1521-0111/12/8103-338–347$25.00
MOLECULAR PHARMACOLOGY
Copyright © 2012 The American Society for Pharmacology and Experimental Therapeutics
Mol Pharmacol 81:338–347, 2012

Vol. 81, No. 3
75952/3747464

A Novel Nonconsensus Xenobiotic Response Element Capable of Mediating Aryl Hydrocarbon Receptor-Dependent Gene Expression

Gengming Huang and Cornelis J. Elferink

Department of Pharmacology and Toxicology, University of Texas Medical Branch, Galveston, Texas

Received September 20, 2011; accepted November 23, 2011

ABSTRACT

The aryl hydrocarbon receptor (AhR) is a mediator of xenobiotic toxicity, best recognized for conveying the deleterious effects of 2,3,7,8-tetrachlorodibenzo-*p*-dioxin (TCDD) exposure. The AhR functions as a ligand-activated transcription factor that binds to a canonical xenobiotic response element (XRE) in association with the heterodimerization partner, the AhR nuclear translocator (Arnt) protein. However, within the repertoire of AhR target genes identified in recent years, many lack a clearly defined XRE highlighting the growing realization that AhR-mediated gene expression seems to involve additional mechanisms distinct from the well characterized process involving the XRE. The present study characterized a novel nonconsensus XRE (NC-XRE) in the promoter of the plasminogen activator inhibitor-1 *(PAI-1*) gene that recruits a novel protein-DNA complex responsible for TCDD-inducible expression. DNA binding studies and reporter assays identified key residues in the NC-XRE necessary for protein-DNA binding and function, respectively. Functional studies with AhR expression constructs confirm that TCDD-inducibility is AhR-dependent and requires direct AhR-DNA binding to the NC-XRE. Chromatin immunoprecipitation and RNA interference studies reveal that the Arnt protein is not a component of the NC-XRE-bound AhR complex, suggesting that in contrast to the XRE, AhR-dependent gene expression mediated through the NC-XRE may involve a new DNA binding partner.

Introduction

The eukaryotic Per-Arnt-Sim (PAS) domain protein family contains several members that function as sensors of extracellular signals and environmental stresses affecting growth and development (Gu et al., 2000). Within this family, the aryl hydrocarbon receptor (AhR) regulates adaptive and toxic responses to a variety of chemical pollutants, including polycyclic aromatic hydrocarbons and polychlorinated dioxins, most notably 2,3,7,8-tetrachlorodibenzo-*p*-dioxin (TCDD). Studies on the AhR have in the past focused their efforts toward understand the molecular basis for TCDD toxicity, which manifests as a broad spectrum of biological responses that include tumor promotion, immuno- and hepatotoxicity, teratogenesis, a wasting syndrome, and endocrine disturbances (Poland and Knutson, 1982). Evidence obtained using AhR-defective mouse models confirmed that TCDD toxicity is AhR-dependent, requiring the AhR to function as a soluble cytosolic ligand-activated transcription factor that translocates into the nucleus after agonist activation. Upon nuclear entry, the AhR binds to DNA response elements known as xenobiotic responsive elements (XRE) in conjunction with the heterodimerization partner, the AhR nuclear translocator protein (Lees and Whitelaw, 1999).

To better understand TCDD toxicity, several groups sought to identify AhR target genes through DNA microarray studies using cell culture and whole animal models (Puga et al., 2000a; Frueh et al., 2001; Boverhof et al., 2005; Tijet et al., 2006; C. J. Elferink, unpublished observations). Functional clustering identifies numerous TCDD-regulated genes associated with various physiological responses, which underscores the pleiotropic nature of TCDD toxicity but fails to provide an unambiguous mechanistic explanation for most of the deleterious outcomes associated with TCDD exposure. A second general observation made is that despite computa-

This work was supported by the National Institutes of Environmental Health Sciences [Grants R01-ES07800, P30-ES06676].

Article, publication date, and citation information can be found at http://molpharm.aspetjournals.org.

http://dx.doi.org/10.1124/mol.111.075952.

ABBREVIATIONS: PAS, Per-Arnt-Sim (periodicity/aryl hydrocarbon receptor nuclear translocator/single-minded); AhR, aryl hydrocarbon receptor; TCDD, 2,3,7,8-tetrachlorodibenzo-*p*-dioxin; XRE, xenobiotic responsive element; PAI-1, plasminogen activator inhibitor-1; Arnt, aryl hydrocarbon receptor nuclear translocator; CKO, conditional knockout; PAGE, polyacrylamide gel electrophoresis; CHX, cycloheximide; RT-PCR, real-time polymerase chain reaction; C_T, cycle threshold; ChIP, chromatin immunoprecipitation; bp, base pair(s); EMSA, electrophoretic mobility shift assay; NC-XRE, nonconsensus XRE; MOI, multiplicity of infection; GFP, green fluorescent protein.

tional analyzes spanning 3 kilobases (Boverhof et al., 2005) or 6 kilobases (Tijet et al., 2006) of the DNA sequence flanking the transcription start sites of responsive genes, many did not contain a readily identifiable XRE based on the consensus sequence. One possible explanation is that expression of genes lacking a XRE reflects indirect AhR-mediated signaling and, indeed, such changes in expression may be attributed to latent secondary effects. However, it is necessary to consider the possibility that the AhR is altering transcription directly through a site(s) distinct from the consensus XRE. For instance, the ligand-activated AhR/Arnt dimer can interact directly with the unliganded estrogen receptor and promote formation of a transcriptionally active complex binding to estrogen response elements (Ohtake et al., 2003). Correspondingly, the AhR can form a quaternary complex with p300, pRb, and E2F to suppress S-phase gene expression (Puga et al., 2000b; Marlowe et al., 2004) or with an unknown protein(s) upstream of the *CYP1A2* gene (Sogawa et al., 2004). Evidence is also accumulating for direct AhR-DNA binding in conjunction with the RelB protein to a distinct response element located in the interleukin-8 gene regulatory region (Vogel et al., 2007).

The plasminogen activator inhibitor-1 (*PAI-1*) gene was shown to be a TCDD-responsive gene in several DNA microarray studies (Puga et al., 2000a; Frueh et al., 2001; Boverhof et al., 2005; Tijet et al., 2006; C. J. Elferink, unpublished observations). It is noteworthy that the *PAI-1* gene represents an example in which TCDD responsiveness is attributed to a regulatory region devoid of a canonical XRE (Son and Rozman, 2002). Analysis of the PAI-1 promoter using a luciferase reporter system in mouse hepatoma cells demonstrated that a 200-base-pair region of the PAI-1 promoter lacking a clearly recognizable XRE (GCGTG) motif conferred AhR-dependent TCDD inducibility. The evidence presented in this report extends upon the previous finding by identifying and characterizing a novel nonconsensus XRE (NC-XRE) located within this PAI-1 promoter that supports direct DNA binding and function by the AhR independently of the Arnt protein. This discovery may help to reconcile some of the confounding results obtained in earlier studies examining the AhR-regulated transcriptome and serves to illustrate the growing awareness of the complexity associated with AhR biology.

Materials and Methods

Reagents. Anti-AhR (rabbit polyclonal antibody) was obtained from Enzo Life Sciences, Inc. (Farmingdale, NY). Hypoxia-inducible factor-1β/Arnt1 antibody was purchased from BD Biosciences (San Jose, CA). Mouse anti-actin monoclonal antibody was purchased from Millipore Bioscience Research Reagents (Temecula, CA). [γ-^{32}P]GTP was acquired from GE Healthcare (Chalfont St. Giles, Buckinghamshire, UK). Anti-rat CYP1A1 was obtained from Daiichi Pure Chemicals Co., Ltd. (Tokyo, Japan). The purified rabbit anti-rat PAI-1 was obtained from Torrey Pines Biolabs, Inc. (Houston, TX). Goat anti-recombinant rat PAI-1 was acquired from American Diagnostica Inc. (Greenwich, CT). Species-specific horseradish peroxidase-conjugated secondary antibodies were purchased from Zymed Laboratories (South San Francisco, CA). TCDD was obtained from the National Cancer Institute Chemical Carcinogen Reference Standard Repository (Kansas City, MO). 1-(1-Propynyl)pyrene was custom synthesized by the UTMB Center in Environmental Toxicology Synthetic Organic Chemistry Core. Micrococcal nuclease was obtained from Worthington Biochemicals (Lakewood, NJ). H3 antibody was obtained from Abcam (Cambridge, MA). Protein-G Agarose, salmon sperm DNA, and sheep IgG were purchased from upstate (Lake Placid, NY). Protein-G coupled Sepharose resin was from Invitrogen (Carlsbad, CA). Ribonuclease A, Dulbecco's modified Eagle's medium, glass beads, and Sybr Green were obtained from Sigma-Aldrich (St. Louis, MO). [^{35}S]Methionine was obtained from GE Healthcare Oligonucleotides were purchased from Sigma-Genosys (The Woodlands, TX).

Production of Adenoviruses. Generation of the virus AdAhRFL (encoding a full-length wild-type rat AhR) and control AdGFP and AdRFP viruses was described previously (Elferink et al., 2001; Huang and Elferink, 2005). Generation of the DNA-binding defective AhR virus construct (AdAhR-R39/41A) and virus construct used in RNA interference (AdiArnt, encoding a short hairpin RNA) was described previously (Huang and Elferink, 2005).

