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PPARα-independent transcriptional targets of perfluoroalkyl acids revealed by transcript profiling

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Abstract

Perfluoroalkyl acids (PFAAs) are ubiquitous and persistent environmental contaminants. Compounds such as perfluoroocanoic acid (PFOA), perfluorooctane sulfonate (PFOS), perfluorononanoic acid (PFNA), and perfluorohexane sulfonate (PFHxS) are readily found in the tissues of humans and wildlife. While PFOA and PFOS have been the subject of numerous studies since they were first described over a decade ago, less is known about the biological activity of PFHxS and PFNA. Most PFAAs are activators of peroxisome proliferator-activated receptor a (PPARa), although the biological effects of these compounds are likely mediated by other factors in addition to PPARa. To evaluate the effects of PFHxS and PFNA, male wild-type and PPARanull mice were dosed by oral gavage with PFHxS (3 or 10 mg/kg/day), PFNA (1 or 3 mg/kg/day), or vehicle for 7 days, and liver gene expression was evaluated by full-genome microarrays. Gene expression patterns were then compared to historical in-house data for PFOA and PFOS in addition to the experimental hypolipidemic agent, WY-14,643. While WY-14,643 altered most genes in a PPARa-dependent manner, approximately 11-24% of regulated genes in PFAA-treated mice were independent of PPARa. The possibility that PFAAs regulate gene expression through other molecular pathways was evaluated. Using data available through a microarray database, PFAA gene expression profiles were found to exhibit significant similarity to profiles from mouse tissues exposed to agonists of the constitutive activated receptor (CAR), estrogen receptor a (ERa), and PPAR γ . Human PPAR γ and ERa were activated by all four PFAAs in trans-activation assays from the ToxCast screening program. Predictive gene expression biomarkers showed that PFAAs activate CAR in both genotypes and cause feminization of the liver transcriptome through suppression of signal transducer and activator of transcription 5B (STAT5B). These results

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Author contributions:

MBR, JR and JCC analyzed the microarray data. KPD performed animal experiments

MBR, CL, and JCC conceived of the study, participated in study design MBR and JCC helped draft manuscript. All authors read and approved the final manuscript.

indicate that, in addition to activating PPARa as a primary target, PFAAs also have the potential to activate CAR, PPAR γ , and ERa as well as suppress STAT5B.

Keywords

perfluoroalkyl acid; transcript profiling; liver; ToxCast; peroxisome proliferator-activated receptor α ; estrogen receptor alpha; constitutive activated receptor; peroxisome proliferator; activated receptor γ ; STAT5B

1. Introduction

Perfluoroalkyl acids (PFAAs) are stable man-made chemicals that have been used for over 50 years in the manufacture of a wide range of industrial and consumer products. Health concerns related to this class of chemicals have been raised because widespread environmental distribution (Yamashita et al., 2005; Ellis et al., 2004; Wei et al., 2007; Boulanger et al., 2005) and bioaccumulation (reviewed by Houde et al., 2006) have been demonstrated. Contributing to these concerns are the long elimination half-lives in humans for certain PFAAs which can be in the order of years (Olsen et al., 2007). While perfluorooctanoic acid (PFOA) and perfluorooctane sulfonate (PFOS), the two most prevalent PFAAs in the environment, have attracted the greatest attention, additional PFAAs are known to contribute to the chemical body burden in humans. Data for 12 perfluorinated compounds, for example, were included in the most recent exposure report from the National Health and Nutrition Examination Survey (National Center for Health Statistics, 2014). This group included perfluorononanoic acid (PFNA) and perfluorohexane sulfonate (PFHxS), both of which have been measured in human sera at concentrations that are approximately 33–50% of that reported for PFOA (Kato et al., 2011). While serum levels of PFOS, and possibly PFOA, have begun to decline in the general population due to cessation of production by US manufacturers, levels of PFNA and PFHxS appear to be increasing (Kato et al., 2011; Olsen et al., 2011).

A number of PFAAs activate peroxisome proliferator-activated receptor α (PPARα) (Maloney and Waxman, 1999; Wolf et al., 2008a; Wolf et al., 2012). Like other PPARα activators, PFAAs induce liver tumors in rodents (Gonzalez and Shah, 2008). A comprehensive review concluded that the liver tumors that occur by this MOA are either not relevant or not likely to be relevant to humans (Corton et al., 2014). In addition to liver tumor formation, immune system modulation associated with exposure to PFOA and PFOS (reviewed by Dewitt et al., 2009) or PFNA (Rockwell et al., 2013) has been reported in animal studies. Further observations in laboratory animals include changes in mammary development and body composition related to altered endocrine function (reviewed by White et al., 2011), altered brain development (Johansson et al., 2008; Johansson et al., 2009; Onishchenko et al., 2011), and testicular toxicity (Shi et al., 2010) including in vitro effects of PFNA on either rat primary Sertoli cells or mixed testicular cells (Feng et al, 2010; Lindeman et al., 2011). Developmental toxicity has also been reported in rodents for a number of the long chain PFAAs (reviewed by Lau et al., 2007). PFNA was found to delay development and reduce neonatal survival in 129S1/SvlmJ mice based on a PPARa-

dependent mode of action (Wolf et al., 2010), and this has also been shown in the CD-1 mouse (Das et al., 2015). Long term effects on blood pressure have been demonstrated in rats exposed to PFNA or PFOS during pregnancy as well (Rogers et al., 2014). PFHxS, on the other hand, has not been shown to be a reproductive or developmental toxicant in the rat (Butenhoff et al., 2009), although the number of laboratory studies conducted using PFHxS has been limited presumably due to compound availability.

