Cytochrome P450 Regulation by α-Tocopherol in Pxr-null and Humanized-PXR mice

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Running Title: The regulation of CYP gene expression by α-tocopherol

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Abstract

The pregnane X receptor (PXR) has been postulated to play a role in the metabolism of α-tocopherol due to the upregulation of hepatic cytochrome P450 (CYP) 3A in human cell lines and murine models after α-tocopherol treatment. However, in vivo studies confirming the role of PXR in α-tocopherol metabolism in humans presents significant difficulties and has not been performed. PXR-humanized (hPXR), wild-type and Pxr-null mouse models were used to determine whether α-tocopherol metabolism is influenced by species-specific differences in PXR function in vivo. No significant difference in the concentration of the major α-tocopherol metabolites was observed between the hPXR, wild-type, and Pxr-null mice through mass spectrometry-based metabolomics. Gene expression analysis revealed significantly increased expression of Cyp3a11 as well as several other cytochrome P450s only in wild-type mice, suggesting species-specificity for α-tocopherol activation of PXR. Luciferase reporter assay confirmed activation of mouse PXR by α-tocopherol. Analysis of the Cyp2c family of genes revealed increased expression of Cyp2c29, Cyp2c37 and Cyp2c55 in wild-type, hPXR and Pxr-null mice suggesting PXR-independent induction of Cyp2c gene expression. This study revealed that α-tocopherol is a partial agonist of PXR and that PXR is necessary for Cyp3a induction by α-tocopherol. The implications of a novel role for α-tocopherol in Cyp2c gene regulation are also discussed.
Introduction

α-Tocopherol is not accumulated in the body like other lipid-soluble vitamins; it is transported to the liver and, through a series of oxidation reactions, converted to α-carboxyethyl hydroxycroman (α-CEHC) (Scheme 1). It is then conjugated and excreted from the body. Metabolism to α-CEHC involves an initial ω-oxidation step that converts tocopherol to 13’-hydroxy-α-tocopherol. It was reported that cytochrome P450 (CYP) enzymes induced after α-tocopherol dosing carry out this ω-oxidation step (Birringer et al., 2001). However, contradictory studies have failed to ascertain which enzymes and regulatory mechanisms are involved. For example, CYP4F2 was increased after α-tocopherol dosing in cell culture models (Sontag and Parker, 2002), but no change in CYP4F2 was seen in rats injected with α-tocopherol (Mustacich et al., 2006). The same rats however, showed increases in CYP3A, CYP2B, and CYP2C protein. Cyp3a11 (the murine homologue of human CYP3A4) gene expression was increased in C57BL/6 mice dosed with α-tocopherol (Mustacich et al., 2009) but the expression of other Cyp3a subfamily members as well as Cyp2b13, Cyp2c44, and Cyp2e1 genes was not changed. A further study showed an increase of hepatic CYP3A protein in C57BL/6 mice fed an α-tocopherol diet (Traber et al., 2005). These studies revealed that CYP3A enzymes appear to be involved in rodent ω-oxidation of α-tocopherol but the activity of the other CYP enzymes are not conclusive.