Cell Culture, Infections, and Transfections. Mouse primary hepatocytes were isolated by the collagenase type IV perfusion from wild-type C57BL/6 mice as described previously (Park et al., 2005). Cells (5×10^5) were plated in 35-mm plates in Williams' E medium containing penicillin (100 U/ml), streptomycin (100 μg/ml), insulin (5 μg/ml), bovine serum albumin (1 mg/ml), and 5% fetal bovine serum. AhR-defective BP8 cells were grown as subconfluent monolayers in medium consisting of Dulbecco's modified Eagle's medium containing 10% fetal bovine serum, 100 U/ml penicillin, and 100 μg/ml streptomycin. Both cells were incubated in 5% CO_2 atmospheres at 37°C. For viral infection, BP8 cells at 5×10^5 cells per 35-mm dish were infected with a multiplicity of infection of 100 and the infection efficiency monitored using GFP coexpression. Where appropriate, primary hepatocytes and BP8 cells were cotransfected with the indicated plasmids using the Lipofectamine 2000 (Invitrogen) in accordance with the manufacturer's recommendations.

Animal Treatment. All experiments were performed in compliance with the standards established for the care and use of laboratory animals at the University of Texas Medical Branch. TCDD was dissolved in anisole and diluted in peanut oil. Male adult C57BL/6 mice (10 weeks old, weighing 25 g) were administered via gavage with TCDD at 20 μg/kg body weight. Control mice received peanut oil spiked with an equivalent amount of anisole. Mice were treated with TCDD or vehicle for the indicated period before liver harvest. $Ahr^{fx/fx}$ mice [mice containing loxP sites that flank exon 2 of the AhR allele (Walisser et al., 2005)], and mice harboring an albumin promoter-driven *Cre* recombinase on a C57BL/6 background (Cre^{Alb} mice) were purchased from The Jackson Laboratory (Bar Harbor, ME). $Ahr^{fx/fx}$ mice were crossed with Cre^{Alb} mice to produce conditional knockout (CKO) offspring in which the $Ahr^{fx/fx}$ allele is excised in parenchymal hepatocytes, effectively eliminating AhR protein expression in these cells after birth. Excision of the AhR allele was verified at the genomic level (data not shown). Animals were housed in microisolator cages in a temperature- and light-controlled facility with free access to water and diet. Mice were euthanized at the indicated time by isoflurane overdose followed by cervical dislocation.

Immunoprecipitation and Western Blotting. For assessment of PAI-1 expression, secreted PAI-1 from BP8 cell-conditioned media was incubated with goat anti-recombinant rat PAI-1 antibody for 4 h on ice, followed by precipitation with protein-G resin. Beads were washed four times in radioimmunoprecipitation assay buffer. Both immunoprecipitated proteins and total cell lysates were fractionated by 10% SDS-PAGE, transferred to the polyvinylidene difluoride membrane, and blocked with 5% BLOTTO in Tris-buffered saline containing 0.1% Tween 20. Filters were probed with antibodies against the PAI-1, Arnt protein, P4501A1, and Actin for 4 h at room temperature, followed by the appropriate horseradish peroxidase-conjugated secondary antibody at room temperature. Immunoreactivity was visualized at room temperature using the enhanced chemiluminescence Western blot detection reagent (GE Healthcare).

Bands were visualized and quantified by using ChemiImager 5500 2.03 software (Alpha Innotech, San Leandro, CA).

Cycloheximide Treatment and Examination of Protein Synthesis. Before treatment with TCDD, BP8 cells infected with AdAhRFL or AdGFP at a multiplicity of infection of 100 were exposed to cycloheximide (CHX) (10 μg/ml) for 1 h. To confirm cessation of nascent protein synthesis, BP8 cultures with or without CHX where pulsed for 4 h with 0.5 mCi/ml [^{35}S]methionine in methionine-depleted media in the presence of 6 nM TCDD or vehicle (dimethyl sulfoxide). Cells were harvested and processed for SDS-PAGE and autoradiography to monitor nascent protein synthesis or total RNA isolation for real-time polymerase chain reaction (RT-PCR), as described below.

RNA Isolation and Analysis. Total RNA was isolated from liver tissue, mouse primary hepatocytes, or BP8 cells using RNAqueous (Ambion, Inc., Austin, TX), and quantitative (q) RT-PCR was performed by the Sealy Center for Cancer Cell Biology and Real-Time PCR Core Facility at the University of Texas Medical Branch. We used Applied Biosystems assays-on-demand 20 assay mix of primers and TaqMan MGB probes (5-carboxyfluorescein dye-labeled) for *PAI-1* gene and predeveloped 18S rRNA (VIC-dye labeled probe) TaqMan assay reagent for an internal control. The primers were designed to span exon-exon junctions so as not to detect genomic DNA. Validation experiments were performed to test the efficiency of the target and reference amplifications. The absolute value of the slope of log input amount versus C_T was <0.1. Separate tubes (singleplex) one-step RT-PCR was performed with 40 ng of RNA for both target genes and endogenous control. The reagent used was TaqMan one-step RT-PCR master mix reagent kit (Applied Biosystems, Foster City, CA). The cycling parameters for one-step RT-PCR were as follows: reverse transcription at 48°C for 30 min, AmpliTaq activation at 95°C for 10 min, denaturation at 95°C for 15 s, and annealing/extension at 60°C for 1 min (repeat 40 times) on an ABI 7000. Triplicate C_T values were analyzed in Microsoft Excel (Microsoft Corp., Redmond, WA) using the comparative C_T ($\Delta\Delta C_T$) method as described by the manufacturer (Applied Biosystems). The amount of target ($2^{-\Delta\Delta C_T}$) was obtained by normalized to endogenous reference (18S rRNA) and relative to a calibrator (one of the experimental samples).

Genomic DNA Extraction and Constructs and Luciferase Report Assays. Genomic DNA extraction was described previously (Laird et al., 1991). The mouse PAI-1 promoter (−116/+1) sequence was generated by PCR using Taq polymerase, genomic DNA and primers 1 and 2 (Table 1). The PCR product was subcloned into pCR 4-Topo vector (Invitrogen), and DNA was sequence-verified. The PCR product was subcloned into the KpnI and BglII sites of the firefly luciferase reporter vector pGL3-Basic (Promega Corporation, San Luis Obispo, CA) to generate the resultant plasmid construct pPAI-1/116Luc. The NC-XRE (pGL3-NC-XRE) and mutant constructs (pGL3-M3, pGL3-M4, and pGL3-M5) were generated by PCR using Taq polymerase, pPAI-1/116Luc DNA, and primers 3 and 4 (NC-XRE), 3 and 5 (M4), 3 and 6 (M5), and 7 and 8 (M3) (Table 1). The PCR products were subcloned into pCR 4-Topo vector, and the DNA was sequence-verified. The PCR products were subsequently cloned into the KpnI and BglII sites of the vector pGL3-Promoter.

For transfection experiments, the cells were cultured in six-well plates and transiently cotransfected with the firefly luciferase constructs and the *Renilla reniformis* luciferase-encoding pRL-SV40 vector (Promega), used as an internal control, according to the Lipofectamine 2000 method (Invitrogen). In brief, 500 μl of transfection medium containing 200 ng of luciferase reporter plasmid was added per well of 90% of appropriate cells along with 20 ng of the pRL-SV40 plasmid and 10 μl of Lipofectamine 2000. After a 24-h period, cells were exposed to TCDD for a further 24 h. Dual luciferase assays (firefly and *R. reniformis*) were performed with a Promega kit according to the manufacturer's instructions.

Chromatin Immunoprecipitation Assays. Chromatin immunoprecipitation (ChIP) assays on whole-liver tissues were performed as described previously (Nguyen et al., 2005). In brief, liver tissues from C57BL/6 mice were isolated, finely diced, and cross-linked with 1% formaldehyde in phosphate-buffered saline at room temperature for 10 min. Sonication of the cross-linked chromatin was performed with glass beads followed by digestion with micrococcal nuclease to generate fragments with a median length of 400 to 500 bp, as determined empirically by agarose gel electrophoresis of fragmented chromatin samples. The fragmented chromatin lysate was incubated with nonspecific IgG for 1 h to preclear the lysate. The precleared lysate was divided equally among all samples and incubated overnight at 4°C with 1 μg of the following antibodies: anti-AhR, hypoxia-inducible factor-1β/Arnt1, H3 antibodies (as a positive control and a measure of chromatin recovery for each lysate), and normal sheep IgG (negative control). Protein G-Sepharose beads with salmon sperm DNA were added and incubated for 1 h, followed by recovery of antibody precipitates.

The recovered DNA was subjected to PCR using primers 9 and 10 or 11 and 12 (Table 1) to generate a 234-bp (spanning the PAI-1 promoter NC-XRE) and a 357-bp (Cyp1a1 promoter region spanning several XRE sequences) PCR product, respectively. Twenty-eight PCR cycles were performed for each bound DNA fraction and input. PCR products were separated on 6% polyacrylamide gels and stained with SYBR Green. DNA bands were visualized and quantified by using ChemiImager 5500 2.03 software. The bound fraction values were calculated as a percentage of the input DNA used in the immunoprecipitation representing 100%.

Electrophoretic Mobility Shift Assays. Nuclear extracts were isolated from mouse liver tissue as described previously (Schwartz and Schlaepfer, 1996). Mice were treated with 20 μg/kg TCDD or vehicle (peanut oil) by gavage 2 h before harvest of liver tissue, and electrophoretic mobility shift assay (EMSA) was performed using a [γ-^{32}P]GTP end-labeled double-stranded DNA probe containing an AhR-binding site as described by Shen et al. (1991).

Statistical Analyses. Statistical analyses were performed using Prism (version 4.0; GraphPad Software, San Diego, CA). Data were evaluated by two-way analysis of variance. p values < 0.05 were considered statistically significant.

