, 2C19, 2D6, 2E1, 3A4, and 3AS. On the other hand, PL increased expression level of CYP2E1 mRNA with corresponding increases in CYP2E1 protein and activity levels. Results from hepatocytes and HepaRG cells indicate that PL does not affect the expression or activity of HNF1α, the known transcriptional activator of basal CYP2E1 expression. Furthermore, transient transfection studies and Western blot results showed that STAT signaling, the previously known mediator of PL actions in certain tissues, does not play a role in CYP2E1 induction by PL. A chemical inhibitor of PI3-kinase signaling significantly repressed the CYP2E1 induction by PL in human hepatocytes, suggesting involvement of PI3-kinase pathway in CYP2E1 regulation by PL. CYP2E1-humanized mice did not exhibit enhanced CYP2E1 expression during pregnancy, potentially because of interspecies differences in PL physiology. Taken together, these results indicate that PL induces CYP2E1 expression via PI3-kinase pathway in human hepatocytes.

**Introduction**

Cytochrome P450 (P450, CYP450) enzymes are responsible for eliminating approximately 75% of marketed drugs, and pregnancy is known to alter P450-mediated hepatic drug metabolism. Results from clinical studies indicate that during pregnancy, elimination of drugs metabolized by CYP2A6, CYP3A4, CYP2D6, and CYP2C9 is decreased, whereas elimination of the CYP1A2 and CYP2C19 substrate drugs is decreased (Hodge and Tracy, 2007). Pregnancy is also accompanied by increases in plasma concentrations of multiple hormones including estrogen, progesterone, and corticosteroids, and these hormones may be in part responsible for altered drug metabolism during pregnancy. For example, results from previous studies indicate that rising concentrations of estrogen and progesterone may lead to increased elimination of CYP2B6 and CYP3A4 substrate drugs during pregnancy (Koh et al., 2012; Choi et al., 2013; Papaeeorgiou et al., 2013).

Prolactin (PRL), placental lactogen (PL), and growth hormone variant (GH-v) are peptide hormones belonging to the growth hormone family, and their plasma concentrations increase during pregnancy. For example, plasma concentration of PRL rises >10-fold during pregnancy compared with the basal level in nonpregnant women. PL and GH-v are pregnancy-specific somatotropins produced from placenta. PL secretion rate is about 1.0 g/day at term, a rate considerably greater than that of any other peptide hormones (Handwerger and Freemark, 2000). GH-v is the predominant growth hormone in the systemic circulation of pregnant women because of decreased pituitary production of native growth hormone during pregnancy. These peptide hormones share similar genetic, structural, binding, and functional properties (Handwerger and Freemark, 2000). PRL, PL, and GH-v show 16, 84, and 93% similar genetic, structural, binding, and functional properties (Handwerger and Freemark, 2000). PRL, PL, and GH-v show 16, 84, and 93% amino acid homology to the pituitary growth hormone, respectively. The major biologic function of GH-v and PL is to modulate nutrient metabolism (Handwerger and Freemark, 2000), whereas prolactin is primarily involved in mammary gland development and lactation.

In the rat liver, PRL has been shown to modulate drug elimination. In ovariectomized rats, ovine PRL increases the activity of glutathione S-transferase (Luquita et al., 1999) and UDP-glucuronosyltransferase (Luquita et al., 1996). However, significant interspecies differences in amino acid sequences and biologic activities of PRL (Forzsry and Wallis, 2002; Ben-Jonathan et al., 2008) render extrapolation to humans difficult. GH-v was recently shown to have insignificant effects on the expression and activity of the major drug-metabolizing enzyme...
CYP3A4 in human hepatocytes (Papageorgiou et al., 2013), but whether GH-v influences expression of other P450 isoforms is unclear. The effects of PL on human P450 expression and activity are completely unknown.