Human CYP3A isoforms are involved in the metabolism of over 50% of drugs. In cellular and rodent models α-tocopherol supplementation may interfere with drug metabolism through the induction of CYP3A4, which is regulated by pregnane X receptor (PXR). α-
Tocopherol was shown to act as a ligand for PXR in HepG2 cells (Landes et al., 2003). Thus, it could potentially induce its own metabolism by increasing the expression of CYP3A4 and ω-oxidation to 13’-hydroxy-α-tocopherol. However, another study revealed that activation of PXR in wild-type mice by pregnenolone 16α-carbonitrile (PCN) or in PXR-humanized (hPXR) mice by rifampicin decreased vitamin E metabolism compared to Pxr-null mice (Cho et al., 2009). This may have been due to downregulation of β-oxidation by PCN and rifampicin. The contradictory observations in previous studies could primarily be due to different model systems used for comparison. Indeed, it is known that mouse PXR does not have the same response as human PXR to ligands. The DNA-binding domain for PXR is 95% homologous between humans and mice yet they only share between 75-80% of amino acids in the ligand-binding domain (LeCluyse, 2001). Therefore, although mouse models can be ideal for biological research, the genetic differences that exist between mice and humans can have a major impact on drug metabolism. To overcome this problem hPXR and Pxr-null mice can be used to show the species-specific response. The National Health and Nutrition Examination Survey (NHANES) in 1999–2000 showed that ~ 10% of U.S adults took a vitamin E supplement (Picciano and McGuire, 2009), and as PXR is also involved in the detoxication of a large number of drugs from the body, it is essential to characterize α-tocopherol modulation of PXR and the downstream effects on the expression of drug-metabolizing enzymes in appropriate mouse models. Thus, the expression of hepatic CYP genes were analyzed in hPXR, Pxr-null and wild-type mice after α-tocopherol dosing to determine whether α-tocopherol metabolism is influenced by species-specific differences in PXR function. Ultra-performance liquid chromatography-mass spectrometry (UPLC-MS)-based metabolomics was also used to identify and quantitate the
urinary metabolites of \( \alpha \)-tocopherol. This was to determine whether species-specific differences in PXR would affect the metabolic end-products of \( \alpha \)-tocopherol. This study could potentially shed light on the possibility for drug-drug interactions when supplementing the diet with \( \alpha \)-tocopherol.
Materials and Methods

Reagents. Pregnenolone 16α-carbonitrile (PCN), corn oil, rifampicin, and chlorpropamide were obtained from Sigma Aldrich (St. Louis, MO). All other chemicals required for UPLC-MS were obtained from Fisher Scientific (Waltham, MA), and were of the highest purity grade.

Animals, diets and experimental design. All animal studies were conducted in accordance with Institute of Laboratory Animal Resource (ILAR) guidelines and approved by the National Cancer Institute Animal Care and Use Committee. From three weeks of age, male hPXR (n=13), Pxr-null (n=13), and wild-type (n=9) mice bred at NCI-Bethesda were maintained under a standard 12 h light/12 h dark cycle with water. Mice were fed ad libitum a purified diet containing vitamin free casein, sucrose, cornstarch, dyetrose, L-cystine, cellulose, tocopherol stripped soybean oil, mineral mix (Cat#210050, Dyets, Inc, Bethlehem, PA), vitamin mix with no vitamin E (Cat# 319508, Dyets, Inc) and choline bitartrate. The mineral mix consisted of: calcium carbonate, potassium citrate, potassium phosphate monobasic, sodium chloride, potassium sulfate, magnesium oxide, ferric citrate, zinc carbonate, manganous carbonate, cupric carbonate, potassium iodate, sodium selenate, ammonium vanadate and sucrose. The vitamin mix consisted of: niacin, calcium pantothenate, pyridoxine HCl, thiamine HCl, riboflavin, folic acid, biotin, vitamin B12, vitamin A palmitate, vitamin D3, vitamin K2/dextrose mix and sucrose. For acclimatization purposes, the mice were placed in individual metabolic cages for 24 h at six and seven weeks of age. At eight weeks of age the mice were placed in metabolic cages for a 24 h predose urine collection. After urine collection, half of the mice were switched to the same vitamin E deficient base diet but supplemented with 500 mg/kg DL-α-tocopheryl acetate (Glanbia Nutrition, Carlsbad, CA); the remaining half continued on the vitamin E deficient diet.
This dose was chosen to be equivalent to the dose received by a 70 kg human taking vitamin E supplements. These supplements typically contain 400-600 mg of α-tocopherol. For a 70 kg human this equates to approximately 5.7-8.6 mg a-tocopherol/kg human weight. Therefore for a 30 g mouse who eats 5 g vitamin E enriched diet/day they will ingest 2.5 mg of α-tocopherol. At nine and 10 weeks of age, the mice were placed in metabolic cages for 24 h urine collection and then euthanized under CO₂. Livers were harvested, flash frozen in liquid N₂, and stored at -80ºC.