The biological activity of PFAAs is not limited to activation of PPARa. There is evidence of PPARa-independent transcript regulation in mammals including activation of the constitutive androstane receptor (CAR) (Rosen et al., 2008a,b; Cheng and Klaassen 2008; Ren et al., 2009). Activation of estrogen receptor a (ERa) by various PFAAs has also been demonstrated in rainbow trout (Tilton et al., 2008; Benninghoff et al., 2011; Benninghoff et al., 2012) and was recently suggested in PFOA-exposed human primary hepatocytes (Buhrke et al, 2015). Bjork et al. (2011) utilized cultured primary rat and human hepatocytes and found that exposure to moderately high concentrations of either PFOA or PFOS could increase the expression of specific marker genes for not only PPARa, but CAR, pregnane X receptor (PXR), and liver X receptor (LXR). These investigators suggested that triggering these additional signaling pathways may be secondary to the metabolic remodeling which was initiated by activation of PPARa. Using a proteomic approach, Scharmach et al. (2012) was able to show that PFOA is an inhibitor of the HNF4a pathway in HepG2 cells. This same group came to a similar conclusion based on transcript analysis of human primary hepatocytes (Buhrke et al., 2015). A more recent study showed that human hepatocytes treated with PFOA or PFOS at a concentration relevant to occupational exposure caused a decrease in HNF4a protein without affecting HNF4a mRNA or causing cell death (Beggs et al., 2016). One of the more intriguing observations in treated *Ppara*-null mice is dysregulation of genes associated with fatty acid metabolism (Rosen et al., 2008a,b; Rosen et al., 2010). While such a result is generally associated with transactivation of PPARa, it is not clear why this outcome could occur in the absence of a functional PPARa. In the past, our group has speculated that activation of PPAR γ or PPAR β could be involved (Rosen et al., 2008). Indeed, based on gene array data, Buhrke et al. (2015) suggested that PPAR γ was activated in human primary hepatocytes exposed to PFOA. Teasing apart the effects of the various PPAR subtypes based on gene expression data, however, is difficult given the potential overlap in target genes among these nuclear receptors. Cell-based reporter assays have not provided convincing support for the role of PPAR γ or PPAR β . Vanden Heuvel et al. (2006) and Taxvig et al. (2012) found only modest activation of PPAR γ by either PFOA or PFOS, while other publications have generally been negative (Maloney and Waxman, 1999). Takacs and Abbott (2007) did observe significant activation of murine PPARβ by either PFOA or PFOS but neither compound was found to activate mouse or human PPAR γ .

Here, we examine the transcript profiles of PFNA and PFHxS in the livers of both wild-type and *Ppara*-null mice. The goal of this study was to evaluate these PFAAs within the context of historical data generated by our group for PFOA and PFOS. The Nextbio database (Illumina, San Diego, CA) was utilized to allow for comparisons to microarray datasets associated with activation or inhibition of various nuclear receptors. ToxCast data (http://actor.epa.gov/dashboard/) was utilized as well. Emphasis was placed on identifying those effects that were independent of PPARa.

2. Materials and Methods

2.1. Animals and dosing

In-house studies were approved by the U.S. EPA ORD/NHEERL Institutional Animal Care and Use Committee. The facilities and procedures used followed the recommendations of the 1996 NRC "Guide for the Care and Use of Laboratory Animals", the Animal Welfare Act, and the Public Health Service Policy on the Humane Care and Use of Laboratory Animals. Ppara-null mice (129S4/SvJae-Pparatm1Gonz/J, stock #003580) and wild-type mice (129S1/SvlmJ, stock #002448) were purchased from The Jackson Laboratory (Bar Harbor, ME) and maintained as an inbred colony on the 129/Sv background at the U.S. EPA, Research Triangle Park, NC. Animals were housed 4 per cage and allowed to acclimate for a period of one week prior to the conduct of the study. Commercial lab chow and municipal tap water were provided ad libitum. Animal facilities were controlled for temperature (20-24°C), relative humidity (40–60%), and kept under a 12 hr light-dark cycle. *Ppara*-null and wild-type male mice at 6-9 months of age were dosed by gavage for 7 consecutive days with either 0, 3, or 10 mg/kg PFHxS or 0, 1, or 3 mg/kg PFNA (#394459, Sigma-Aldrich, St, Louis, MO) in water. PFHxS (CAS # 355-46-4) was kindly provided by 3M Corp (St. Paul, MN). Dosing was based on previous work from our laboratory (PFNA, Das et al., 2015; PFHxS, based on a related chemical, PFOS, Rosen et al., 2010). All dose levels reflected exposures that produce hepatomegaly in wild-type adult mice without inducing overt toxicity. Four biological replicates consisting of individual animals were included in each dose group. Dose levels reflected exposures that produce hepatomegaly in adult mice without inducing overt toxicity. All dosing solutions were freshly prepared each day. At the end of the dosing period, animals were euthanized by CO₂ asphyxiation and tissue was collected from the left lobe of the liver for preparation of total RNA as detailed below.

2.3. RNA preparation

Collected liver from PFNA and PFHxS treated mice (50 mg) was immediately placed in 1 ml RNA*later* (Thermo Fisher/Life Technologies, Grand Island, NY) and stored at -20°C. Total RNA preparations for microarray analysis were then prepared using the *mir*VANA miRNA isolation kit (Thermo Fisher/Life Technologies) according to the manufacturer's protocol without further enrichment for small RNAs. All samples used in the study were quantified by determining the ratio of absorbance at 260 and 280 nm using a NanoDrop ND-1000 spectrophotometer (Thermo Fisher, Waltham, MA). RNA quality was evaluated using a 2100 Bioanalyzer (Agilent, Palo Alto, CA) which calculates the RNA Integrity number. Only samples with an RNA Integrity number 7.5 were included in the study (2100 Expert software, version B.01.03).

2.4. Microarray data collection and analysis

In-house microarray hybridization and scanning was conducted at the U.S. EPA NHEERL Genomics Research Core Facility using Affymetrix 430_2 expression GeneChips according to the protocols recommended by the manufacturer (Manual #701021 rev. 5, Affymetrix, Santa Clara, CA). Sample labeling and microarray hybridization were conducted as a single block to minimize technical variation. In addition to PFHxS and PFNA (archived in Gene

Expression Omnibus as GSE55756), three additional studies were analyzed to allow for examination of similarities and differences across five chemicals:

- 1. PFOA administered by gavage (3 mg/kg) for 7 days (GSE9786) (Rosen et al., 2008b).
- 2. PFOS administered by gavage (10 mg/kg) for 7 days (GSE22871) (Rosen et al., 2010).
- **3.** WY-14,643 (0.1% w/w) mixed in the food and fed for 5 days (GSE8295) (Rakhshandehroo et al., 2007).

All studies were conducted using similar background genotypes of male mice. All but the WY study was conducted in the Lau lab. The microarray platform for all studies consisted of the Affymetrix mouse 430_2 chip. All Affymetrix .cel files were processed using the standard procedures described in Kuperschmidt et al. (2010). Robust multichip average was used to normalize the data. To address the potential unreliability of the fold-change metric at low intensity levels, genes with signals lower than a 20th percentile cutoff in both control and test groups were discarded. A Welch's paired t-test was used to identify significantly altered genes with a p-value significance cutoff of 0.05 and a minimum absolute fold-change cutoff of 1.2. For comparisons of the gene lists to each other and for analysis in Ingenuity Pathways Analysis (IPA), the lists were further filtered for those genes with a false discovery rate of p < 0.05 and an absolute fold-change cutoff of 1.5.