TABLE 1
Oligonucleotides used in PCR and as EMSA probe sets

Oligonucleotide	Sequence (5′→3′)
Cloning primers	
1	GGGGTACCGTCACTGGGAGGGAGGGAGGG
2	GGAAGATCTAACTCATGTTCCAGCCCCACCCACTTTC
3	GGGTACCGTCCCAGCAAGTCACTGGGAG
4	GGAAGATCTCTCCCCCCCCTCCCTCCCTC
5	GGAAGATCTCTCCCCCCCCTCCCCTTCTC
6	GGAAGATCTCTCCCCCCCCTCTTTCCCTC
7	GGGTACCGTCCCAGCAAGTCACTGGAGAG
8	GGAAGATCTCTCCCCCCCCTCCCTCCTCT
ChIP assay PCR primers	
9	GTCCCAGCAAGTCACTGGGAGG
10	CTGGAGGCGGGTGTGCGGCG
11	CTATCTCTTAAACCCCACCCCAA
12	CTAAGTATGGTGGAGGAAAGGGTG
EMSA oligonucleotides	
13	GTCCCAGCAAGTCACTGGGAGGGAGGGAGGGGGGGGAG
	CTCCCCCCCCTCCCTCCCTCCCAGTGACTTGCTGGGAC
14	GTCCTGAACGACCACTGGGAGGGAGGGAGGGGGGGGAG
	CTCCCCCCCCTCCCTCCCTCCCAGTGGTCGTTCAGGAC
15	GTCCCAGCAAGTCACTGGCACCCACCGAGGGGGGGGAG
	CTCCCCCCCCTCGGTGGGTGCCAGTGACTTGCTGGGAC
16	GTCCCAGCAAGTCACTGGAGAGGAGGGAGGGGGGGGAG
	CTCCCCCCCCTCCCTCCTCTCCAGTGACTTGCTGGGAC
17	GTCCCAGCAAGTCACTGGGAGAAGGGGAGGGGGGGGAG
	CTCCCCCCCCTCCCCGGCTCCCAGTGACTTGCTGGGAC
18	GTCCCAGCAAGTCACTGGGAGGGAAAGAGGGGGGGGAG
	CTCCCCCCCCCTCTTTCCCTCCCAGTGACTTGCTGGGAC
19	GATCTGAGCTCGGAGTTGCGTGAGAAGAGCCG
	GATCCGGCTCTTCTCACGCAACTCCGAGCTCA

Results

Several previous DNA microarray reports documented that PAI-1 expression could be induced by TCDD (Puga et al., 2000a; Frueh et al., 2001; Boverhof et al., 2005; Tijet et al., 2006). In microarray studies performed by us, PAI-1 expression was induced 5- to 9-fold in rat 5L hepatoma cells treated with TCDD for 4 h. In primary mouse hepatocytes exposed to TCDD for 12 h, PAI-1 expression increased by a more modest 3-fold (Fig. 1A), similar to that observed in HepG2 (Puga et al., 2000a; Frueh et al., 2001) and Hepa1 cells (Son and Rozman, 2002). By contrast, in vivo liver PAI-1 expression increased by more than 40-fold after 12 h of TCDD exposure (Fig. 1B). The data clearly identify PAI-1 as a TCDD-responsive gene in liver derived tissues and cells.

To establish that PAI-1 induction is AhR-dependent, we infected BP8 cells—a variant of the 5L cell line lacking detectable AhR expression (Weiss et al., 1996)—with an adenovirus expressing the AhR (Elferink et al., 2001). A multiplicity of infection of 100, sufficient to infect 100% of the cells was used, and the infection rate was monitored through coexpression of a GFP protein (Fig. 2A). A virus (AdGFP) expressing only the GFP served as a control. Activation of the AhR relied on treatment with 1-(1-propynyl)pyrene as previously reported by us (Levine-Fridman et al., 2004). PAI-1 is a secreted protein; therefore, its expression was measured after immunoprecipitation of the culture medium at the indicated times. P4501A1 expression was determined concomitantly using the cell lysates. The evidence reveals that increases in secreted PAI-1 are first detectable at 4 h and peak by 8 h. P4501A1 levels are clearly evident within 4 h after 1-(1-propynyl)pyrene administration. Because expression of both PAI-1 and P4501A1 is restricted to the BP8 cells infected with AdAhRFL, the evidence clearly illustrates that PAI-1 induction is AhR-dependent. This finding extends upon an earlier observation that TCDD could not induce PAI-1 expression in the AhR-defective Hepa1 variant cell line (Son and Rozman, 2002), by confirming the requirement for the AhR.

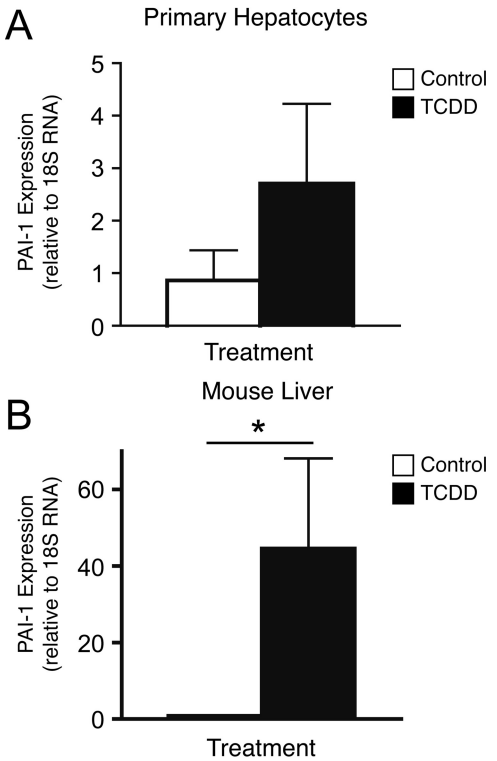


Fig. 1. TCDD inducible PAI-1 expression in the mouse liver tissue and primary hepatocytes. A, mouse primary hepatocytes were cultured in the presence of 6 nM TCDD or vehicle (Control) for 4 h. PAI-1 mRNA expression (normalized to 18s RNA) was then analyzed using quantitative RT-PCR. The data presented are the average of two independent experiments (± S.E.M.). B, adult C57BL/6 mice were treated with 20 μg/kg TCDD or vehicle (peanut oil) by gavage. After 12 h, total RNA was isolated, and PAI-1 mRNA levels were analyzed by quantitative RT-PCR. The data shown are representative of three independent experiments. *, $p < 0.05$, significant difference compared with vehicle group.

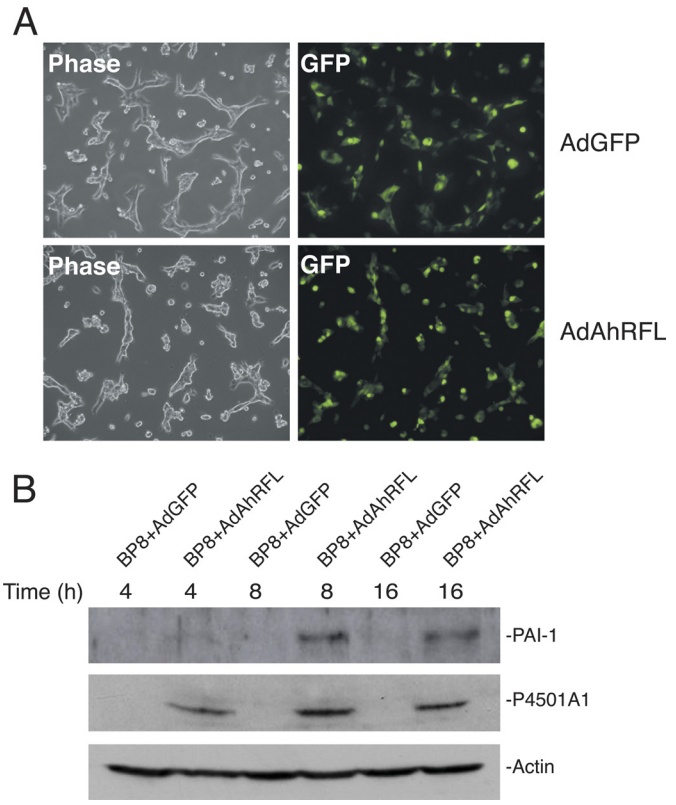


Fig. 2. PAI-1 induction is AhR-dependent. A, AhR-negative BP8 cells were infected with a control adenovirus (AdGFP) or a virus expressing the rat AhR (AdAhRFL) at a MOI of 90 for 24 h as described previously (Elferink et al., 2001). GFP expression was used to monitor infection efficiency. B, cultures were treated with 1 μM 1-(1-propynyl)pyrene to activate the AhR for the indicated time, and Western blotting was performed on immunoprecipitated PAI-1 from the culture media to measure the secreted PAI-1 protein and on total cell lysates to assay for P4501A1 expression. Analysis of actin was used as a loading control.