A second set of mice were gavaged with strong PXR activators to compare the expression of PXR activated genes with those induced by α-tocopherol. From three weeks of age, hPXR (n=9), Pxr-null (n=9), and wild-type (n=10) mice bred at NCI-Bethesda, were maintained under a standard 12 h light/12 h dark cycle with water and fed ad libitum the vitamin E deficient diet. At six weeks of age, wild-type (n=5), Pxr-null (n=4), and hPXR (n=4) mice were gavaged with 100 μl corn-oil daily for four days. The remaining wild-type (n=5) and Pxr-null (n=5) mice were gavaged with PCN (50 mg/kg/mouse dissolved in corn oil), and the hPXR (n=5) mice with rifampicin (10 mg/kg/mouse dissolved in corn oil) daily for four days. On day five, the mice were killed by CO₂ asphyxiation and their livers harvested, flash frozen in liquid N₂ and stored at -80ºC.

**Chemical Synthesis.** In order to verify the identities of α-CEHC acyl glucuronide, α-CEHC ether glucuronide and α-CEHC glycine, standards were synthesized in-house as described previously (Johnson et al., 2012).

**Urine preparation for UPLC-ESI-QTOFMS-based metabolomics.** Urine samples were thawed and 50 μl added to a microcentrifuge tube containing 50 μl acetonitrile:water (50:50 v/v)
and 5 µM chlorpropamide stored at 4°C. The samples were vortexed for 1 min each and centrifuged at 14,000 x g for 20 min at 4°C to remove proteins and particulates. The supernatant was transferred to an UPLC vial (Waters Corp, Milford, MA). Pooled samples were also made for quality control containing 5 µl of each sample. The samples were then randomized and analyzed by UPLC-ESI-QTOFMS as described previously (Johnson et al., 2011) using a reverse-phase 50 x 2.1 mm ACQUITY® 1.7 µm BEH C18 column (Waters Corp, Milford, MA) and an ACQUITY® UPLC system (Waters Corp, Milford, MA). Mass spectrometry was performed on a Waters® QTof-Premier™-MS operating in ESI− and ESI+ mode. The mass spectral data were centroided, integrated, and deconvoluted to generate a multivariate data matrix using MarkerLynx® (Waters Corp, Milford, MA). Peak picking, alignment, deisotoping, and integration were performed automatically by the software and then were transformed into a multivariate matrix containing aligned peak areas with matched mass-to-charge ratios (m/z) and retention times. The data were normalized to the peak area of the internal standard chlorpropamide which appeared at a retention time of 5.3 min, 275.024 [M-H]− and 277.041 [M+H]+ and imported to SIMCA-P+ software (Umetrics, Kinnelon, NJ) for multivariate data analysis. The ESI− and ESI+ data were Pareto-scaled and analyzed by partial least squares discriminant analysis (PLS-DA) and orthogonal partial least squares discriminant analysis (OPLS-DA). For identification of metabolites OPLS-DA models were constructed comparing predose to postdose samples. Ions with a p(corr) value above 0.8 and peak area above 100 were subjected to tandem MS. Further confirmation of identity was then carried out by repeating the tandem MS fragmentation using authentic standards at 100 µM in water and in urine.
Biomarkers were quantitated by multiple reaction monitoring (MRM) on an Acquity UPLC coupled to a XEVO triple-quadrupole tandem MS (QqQMS) (Waters Corp, Milford, MA), to obtain the actual concentration of each metabolite normalized to the endogenous creatinine concentration. Standard calibration curves were made and the following MRM transitions were monitored for creatinine (114.0 → 86.1 m/z ESI⁺), α-CEHC ether glucuronide (455.2 → 279.2 m/z ESI⁺), α-CMBHC ether glucuronide (497.1 → 165.1 m/z ESI⁺) and α-CEHC glycine (336.2 → 261.2 m/z ESI⁺), using authentic standards. Urines were deproteinized in 50% acetonitrile and diluted 1:2. An internal standard of chlorpropamide (277.1 → 110.9 m/z ESI⁺) was added to each sample with final concentration 1 μM. The samples were quantitated using TargetLynx (Waters Corp, Milford, MA) software.

**Gene expression analysis.** cDNA was synthesized from 1 μg total RNA using Superscript II reverse transcriptase kit (Invitrogen, Carlsbad, CA). For qPCR analysis, primers were designed using the Primer Express software (Applied Biosystems, Foster City, CA) based on GenBank sequence data and crossed exon-exon junctions. qPCR reactions contained 25 ng of cDNA, 150 nM of each primer and 5 μl of SYBR Green PCR Master Mix (Applied Biosystems, Foster City, CA) in a total volume of 10 μl. All reactions were performed in triplicate on an Applied Biosystems Prism 7900HT Sequence Detection System. Relative mRNA levels were calculated by the comparative threshold cycle method using β-actin as the internal control.