2.5. Comparison of PFAA data to a gene expression database.

A rank-based nonparametric analysis strategy called the Running Fisher test implemented within the NextBio database (Illumina, San Diego, CA) was used to compare gene lists derived from PFAA treated mice to other gene lists in the database. This normalized ranking approach enables comparability across data from different studies, platforms, and analysis methods by removing dependence on absolute values of fold-change, and minimizing some of the effects of normalization methods used, while accounting for the level of genome coverage by the different platforms. The Running Fisher algorithm computes statistical significance of similarity between ranked fold-change values of two gene lists using a Fisher's exact test (Kupershmidt et al., 2010). A p-value 1E-4 was selected as our cutoff for significance based on prior evaluation of the cutoff as predictive of activation of a number of transcription factors (Oshida et al., 2015a,b,c; Oshida et al., 2016a,b; Ryan et al., 2016). The PFAA gene lists were compared to gene lists from a number of studies that were analyzed in NextBio:

- Livers of wild-type or CAR-null mice exposed to 100 mg/kg phenobarbital for three days (GSE40120).
- Livers from ovariectomized wild-type and ERa-null mice exposed to the ERa non-steroidal agonist PPT (4,4',4''-(4-Propyl-[1H]-pyrazole-1,3,5-triyl)trisphenol) for 3 days (Pedram et al., 2013) (GSE45346).
- Livers from Lepr (db/db) mice fed for 18d 280umol/kg/d the PPARγ agonist rosiglitazone (Le Bouter et al., 2010) (GSE19896).

- Mouse 3T3-L1 adipocytes exposed to four PPARγ full agonists (COOH, rosiglitazone, Full agonist2, Full agonist4) or an LXR agonist ("LXR agonist 1") for 24 hours at 10uM (Tan et al., 2012) (GSE31222).
- Mouse 3T3-L1 adipocytes were treated with a control siRNA or a siRNA targeting the *Pparg* gene (Schupp et al., 2009) (GSE14004)

2.6. Additional data analysis.

Liver weight was analyzed by genotype using one-way ANOVA followed by Tukey-Kramer honest significant difference (HSD) test to compare individual means (SAS JMP, ver.7.0). Significant probe sets were further evaluated for relevance to biological pathway and function using Ingenuity Pathway Analysis software (https://analysis.ingenuity.com). Hierarchical clustering and heat maps were generated using Eisen Lab Cluster and Treeview software (http://bonsai.hgc.jp/~mdehoon/software/cluster/software.htm). ToxCast data came from a Dashboard download (Dashboard_Export_08_31_15) from the ToxCast data website (http://actor.epa.gov/dashboard/) and filtered for data derived from exposures to the four PFAAs. The ability of the PFAAs to activate PPAR subtypes and ERa were evaluated using the trans-activation assays from Attagene, Inc. (Durham, NC) in which the ligand binding domains of each nuclear receptor were linked to the GAL4 DNA binding domain. The chemicals were also examined for ability to activate an estrogen responsive element (ERE) linked to a reporter gene. The ToxCast analysis pipeline fits dose response curves to data generated in over 700 in vitro high throughput screening assays (Judson et al 2010, Kavlock et al 2012). Constant, hill, and gain-loss models are fit to the data, and the best fitting model as determined by Akaike information criterion (AIC) is used to make hit calls and generate modeled AC50 values, hill slopes and maximal activities of predicted active chemicals. Baseline values for each assay are determined from DMSO (negative) controls, and a fold induction increase in signal cutoff (usually 3X the baseline median absolute deviation) is used to determine hit calls. Details of the analysis pipeline ("ToxCast Data Pipeline Overview") are available on the ToxCast website at: http://www2.epa.gov/chemicalresearch/toxicity-forecaster-toxcasttm-data (accessed October 13, 2016).

3. Results

3.1. PFAA induction of hepatomegaly

Mice were treated for one week with daily gavage exposures of PFNA (1 and 3 mg/kg), PFHxS (3 and 10 mg/kg), or control vehicle. The effects of treatment on body and liver weights are shown in Tables 1 and 2. No change in body weight was observed with either compound. Increased relative liver weight was apparent in wild-type mice at both doses of PFNA or PFHxS, although the effect of PFHxS at the low dose was modest. In *Ppara*-null mice, liver weight increase was limited to the highest dose of either compound.

3.2. PFAA-regulated gene expression is dominated by PPARa-dependent effects

Changes in gene expression induced by PFHxS and PFNA were examined by microarray analysis. In order to facilitate the identification of factors which alter gene expression by other PFAAs, changes induced by PFOA and PFOS were examined using data that were

previously collected by our lab under similar experimental conditions. In addition, a study in which wild-type and *Ppara*-null mice were treated with the specific PPARa agonist, WY-14,643 (WY) was included to allow PFAA-specific effects to be distinguished from those mediated by a more specific PPARa activator. Fig. 1A shows the number of genes that exhibited significant increased or decreased expression in each of the treatment groups (False Discovery Rate 0.05; |fold change| 1.5). Dose-dependent changes in differentially regulated genes were observed for PFHxS and PFNA in both wild-type and *Ppara*-null mice but fewer differentially regulated genes were observed in *Ppara*-null mice. PFOA also altered fewer genes in *Ppara*-null mice compared to wild-type mice. A greater percentage of total genes were altered by PFOS in *Ppara*-null mice compared to the other PFAAs. WY treatment altered the greatest number of genes in wild-type mice but also affected the fewest genes in *Ppara*-null mice. The complete list of genes altered by the treatments and pathway analysis is provided in Supplemental File 1.

Earlier studies showed that PFOA and PFOS regulate the majority of genes in the mouse liver in a *Ppara*-dependent manner (Rosen et al., 2008a; Rosen et al., 2008b; Rosen et al., 2010). To determine if that was also the case for PFHxS and PFNA, gene expression was compared between the genotypes. Genes were divided into groups based on their expression behavior in the two genotypes. Class I genes were defined as completely dependent on PPARa for regulation in wild-type mice (i.e., no regulation in the same direction in Pparanull mice compared to wild-type mice). Class II genes exhibited regulation in the same direction in both genotypes. Class III genes were regulated only in the Ppara-null mice. Genes were rank-ordered by fold-change in each group and summarized as heat maps for each chemical-dose treatment (Fig. 1B). Each chemical-dose pair altered the expression of different proportions of class I-III genes. The lowest dose of PFHxS regulated the smallest proportion of Ppara-dependent genes while WY regulated almost all genes in a Pparadependent manner. In the absence of PPARa, PFAA exposure led to a unique set of gene targets (class III genes). PFHxS and PFOS, the two sulfonated PFAAs, had the greatest proportion of class III genes relative to class II genes when compared to the non-sulfonated PFAAs.