Son and Rozman (2002) ascertained that a region of the murine PAI-1 promoter spanning nucleotides −116 to +73 conferred TCDD inducibility upon a luciferase reporter. Our preliminary findings narrowed this region down to the first 116 nucleotides upstream of the transcription start site (Fig. 3). In primary mouse hepatocytes and in BP8 cells infected with AdAhRFL, this promoter sequence mediated TCDD inducible reporter expression. This region also increased basal expression, suggesting that other regulatory factors may be interacting with this promoter sequence. Subsequent studies using CHX to inhibit nascent protein synthesis in BP8 cells demonstrated that the AhR-dependent induction persisted in the absence of new protein synthesis (Fig. 4), suggesting that the increased expression is a direct

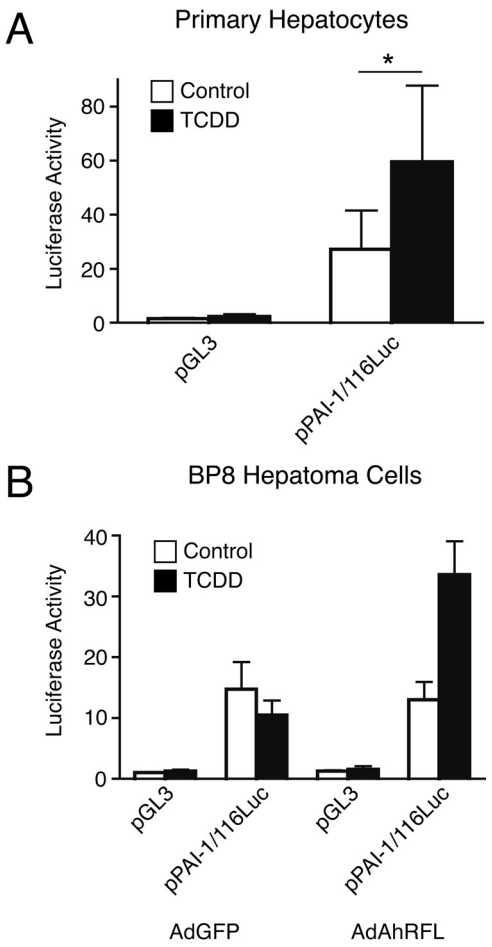


Fig. 3. The AhR is required for TCDD-induced PAI-1 expression. A, mouse primary hepatocytes isolated as described under *Materials and Methods* were transfected with the pGL3 control vector or the pPAI-1/116Luc firefly luciferase reporter construct under the control of the 116-bp PAI-1 promoter region. Cells were cotransfected with the pRL-SV40 vector encoding *R. reniformis* luciferase as a transfection control. Cells were treated with vehicle (Control, open bars) or 6 nM TCDD (TCDD, solid bars) for 24 h, and dual luciferase assays (firefly and *R. reniformis*) were performed. The data are presented as means ± S.E.M of four independent experiments for firefly luciferase activity normalized against pRL-SV40 *R. reniformis* luciferase activity. The asterisk indicates a significant difference ($p < 0.05$). B, subconfluent cultures of asynchronous BP8 cells (AhR-negative) were infected with the AdGFP or AdAhRFL at a MOI of 100 for 24 h. The cells were subsequently cotransfected with pGL3 or pPAI-1/116 and pRL-SV40 and treated with vehicle (Control, open bars) or 6 nM TCDD (TCDD, solid bars) for a further 24 h. Dual luciferase activity was determined and the data are expressed as means ± S.E.M of two independent experiments.

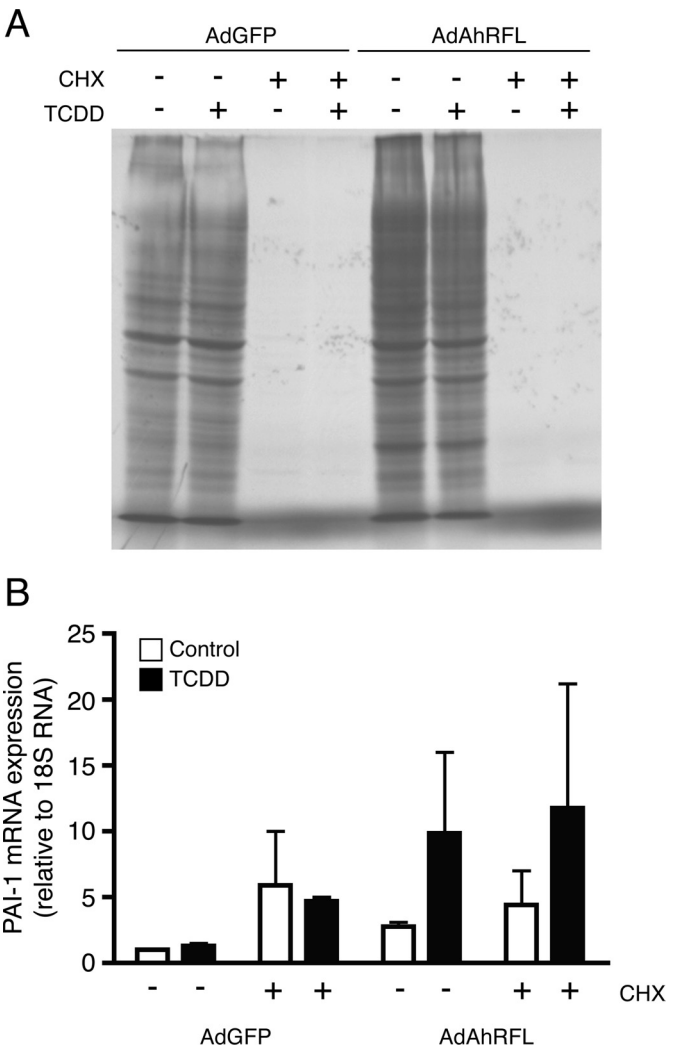
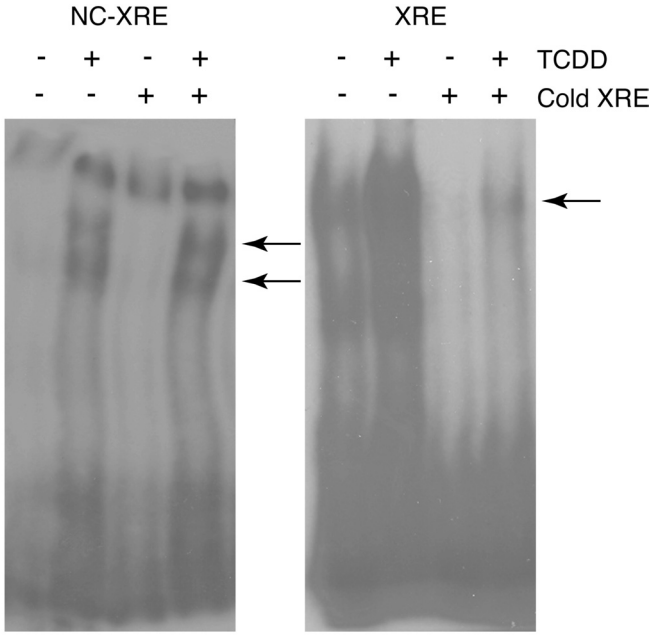


Fig. 4. TCDD induction of PAI-1 does not require new protein synthesis. A, BP8 (AhR-negative) cells were infected with AdAhRFL or AdGFP at an MOI of 100 for 24 h before treatment with PBS (−CHX) or 10 μg/ml cycloheximide (+CHX) for 1 h. Subsequently, the cells were labeled with 0.5 mCi/ml [^{35}S]methionine (±CHX) as described under *Materials and Methods* in the vehicle (−TCDD) or 6 nM TCDD (+TCDD) for an additional 4 h. Cells were harvested to monitor nascent protein synthesis by 10% SDS-PAGE and autoradiography. B, duplicate cultures of BP8 cells were prepared as described for A, except that they were not radioactively labeled with [^{35}S]methionine. Total RNA was isolated, and quantitative RT-PCR was performed to measure PAI-1 mRNA levels (normalized to 18S rRNA). The data are presented as the mean (± S.E.M.) of two independent experiments.

rather than indirect response to TCDD, consistent with a direct role for the AhR reminiscent of a canonical XRE-mediated induction response.

Identification and Characterization of the Nonconsensus XRE. The evidence indicates that AhR-mediated induction of the *PAI-1* gene is a direct response involving a DNA region proximal to the promoter. However, this region lacks an obvious consensus XRE (5′-GCGTG-3′). EMSAs were performed using mouse liver nuclear extracts and overlapping 40-nucleotide probes to interrogate the 116-bp region for a site capable of forming a TCDD-inducible protein-DNA complex (data not shown). These studies identified a single oligonucleotide spanning residues −116 to −76 of the PAI-1 promoter that conferred a TCDD-inducible EMSA complex (Fig. 5). The DNA sequence designated as an NC-XRE forms two distinct inducible complexes that are refractory to competition by a 10-fold molar excess of unlabeled XRE (Fig. 5, lanes 1–4). In contrast, the unlabeled XRE readily competes for the inducible complex detected using a radiolabeled XRE (Fig. 5, lanes 5–8).

A further characterization of the NC-XRE sought to resolve the precise binding site by identifying important residues for complex formation (Fig. 6). Using the UCSC Genome Browser (http://genome.ucsc.edu/cgi-bin/hgGateway), examination of the PAI-1 promoter encompassing this region among several mammalian species (human, mouse rat, orangutan, dog) identified two conserved sequences that were independently mutated and analyzed by EMSA (Fig. 6A). The results show that direct binding of the TCDD inducible protein-DNA complex occurred with both the wild-type NC-XRE and M1 mutant oligonucleotide, but not with



XRE 5'-GATCTGAGCTCGGAGTTGCGTGAGAAGAGCCG-3'

NC-XRE 5'-GTCCCAGCAAGTCACTGGGAGGGAGGGAGGGAGGGGGAG-3'

Fig. 5. EMSA on the NC-XRE and XRE reveals distinct protein-DNA complexes. Whole-liver nuclear extracts were prepared from vehicle-treated mice (i.e., peanut oil administered by gavage, −TCDD) or mice treated with 20 μg/kg TCDD for 2 h (+TCDD). EMSA using the nuclear extracts was performed with ^{32}P-labeled NC-XRE and XRE oligonucleotide probes as indicated. Competition experiments used a 10-fold molar excess of the unlabeled (Cold) XRE probe containing the consensus AhR-binding site, as described under *Materials and Methods*. The arrows denote the position of the TCDD-inducible protein-DNA complexes for each oligonucleotide.

the M2 sequence. Therefore, the sequence altered in M2 seems to map the NC-XRE binding site. A striking feature associated with this sequence is the repeated 5′-GGGA-3′ tetranucleotide motif (Fig. 6B). Subsequent competition EMSA experiments further resolved the key residues involved in protein-DNA binding (Fig. 6C). The evidence suggests that the second tetranucleotide motif is preferentially involved in protein binding because akin to the M2 mutant, the M4 mutant NC-XRE fails to effectively compete for the EMSA complex. In contrast, unlabeled M3 and M5 mutant oligonucleotides proved as effective as the wild-type NC-XRE in competing for binding. Because the unaltered tetranucleotide motifs in the M4 oligonucleotide failed to compete effectively for the complex, we conclude that they do not contribute substantially to protein-DNA binding. In addition, the evidence suggests that the slower migrating complex (Fig. 6C, upper arrow) exhibits higher affinity binding because it persisted despite challenge with a 100-fold molar excess of the mutant M2 and M4 oligonucleotides. The composition of the protein-DNA complexes bound to the NC-XRE remains undetermined.