**Transient Transfection Assay.** HepG2 cells (ATCC, Manasses, VA) were plated in 12-well plates and cultured in DMEM + 10% fetal bovine serum (FBS). Cells were transfected with 10 ng mouse PXR, 100 ng of the firefly luciferase DR3 reporter construct (kind gift of Grace Guo, University of Kansas Medical Center), and 2 ng of the control Renilla plasmid pRL-Sv40 with
FuGENE Transfection Reagent (Promega, Madison, WI). Twenty-four hours post-transfection, media was removed and replaced with media containing 10 μM PCN (in DMSO) or increasing concentrations of α-tocopherol. For α-tocopherol dosing, α-tocopherol stock solution in ethanol was added drop-wise to FBS and stored for 4 hrs at 4 °C as described (Parker and Swanson, 2000). This α-tocopherol-enriched FBS was then diluted 1:10 with DMEM prior to addition to the cells. Twenty-four hours after treatment, cells were lysed and luciferase assay was performed using the Dual Luciferase Assay Kit (Promega). Firefly luciferase values were normalized to *Renilla* values for each well and represented as fold over control treatment (DMSO).

**Statistical Analysis.** Concentrations of α-tocopherol metabolites, gene expression fold change and gene relative expression were expressed as mean ± standard error of the mean (SEM) after Student’s t-test on unpaired samples using GraphPad Prism v5.00 (GraphPad Software, San Diego, CA) with the assumption that there was a normal population distribution. A comparison with a *P*-value <0.05 was statistically significant and noted on each graph. Mann-Whitney U-test was also carried out due to the low sample number in each group which confirmed that each comparison was significant (data not shown).
RESULTS

**Metabolomics analysis:** UPLC-ESI-QTOFMS analysis was carried out on urine samples collected from mice pre- and post-dosing with α-tocopherol deficient and enriched diets. PLS-DA models were constructed for each mouse strain that clearly showed clustering based on the diet the mice were fed (Figure 1A-C). OPLS-DA models were then generated for each mouse strain comparing urine from mice fed the α-tocopherol deficient diets to 7 days of α-tocopherol supplementation or 14 days of α-tocopherol supplementation. Ions that were highly correlated to α-tocopherol dosing were subjected to tandem MS and compared against authentic standards that were synthesized in-house. The ions were confirmed as α-CEHC ether glucuronide, α-CMBHC ether glucuronide and α-CEHC glycine. The urinary concentrations of these metabolites were quantitated using MRM revealing no significant difference in the concentration of each urinary metabolite between the wild-type, \(P_{xr}\)-null and \(hPXR\) mice (Figure 2). There was also no significant difference between day 7 and 14 for each mouse strain in the excretion of the metabolites.

**CYP gene expression.** Gene expression analysis was performed on a number of hepatic CYPs from mice fed the α-tocopherol deficient and enriched diets (Figure 3A). Induction of \(Cyp3a11\) by α-tocopherol was confirmed in wild-type mice; however, \(Cyp3a11\) expression was unchanged in the \(P_{xr}\)-null and \(hPXR\) mice. In wild-type mice, \(Cyp4f13\) was induced 1.6-fold \((P=0.001)\), after α-tocopherol supplementation, while no changes were observed in \(P_{xr}\)-null or \(hPXR\) mice. \(Cyp4f14\), \(Cyp4f15\), \(Cyp4f16\) and \(Cyp4f18\) expression was unaffected by α-tocopherol supplementation in all mouse strains studied. In order to determine if α-tocopherol could
upregulate other drug metabolizing CYP enzymes, gene expression analysis was carried out on mRNAs encoded by Cyp1a2, Cyp2e1, Cyp2b10 and Cyp4a10. Of these genes, Cyp1a2, Cyp2e1, and Cyp2b10 were upregulated only in the wild-type mice, 1.5-fold ($P=0.027$), 1.9-fold ($P=0.027$) and 7.3-fold ($P=0.022$) respectively. Cyp4a10 was significantly decreased in hPXR mice 2.4-fold ($P=0.017$).