The percentage of PPARa-independent genes regulated specifically in wild-type mice (Class II genes) is summarized in Fig. 1C. This was expressed as the number of class II genes as a percent of the total number of differentially expressed genes in wild-type mice. Both doses of PFHxS altered the greatest percentage of PPARa-independent genes (24% and 22% for 3 and 10 mg/kg, respectively). The other PFAAs exhibited PPARa-independence between 10 and 17%. In contrast, only approximately 2% of WY-regulated genes were PPARa-independent. These results indicate that greater than ~75% of all genes regulated by PFAAs in wild-type mice are PPARa-dependent, and the degree of dependence varies by dose and chemical. Additionally, in the absence of PPARa, each PFAA regulated an additional set of genes unique from those regulated in wild-type mice.

3.3. Common activation of CAR by PFAAs

Earlier studies indicated that CAR is activated by exposure to PFOA and PFOS (Ren et al., 2009; Rosen et al., 2008b, 2010; Oshida et al., 2015b). If that is the case, similarities in the

expression patterns between various PFAAs and the prototypical activator of CAR, phenobarbital, should be apparent. To test this hypothesis, gene lists derived from PFAA-treated mice were compared to lists derived from the livers of wild-type or *CAR*-null mice exposed to 100 mg/kg phenobarbital for three days (Chua and Moore, 2005). A Running Fisher Test was used to provide a similarity statistic for overlapping genes using pairwise comparisons. The same level of significance was used at that in previous studies (|–log(p-value)| 4; Oshida et al., 2015a,b,c). All PFAA treatment groups except the low dose of PFHxS and PFNA in *Ppara*-null mice exhibited significant similarity to wild-type mice treated with phenobarbital (Fig. 2A). In contrast, there was no positive similarity to phenobarbital treatment in *Car*-null mice. WY-treatment in wild-type or *Ppara*-null mice also did not exhibit similarity to phenobarbital treatment, as expected. Significant similarity between PFAA-treatment and a phenobarbital time course of up to 28 days in wild-type mice (Thomson et al., 2013) was also observed (data not shown).

PFAA gene lists were also compared to a previously described gene expression biomarker shown to accurately predict CAR activation (Oshida et al., 2015b). Fig. 2B (top) shows the expression of the 83 CAR biomarker genes after PFAA or WY treatment. Many genes in the biomarker set were regulated by PFAA treatment in a pattern that was similar to that of the CAR biomarker itself. The results of the statistical test are shown in Fig. 2B (bottom). All PFAA groups except low dose PFHxS in wild-type mice exhibited significant similarity to the CAR biomarker set (–log(p-value) 4). PFOA treatment in *Ppara*-null mice exhibited the greatest significance. These results demonstrate that all PFAAs examined activate CAR independently of PPARa and that in most cases except PFHxS, CAR is activated to greater extents in *Ppara*-null mice compared to wild-type mice at at least one dose level.

3.4. Similarities between the PFAA profiles and those altered by estrogen receptor agonists

There is evidence that PFAAs affect the activity of the estrogen receptor (Tilton et al., 2008; Benninghoff et al., 2011; Benninghoff et al., 2012). Assessment of estrogen as well as androgen receptor activity was evaluated using available ToxCast data. All ToxCast assays were evaluated for dose-response trans-activation assays carried out in the human hepatocyte HepG2 cell line showed that all PFAAs, except PFHxS, activate ERa (Table 3, top). ERa activation was also suggested for all compounds based on a cis-activation assay in which activation of an ERE-linked reporter was driven by an exogenously expressed ERa (Table 3, bottom). By contrast, none of the PFAAs were found to activate the androgen receptor (data not shown).

We also compared our PFAA gene expression profiles to those induced by the ERa nonsteroidal agonist PPT (4,4',4''-(4-Propyl-[1*H*]-pyrazole-1,3,5-triyl)*tris*phenol) following a 3 day exposure in ovariectomized wild-type and ERa-null mice (Pedram et al., 2013). Using the Running Fisher Test, most PFAA treatment groups from wild-type mice exhibited significant similarity to the profile induced by PPT in the livers of wild-type mice (Fig. 3A). Based on the data in *Ppara*-null mice, this response was partially or completely dependent upon PPARa for all of the PFAAs except PFHxS and WY (Fig. 3A, **blue bars**). Many of the

comparisons to the PPT-treated ERa-null mice exhibited a negative relationship with the PFAA data.

It is possible that the observed transcript similarity between PPT and the PFAAs may be due to factors that are downstream of ERa activation. Therefore, we also evaluated whether PFAA treatment had an effect on the growth hormone (GH)-regulated transcription factor STAT5B. This transcription factor determines sexually-dimorphic differences in hepatic gene expression in mice (Udy et al., 1997). In previous studies, we characterized a gene expression biomarker that accurately predicts activation or suppression of STAT5B. A group of male-dominant up-regulated genes were identified that positively correlated with activation of STAT5B, whereas, a second group of female-dominant down-regulated genes were associated with disruption of STAT5B (Oshida et al., 2016a,b). Evaluation of this biomarker in PFAA-treated mice indicated decreased expression of the male-specific genes along with increased expression of the female-specific genes (Fig. 3B, upper panel). PFHxS at 3 mg/kg, PFNA at 1 mg/kg, PFOA, and WY were found to regulate this group of genes in a PPARa-dependent manner, while the other PFAAs lost some but not all significance in *Ppara*-null mice (Fig. 3B, lower panel). Taken together, the results indicate that there were changes in the gene expression profiles of PFAA-treated mice indicative of feminization of the liver.

3.5. PFAAs induce fatty acid β -oxidation genes in Ppara-null mice similar to that of PPAR γ agonists

Our analysis above indicated that there are genes similarly regulated by PFAAs in both genotypes of mice (class II genes). Fig. 4 shows one-way hierarchical clustering of 67 common class II genes that exhibited increased expression in at least 11 of the 12 PFAA treatment groups. A number of genes in this group encode for proteins involved in fatty acid β -oxidation including *Acox1*, a gene often used as a marker of PPARa activation. These results indicate that not all genes known to be regulated by PPARa are necessarily suitable indicators of PPARa activation. Also included in this group were genes regulated by CAR (*Cyp2c55, Cyp2b10, Cyp2c65, Gstm3*), which segregated to a different hierarchical clade due to down-regulation of these transcripts in wild-type mice by WY.