To examine the functionality of the mutant NC-XRE sequences, constructs harboring a single copy of the wild-type NC-XRE, M3, M4 or M5 mutant, were introduced into the promoter of a luciferase reporter plasmids and transfected into primary mouse hepatocytes (Fig. 7). The result reveals that the NC-XRE and mutant M3 and M5 binding sites conferred significant TCDD inducibility upon the luciferase reporter, whereas the mutant M4 was unable to confer induced gene expression. The diminished induction seen with the M3 and M5 mutants may reflect a partial disruption in protein-DNA binding, but insufficient to fully abolish function. Therefore, the functional evidence corroborates the in vitro protein-DNA binding observations.

AhR Binding to the PAI-1 Promoter Is Arnt-Independent. Son and Rozman (2002), using the Hepa1 cell variants, surmised that TCDD induction of the PAI-1 gene required both the AhR and Arnt protein, because neither the AhR- nor Arnt-defective variant cell lines responded to TCDD. Although the composition of the protein complex binding to the NC-XRE is unknown, the characteristics of the binding site strongly suggest that the NC-XRE does not recruit the typical AhR/Arnt protein heterodimer known to bind to the XRE. Attempts to interrogate the in vitro EMSA complex with antibodies against the AhR or Arnt protein did not produce a supershift complex or disrupt complex formation (data not shown). However, ChIP experiments performed using the whole mouse liver nevertheless revealed a TCDD-inducible association of the AhR with the PAI-1 promoter in vivo (Fig. 8). It is noteworthy that a corresponding association of the Arnt protein was not evident, whereas concomitant analysis of the Cyp1a1 promoter region harboring XREs confirmed TCDD-inducible binding by both the AhR and Arnt protein as expected. Therefore, the data suggest that AhR binding to the PAI-1 NC-XRE is Arnt protein-independent.

Given the dissimilarity between the NC-XRE and canonical XRE, and the inability to detect Arnt protein binding to the PAI-1 promoter by ChIP, there is some question about the nature of the AhR-NC-XRE interaction. Specifically, does the receptor binds to the DNA directly, or does it reside within a quaternary complex through a protein-protein interaction in the absence of direct DNA binding? Indeed, the AhR's association with the E2F/DP complex provides a precedent for the latter scenario (Marlowe et al., 2004). To examine this, we tested whether an AhR harboring point mutations in the basic (DNA-binding) domain designed to specifically and exclusively abolish DNA binding (Huang and Elferink, 2005) could still induce PAI-1 expression (Fig. 9). Primary hepatocytes were isolated from Ahr$^{fx/fx}$Cre^{Alb} CKO mice—lacking the AhR—and infected with a control adenovirus (AdGFP), a virus expressing a wild-type AhR (AdAhRFL), or a virus expressing the DNA binding defective mutant receptor (AdAhR-R39/41A). After TCDD treatment, RT-PCR was performed on total RNA to monitor AhR expression and PAI-1 and Cyp1a1 inducibility (Fig. 9A). qRT-PCR was performed to quantify the induction of PAI-1 and Cyp1a1 (Fig. 9B). Collectively, the evidence demonstrates that TCDD induction of both target transcripts is abolished in the cell expressing the mutant AhR, suggesting that NC-XRE-mediated PAI-1 induction depends on direct DNA binding by the AhR but seems independent of the Arnt protein.

To verify that TCDD induction of the *PAI-1* gene is indeed independent of the Arnt protein, BP8 cells were coinfected with adenoviruses expressing the AhR and RFP (as a control), or coinfected with viruses expressing the AhR and a short hairpin RNA to knock-down Arnt protein expression by RNA interference, as previously reported (Huang and Elferink, 2005). The virus-infected cells were subsequently tran-

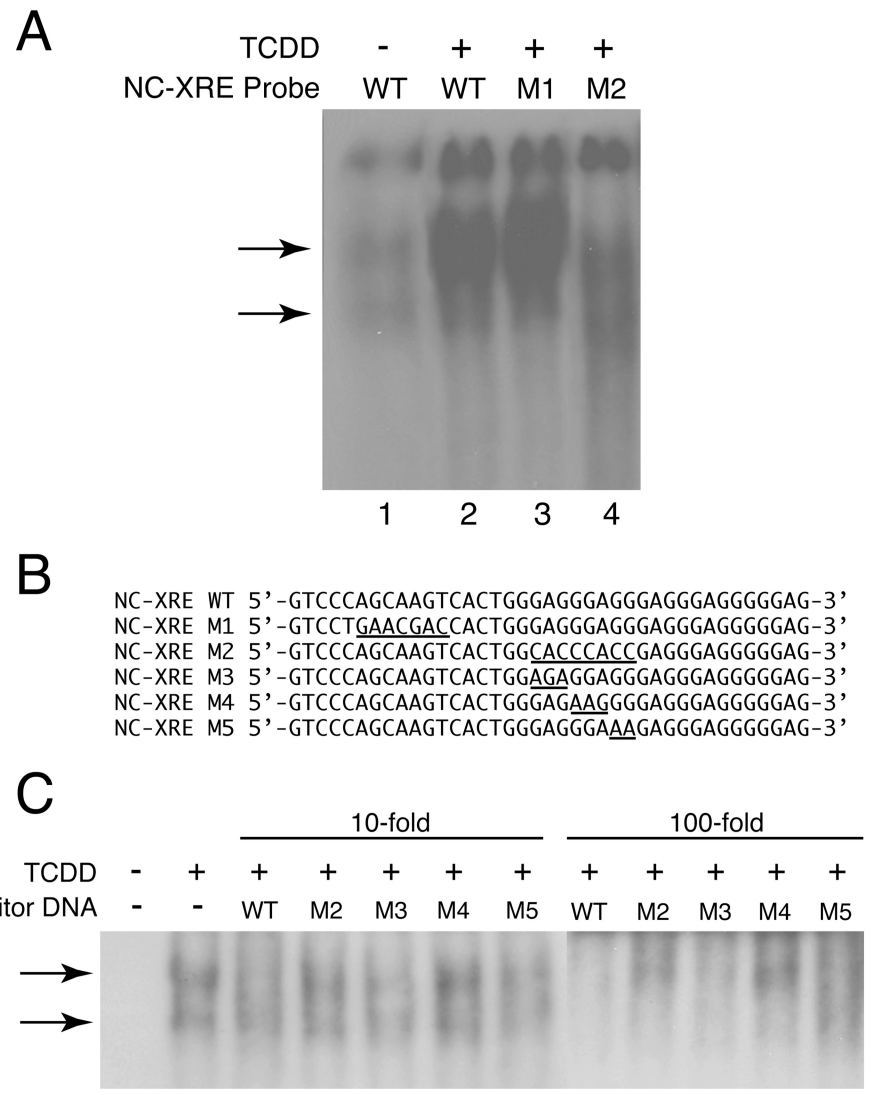


Fig. 6. Characterization of the NC-XRE binding site. A, whole liver nuclear extracts were prepared from vehicle-treated mice (i.e., peanut oil administered by gavage, -TCDD) or mice treated with 20 μg/kg TCDD for 2h (+TCDD). EMSA using the nuclear extracts was performed with ^{32}P-labeled NC-XRE (WT) and two mutant oligonucleotide probes (M1 and M2) depicted in B. B, depicts the sequences of the wild-type and mutant NC-XRE oligonucleotides used in the EMSA analysis. C, competition EMSA was performed using the ^{32}P-labeled NC-XRE (WT) with the indicated unlabeled competitor oligonucleotides (at a 10- and 100-fold molar excess) and nuclear extracts from vehicle-treated (−TCDD) and TCDD-treated (+TCDD) mice. Arrows denote the position of the TCDD-inducible complexes.

siently transfected with a control luciferase reporter construct (pGL3) or the construct containing the 116-bp PAI-1 promoter (pPAI-1/116Luc) and induced with TCDD for 24 h (Fig. 10). As anticipated, partial knock-down of Arnt protein expression caused a marked (>2-fold) attenuation in TCDD induction of the endogenous *Cyp1a1* gene (Fig. 10A). However, TCDD-inducible luciferase activity driven by the PAI-1 promoter is unaltered despite the marked decrease in Arnt protein expression. These results complement those ChIP data (Fig. 8) and strongly imply that AhR-mediated PAI-1 induction through the NC-XRE is indeed Arnt protein-independent.