As members of the CYP2C family have been identified as PXR and CAR targets, the expression of several CYP2C family members was investigated (van Waterschoot et al., 2009; Konno et al., 2010). Cyp2c29 was increased 2.4-fold ($P=0.040$), 1.5-fold ($P=0.002$) and 1.8-fold ($P=0.044$) in the wild-type, Pxr-null, and hPXR mice, respectively, in mice fed the α-tocopherol enriched diet, compared to the deficient diet. The relative expression of this gene was highest compared to other genes in the Cyp2c family (Figure 3B). Cyp2c55 was increased 2.2-fold ($P=0.007$) and 2.9-fold ($P=0.007$) in Pxr-null and hPXR mice; however the relative gene expression was very low. In addition, Cyp2c37 was increased 2.0–fold ($P=0.005$) in the hPXR mice. Cyp2c44 showed an increased trend in Pxr-null mice fed the α-tocopherol enriched diet (1.4-fold, $P=0.052$) while the expression of Cyp2c39 was not affected by α-tocopherol in any of the mouse strains.

Gene expression analysis was also carried out on the same hepatic phase I drug metabolizing enzymes in mice gavaged with strong PXR activators (Figure 4). PCN was given by oral gavage to wild-type and Pxr-null mice, and rifampicin to hPXR mice. This was carried out in order to compare the expression of PXR activated genes with those induced by α-tocopherol. PCN gavage to wild-type mice resulted in the upregulation of the following genes; Cyp3a11, 20.9-fold ($P<0.001$), Cyp2b10, 160-fold ($P=0.001$), Cyp2c29, 9.2-fold ($P=0.001$), and
Cyp2c55, 303.3-fold ($P=0.001$). Following rifampicin gavage to hPXR mice, Cyp3a11 was upregulated 4.5-fold ($P<0.001$), Cyp2b10, 16.5-fold ($P=0.005$), Cyp2c29, 3.7-fold ($P=0.001$), Cyp2c55, 171.9-fold ($P=0.002$) and Cyp2c37 1.9-fold ($P=0.001$). However, in the Pxr-null mice, only Cyp2c29 was increased after PCN gavage, 1.6-fold ($P=0.035$).

In order to determine whether $\alpha$-tocopherol can activate mouse PXR, in vitro reporter gene assays were carried out. $\alpha$-Tocopherol was administered at doses of 2.5, 25, and 50 $\mu$M. PXR was activated 1.7-fold ($P<0.001$) and 1.6-fold ($P=0.015$) at 50 $\mu$M and 2.5 $\mu$M doses of $\alpha$-tocopherol respectively (Figure 5). As a positive control, PCN activated PXR 9.5-fold ($P=0.005$).

**UGT gene expression analysis.** As glucuronide conjugates of $\alpha$-CEHC and $\alpha$-CMBHC were identified in mouse urine after dietary supplementation with $\alpha$-tocopherol, and UDP glucuronosyltransferase (UGT) genes are regulated by PXR (Buckley and Klaassen, 2009; Mackenzie et al., 2010), gene expression analysis of the major hepatic UGT isoforms was carried out. There was no difference in the expression of the major Ugt isoforms between the mice fed the $\alpha$-tocopherol deficient and enriched diets (Figure 6A).

However, PCN gavage to wild-type mice did induce the expression of; Ugt1a10, 2.8-fold ($P=0.001$), Ugt1a1, 3.1-fold ($P<0.001$), Ugt2b34 3.2-fold ($P<0.001$), Ugt1a9, 9.4-fold ($P<0.001$) and Ugt2b5, 1.4-fold ($P=0.005$) (Figure 6B). PCN gavage to Pxr-null mice resulted in the upregulation of one gene, Ugt1a10, 1.8-fold ($P=0.015$). Rifampicin dosing to hPXR mice upregulated; Ugt1a10, 2.7-fold ($P=0.009$), Ugt1a1, 1.5-fold ($P=0.025$), Ugt2b34, 2.5-fold ($P=0.038$), Ugt1a9, 8.4-fold ($P=0.009$) and Ugt1a7c 2.1-fold in hPXR mice ($P=0.007$). The Ugt1a6 genes were downregulated after PCN or rifampicin dosing; Ugt1a6b, 1.3-fold ($P=0.025$)
in wild-type mice and 1.8-fold ($P=0.005$) in hPXR mice, $Ugt1a6a$, 2.0-fold in hPXR mice ($P=0.007$).
Discussion