The biologic action of GH-v and PRL is initiated by hormone binding to the growth hormone receptor or the PRL receptor (PRLR), respectively, on cell membranes. Of these two membrane receptors, PL is known to bind preferentially to PRLR (Handwerger and Freemark, 2000). The hormone binding to the receptor triggers activation (i.e., phosphorylation) of a number of signaling proteins, including signal transducers and activators of transcription (STAT). A previous study showed that STAT5a and STAT5b were activated by ovine PRL, mouse PL, and rat growth hormone in primary rat hepatocytes (Cao et al., 2001).

In this study, we examined whether PRL, PL, and GH-v modulate expression and/or activity of major drug-metabolizing P450 enzymes in human hepatocytes. The results demonstrated that PL significantly induces hepatic expression of CYP2E1. Potential molecular mecha-
nisms underlying CYP2E1 induction by PL are presented.

Materials and Methods

Reagents. PRL, PL, and GH-v were obtained from the National Hormone and Peptide Program (Torrance, CA). Antibodies against CYP2E1 and β-actin were purchased from ProteinTech (Chicago, IL) and Sigma-Aldrich (St. Louis, MO), respectively. Antibodies against phosphorylated STAT1, 3, 6, phosphorylated AKT, and native AKT were purchased from Cell Signaling Technology (Danvers, MA). Chlorzoxazone, 6-hydroxychlorzoxazone, and interleukin (IL)-6 were purchased from Sigma-Aldrich. INF-γ, U0126, and SB202190 were purchased from Toronto Research Chemical (Ontario, Canada).

Animals. CYP2E1-humanized transgenic mice were previously characterized (Cheung et al., 2005). All mice were housed in temperature-controlled animal facilities with 12-hour light/12-hour dark cycles and were permitted consumption of tap water and standard rodent chow ad libitum. Adult female (8–10 weeks) mice were mated with male mice of similar age. The 2nd day after mating was assigned as gestational day 1 for the mice showing sperm plug. At gestational days 7 and 17 and 30 days after delivery, the female mice after mating was assigned as gestational day 1 for the mice showing sperm plug. All procedures were approved by the Institutional Animal Care and Use Committee at the University of Illinois at Chicago.

Cell Culture. HepG2 cells from the American Type Culture Collection (ATCC, Manassas, VA) were cultured in complete Dulbecco’s modified Eagle’s medium supplemented with 10% fetal bovine serum (Gemini, Woodland, CA), 2 mM L-glutamine, 100 U penicillin/ml, 100 μg streptomycin/ml, and 1% minimum Eagle’s medium nonessential amino acids. HepaRG cells were purchased from Biopredic international (Rennes, France) and maintained in 25-
cm² culture flask in William’s E medium supplemented with 10% fetal bovine serum, 100 U penicillin/ml, 100 μg streptomycin/ml, 5 μg/ml insulin, 2 mM L-glutamine, and 50 μM hydrocortisone. Then the cells were seeded onto 12-well plates at a density of 2×10⁵ cells/ml and cultured for 14 days, after which the cells were used for experiments.

Primary Hepatocyte Culture. Freshly isolated human hepatocytes from female donors of age 18–50 years were obtained from Life Technologies (Pittsboro, NC), BD biosciences (San Jose, CA), and Liver Tissue Cell Distribution System (Pittsburgh, PA). Briefly, human hepatocytes were shipped overnight in cold preservation media. Upon receipt, the media were replaced with serum-free Williams’ E media (without phenol red) containing 0.1 μM dexamethasone, 100 U penicillin/ml, 15 mM HEPES, 2 mM L-glutamine, 5 μg/ml transferrin, and 5 ng/ml sodium selenite. Cells were allowed to recover from shipping for 18 hours at 37°C in an atmosphere containing 5% CO₂ and used for experiments on the next day. Mouse hepatocytes were isolated from the livers of CYP2E1-humanized mice as previously described (Swift and Brouwer, 2010) and cultured as described above for human hepatocytes.