Discussion

PAI-1 is almost ubiquitously expressed with the highest levels found in endothelial cells, adipocytes and hepatocytes. PAI-1 is a member of the serpin (serine protease inhibitor) family responsible for suppressing the activity of the urokinase-type and tissue-type plasminogen activators that in turn, convert plasminogen to plasmin. Plasmin possesses broad substrate specificity, including extracellular matrix proteins, blood clot fibrin, growth factor precursors, and other proteases (Durand et al., 2004) involved in processes important for angiogenesis, wound healing, tumor metastasis, and liver regeneration (Michalopoulos and DeFrances, 1997; Irigoyen et al., 1999). Hence, plasmin formation and action are highly dependent on PAI-1 levels. In particular, PAI-1 inhibits liver regeneration by forming a complex with the urokinase-type plasminogen activator, thus preventing the activation of hepatocyte growth factor, a key protein in the regenerative process. Because our previous studies showed that TCDD could arrest liver regeneration (Mitchell et al., 2006), it is conceivable that PAI-1 is involved in the TCDD-induced liver growth arrest. As a prelude to this hypothesis, we sought to further investigate the finding that PAI-1 is a TCDD-responsive gene (Puga et al., 2000a; Frueh et al., 2001; Boverhof et al., 2005; Tijet et al., 2006; Fig. 1), particularly because the promoter lacks a definable XRE (Son and Rozman, 2002).

Extending upon earlier reported findings (Son and Rozman, 2002), the evidence presented here confirm that the AhR can induce PAI-1 expression through a nonconsensus XRE (NC-XRE) devoid of sequence homology with the well characterized XRE known to regulate CYP1A1 expression (Figs. 5 and 6). The studies further show that AhR activity inducing PAI-1 expression is a direct response that is not reliant on nascent protein

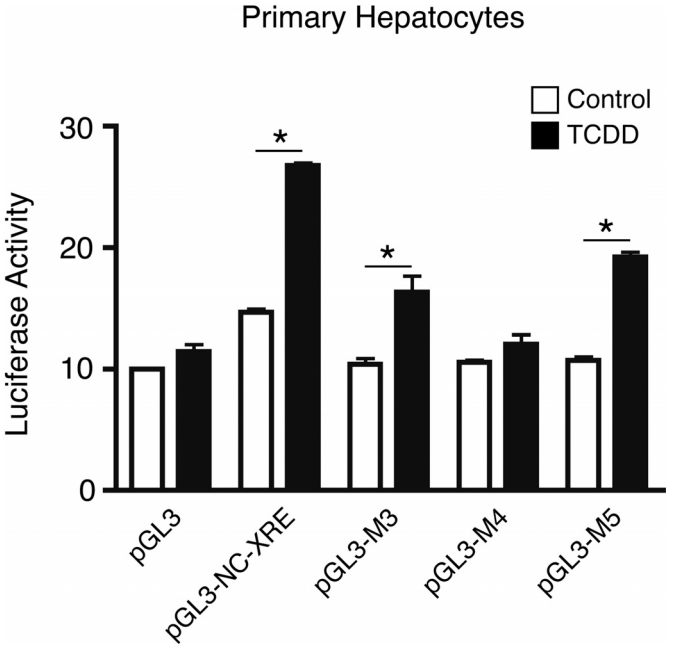


Fig. 7. Functional analysis of the mutant NC-XRE binding sites. A, mouse primary hepatocytes were cotransfected with pRL-SV40 and reporter constructs lacking a NC-XRE (pGL3) or containing a single copy of the wild-type NC-XRE (pGL3-NC-XRE) or the mutant NC-XREs identified in Fig. 6B (pGL3-M3, M4 and M5). Cells were cultured in the presence of vehicle (Control) or 6 nM TCDD for 24 h before assaying for luciferase expression (firefly and *R. reniformis*). The data are expressed as means ± S.E.M of three independent experiments. *, $p < 0.001$, significant difference compared with the control.

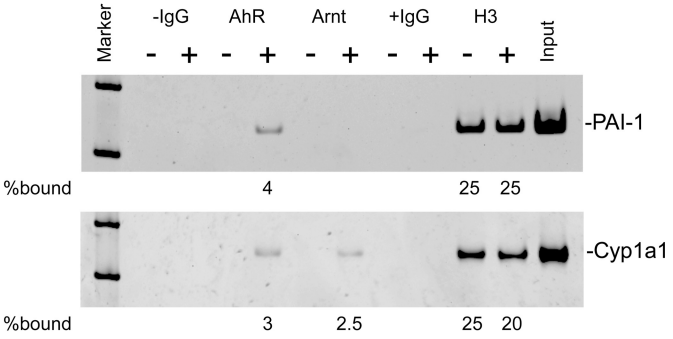


Fig. 8. TCDD-dependent AhR binding to the PAI-1 promoter is Arnt protein-independent. ChIP analysis of AhR and Arnt protein binding to the PAI-1 promoter region or Cyp1a1 enhancer in liver tissue from mice treated with vehicle (−) or 20 μg/kg TCDD (+) for 2 h. IgG and histone H3 antibodies were used as negative and positive controls, respectively. PCR products were fractionated by 6% PAGE and stained with SYBR Green, and quantitation was presented as a percentage of the input DNA. The data shown are representative of three independent experiments.

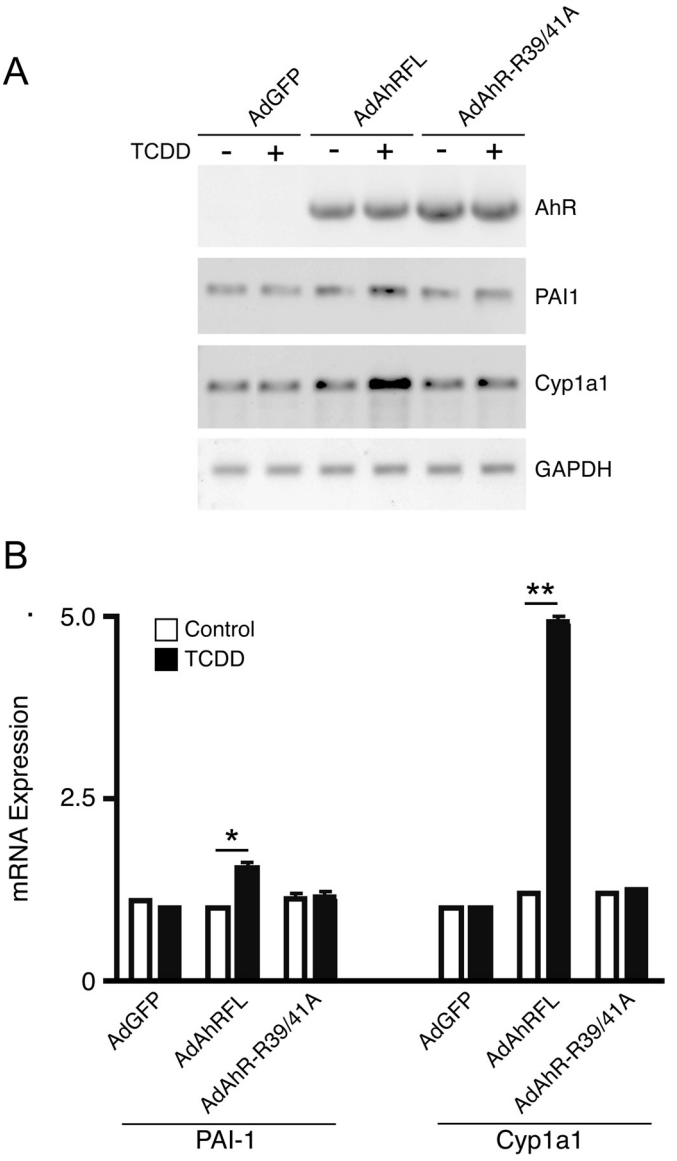


Fig. 9. PAI-1 induction requires direct DNA binding by the AhR. A, primary hepatocytes were isolated from $Ahr^{fx/fx}Cre^{Alb}$ CKO mice and infected with a control adenovirus (AdGFP), a virus expressing a wild-type AhR (AdAhRFL), or a virus expressing the DNA binding defective mutant receptor (AdAhR-R39/41A) at a MOI of 100. After 24 h in culture, the hepatocytes were treated with vehicle (−) or 6 nM TCDD (+) for 8 h and AhR, PAI-1, Cyp1a1, and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA levels measured by RT-PCR. B, primary hepatocytes were prepared as described above, and PAI-1 and Cyp1a1 mRNA were measured by qRT-PCR. The data are expressed as means ± S.E.M of three independent experiments. *, $p < 0.05$; **, $p < 0.001$.

synthesis (Fig. 4), requires direct DNA binding to the NC-XRE (Fig. 9), but is independent of the Arnt protein (Figs. 8 and 10). It is noteworthy that Son and Rozman (2002) assigned a role for the Arnt protein in TCDD-induced PAI-1 induction, based on the observation that induction was not detected in Arnt-defective Hepa 1 mutant cells. Because the cell line was isolated for its resistance to benzo[*a*]pyrene toxicity after exposure to this potent genotoxin (Miller et al., 1983), it is conceivable that among the numerous uncharacterized genetic lesions existing within this cell line, are mutations affecting AhR-mediated PAI-1 induction unrelated to Arnt protein function. In this regard, several features argue against a role for the Arnt protein: 1) the PAI-1 promoter region conferring TCDD responsiveness lacks a canonical XRE capable of binding the AhR/Arnt protein heterodimer, 2) the ChIP assay fails to detect an Arnt protein association with the PAI-1 promoter even though Arnt protein binding to the Cyp1a1 promoter is readily observed (Fig. 8), and 3) the PAI-1 promoter retains TCDD responsiveness when Arnt protein expression—and concomitant P4501A1 protein induction—is suppressed by RNA interference (Fig. 10). The implication for AhR binding to the NC-XRE independently of the Arnt protein imputes a role for a new binding AhR DNA binding partner. Indeed, the AhR is known to interact with other transcription factors, including the retinoblastoma tumor suppressor protein (Ge and Elferink, 1998), E2F1 (Marlowe et