MS-based metabolomics was used to reveal three urinary α-tocopherol metabolites in wild-type, Pxr-null and hPXR mice: α-CEHC ether glucuronide, α-CMBHC ether glucuronide and α-CEHC glycine. These metabolites were produced via an initial ω-hydroxylation step that converts α-tocopherol into 13’-hydroxy-α-tocopherol and then a series of β-oxidation steps to produce α-CMBHC and α-CEHC. Earlier studies revealed that the ω-hydroxylation step was carried out by CYPs, predominantly CYP3A4 in HepG2 cells, or Cyp3a11 in mouse models (Birringer et al., 2001; Birringer et al., 2002; Traber et al., 2005; Mustacich et al., 2009). This enzyme is regulated by PXR (Bertilsson et al., 1998). It was also hypothesized that α-tocopherol could be a ligand for PXR, thus inducing its own metabolism (i.e. autoinduction). After dosing with α-tocopherol, Cyp3a11 was upregulated only in wild-type mice, while dosing with known murine and human PXR-specific ligands upregulated Cyp3a11 in both the wild-type and hPXR mice. The possibility does exist that α-tocopherol activates human PXR but that this form of activated PXR is not able to transactivate the murine Cyp3a11 promoter while a strong human PXR agonist like rifampicin is able to activate Cyp3a11. The activation of murine PXR by α-tocopherol was confirmed through luciferase reporter assay, although PXR activation by α-tocopherol was minimal (Figure 5). Previously, species-specific responses to ligand activation by human and mouse PXR were seen for a number of xenobiotics (Lehmann et al., 1998; Cheng et al., 2011). Although α-tocopherol induces Cyp3a11 expression, no significant difference in the concentration of α-tocopherol urinary metabolites was observed between wild-type and Pxr-null mice. Therefore, the basal protein level of CYP3A may be sufficient to metabolize α-tocopherol
in wild-type, \(hPXR\), and \(Pxr\)-null mice. Indeed, there is no difference in basal CYP3A expression between wild-type, \(hPXR\), and \(Pxr\)-null mice (Ma et al., 2007).

The CYP4F family was postulated to be involved in \(\omega\)-hydroxylation of \(\alpha\)-tocopherol (Sontag and Parker, 2002; Sontag and Parker, 2007), and studies have linked the regulation of this family to PPAR\(\alpha\) (Issemann and Green, 1990; Kalsotra and Strobel, 2006). Substrates for human CYP4F enzymes are leukotriene B\(_4\) (Chen and Hardwick, 1993), arachidonic acid, and \(\alpha\)-tocopherol (Sontag and Parker, 2007), however, limited substrates have been found for mouse CYP4F enzymes (Kalsotra and Strobel, 2006). A recent study revealed that \(Cyp4f14\) is the major vitamin E \(\omega\)-hydroxylase in mice (Bardowell et al., 2012). However \(Cyp4f13\) was the only \(Cyp4f\) gene upregulated in the present study in wild-type mice, and no \(Cyp4f\) genes were increased in the \(Pxr\)-null or \(hPXR\) mice after \(\alpha\)-tocopherol dosing. In contrast to the upregulation of \(Cyp4f13\) in wild-type mice after \(\alpha\)-tocopherol dosing, the known PPAR\(\alpha\) target gene \(Cyp4a10\) was repressed in \(hPXR\) mice after \(\alpha\)-tocopherol dosing, suggesting a complex role for \(\alpha\)-tocopherol in PPAR\(\alpha\) signalling.