A number of genes commonly regulated across PPAR subtypes are associated with fatty acid β -oxidation (DeLuca et al., 2000; Rosen et al. 2008a,b; Rosen et al., 2010); hence, teasing apart the activity of the various PPAR subtypes based on transcript data can be a challenge. To address this, we initially evaluated ToxCast high throughput screening data for evidence of either PPAR γ or PPAR β activation. All four PFAAs represented by 6 discrete chemicals were examined in trans-activation assays carried out in HepG2 cells. AC50 values derived from these experiments were positive for activation of PPAR α and PPAR γ in human cells (Table 4). In contrast, activation of PPAR β was not observed (data not shown).

We further hypothesized that the pattern of gene expression in treated mice would be similar to activators of PPAR γ . To test this hypothesis, gene lists from PFAA-treated mice were compared to gene expression profiles derived from three experiments. In the first comparison, the PPAR γ agonist rosiglitazone was administered to *Lepr (db/db)* mice and evaluated for liver gene expression (Le Bouter et al., 2010). The profile from the

rosiglitazone-treated mice exhibited significant similarity (-log(p-value) 4) to profiles from PFAA-treated wild-type mice (Fig. 5A). Although diminished, significance was also observed in most treated *Ppara*-null mice. Only WY or PFHxS (3 mg/kg) treatment in Ppara-null mice lacked significance. In a second experiment, comparisons were made to genes altered in mouse 3T3-L1 adipocytes by four PPAR γ full agonists following a 24 hour exposure (Tan et al., 2012). Treatment with each of the PFAAs or WY exhibited similarity to all four PPAR γ agonists in wild-type mice but not to a LXR agonist included as a negative control (Fig. 5B). All PFAAs retained similarity to most, if not all of the PPAR γ agonists in *Ppara*-null mice, although the significance was not as great as in the wild-type groups. WY treatment in Ppara-null mice lacked similarity. In a third experiment, profiles were compared to those observed in 3T3-L1 cells after interference with PPAR γ signaling by RNAi against the *Pparg* gene (Schupp et al., 2009). A negative relationship was found in all treated wild-type mice along with similar but muted effects in *Ppara*-null mice exposed to PFHxS, PFOA, and PFOS (Fig 5C). PFNA (1 mg/kg) was marginally significant in Pparanull mice $(-\log(p-value) \sim -4)$, whereas, WY treatment did not reach significance in the nulls. Finally, we compared the gene expression data from PFAA-treated mice to direct targets of PPARs. We focused on 34 mitochondrial and peroxisomal fatty acid β -oxidation genes, most if not all of which are regulated by PPARs through interactions with peroxisome proliferator response elements (PPREs) (Kersten, 2014). Using two-dimensional unsupervised hierarchical clustering, *Ppara*-null mice treated with three of the PFAAs (high dose PFHxS, PFOA, both doses of PFNA) segregated with all four of the PPAR γ agonists (Fig 5D). Low dose PFHxS, PFOS and WY treatment in *Ppara*-null mice segregated with the wild-type groups rather than the PPAR γ agonists. Taken together, the results from these analyses support the plausibility of genes being regulated by PPAR γ in PFAA-treated *Ppara*-null mice.

4. Discussion

PFHxS, PFNA, PFOA and PFOS represent environmental contaminants readily identified in human biomonitoring data (National Report on Human Exposure to Environmental Chemicals, 2014). PFOA and PFOS are no longer being manufactured in the US while PFHxS and PFNA continue to be used as replacements. To gain insight into common and chemical-specific effects, we examined the gene expression profiles associated with these PFAAs in the murine liver and compared them to prototypical activators of PPARa, CAR, ERa, and PPAR γ using a microarray database. In addition, ToxCast data was mined to further evaluate these compounds for PPARa-independent effects. While transcriptional effects of PFOA and PFOS have been reported earlier, the present analysis is the first comprehensive examination of gene expression changes caused by PFHxS and PFNA and is the first comprehensive comparison of the transcriptional effects of all four chemicals.

4.1. PPARa mediates most of the transcriptional effects of PFAAs in the liver

PPARa-dependent and -independent transcriptional effects were considered across four PFAAs. For each treatment group, regulated genes were divided into three classes based on regulation in wild-type or *Ppara*-null genotypes. PPARa-independence in wild-type mice was estimated by considering the number of similarly-regulated genes in both genotypes

(defined as class II genes) divided by the total number of genes regulated in wild-type mice. PFHxS exhibited the greatest percentage of PPARa-independent genes (24% and 22% for 3 and 10 mg/kg, respectively) (Fig. 1). PPARa-independence for the other PFAAs was estimated to be between 10 and 17%. In contrast, only 2% of the genes regulated by WY were PPARa-independent. These results indicate that the majority of genes (> ~75%) regulated by PFAAs in wild-type mice are PPARa-dependent, and that the degree of dependence is contingent upon chemical and dose. Other chemicals have been profiled in wild-type and *Ppara*-null mice, but only one, di(2-ethyl)hexyl phthalate (DEHP), has been similarly evaluated for PPARa-independence. Ren et al. (2010) found that only ~6% of genes were regulated by DEHP in a PPARa-independent manner. Based on these results, it is likely that other environmental contaminants identified as activators of PPARa (unlike marketed or experimental drugs designed specifically to target PPARa such as WY) regulate PPARa-independent molecular pathways, albeit to different extents.

The fact that PPARa is the major regulator of PFAA effects in the mouse liver leads to the question of human relevance of the PPARa mode of action as detailed in a number of reviews (Klaunig et al., 2003; Corton et al., 2014). Prior studies have shown that there is lower expression of the receptor compared to mouse and rat livers (summarized in Corton et al., 2014). Recently, Thomas et al. extensively characterized the mRNA and protein levels of a truncated splice variant of PPARa (*Ppara*-tr) in 150 human liver samples and found that on average there was ~3-fold lower expression of PPARa-tr protein compared to PPARa-wt and that the truncated form can suppress the expression of proliferative and pro-inflammatory genes (Thomas et al., 2015). Expression of the PPARa-tr protein which is not observed in responsive species could help explain the inability of human primary hepatocytes to mount a proliferative response to PPARa activators (Corton et al., 2014). A large body of evidence including these differences in the PPARa expression and activity does not support the human relevance of rodent liver tumors that are mediated by PPARa, and for compounds such as the PFAAs shifts the focus of research to other pathways altered by PFAAs in the liver that may be more relevant for human toxicity.

