



Published in final edited form as:

J Hazard Mater. 2022 March 15; 426: 128084. doi:10.1016/j.jhazmat.2021.128084.

The aryl hydrocarbon receptor: a predominant mediator for the toxicity of emerging dioxin-like compounds

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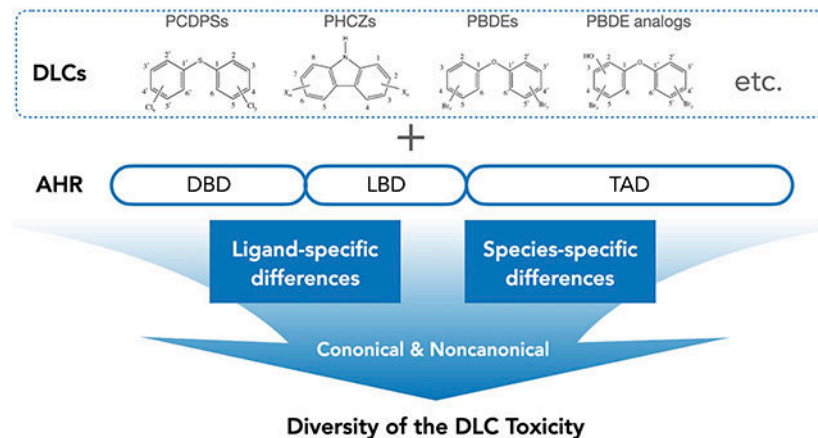
Abstract

The aryl hydrocarbon receptor (AHR) is a member of the basic helix-loop-helix/Per-ARNT-Sim (bHLH-PAS) family of transcription factors and has broad biological functions. Early after the identification of the AHR, most studies focused on its roles in regulating the expression of drug-metabolizing enzymes and mediating the toxicity of dioxins and dioxin-like compounds (DLCs). Currently, more diverse functions of AHR have been identified, indicating that AHR is not just a dioxin receptor. Dioxins and DLCs occur ubiquitously and have diverse health/ecological risks. Additional research is required to identify both shared and compound-specific mechanisms, especially for emerging DLCs such as polyhalogenated carbazoles (PHCZs), polychlorinated diphenyl sulfides (PCDPSs), and others, of which only a few investigations have been performed at present. Many of the toxic effects of emerging DLCs were observed to be predominantly mediated by the AHR because of their structural similarity as dioxins, and the *in vitro* TCDD-relative potencies of certain emerging DLC congeners are comparable to or even greater than the WHO-TEFs of OctaCDD, OctaCDF, and most coplanar PCBs. Due to the close relationship between AHR biology and environmental science, this review begins by providing novel insights into AHR signaling (canonical and non-canonical), AHR's biochemical properties (AHR structure, AHR-ligand interaction, AHR-DNA binding), and the variations during AHR transactivation. Then, AHR ligand classification and the corresponding mechanisms are discussed, especially

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the shared and compound-specific, AHR-mediated effects and mechanisms of emerging DLCs. Accordingly, a series of *in vivo* and *in vitro* toxicity evaluation methods based on the AHR signaling pathway are reviewed. In light of current advances, future research on traditional and emerging DLCs will enhance our understanding of their mechanisms, toxicity, potency, and ecological impacts.

Graphic Abstract



Keywords

aryl hydrocarbon receptor; AHR ligands; dioxin-like compounds; molecular mechanisms; toxicity evaluation

1. Introduction

The aryl hydrocarbon receptor (AHR, also called dioxin receptor), a member of the basic helix-loop-helix/Per-ARNT-Sim (bHLH-PAS) family of transcription factors, was identified more than four decades ago and is well known for its ability to mediate a series of biological and toxic effects caused by environmental contaminants, including polychlorinated dibenzo-*p*-dioxins and polychlorinated dibenzofurans (PCDD/Fs) and many other halogenated aromatic hydrocarbons (HAHs), often referred to as ‘dioxin-like compounds (DLCs)’^{1–3}. These compounds occur ubiquitously in various environmental matrices, and many of them undergo bioaccumulation and biomagnification^{4–6}. The toxicity of PCDD/Fs and dioxin-like polychlorinated biphenyls (DL-PCBs) has been extensively investigated, but our understanding remains incomplete, with many adverse effects being continuously revealed^{7–9}. A variety of emerging DLCs such as polyhalogenated carbazoles (PHCZs) and polychlorinated diphenyl sulfides (PCDPSs) are being found to act by a similar mechanism to dioxins via AHR, but there are many compound-specific effects and detailed mechanisms remain largely unknown. Research on human samples has indicated the occurrence of emerging DLCs and has suggested their potential risk to human health^{10–12}. Due to DLCs’ adverse effects like that of the dioxins, and the importance of AHR as a key mediator, much research has been performed to evaluate their toxicity and obtain preliminary mechanistic knowledge^{13, 14}. Indeed, the understanding of DLC toxicity largely depends on the current

knowledge of AHR biology; thus, advances in AHR biology (e.g., structural insights into AHR-DNA binding or detailed transactivation mechanisms^{15, 16}) would benefit future research on DLC-AHR interactions and their downstream effects.