Regulation of other cytochrome P450s that are under the control of various nuclear receptors were investigated including constitutive androstane receptor (CAR), and the aryl hydrocarbon receptor (AhR). Expression of the AhR target gene \(Cyp1a2\) and CAR target gene \(Cyp2b10\) were significantly upregulated in the wild-type mice after \(\alpha\)-tocopherol dosing, revealing possible novel roles for \(\alpha\)-tocopherol in regulation of these enzymes. The \(Cyp2c\) family of genes was also upregulated after \(\alpha\)-tocopherol treatment.
The Cyp2c family is regulated by PXR (Cyp2c55) (van Waterschoot et al., 2009; Konno et al., 2010) and CAR in mice (Cyp2c37, Cyp2c29) (Jackson et al., 2004; Jackson et al., 2006; van Waterschoot et al., 2009; Konno et al., 2010). However human CYP2C9 regulation was shown to be carried out by PXR, CAR (Al-Dosari et al., 2006), vitamin D receptor (Drocourt et al., 2002), hepatocyte nuclear factor 4α (HNF4α) (Ibeanu and Goldstein, 1995), HNF3γ (Bort et al., 2004), glucocorticoid receptor (Gerbal-Chaloin et al., 2002), and CCAAT/enhancer binding protein α (Jover et al., 1998; Al-Dosari et al., 2006). The activation of PXR by PCN reveals that Cyp2c29 and Cyp2c55 are regulated by mouse PXR while Cyp2c29, Cyp2c55 and Cyp2c37 are regulated by rifampicin-activated human PXR. The results show that activation of PXR can not only induce Cyp3a11 but also Cyp2b10. Cyp2b10 is induced by CAR, but it has been shown that PXR can regulate Cyp2b genes and in turn CAR can regulate Cyp3a genes (Xie et al., 2000). Therefore it is apparent that there is cross-talk between PXR and CAR-mediated gene regulation and regulation of the Cyp2c gene family by α-tocopherol may involve both PXR and CAR. Indeed, the increased expression of Cyp2b10 in α-tocopherol treated wild-type mice and Cyp2c29, Cyp2c55, and Cyp2c37 in the Pxr-null mice dosed with α-tocopherol indicates that α-tocopherol may activate CAR.

As PXR can also upregulate UGT’s (Xie et al., 2003; Buckley and Klaassen, 2009), gene expression analysis of the major hepatic Ugt isoforms were carried out. There was no significant change in Ugt expression after α-tocopherol dosing (Figure 6). The same isoforms were also analysed from mice dosed with PCN or rifampicin, and some Ugts were induced, including the known PXR target gene Ugt1a1 (Xie et al., 2003). However the induction was not as robust as
was seen with the Cyp genes suggesting that Ugt genes are not as responsive to xenobiotic induction.

Previously Cyp3a11 and Cyp2b10 have been shown to be activated by PCN in wild-type mice, but a much larger increase in Cyp2b10 was seen after induction of CAR by 1,4-bis[2-(3,5-dichloropyridyloxy)]benzene, showing that CAR has a greater effect on Cyp2b10 expression than PXR (Maglich et al., 2002). Others (Mustacich et al., 2009) have proposed that α-tocopherol regulates drug metabolizing enzyme expression through CAR rather than PXR due to low PXR activation in HepG2 cells (Landes et al., 2003) and primary hepatocytes (Zhou et al., 2004). The induction of Cyp3a11 and Cyp2b10 by α-tocopherol is lost in Pxr-null mice indicating that PXR is the primary nuclear receptor involved in α-tocopherol induction of these genes. However the involvement of CAR in induction of Cyp2c29 cannot be ruled out due to the induction observed in Pxr-null mice after α-tocopherol dosing. The absence of Cyp3a11 induction in hPXR mice indicates that α-tocopherol is a mouse PXR partial agonist and the induction of the Cyp2c genes in all three mouse strains studied is linked to CAR or another transcription factor.

In humans CYP2C9, CYP2C8 and CYP2C19 metabolize approximately 20% of pharmaceutical drugs. Therefore, co-administration of α-tocopherol with other xenobiotics could result in faster clearance and lower plasma levels of a therapeutic drug. There have been numerous clinical trials of vitamin E for disease amelioration resulting in contradictory data. There are at least two known polymorphisms in the CYP2C9 promoter which allows for the possibility of reduced response to transcriptional activation by PXR that could contribute to inter-individual variation (Yin et al., 2008). CYP3A4 is also highly polymorphic with known
mutations of varying prevalence in different ethnic groups in the promoter region as well as the coding region that could affect \( \alpha \)-tocopherol induction of \( CYP3A4 \) as well as the metabolism of \( \alpha \)-tocopherol (McGraw and Waller, 2012). Therefore, genetic polymorphisms and co-administration with other xenobiotics could be routes for further investigation when investigating disparities seen in trials of the therapeutic value of vitamin E supplementation.
Authorship Contributions