4.2. Role for CAR in mediating PFAA effects

Many genes regulated by PFAAs encode for enzymes catalyzing xenobiotic metabolism, indicating involvement of one or more transcription factors which could include PXR, Ah receptor (AhR), NFE2L2 (Nrf2), and CAR. As previously reported, there is no evidence that PFAAs activate AhR (Oshida et al., 2015a). Nrf2 is a principal regulator of the oxidative stress response and activation of this factor has been previously suggested in mice exposed to perfluorodecanoic acid (PFDA) (Maher et al., 2008). Oxidative stress has also been reported at higher micromolar concentrations of PFOA in HepG2 cells (Yao and Zhong, 2005), although Eriksen et al. (2010) observed only modest effects for various PFAAs in HepG2 cells. Oxidative stress has been reported in the murine liver following relatively high PFOA exposure levels as well (Yang et al., 2014). Activation of CAR by PFOA and PFOS has previously been demonstrated in either rodents or by in vitro studies (Cheng and Klaassen, 2008; Ren et al., 2009; Elcombe et al., 2010; Bjork et al., 2011; Elcombe et al., 2012). In the current study, when comparisons were made with the gene expression profiles of wild-type or *Car*-null mice exposed to phenobarbital, significant similarity was observed

only to those profiles from PB-treated wild-type mice (Fig. 2A). A CAR gene expression biomarker that accurately predicts CAR modulation (Oshida et al., 2015b) was used to show CAR activation by all four PFAAs but not by WY (Fig. 2B). Furthermore, significance of the overlap with the CAR biomarker was found to increase in *Ppara*-null mice for PFNA, PFOA and PFOS compared to treated wild-type mice. The phenomenon of increased activation of CAR in the absence of PPARa has been discussed in Corton et al. (2014) and may be due to a number of overlapping mechanisms including competition for shared co-activators.

4.3. Feminization of the liver transcriptome by PFAAs

There is increasing evidence that PFAAs activate ERa. Our evaluation of ToxCast trans- and cis-activation assays indicated that ERa is activated by all four PFAAs (Table 3). Using a human reporter gene assay, Benninghoff et al. (2011) found that PFOA, PFNA, PFDA, perfluoro-n-undecanoic acid (PFUnDA), and PFOS significantly increase human ERadependent transcriptional activation at concentrations ranging from 10–1000 nM. This group also showed that all PFAAs weakly bind to rainbow trout liver ERa with half maximal inhibitory concentration (IC50) values of 15.2-289 µM. PFHxS, PFOS and PFOA induced ERa trans-activation in the human breast cancer cell line, MCF-7, as well (Kjeldsen and Bonefeld-Jørgensen, 2013). Furthermore, Du et al. (2013) found that PFOS acts as an ERa agonist in either in an in vitro reporter cell line or a zebrafish-based in vivo assay. In contrast, PFOA treatment of a stable human cell line containing an ERa-dependent luciferase reporter construct (the human ovarian carcinoma cell line BG1-Luc4E2 recently renamed VM7Luc4E2 cells because they were found to be a variant of MCF-7 cells; https:// ntp.niehs.nih.gov/iccvam/methods/endocrine/bg1luc/bg1luc-vm7luc-june2016-508.pdf) caused no change in ERa-dependent luciferase activity (Yao et al., 2014). It is possible that study differences were due to the underlying differences in the expression of the ER subtypes in these two MCF-7 variants.

Only one rodent study tested the hypothesis that ERa is perturbed upon PFAA exposure. Exposure to PFOA at up to 1 mg/kg in the mouse uterotrophic assay had no effect on uterine weight (Yao et al., 2014). We compared PFAA gene expression profiles to those from the livers of mice treated with the nonsteroidal ERa agonist, PPT (Pedram et al., 2013). Profiles from PFAA-treated wild-type mice exhibited significant similarity to those from PPT-treated wild-type mice but not PPT-treated ERa-null mice indicating that a set of genes regulated by PFAAs overlapped with those that were ERa-dependent (Fig. 3A). Interestingly, WY exhibited similarity in wild-type mice as well, an effect that became greatly diminished in *Ppara*-null mice. These data suggest that PFAAs alter gene expression in the mouse liver in a manner similar to ERa agonists. The observation that WY induced comparable changes to that of the ERa agonists suggests that this effect may be common to activators of PPARa and may not be specific to PFAAs. Assessment of ER activation in zebrafish using clofibrate, a well described hypolipidemic activator of PPARa, does not support this conclusion as clofibrate did not act like an ER activator (Tilton et al., 2008; Benninghoff et al, 2012). Given that PFOA did not act like a typical ER agonist in the uterotrophic assay (Yao et al., 2014), but exhibited some ER-like effects in the liver, it is possible that the effects are tissue-specific for an estrogen-like response. Despite the estrogen-like response in

the liver at the transcriptional level, there is a lack of more objective cellular and tissue measures of estrogenicity in other estrogen-responsive tissues.

A murine gene expression biomarker which accurately predicts activation of STAT5B was recently characterized by our group. STAT5B functions downstream of GH to regulate sexually-dimorphic gene expression in the liver. Exposure to testosterone activates STAT5B while exposure to estrogens or genetic interference with GH function results in downregulation of STAT5B and feminization of the liver in male mice (Oshida et al., 2016a,b). In the current study, we determined that all four PFAAs caused significant suppression of STAT5B in wild-type mice. Significance was found to be either partially (PFHxS, PFNA, PFOS) or completely (PFOA, WY) PPARa-dependent (Fig. 3B). Hence, PFAAs interfere with GH signaling as reflected by suppression of STAT5B. Chemical-induced feminization of the liver could occur by disruption of one or more sensitive nodes along the GH hypothalamic-pituitary-liver axis. In one model, antagonism could come about directly in the liver through physical interactions between STAT5B and PPARa. Circumstantial evidence for this model comes from observations of genes co-regulated by PPARa and STAT5B in which absence of one transcription factor leads to increased regulation by the other (Shipley and Waxman, 2004; Stauber et al., 2005). Alternatively, feminization could occur through changes in circulating hormones. Treatment of male mice or rats with estradiol antagonizes hepatic expression of male-specific cytochrome P450 genes (Ishii et al., 2006) and, when administered to neonatal castrated rats, estradiol induces femalespecific liver enzymes (Dannan et al., 1986). High doses of DEHP, for example, increased estradiol levels (Eagon et al., 1994) and caused feminization (Oshida et al., 2016b). Feminization may also occur through decreases in testosterone levels as is observed after castration. PFOA has been shown to decrease testosterone and increase estradiol in the serum of male rats, effects at least partially associated with induction of hepatic aromatase (Cook et al., 1992). Such changes may be due in part to CAR, since CAR regulates a number of cytochrome P450 genes that metabolize testosterone to hydroxylated metabolites (Waxman, 1988). Male Car-null mice have serum levels of testosterone that are 2.5-fold higher than wild-type mice along with decreased constitutive hepatic expression of testosterone hydroxylases Cyp2b9 and Cyp2b10 (Cho et al., 2014). A role for cytochrome P450 activity in decreasing testosterone production is plausible based on suppression of STAT5B with parallel activation of CAR.