It is now widely accepted that AHR has broad functions, including playing roles in human physiology (e.g., development biology, neurobiology, and immunology), diseases (e.g., autoimmune diseases and cancer), and chemical toxicity^{17–20}. Beyond these cellular and physiological aspects, the AHR gene and its functions in most metazoans have both conserved and varied roles, and further study of AHR can enhance the understanding of the toxicology of AHR-active contaminants in distinct species²¹. Organisms in certain areas may suffer from exposure to a particular dioxin/DLC and its potential adverse effects in a species-specific manner, so the role of AHR in different species should be carefully evaluated, including the number of homologs, expression level, predominant form, and AHR sensitivity^{22–24}. Moreover, AHR can be used by environmental scientists as a tool in toxicology research based on ligand-induced AHR activation, with species-specific effects being considered²⁵, such as for developing bioassays for evaluating toxicity or identifying novel ligands/contaminants^{26, 27}.

Since knowledge of AHR biology is rapidly growing, further advances could improve many aspects of environmental science, such as contaminant quantification/screening, toxicity evaluation, species-specific effects, and mechanistic exploration. Recent biochemical and structural research has provided increasing evidence that the physicochemical features of ligands, structural determinants of AHR, and interactions of AHR and ligands could influence its transactivation process (and sometimes its toxic potential)^{15, 28–30}. To provide information for more thorough DLC toxicology research, this review describes recent advances in research on traditional and emerging DLCs by focusing on (i) advances in understanding of the AHR transactivation process (e.g., AHR-ligand interactions, AHR-DNA binding, and nongenomic mechanisms); (ii) variations or uncertainty during the transactivation process (e.g., ligand-specific effects and species-specific effects); (iii) AHR ligands, especially emerging toxic DLCs, and their mechanisms; and (iv) toxicity evaluation assays for potential ligands/DLCs.

2. The AHR pathway

AHR is a nuclear receptor belonging to the bHLH-PAS family and is present in most metazoans. AHR has an evolutionary history of at least 600 million years¹. Vertebrate AHRs are the most well characterized AHRs and were initially believed to sense exogenous molecules, but currently, research has widened the knowledge of the functions of AHR, such as governing many cellular/physiological functions and playing a role in human disease^{17–20}. *Caenorhabditis elegans*, a modern representative of an early-diverging metazoan, has a “protoAHR”¹ that does not bind well-known AHR ligands such as TCDD and BNF^{31, 32} (and may be constitutively active), but maintains some fundamental roles of AHR in neuronal differentiation and migration, and cell fate determination³³. However, at an unknown time, ancient AHR acquired the ability to bind and be activated by many internal and external ligands, especially the high-affinity ligand TCDD and some halogenated aromatic hydrocarbons (HAHs)¹. Thus, the AHR may have evolutionarily conserved,

fundamental biological roles in all animals, as well as species-specific properties. In more recently diverged animals such as vertebrates, the multitasking feature of AHR can be attributed to two major types of molecular mechanisms in cells, the canonical genomic pathway and non-canonical pathways^{34, 35}.

2.1 Canonical genomic pathway

AHR is a ligand-dependent nuclear receptor (Figure 1); when absent from ligands, it is maintained in an inactive form and protected from degradation by complexing with chaperones, including HSP90, p23, and XAP2 (also called Ara9 and AIP)³⁶. At this stage, certain functional sequences and interfaces of AHR (e.g., the nuclear localization sequence (NLS) and ARNT dimerization interface) are blocked, ensuring that AHR is localized in the cytosol¹⁵. Once bound with an agonist ligand, AHR subsequently undergoes a structural transformation and translocates to the nucleus to dimerize with ARNT and bind specific DNA recognition sites with high affinity¹⁵. The DNA binding sites can be consensus or non-consensus sequences (see Section 2.2). The consensus site is a 5'-GCGTG-3' core motif usually named the dioxin response element (DRE) or xenobiotic response element (XRE). Then, the dimer recruits the basal transcription machinery to transcribe its target genes to exert various downstream functions (Figure 1).