Quantitative Real-Time Polymerase Chain Reaction. Total RNA was isolated from human hepatocytes using Trizol (Life Technologies) and used as template for the synthesis of complementary DNA using High Capacity cDNA Archive Kit (Applied Biosystems, Foster City, CA). With the cDNA as template, quantitative real-time polymerase chain reaction (qRT-PCR) was performed using StepOnePlus Real-Time PCR System and TaqMan Gene expression assays (Applied Biosystems). The fold change in mRNA levels of P450 isoforms was determined after normalizing the gene expression levels to those of GAPDH (2⁻ΔΔCt method).

Precursor RNA Analysis. RNA was prepared from hormone-treated cells and treated with DNase I. The RNA was then reverse-transcribed using an intron 6-specific CYP2E1 primer (5’-GAC TACAT TTGACC CATCT-3’), and qRT-PCR was performed using a primer set that can detect intron 5 and exon 6 of CYP2E1 (Life Technologies; Hs01666884_cn). As a loading control, precursor RNA level of GAPDH was used. To this end, an intron 6-specific glyceraldehyde-3-phosphate dehydrogenase (GAPDH) primer (5’-CGGCC ATTCAC GCCAC AGTTT-3’) and a primer set that can detect exon 5 and intron 5 of GAPDH (Life Technologies; Hs00983422_cn) were used for reverse-transcription and qRT-PCR, respectively. The fold change in the precursor RNA levels of CYP2E1 was determined after normalizing the gene expression levels to those of GAPDH (2⁻ΔΔCt method).

Western Blot Analysis. Cell lysates were prepared from drug-treated human hepatocytes, and proteins (30 μg) were separated using 12% SDS-polyacrylamide gel electrophoresis and transferred onto a nitrocellulose membrane. Blots were blocked with 5% skim milk/Triton buffered saline containing 0.1% Tween 20 (TBST) for 1 hour at room temperature and incubated overnight at 4°C with primary antibodies against CYP2E1 or β-actin diluted according to the manufacturer’s specifications in 1% skim milk/TBST. The membranes were then washed in TBST before incubation with horseradish peroxidase-coupled anti-rabbit IgG or anti-mouse IgG antibodies for 1 hour at room temperature. The membranes were visualized by an enhanced chemiluminescence detection system (SuperSignal West Pico; Pierce Biotechnology, Rockford, IL) and FluorChem E imager (Cell Biosciences, Santa Clara, CA). The intensities of bands were measured by densitometry using AlphaView Software 3.2.3.0 (Cell Biosciences).

Measurement of CYP2E1 Activity. Human hepatocytes were treated with PL for 72 hours, and the media were replaced with fresh media containing chlorozoxone (100 μM), a CYP2E1 probe drug (Ogilvie et al., 2008). Media were sampled at various time points (up to 5 hours). The concentrations of metabolite (6-hydroxychlorzoxone) were determined by liquid chromatography–tandem mass spectrometry. Liquid chromatography–tandem mass spectrometry system consisted of an HP1100 high-performance liquid chromatography system (Agilent Technologies) with an AB Sciex 3200 Q-trap mass spectrometer (Applied Biosystems) equipped with an electrospray ionization source. Hydroxytolbutamide was used as an internal standard. The multiple reaction monitoring detection method was employed for quantification of metabolite and internal standard. Multiple reaction monitoring pairs for 6-hydroxychlorzoxone and hydroxytol-
butamide were m/z 183.9/120.0 and m/z 285.1/186.0, respectively. Standard curves of 6-hydroxychlorzoxone were linear over the range studied with r > 0.998. The limit of quantitation for 6-hydroxychlorzoxone was 27 nM (i.e., 5 ng/ml).

Luciferase Reporter Assays. HepG2 cells were seeded in 24-well plates at a density of 5×10⁴ cells/ml. On the next day, the cells were transfected with 0.2 μg of luciferase construct, 0.15 μg of expression plasmid, and 0.001 μg of CMV-
Renilla expression plasmid using Fugene HD transfection reagent (Roche Applied
Results

PL Induces CYP2E1 Expression. To determine the effects of PRL, PL, and GH-v on the expression of major P450 enzymes, human hepatocytes were treated with PRL (150 ng/ml), PL (6 μg/ml), or PBS (vehicle). On the next day, cells were harvested, and firefly and Renilla luciferase activities were measured using assay kits from Promega. Firefly luciferase activity was normalized to the Renilla luciferase activity.