4.4. Role of PPAR γ in mediating the transcriptional effects of PFAAs in the liver

In previous studies, we hypothesized that either PPAR γ or PPAR β may regulate genes in *Ppara*-null mice exposed to PFOS or PFOA (Rosen et al., 2008a,b; Rosen et al., 2010). Our current study indicates that all four compounds similarly regulate genes involved in lipid homeostasis in both genotypes, including those involved in fatty acid β -oxidation, lipid catabolism, lipid synthesis, and lipid transport. Our studies provided plausibility to regulation of genes by PPAR γ . We compared the expression profiles of PFAA-treated mice to those of PPAR γ agonists administered to either *Lepr (db/db)* mice or to 3T3-L1 adipocytes. Significant similarity was observed between the PPAR γ agonist profiles and PFAAs in both wild-type and *Ppara*-null mice (Fig. 5A,B). Profiles in PFAA-treated mice also exhibited negative correlation to 3T3-L1 adipocytes that were treated by RNAi to

reduce PPAR γ activity (Fig. 5C). As a final test, we focused on a set of fatty acid β oxidation genes, most if not all reported to be regulated in a positive manner by PPAR subtypes through one or more PPREs (Kersten, 2014). Using two-dimensional hierarchical unsupervised clustering, groups from *Ppara*-null mice treated with PFOA, PFNA, and PFHxS segregated with PPAR γ agonists (Fig. 5D).

Evidence against a role for PPAR γ in mediating the effects in PFAA-treated mice have also come from studies using reporter cell lines. These studies have been largely negative, with the exception of modest activation of PPAR γ by PFOA under high exposure conditions (Vanden Heuvel et al. 2006, Taxvig et al., 2012, Maloney and Waxman 1999). Likewise, Takacs and Abbott (2007) did not report activation of either human or mouse PPAR γ by PFOA or PFOS, although significant effects on murine PPAR β were observed. In the current study, however, EPA ToxCast data showed activation of human PPAR γ but not PPAR β by all four PFAAs (Table 4). Our group also found that expression of the *Pparg* gene was increased in both wild-type and *Ppara*-null mice after PFOA exposure while expression of *Pparb* was unchanged (Das et al., 2016). Additional studies indicate the involvement of PPAR γ in mediating the inhibitory effects of PFOA during leukocyte activation in rats (Griesbacher et al., 2008) and in altering spontaneous differentiation of rat embryonic neural stem cells by PFOS (Wan Ibrahim et al., 2013). In summary, there is compelling evidence that PPAR γ may be a target of PFAAs in liver and other tissues.

5.0. Conclusions

We have examined the hepatic gene expression profiles of PFNA and PFHxS in wild-type and *Ppara*-null mice. In order to carry out a comprehensive analysis of PFAA transcriptional effects, historical in-house data for PFOA and PFOS were also included as were data for WY-14,643, a recognized activator of PPARa. These microarray profiles were compared to relevant microarray studies in a database allowing us to assess the involvement of a number of transcription factors. PPARa was found to be the primary molecular target for PFAAs in the mouse liver. Using previously defined predictive gene expression biomarkers, we demonstrated that PFAAs activate CAR in both wild-type and Ppara-null mice and cause feminization of the liver transcriptome through suppression of STAT5B. The suppression of STAT5B could be linked to activation of ERa as there was significant overlap in the genes regulated by PFAAs and an ERa agonist in an ERa-dependent manner. Human PPAR γ and ERa were also found to be activated by all four PFAAs in ToxCast trans-activation assays. These results indicate that, in addition to activating PPARa, PFAAs activate other nuclear receptors including CAR, PPAR γ and ER α , and may function as suppressors of STAT5B. While these data indicate that the PFAAs mediate a limited number of genomic effects through transcription factors other than PPARa, there is little evidence that these PPARaindependent changes are associated with the key events in the PPARa mode of action for liver cancer. Additional studies would be needed to determine if liver cancer can be induced by PFAAs independently of PPARa.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Abbreviations:

AhR	aryl hydrocarbon receptor
CAR	constitutive activated receptor
DEHP	di-(2-ethylhexyl)phthalate
ERa	estrogen receptor a
ERE	estrogen response element
GH	growth hormone
LXR	liver X receptor
Nrf2	nuclear factor erythroid-2-related factor 2
PFAAs	perfluoroalkyl acids
PPARa	peroxisome proliferator-activated receptor a
PPARγ	peroxisome proliferator-activated receptor γ
PFHxS	perfluorohexanesulfonic acid
PFNA	perfluorononanoic acid
PFOA	perfluorooctanoic acid
PFOS	perfluorooctane sulfonate; PFUnDA, perfluoro-n-undecanoic acid
PPREs	peroxisome proliferator response elements
PXR	pregnane X receptor
STAT5B	signal transducer and activator of transcription 5B
Vtg	vitellogenin
WY	WY-14.643

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Fig. 1. PPARa regulates the majority of PFAA-responsive genes. Significantly altered genes (FDR 0.05; |fold change| 1.5) were identified using procedures described in the Methods.

A. Number of genes with increased or decreased expression in each treatment group. Numbers refer to treatment in mg/kg/day.

B. Heat maps of the distribution of genes in wild-type and *Ppara*-null mice. Genes regulated by the PFAAs were divided into three classes: I, PPARa-dependent; II, PPARa-independent and similarly expressed in both genotypes; III, PPARa-independent and expressed only in *Ppara*-null mice. The heat maps are not proportional to the total number of genes that are altered by each treatment.

C. Percentage of genes that were determined to be PPARa-independent. Values were derived by calculating the number of genes in class II/number of genes in class I and II.

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Fig. 2. CAR activation by PFAAs is PPARa-independent.

A. Lists of significant genes from PFAA-treated groups were compared to two gene lists derived from the livers of wild-type or *Car*-null mice exposed to 100 mg/kg phenobarbital for three days (from Chua and Moore, 2005). PFAA treatment groups are indicated in mg/kg/day. WY treatment groups are in %w/w.

B. Comparison of the PFAA gene lists to the CAR biomarker. (Top) Altered regulation of the genes in the CAR biomarker. The expression of the CAR biomarker genes are shown on the far left for reference (B). (Bottom) -Log(p-value)s of the similarity of the gene lists to the CAR biomarker.

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A. Similarity to the profile from PPT-treated wild-type but not PPT-treated ERa-null mice. Lists of significant genes from PFAA-treated groups were compared to the lists derived from the livers of wild-type or ERa-null mice exposed to 100 ug PPT intraperitoneally daily for 3 days (from Pedram et al., 2013).