As an important part of transactivation, the detailed AHR-DNA binding mechanism was revealed by resolving the structure of the core AHR-ARNT-DRE complex, which illuminated the principal role of the bHLH domain of both AHR and ARNT in recognizing the DRE, as well as the key interface for AHR:ARNT dimerization¹⁶. In addition, the two PAS domains have been shown to have distinct functions. The PAS-A domain is involved in ARNT dimerization^{16, 36}. The PAS-B domain is part of the ligand-binding domain (LBD) of AHR and facilitates interactions with HSP90 or other cofactors, such as pRb^{37, 38}.

As the 3D crystal/NMR structure of LBD has not been characterized, which hampers the detailed understanding of AHR-ligand binding³⁴, researchers have built homology models using available PAS domain structures as templates to provide insights into AHR-ligand interactions or for mechanistic exploration of many unidentified forms of AHR in distinct species³⁹⁻⁴². In addition to the LBD, the diversity of transactivation domains (TADs) of AHRs of various species or strains could have a role in determining the AHR activity, as indicated by research on AHRs in the H/W rat and hamster^{43, 44}.

Presently, a more detailed structural exploration of AHR (and the AHR-partner complex) and the molecular dynamics of AHR have yet to be investigated. In environmental science, many emerging DLCs are able to activate the canonical pathway of AHR and induce the prototypical biomarkers CYP1A1 and CYP1B1 (Figure 1)⁴⁵. Although the genomic pathway is canonical in mediating the toxic effects of contaminants (including emerging DLCs), it is noteworthy that even toxic-equivalent doses of ligands may induce rather different effects both *in vitro* and *in vivo*. The reason for these differences may lie in the metabolic liability of distinct ligands, their pharmacokinetic and distributional differences, and the variations in their induced non-canonical crosstalk^{46, 47}. In particular, investigating non-canonical crosstalk would be a good strategy to explain these differences.

2.2 Non-canonical pathways

Non-canonical pathways of AHR action, including crosstalk of AHR with other proteins/pathways, are of increasing interest but are not well understood. Systems biology research has revealed the ligand-specific coregulation and coexpression patterns of AHR with other genes, indicating the potential of AHR to crosstalk with other proteins/pathways⁴⁸. Non-canonical mechanisms of AHR action can be classified into several patterns (Figure 1): (i) AHR associates with other transcription factors and then binds to non-consensus DREs (e.g., RelB⁴⁹ and KLF6⁵⁰) or indirectly binds to the DNA binding site of the associated partner (e.g., ER⁵¹ and E2F1⁵²); (ii) AHR directly binds some functional components, and they cooperatively exert a particular function, such as ubiquitin ligation⁵³; and (iii) AHR interacts with various signaling pathways (e.g., JNK⁵⁴ and Src⁵⁵). Collectively, in most cases of non-canonical signaling, AHR is more like a signaling mediator rather than a transcription factor, and ligand-dependent activation is also not always necessary³⁷.

Non-canonical mechanisms are environmentally relevant because they can contribute to the toxicity of contaminants, including DLCs^{56,57}. For example, it has been found that lipophilic chemicals from diesel exhaust particles, which contain polycyclic aromatic hydrocarbons (PAHs) and numerous unsolved compounds, can trigger calcium responses in human endothelial cells via AHR-dependent nongenomic signaling indicated by pharmacological inhibition and RNA interference⁵⁶. As another example, the uremic toxin indoxyl sulfate (IS) can induce endothelial hyperpermeability via an AHR/Src-dependent pathway⁵⁸. Currently, research on non-canonical crosstalk of AHR is largely focused on a limited number of crosstalk factors/pathways and their effects, especially of dioxins (especially TCDD), which should be extended to other AHR-active DLCs in light of the results of TCDD research.

3. Variation during AHR transactivation

The AHR transactivation has many steps that can be affected by ligands' physicochemical properties. In light of the structural and biochemical research on AHR, DLCs' specific toxicity potential and mechanistic variations can be partly explained, including but not limited to the following aspects.

3.1 Possible ligand-specific structural changes of AHR

During AHR activation, several transitional stages can affect the outcome^{15,34}. AHR activation by a ligand binding initiates a multi-step process of AHR transformation before the AHR:ARNT heterodimer binds to DNA. Although the precise processes are still elusive, recent research has proposed a potential mechanism and described several factors that may influence the transformation process and subsequent transactivation of target genes¹⁵. Between ligand binding and DNA recognition by AHR, there may be two major transitional steps, including 'step one' of switching HSP90 into an open form and exposing the AHR's NLS motif, followed by translocation of the AHR:HSP90 complex to the nucleus; 'step two' is the formation of a ternary complex of AHR:HSP90:ARNT before transforming into the competent state of the AHR:ARNT complex that can bind DNA¹⁵. Both steps are likely altered by the conformational change of PAS-B following ligand binding, which