Inhibition of Cell Signaling. Human hepatocytes were treated with PL or vehicle in the presence or absence of one of the following signaling inhibitors (1 μM): wortmannin, rapamycin, Ro 31-8220, U0126, and SB202190 for inhibition of PI3-kinase, p70 S6 kinase, PKC, MEK, and p38 MAPK, respectively. After 72 hours, cell lysates were collected and analyzed.

Statistical Analysis. Each experiment with primary human hepatocytes was conducted in triplicate, and data were expressed as mean ± S.D. Statistical analysis for human hepatocyte experiments with different hormones was performed by two-way analysis of variance, followed by post hoc Bonferroni test. For luciferase reporter assays, at least two independent experiments were performed in triplicate, and the Student’s t-test was performed for statistically analysis. For cell signaling experiments, one-way analysis of variance was performed, followed by post hoc Dunnett’s test.

To determine whether CYP2E1 induction by PL occurs at the transcriptional level, the effects of PL on the level of CYP2E1 precursor RNA (an immature mRNA before processing) were examined in human hepatocytes from a different donor. The hepatocytes were treated with PL or vehicle, RNA isolated, and the level of precursor RNA measured by qRT-PCR using a primer set that can detect the intron regions of CYP2E1. PL significantly increased the level of CYP2E1 precursor RNA compared with vehicle treatment, accompanied by a similar extent of increase in CYP2E1 mRNA level (Fig. 2D). Together, these results indicate that CYP2E1 induction by PL likely occurs at the transcriptional level.

HNF1α Is Not Involved in CYP2E1 Induction by PL. HNF1α is a known transcriptional activator of the CYP2E1 gene (Liu and Gonzalez, 1995). To determine whether PL affects expression of HNF1α and its dimerization cofactor DCoH (Mendel et al., 1991), their mRNA levels were determined by qRT-PCR in human hepatocytes treated with vehicle or PL for 72 hours. The result showed that PL did not affect the mRNA expression of HNF1α or DCoH in human hepatocytes (Fig. 3, A and B, respectively). To determine whether the transcriptional activity of HNF1α is modulated by PL, HepaRG cells were transiently transfected with a luciferase construct HNF1α-RE-luc where luc gene expression is driven by four copies of HNF1α response element, and its response to PL was examined. HepaRG cells were chosen because the expression levels of hepatic genes (likely including DCoH) in these cells are comparable to those in primary human hepatocytes (Lubberstedt et al., 2011). In the vehicle-treated cells, overexpression of HNF1α significantly increased the luciferase activity, indicating that components for proper HNF1α actions are present and functional in HepaRG cells (Fig. 3C). However, PL did not induce HNF1α-RE-luc activity in the cells (Fig. 3C), indicating a lack of PL effects on HNF1α activity. Together, these results indicate that PL does not affect the expression or activity of HNF1α and that HNF1α likely plays an insignificant role in CYP2E1 induction by PL.

STATs Are Not Involved in CYP2E1 Induction by PL. To examine potential involvement of STAT5 pathway in PL-mediated CYP2E1 induction, luciferase reporter assays were performed. HepG2 cells were cotransfected with expression vectors for PRLR, STAT5a, and a luciferase construct (pGL3-CYP2E1 U1.4kb or pGL4-CISH), treated with vehicle or PL (6 μg/ml), and luciferase assays were performed. pGL3-CYP2E1 U1.4kb harbors 1.4-kb upstream region of CYP2E1 where multiple putative STAT5 binding sites were found (data not shown). pGL4-CISH contains four copies of a verified STAT5 binding site of cytokine-inducible SH-2-containing protein (encoded by CISH gene) that drives luc expression and was used as a positive control. The results showed that PL increased the promoter activity of CISH but not that of CYP2E1 (Fig. 3D). These results suggest that STAT5 does not transactivate the CYP2E1 promoter.