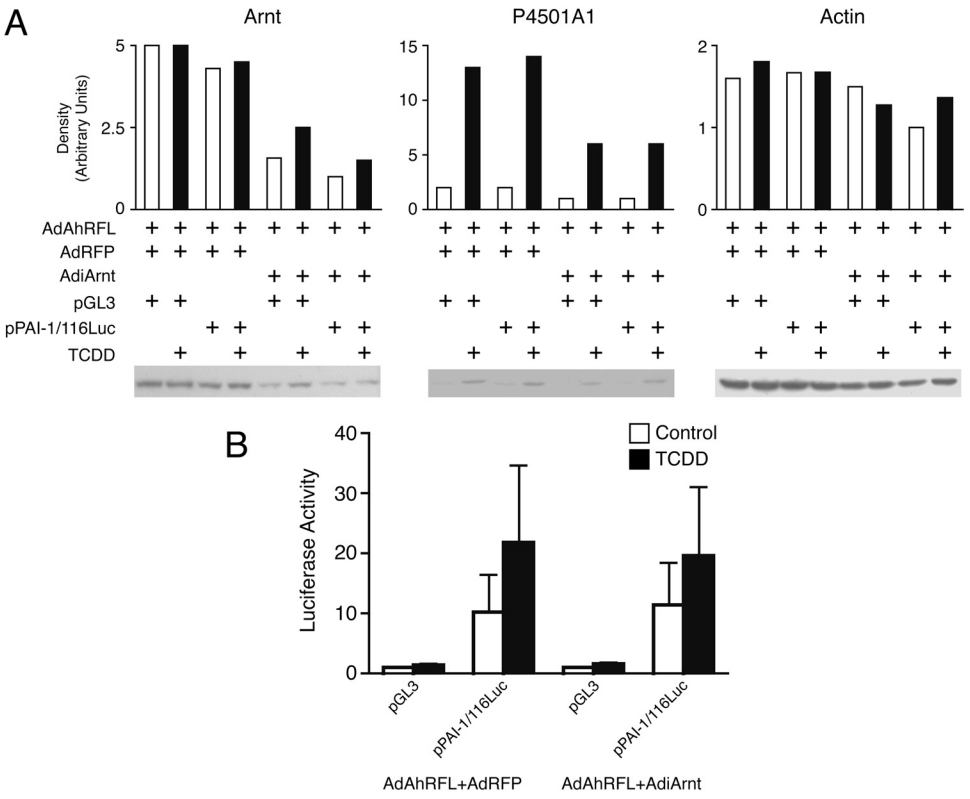


Fig. 10. The Arnt protein is not required for AhR- mediated PAI-1 expression. A, asynchronous subconfluent BP8 (AhR-negative) cultures were infected with AdAhRFL at an MOI of 100 for 24 h before subsequent reinfection with AdRFP or AdiArnt (coexpressing RFP, Huang and Elferink, 2005) at an MOI of 100 for an additional 24 h. Cells were then transiently transfected with pRL-SV40 and pGL3 or pPAI-1/116Luc for 24 h before treatment with dimethyl sulfoxide or 6 nM TCDD (+) for a further 24 h. Total cell lysates were probed for Arnt protein, P4501A1, and Actin by Western blotting, and the band densities were quantified. The data shown are from a single experiment. B, cells treated as described above were assayed for dual luciferase activity and the data expressed as means ± S.E.M of two independent experiments.

al., 2004), and RelB (Vogel et al., 2007). The latter example is noteworthy because the AhR/RelB complex seems to bind DNA directly, although this interaction was not specifically assessed. Moreover, the RelB/AhR response element nucleotide sequence differs markedly from the NC-XRE, suggesting that AhR binding to the NC-XRE depends on an as-yet-unidentified protein partner. Interrogation of the TRANSFAC database however, did not identify the NC-XRE as a known DNA binding site classified by a defined protein-DNA interaction.

Consistent with the previously observations (Son and Rozman, 2002), TCDD induction of both endogenous *PAI-1* gene expression and luciferase reporter expression in the various cultured cell systems is a modest 2- to 3-fold. In contrast, PAI-1 induction in vivo revealed a 40-fold increase in gene expression (Fig. 1B), suggesting that under physiological conditions, AhR regulation of the *PAI-1* gene is indeed robust. This may reflect interplay between multiple transcription factors whose signals are preserved only under in vivo conditions. Of course, gene regulation seldom involves a single transcription factor. Given the involvement of PAI-1 in diverse biological roles, its expression is controlled by several different signals, including hormones, cytokines, and both environmental and mechanical stresses. Underpinning the various signaling pathways are several transcription factors that interact with the PAI-1 regulatory region spanning several kilobases upstream of the transcription start site; these include the following:

- specificity protein 1 (−73 and −42; Chen et al., 1998),
- activator protein 1 (−60 and −52; Al-Nedawi et al., 2004; Vulin and Stanley, 2004),
- serum-induced expression element (−165; White et al., 2000),
- p53 (−136; Parra et al., 2001),
- activator protein 1-like sequence (−62; Guo et al., 2005),
- hepatocyte growth factor-responsive element (−158; Imagawa et al., 2006),
- β-catenin (−425; He et al., 2010),
- E26-like transcription factor 1 (Elk-1) (−42; Wyrzykowska et al., 2010),
- hypoxia-inducible factor-1 (−195 and −3633; Liu et al., 2004; Ahn et al., 2010), and the
- PAS proteins circadian locomotor output cycles kaput (CLOCK) and brain and muscle Arnt-like (BMAL) (−684 and −565, respectively; Maemura et al., 2000; Schoenhard et al., 2003).

Therefore, the significance of AhR mediated PAI-1 regulation will most likely be context dependent, reflecting the integration of multiple signaling pathways to either enhance or stifle AhR action.

What becomes evident from this and other studies is that AhR-mediated transcriptional regulation is more diverse than the repertoire of target genes responding to the AhR/Arnt protein heterodimer. The effect of AhR activity governing gene expression through multiple DNA *cis* elements (e.g., XRE, NC-XRE, RelBAhRE) on TCDD toxicity and normal physiological processes still needs to be resolved. Nukaya et al. (2010) demonstrated, using a conditional knockout Arnt protein mouse line, that loss of Arnt protein expression in hepatocytes prevented the occurrence of several well established toxic endpoints in the liver after TCDD exposure. These findings elegantly show that certain TCDD-induced hepatotoxicities are directly attributable to AhR/Arnt protein activity. Nevertheless, a genomewide analysis of AhR DNA binding target genes (Sartor et al., 2009) revealed that among the hundreds of AhR target genes identified by the ChIP-chip analysis, many did not contain canonical XRE sequences in the region flanking the transcription start site.

Consequently, there is good cause to speculate that non-XRE mediated Arnt-independent transcriptional responses also contribute to adaptive and toxic AhR-regulated responses. The PAI-1 NC-XRE may constitute an important alternative binding site for receptor action and further characterization of the binding partner(s) is a priority for future study.

Authorship Contributions

Participated in research design: Huang and Elferink.
Conducted experiments: Huang.
Contributed new reagents or analytic tools: Huang and Elferink.
Performed data analysis: Huang and Elferink.
Wrote or contributed to the writing of the manuscript: Huang and Elferink.

References

Ahn YT, Chua MS, Whitlock JP Jr, Shin YC, Song WH, Kim Y, Eom CY, and An WG (2010) Rodent-specific hypoxia response elements enhance PAI-1 expression through HIF-1 or HIF-2 in mouse hepatoma cells. *Int J Oncol* **37:**1627–1638.

Al-Nedawi KN, Czyz M, Bednarek R, Szemraj J, Swiatkowska M, Cierniewska-Cieslak A, Wyczolkowska J, and Cierniewski CS (2004) Thymosin beta 4 induces the synthesis of plasminogen activator inhibitor 1 in cultured endothelial cells and increases its extracellular expression. *Blood* **103:**1319–1324.

Boverhof DR, Burgoon LD, Tashiro C, Chittim B, Harkema JR, Jump DB, and Zacharewski TR (2005) Temporal and dose-dependent hepatic gene expression patterns in mice provide new insights into TCDD-mediated hepatotoxicity. *Toxicol Sci* **85:**1048–1063.

Chen YQ, Su M, Walia RR, Hao Q, Covington JW, and Vaughan DE (1998) Sp1 sites mediate activation of the plasminogen activator inhibitor-1 promoter by glucose in vascular smooth muscle cells. *J Biol Chem* **273:**8225–8231.

Durand MK, Bødker JS, Christensen A, Dupont DM, Hansen M, Jensen JK, Kjelgaard S, Mathiasen L, Pedersen KE, Skeldal S, et al. (2004) Plasminogen activator inhibitor-I and tumour growth, invasion, and metastasis. *Thromb Haemost* **91:**438–449.

Elferink CJ, Ge NL, and Levine A (2001) Maximal aryl hydrocarbon receptor activity depends on an interaction with the retinoblastoma protein. *Mol Pharmacol* **59:**664–673.

Frueh FW, Hayashibara KC, Brown PO, and Whitlock JP Jr (2001) Use of cDNA microarrays to analyze dioxin-induced changes in human liver gene expression. *Toxicol Lett* **122:**189–203.