B. Comparison of the PFAA-regulated genes to the STAT5B biomarker. The STAT5B biomarker previously described in Oshida et al. (2016a,b) consists of 144 STAT5B-dependent genes. The gene lists from each of the treatment groups were compared to the biomarker as described in the Methods. (Top) Heat map showing the expression of STAT5B biomarker genes after PFAA treatment. The expression of the STAT5B biomarker genes are shown on the far left for reference (B). In the biomarker the male-dominated upregulated genes are red and female-dominated down-regulated genes are blue. (Bottom) The –log(p-value)s are derived from the Running Fisher test of significance of the correlation in the expression pattern between the biomarker and the gene list.

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Fig. 4. Genes regulated similarly by PFAAs in wild-type and *Ppara*-null mice.

Genes regulated by PFAAs were filtered for those that exhibited regulation in 11 or 12 out of the 12 PFAA treatment groups and clustered by one-dimension hierarchical clustering.





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A. Similarity between PFAA-regulated genes and those regulated by the PPAR γ agonist rosiglitazone. The gene lists derived from PFAA-treated mice were compared to the profiles from livers of db/db mice treated with rosiglitazone (Le Bouter et al., 2010).

B. Similarity between PFAA-regulated genes and those regulated by four PPAR γ agonists. Lists of significantly altered genes derived from exposure to one of the four indicated PPAR γ agonists or a LXR agonist were compared to the PFAA groups. Mouse 3T3-L1

adipocytes were exposed to 10 uM of the indicated PPAR γ agonists or LXR agonist for 24 hrs (Tan et al., 2012).

C. The PFAA profiles exhibit negative correlation to a profile of knockdown of the *Pparg* gene. The PFAA profiles were compared to the profile of 3T3-L1 cells treated with a siRNA against *Pparg* (Schupp et al., 2009).

D. Similarity in the expression pattern of fatty β -oxidation genes between PFAAs in *Ppara*null mice and PPAR γ agonists. The expression of fatty acid β -oxidation genes was compared between the groups by two-dimensional hierarchical clustering and shows greater similarity in the expression pattern between the PPAR γ agonists and PFAA from *Ppara*-null mice than from wild-type mice. Only the hierarchical tree of one dimension is shown.

Table 1.

Body and liver weight in WT and PPARa-null mice exposed to PFNA for 7 days.

	WT			PPARa-null			
	0 mg/kg	1 mg/kg	3 mg/kg	0 mg/kg	1 mg/kg	3 mg/kg	
N	4	4	4	4	4	4	
Body Weight	28.1±1.6	29.2±1.6	29.2±3.0	30.5±8.0	30.3±3.6	30.8±3.4	
Liver Weight	0.94 ± 0.06	1.54±0.14*	1.93±0.16*	1.20±0.24	1.41±0.20	1.83 ± 0.30 *	
Relative Liver Weight	0.034 ± 0.002	0.053 ± 0.002 *	0.066 ± 0.004 *	0.040 ± 0.006	0.047 ± 0.006	0.059±0.004*	

* Significantly different than control (p 0.05)

Table 2.

Body and liver weight in WT and PPARa-null mice exposed to PFHxS for 7 days.

	WT			PPARa-null			
	0 mg/kg	3 mg/kg	10 mg/kg	0 mg/kg	3 mg/kg	10 mg/kg	
N	4	4	4	4	4	4	
Body Weight	29.03±2.00	29.80±0.90	29.15±2.16	30.83±5.00	29.40±3.98	30.23±4.18	
Liver Weight	0.99±0.10	$1.18{\pm}0.08$	1.68±0.14*	1.07 ± 0.16	1.13±0.14	$1.50{\pm}0.08$ *	
Relative Liver Weight	0.034 ± 0.004	0.040 ± 0.004 *	$0.058 {\pm} 0.001$ *	0.035±0.002	0.039 ± 0.006	0.050±0.008*	

* Significantly different than control (p 0.05)

Activation of ERa in trans-activation assays by PFAAs

Assay	Chemical	Hit Call ¹	Modeled Maximum ²	Maximum SD ³	Modeled AC50 ⁴	AC50 SD ⁵
	PFNA	1	1.898	0.124	1.490	0.047
	PFOS	1	0.707	0.070	1.257	0.069
	PFOA	1	2.034	0.029	1.529	0.007
AIG_ERE_CIS_up	PFOS-K	1	1.848	0.762	1.514	0.222
	PFOA, ammonium salt	1	1.708	0.052	1.356	0.013
	PFHS-K	1	1.381	0.449	1.986	0.177
ATG_ERa_TRANS_up	PFNA	1	2.566	0.228	1.330	0.089
	PFOS	1	2.256	0.070	1.590	0.026
	PFOA	1	4.278	1.538	1.674	0.210
	PFOS-K	1	2.159	1.683	1.555	0.397
	PFOA, ammonium salt	1	2.874	0.382	1.650	0.121
	PFHS-K	0	NA	NA	NA	NA

¹ = Hit call: 1 = active, 0 = inactive;

 2 = top asymptote predicted by model (log10 fold induction);

 \mathcal{S} = standard deviation of modeled maximum;

 4 = modeled half maximal concentration (log10 μ M);

5 = standard deviation of AC50.

Table 4.

PPAR subtype activation from ToxCast Attagene assays.

Assay	Chemical	Hit Call ¹	Modeled Maximum ²	Maximum SD ³	Modeled AC50 ⁴	AC50 SD ⁵
	PFNA	1	3.315	0.119	1.157	0.038
	PFOS	1	1.765	0.074	1.770	0.013
	PFOA	1	3.564	0.229	1.339	0.052
AIG_PPAKa_IKANS_up	PFOS-K	1	1.263	0.193	1.234	0.133
	PFOA, ammonium salt	1	2.876	0.170	0.828	0.105
	PFHS-K	1	1.580	0.118	1.051	0.063
ATG_PPARg_TRANS_up	PFNA	1	3.282	0.063	1.638	0.017
	PFOS	1	2.745	0.075	1.426	0.147
	PFOA	1	3.406	0.992	1.695	0.174
	PFOS-K	1	1.829	0.194	1.347	0.116
	PFOA, ammonium salt	1	2.647	0.149	1.339	0.052
	PFHS-K	1	1.987	0.220	1.484	0.161

¹ = Hit call, 1 = active, 0 = inactive;

 2 = top asymptote predicted by model (log10 fold induction);

 \mathcal{S} = standard deviation of modeled maximum;

 4 = modeled half maximal concentration (log10 μ M);

5 = standard deviation of AC50.