To investigate whether other STATs are involved in PL action on CYP2E1 expression, the effect of PL on activation of multiple STATs was examined in human hepatocytes. Human hepatocytes starved of serum for 18 hours were treated with PL or vehicle for 10 or 30 minutes, and phosphorylated STAT proteins were detected by using Western blot. Previously known activators of individual STAT

Sciences) according to the manufacturer’s protocol. The transfected cells were treated with PRL (150 ng/ml), PL (6 μg/ml), or PBS (vehicle) for 24 hours, and then luciferase assays were performed using the assay kits from Promega. Luciferase activity was normalized to the Renilla luciferase activity.

HepaRG cells were seeded in 12-well plates at a density of 8×10⁵ cells/ml and cultured for 2 weeks for differentiation. The differentiated cells were transfected with 1 μg of luciferase construct, 0.6 μg of expression plasmid, and 0.002 μg of CMV-Renilla expression plasmid using Lipofectamine 2000 transfection reagent (Life Technologies) according to the manufacturer’s protocol. The transfected cells were grown for 24 hours and treated with PL (6 μg/ml) or PBS (vehicle). On the next day, cells were harvested, and firefly and Renilla luciferase activities were measured using assay kits from Promega. Firefly luciferase activity was normalized to the Renilla luciferase activity.

Inhibition of Cell Signaling. Human hepatocytes were treated with PL or vehicle in the presence or absence of one of the following signaling inhibitors (1 μM): wortmannin, rapamycin, Ro 31-8220, U0126, and SB202190 for inhibition of PI3-kinase, p70 S6 kinase, PKC, MEK, and p38 MAPK, respectively. After 72 hours, cell lysates were collected and analyzed.

Statistical Analysis. Each experiment with primary human hepatocytes was conducted in triplicate, and data were expressed as mean ± S.D. Statistical analysis for human hepatocyte experiments with different hormones was performed by two-way analysis of variance, followed by post hoc Bonferroni test. For luciferase reporter assays, at least two independent experiments were performed in triplicate, and the Student’s t-test was performed for statistically analysis. For cell signaling experiments, one-way analysis of variance was performed, followed by post hoc Dunnett’s test.
pathways (i.e., INFγ for STAT1, IL-6 for STAT3, and IL-4 for STAT6 activation) were used as positive controls. The results showed that INFγ, IL-6, and IL-4 phosphorylated the respective STAT proteins as expected; however, PL did not activate any of the STATs (Fig. 3E). Taken together, these results indicate that STAT signaling is likely not responsible for CYP2E1 induction by PL.

PI3-Kinase Plays a Key Role in CYP2E1 Induction by PL. In primary rat hepatocytes, insulin was shown to modulate CYP2E1 mRNA expression via activation of PI3-kinase and p70 S6 kinase signaling pathways (Woodcroft et al., 2002). To examine whether one or more intracellular signaling pathways mediating insulin reaction are involved in CYP2E1 induction by PL, human hepatocytes were

Fig. 1. Effects of PL on mRNA expression of major hepatic P450 enzymes. (A) Human hepatocytes (HH) from different donors were treated with PL (6 μg/ml) or vehicle (PBS) for 72 hours. mRNA levels of CYP1A2, 2A6, 2B6, 2C9, 2C19, 2D6, 2E1, 3A4, and 3A5 were determined by qRT-PCR. Results represent mRNA levels of each P450 relative to those in vehicle control (mean ± S.D.; n = 3 or 4). The dotted line represents the relative expression level of 1.0. (B) HepaRG cells were treated with PL (6 μg/ml) or vehicle (PBS) for 72 hours. mRNA levels of CYP2E1 were determined by qRT-PCR *P < 0.05; **P < 0.01; ***P < 0.001 versus vehicle-treated group.