Participated in Research Design: Johnson, Bonzo, Cheng, Krausz, Idle, Gonzalez

Conducted Experiments: Johnson, Bonzo, Cheng, Krausz

Contributed New Reagents: Kang, Luecke

Performed Data Analysis: Johnson, Bonzo

Wrote or contributed to the writing of manuscript: Johnson, Bonzo, Cheng, Idle, Gonzalez
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Footnotes

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Legend for Schemes

**Scheme 1.** Scheme of $\alpha$-tocopherol metabolism.
Legend for Figures.

Figure 1. PLS-DA scores plot from urine samples analyzed by UPLC-ESI-QTOFMS. A: Wild-type mice (R²X = 0.403, R²Y = 0.993, Q² = 0.859) B: Pxr-null (R²X = 0.218, R²Y = 0.856 Q² = 0.531), C: hPXR (R²X = 0.301, R²Y = 0.948, Q² = 0.731); □ predose α-tocopherol deficient diet, △ day 7 α-tocopherol deficient diet, ◇ day 14 α-tocopherol deficient diet, ▣ predose α-tocopherol enriched diet, ▾ day 7 α-tocopherol enriched diet, ◆ day 14 α-tocopherol enriched diet.

Figure 2. Mean concentrations of α-tocopherol metabolites identified in urine. Urinary α-tocopherol metabolite concentrations were normalised to urinary creatinine and expressed as μmol of metabolite per mmol of creatinine. No α-tocopherol metabolites were detected in α-tocopherol deficient diet fed mice. Error bars are SEM after two-tailed Student’s t-test. No statistical significance was observed between mouse strains for the excretion of each metabolite.

Figure 3. A: Hepatic gene expression analysis by qPCR from mice fed α-tocopherol deficient and enriched diets, B: Relative hepatic gene expression of Cyp2c genes by qPCR from mice fed α-tocopherol deficient and enriched diets. All values were normalized to β-actin and expressed as fold change. Error bars are SEM, significance as determined by two-tailed Student’s t-test between α-tocopherol deficient diet and α-tocopherol enriched diets. P-value: **P<0.01, *P<0.05

Figure 4. Hepatic gene expression analysis by qPCR from wild-type and Pxr-null mice gavaged with corn oil or PCN, and hPXR mice gavaged with corn oil or rifampicin. All values were normalized to β-actin and expressed as fold change. Error bars are SEM, significance as
determined by two-tailed Student’s t-test between corn oil gavage and PCN/rifampicin. \( P \)-value:

\[ **P < 0.001, ***P < 0.001, **P < 0.01, *P < 0.05 \]

**Figure 5.** Activation of mouse PXR by \( \alpha \)-tocopherol. HepG2 cells were transfected with mouse PXR, DR3 reporter luciferase, and pRL-SV40 constructs. Cells were treated with 10 \( \mu \)M PCN or 2.5, 25, or 50 \( \mu \)M \( \alpha \)-tocopherol for 24 hrs. The firefly luciferase value was normalized to Renilla luciferase value and expressed as fold change over DMO. PCN/rifampicin. \( P \)-value: ***\( P < 0.001, *P < 0.05 \)

**Figure 6.** Hepatic gene expression analysis of UGT’s by qPCR. A: Wild-type, \( Pxr \)-null, and h\( PXR \) mice fed \( \alpha \)-tocopherol deficient and enriched diets. B: Wild-type and \( Pxr \)-null mice gavaged with corn oil or PCN, and h\( PXR \) mice gavaged with corn oil or rifampicin. All values were normalized to \( \beta \)-actin and expressed as fold change. Error bars are SEM, significance as determined by two-tailed Student’s t-test between corn oil gavage and PCN/rifampicin. \( P \)-value:

\[ **P < 0.001, ***P < 0.001, **P < 0.01, *P < 0.05 \]
Scheme 1

α-tocopherol

CYP-mediated ω-hydroxylation

13'-hydroxy-α-tocopherol

β-hydroxylation steps

α-carboxyethylhydroxychroman
Figure 1

A

Wild-type

B

Pxr-null

C

hPXR