Ge NL and Elferink CJ (1998) A direct interaction between the aryl hydrocarbon receptor and retinoblastoma protein. Linking dioxin signaling to the cell cycle. *J Biol Chem* **273:**22708–22713.

Gu YZ, Hogenesch JB, and Bradfield CA (2000) The PAS superfamily: sensors of environmental and developmental signals. *Annu Rev Pharmacol Toxicol* **40:**519–561.

Guo B, Inoki K, Isono M, Mori H, Kanasaki K, Sugimoto T, Akiba S, Sato T, Yang B, Kikkawa R, et al. (2005) MAPK/AP-1-dependent regulation of PAI-1 gene expression by TGF-beta in rat mesangial cells. *Kidney Int* **68:**972–984.

He W, Tan R, Dai C, Li Y, Wang D, Hao S, Kahn M, and Liu Y (2010) Plasminogen activator inhibitor-1 is a transcriptional target of the canonical pathway of Wnt/beta-catenin signaling. *J Biol Chem* **285:**24665–24675.

Huang G and Elferink CJ (2005) Multiple mechanisms are involved in Ah receptor-mediated cell cycle arrest. *Mol Pharmacol* **67:**88–96.

Imagawa S, Fujii S, Dong J, Furumoto T, Kaneko T, Zaman T, Satoh Y, Tsutsui H, and Sobel BE (2006) Hepatocyte growth factor regulates E box-dependent plasminogen activator inhibitor type 1 gene expression in HepG2 liver cells. *Arterioscler Thromb Vasc Biol* **26:**2407–2413.

Irigoyen JP, Muñoz-Cánoves P, Montero L, Koziczak M, and Nagamine Y (1999) The plasminogen activator system: biology and regulation. *Cell Mol Life Sci* **56:**104–132.

Laird PW, Zijderveld A, Linders K, Rudnicki MA, Jaenisch R, and Berns A (1991) Simplified mammalian DNA isolation procedure. *Nucleic Acids Res* **19:**4293.

Lees MJ and Whitelaw ML (1999) Multiple roles of ligand in transforming the dioxin receptor to an active basic helix-loop-helix/PAS transcription factor complex with the nuclear protein Arnt. *Mol Cell Biol* **19:**5811–5822.

Levine-Fridman A, Chen L, and Elferink CJ (2004) Cytochrome P4501A1 promotes G1 phase cell cycle progression by controlling aryl hydrocarbon receptor activity. *Mol Pharmacol* **65:**461–469.

Liu Q, Möller U, Flügel D, and Kietzmann T (2004) Induction of plasminogen activator inhibitor I gene expression by intracellular calcium via hypoxia-inducible factor-1. *Blood* **104:**3993–4001.

Maemura K, de la Monte SM, Chin MT, Layne MD, Hsieh CM, Yet SF, Perrella MA, and Lee ME (2000) CLIF, a novel cycle-like factor, regulates the circadian oscillation of plasminogen activator inhibitor-1 gene expression. *J Biol Chem* **275:**36847–36851.

Marlowe JL, Knudsen ES, Schwemberger S, and Puga A (2004) The aryl hydrocarbon receptor displaces p300 from E2F-dependent promoters and represses S phase-specific gene expression. *J Biol Chem* **279:**29013–29022.

Michalopoulos GK and DeFrances MC (1997) Liver regeneration. *Science* **276:**60–66.

Miller AG, Israel D, and Whitlock JP Jr (1983) Biochemical and genetic analysis of variant mouse hepatoma cells defective in the induction of benzo(a)pyrene-metabolizing enzyme activity. *J Biol Chem* **258:**3523–3527.

Mitchell KA, Lockhart CA, Huang G, and Elferink CJ (2006) Sustained aryl hydrocarbon receptor activity attenuates liver regeneration. *Mol Pharmacol* **70:**163–170.

Nguyen TT, Cho K, Stratton SA, and Barton MC (2005) Transcription factor interactions and chromatin modifications associated with p53-mediated, developmental repression of the alpha-fetoprotein gene. *Mol Cell Biol* **25:**2147–2157.

Nukaya M, Walisser JA, Moran SM, Kennedy GD, and Bradfield CA (2010) Aryl hydrocarbon receptor nuclear translocator in hepatocytes is required for aryl hydrocarbon receptor-mediated adaptive and toxic responses in liver. *Toxicol Sci* **118:**554–563.

Ohtake F, Takeyama K, Matsumoto T, Kitagawa H, Yamamoto Y, Nohara K, Tohyama C, Krust A, Mimura J, Chambon P, et al. (2003) Modulation of oestrogen receptor signalling by association with the activated dioxin receptor. *Nature* **423:**545–550.

Park KT, Mitchell KA, Huang G, and Elferink CJ.-T., Mitchell K, Huang G, and Elferink CJ (2005) The aryl hydrocarbon receptor predisposes hepatocytes to Fas-mediated apoptosis. *Mol Pharmacol* **67:**612–622.

Parra M, Jardí M, Koziczak M, Nagamine Y, and Muñoz-Cánoves P (2001) p53 phosphorylation at serine 15 is required for transcriptional induction of the plasminogen activator inhibitor-1 (PAI-1) gene by the alkylating agent N-methyl-N′-nitro-N-nitrosoguanidine. *J Biol Chem* **276:**36303–36310.

Poland A and Knutson JC (1982) 2,3,7,8-tetrachlorodibenzo-p-dioxin and related halogenated aromatic hydrocarbons: examination of the mechanism of toxicity. *Annu Rev Pharmacol Toxicol* **22:**517–554.

Puga A, Maier A, and Medvedovic M (2000a) The transcriptional signature of dioxin in human hepatoma HepG2 cells. *Biochem Pharmacol* **60:**1129–1142.

Puga A, Barnes SJ, Dalton TP, Chang C, Knudsen ES, and Maier MA (2000b) Aromatic hydrocarbon receptor interaction with the retinoblastoma protein potentiates repression of E2F-dependent transcription and cell cycle arrest. *J Biol Chem* **275:**2943–2950.

Sartor MA, Schnekenburger M, Marlowe JL, Reichard JF, Wang Y, Fan Y, Ma C, Karyala S, Halbleib D, Liu X, et al. (2009) Genomewide analysis of aryl hydrocarbon receptor binding targets reveals an extensive array of gene clusters that control morphogenetic and developmental programs. *Environ Health Perspect* **117:**1139–1146.

Schoenhard JA, Smith LH, Painter CA, Eren M, Johnson CH, and Vaughan DE (2003) Regulation of the PAI-1 promoter by circadian clock components: differential activation by BMAL1 and BMAL2. *J Mol Cell Cardiol* **35:**473–481.

Schwartz ML and Schlaepfer WW (1996) Neuronal promoter analysis by in vitro transcription using nuclear extracts from rat brain. *Methods* **10:**320–327.

Shen ES, Elferink CJ, and Whitlock JP Jr (1991) Use of gel retardation to analyze protein-DNA interactions upstream of CYP1A1 gene. *Methods Enzymol* **206:**403–408.

Sogawa K, Numayama-Tsuruta K, Takahashi T, Matsushita N, Miura C, Nikawa J, Gotoh O, Kikuchi Y, and Fujii-Kuriyama Y (2004) A novel induction mechanism of the rat CYP1A2 gene mediated by Ah receptor-Arnt heterodimer. *Biochem Biophys Res Commun* **318:**746–755.

Son DS and Rozman KK (2002) 2,3,7,8-Tetrachlorodibenzo-*p*-dioxin (TCDD) induces plasminogen activator inhibitor-1 through an aryl hydrocarbon receptor-mediated pathway in mouse hepatoma cell lines. *Arch Toxicol* **76:**404–413.

Tijet N, Boutros PC, Moffat ID, Okey AB, Tuomisto J, and Pohjanvirta R (2006) Aryl hydrocarbon receptor regulates distinct dioxin-dependent and dioxin-independent gene batteries. *Mol Pharmacol* **69:**140–153.

Vogel CF, Sciullo E, Li W, Wong P, Lazennec G, and Matsumura F (2007) RelB, a new partner of aryl hydrocarbon receptor-mediated transcription. *Mol Endocrinol* **21:**2941–2955.

Vulin AI and Stanley FM (2004) Oxidative stress activates the plasminogen activator inhibitor type 1 (PAI-1) promoter through an AP-1 response element and cooperates with insulin for additive effects on PAI-1 transcription. *J Biol Chem* **279:**25172–25178.

Walisser JA, Glover E, Pande K, Liss AL, and Bradfield CA (2005) Aryl hydrocarbon receptor-dependent liver development and hepatotoxicity are mediated by different cell types. *Proc Natl Acad Sci USA* **102:**17858–17863.

Weiss C, Kolluri SK, Kiefer F, and Göttlicher M (1996) Complementation of Ah receptor deficiency in hepatoma cells: negative feedback regulation and cell cycle control by the Ah receptor. *Exp Cell Res* **226:**154–163.

White LA, Bruzdzinski C, Kutz SM, Gelehrter TD, and Higgins PJ (2000) Growth state-dependent binding of USF-1 to a proximal promoter E box element in the rat plasminogen activator inhibitor type 1 gene. *Exp Cell Res* **260:**127–135.

Wyrzykowska P, Stalińska K, Wawro M, Kochan J, and Kasza A (2010) Epidermal growth factor regulates PAI-1 expression via activation of the transcription factor Elk-1. *Biochim Biophys Acta* **1799:**616–621.

Address correspondence to: Cornelis J. Elferink, Department of Pharmacology and Toxicology, University of Texas Medical Branch, 301 University Boulevard, Galveston, TX 77555-0654. E-mail: coelferi@utmb.edu