Fig. 2. Transcriptional regulation of CYP2E1 expression by PL. (A) Human hepatocytes from HH #2 were treated with various concentration of PL (0–10 μg/ml) for 72 hours, and mRNA expression level of CYP2E1 was determined by qRT-PCR. Results represent fold changes in mRNA levels of P450 isozyme relative to vehicle control. (B) CYP2E1 protein expression was determined by using Western blot in human hepatocytes from HH #2 treated with PL (6 μg/ml) or vehicle for 72 hours. The numbers represent the signal of CYP2E1 normalized by that of β-actin. (C) the amount of 6-hydroxychlorzoxazone was measured in human hepatocytes from HH #1 treated with PL (6 μg/ml) or vehicle for 72 hours. *P < 0.05; **P < 0.01; ***P < 0.001 versus vehicle-treated group. (D) The level of CYP2E1 precursor RNA was measured in human hepatocytes from HH #4 treated with PL (6 μg/ml) for 72 hours. NS, not significant.
treated with vehicle or PL for 72 hours in the presence of signaling inhibitors (wortmannin for PI3-kinase, rapamycin for p70 S6 kinase, Ro 31-8220 for PKC, U0126 for MEK, and SB202190 for p38 MAPK inhibition), and CYP2E1 mRNA levels were determined by qRT-PCR. In human hepatocytes, the enhanced CYP2E1 expression by PL was significantly attenuated by wortmannin but not by any of the remaining inhibitors (Fig. 4A), suggesting significant roles of PI3-kinase in mediating CYP2E1 induction by PL.

AKT, a serine/threonine specific protein kinase, is known to be a key mediator for PI3-kinase signaling pathway (Fayard et al., 2010). To further verify the involvement of PI3-kinase in PL action, whether PL activates AKT was examined. Human hepatocytes or HepaRG cells were treated with vehicle or PL for 30 minutes, and activated (i.e., phosphorylated) AKT was detected by Western blot. The result showed that the level of phosphorylated AKT was increased upon treatment with PL (Fig. 4B). Wortmannin abolished AKT phosphorylation, verifying that AKT is a downstream effector of PI3-kinase. Together, these data indicate that PL activates PI3-kinase/AKT signaling pathway.

CYP2E1 Expression Is Not Increased in CYP2E1-Humanized Mice during Pregnancy. To determine whether PL effects on CYP2E1 lead to enhanced CYP2E1 expression during pregnancy, a CYP2E1-humanized mouse line was used. The genome of CYP2E1-humanized mice harbors the complete human CYP2E1 gene along with 2.7-kb of upstream region of the CYP2E1 gene (Cheung et al., 2005). Liver samples were collected from the mice at prepregnancy, 7 or 17 days of pregnancy, and 30 days postpartum, and the level of CYP2E1 mRNA was determined by qRT-PCR. Results showed that CYP2E1 mRNA level was significantly decreased at 7 days of pregnancy in CYP2E1-humanized mice (Fig. 5), apparently inconsistent with the PL-mediated induction of CYP2E1 in human hepatocytes.

Discussion
In this study, we examined the effects of PRL, PL, and GH-v on expression of hepatic drug-metabolizing enzymes in human hepatocytes and investigated the underlying regulatory mechanisms. The results demonstrated that PL enhances CYP2E1 expression in primary human hepatocytes, in part by activation of PI3-kinase signaling pathways. CYP2E1 contributes to a small portion (i.e., 5–10%) of overall P450-mediated metabolism, but the significance of this enzyme cannot...
be overlooked because of its toxicological role in the metabolic activation of many carcinogenic and toxic chemicals as well as the production of reactive oxygen species (Lu and Cederbaum, 2008). Potentially because of its physiologic significance, CYP2E1 expression is highly regulated. Several regulatory mechanisms for CYP2E1 expression have been reported, including transcriptional regulation (Umeno et al., 1988; Vieira et al., 1996), post-transcriptional mechanisms (Song et al., 1987; Yang and Cederbaum, 1997; Khalighi et al., 1999), and post-translational protein stabilization (Song et al., 1989). Our results showed that in human hepatocytes, PL increases the precursor RNA levels of CYP2E1, suggesting that PL induces CYP2E1 via transcriptional activation of the gene.

It was previously demonstrated that HNF1α is a transcription activator of CYP2E1 through direct binding to the promoter (Liu and Gonzalez, 1995; Cheung et al., 2003). Of note, the transcriptional activity of HNF1α can be modulated without any changes in HNF1α expression, by post-translational modification of HNF1α (Lim et al., 2002) or by altered expression of its cofactor DCoH (Mendel et al., 1991). Our results from qRT-PCR and luciferase reporter assays indicate that PL does not influence expression of HNF1α or DcoH or the transcriptional activity of HNF1α. This suggests that although HNF1α may be a key transcription regulator of basal CYP2E1 expression, HNF1α does not play a role in CYP2E1 induction by PL in human hepatocytes. This finding is in part consistent with previously published results indicating the presence of other regulatory mechanisms for CYP2E1 expression (Hakkola et al., 2003; Sekine et al., 2006). For example, transgenic mice with liver-specific disruption of the β-catenin gene showed an almost complete loss of CYP2E1 mRNA expression (>90%), although HNF1α expression did not change (Sekine et al., 2006).

The results from this study demonstrate that PL enhances CYP2E1 expression by activating PI3-kinase in human hepatocytes. Of interest, a previous study showed that activation of PI3-kinase by insulin leads to repressed CYP2E1 expression (Woodcroft et al., 2002), whereas in this study, activation of PI3-kinase by PL led to enhanced CYP2E1 expression. Although detailed underlying mechanisms for the differential actions of PL and insulin warrant comparative studies, this seemingly conflicting data may be explained by the complexity of intracellular signaling pathways. For example, insulin is known to activate PI3-kinase and the downstream AKT signaling, but transgenic mice with decreased PI3-kinase function (via liver-specific deletion of a major regulatory subunit of PI3-kinase) exhibit increased AKT activation (Taniguchi et al., 2006), suggesting that insulin may
modulate other signaling pathways, the net result of which is AKT activation. Similarly, it appears plausible that PL activates a distinct set of multiple intracellular signaling pathways (including PI3-kinase), a net result of which is the CYP2E1 induction. The additional signaling pathways activated by PL remain to be identified.

Humans and mice have shown significant interspecies differences in the directional changes in P450-mediated drug metabolism during pregnancy. For example, CYP2D6-mediated drug metabolism increases during pregnancy in humans (Hodge and Tracy, 2007), whereas expression of CYP2D homologs decreases in mice (Koh et al., 2011). This is potentially caused by DNA sequence differences in the upstream regulatory region of P450 genes between humans and mice. In this regard, humanized mice whose genomes harbor the human structural gene along with the upstream regulatory region have been proven to be useful as an in vivo model by recapitulating altered P450 expression during human pregnancy (Koh et al., 2014). Based on data indicating CYP2E1 induction by PL in human hepatocytes, we hypothesized that pregnancy enhances CYP2E1 expression. In CYP2E1-humanized mice, however, the CYP2E1 expression was decreased during pregnancy. Interspecies differences in hormone physiology may have contributed to the finding. For example, although the human placenta produces one form of PL, the mouse placenta produces two different forms of PL (mPPL1 and mPPL2) whose mRNA sequences share less than 50% homology with those of human PL. Whether pregnancy indeed affects CYP2E1 expression and activity remains to be determined in humans.

Many CYP2E1 substrates are known to produce toxic metabolites. For example, CYP2E1 metabolizes isoniazid to acetylhydrazine that triggers hepatitis (Yue et al., 2004). Of interest, pregnant women are four times more likely to develop isoniazid-mediated hepatitis than are nonpregnant women (Kawamoto et al., 1999), suggesting that expression and activity of CYP2E1 may increase during pregnancy. CYP2E1 plays a major role in metabolizing acetaminophen (a commonly used analgesic during delivery and postpartum). Br J Clin Pharmacol 78:850–860.


Address correspondence to: Dr. Hyunyoung Jeong, Department of Pharmacy Practice (MC 886), College of Pharmacy, University of Illinois at Chicago, 833 S. Wood Street, Chicago, IL 60612. E-mail: yjeong@uic.edu