may subsequently influence the efficiency of ARNT recruitment after ‘step one’ and HSP90 dissociation in ‘step two’¹⁵. These steps are essential for AHR activation and may occur in a ligand-specific manner. There is evidence that binding of agonists and antagonists result in different AHR structures⁵⁹. Moreover, the subsequent efficiency of AHR transformation and DRE binding can also be specifically influenced by binding distinct ligands⁶⁰. This suggested that the varied effects of ligands may result from ligand-induced overall structural alterations of AHR or the AHR:ARNT heterodimer (or perhaps a heterodimer of AHR and other partners), therefore affecting subsequent DRE recognition and cofactor recruitment³⁴. However, the true mechanism may involve one or several of the aspects discussed above. At present, there are still no direct observations of ligand-specific AHR structural changes, which therefore should continue to be investigated.

3.2 Variations during AHR-DNA recognition

In addition to AHR transformation, subsequent DNA binding is another influential process. A recent study on the AHR:ARNT:DRE structure has provided insights into the DRE recognition process and a new avenue to investigate the ligand-specific effects induced by different DRE binding efficiencies or priorities^{16, 60}. As mentioned in Section 2.2, the DRE is an essential factor for AHR-DNA recognition. The classic binding mode is that AhR:ARNT heterodimer binds to a consensus DRE sequence (5'-GCCGTG-3') in the target gene promoter (Figure 1)^{61, 62}. Genome-wide analysis of DREs indicates that most TCDD-inducible genes contain DREs within the 10 kb upstream or transcribed regions^{63, 64}. Alternatively, other sequence(s) (e.g., XRE II) unlike the consensus DRE, can be recognized by AHR-interacting factors and govern the gene expression⁶⁵. Here, the AHR acts more like a coactivator.

Initial evidence indicated ligand-specific DNA recognition by the AHR:ARNT heterodimer^{66, 67}, but later research has not confirmed these results using similar experimental models, suggesting that AHR likely does not utilize a ligand-specific DNA recognition mechanism in its signaling⁶⁸. However, the efficacy of a particular ligand in stimulating AHR transformation/DNA binding can vary⁶⁹. Indirubin, for example, has high efficacy/potency with the human AHR⁶⁰.

To explore the functional domain/region determining species differences in DRE binding by indirubin-activated AHR, swapping the LBD from a human AHR to a mouse AHR made the chimera more efficient at binding the DRE than the wild-type mouse AHR. However, the efficacy of indirubin with the chimera was also not the same as that with human AHR, which indicates that AHR regions outside of the LBD may have a role in ligand-specific DRE binding⁶⁰, as well as the importance of PAS-B conformational changes upon ligand binding for subsequent cofactor recruitment, DRE binding, and AHR activation. Therefore, for DLCs' toxicity evaluation, DRE recognition or efficacy is vital to indicate their toxic potentials. But the DLCs-induced DRE binding now has not been much investigated, although some indirect evidence has revealed the DLCs' DRE binding potential using DRE-driven reporter gene assays (i.e., polyhalogenated carbazoles)¹⁴.

3.3 AHR pathway self-regulation

As a vital aspect of AHR pathway, its regulation or self-regulation (e.g., AHR, ARNT, AHR repressor (AHRR), and AHR target genes) by environmental contaminants have been frequently reported⁷⁰. Regarding transcription, the biochemical state of AHR, ARNT, or CYP1A promoters plus their whole gene body could potentially influence their expression^{71–73}. For instance, exposure to environmental contaminants exerts epigenetic regulation through the AHR promoter (i.e., histone modifications, such as the notably decreased trimethylation of histone 3, lysine 27)⁷⁰ or results in biochemical changes in the AHR protein as a feedback (e.g., ubiquitination and phosphorylation)^{74, 75}. In addition to transient biochemical changes, in ecology, decades of exposure to PCBs causes selective pressure on certain regions of genes involved in the AHR pathway in wild species, thus having a long-term influence on their expression or function^{22, 76–79}.

Besides transcriptional or posttranslational regulation, feedback loop mechanisms are essential for cellular homeostasis (Figure 1)^{80, 81}. One of the most potent patterns is the induction of the AHRR, which is a target gene of AHR^{82, 83}. The AHRR can be sensitively upregulated (~150-fold induction) to exert robust suppression of AHR by forming a heterodimer with ARNT and competing with AHR-ARNT complexes for DRE binding, thus suppressing the canonical genomic response^{30, 81}. More than competing for DRE occupancy, AHRR also inhibits DRE-mediated transcription by influencing the chromatin structure around the promoters of CYP1A1 and presumably those related DRE-driven genes^{84, 85}. As another AHR target gene, TIPARP can ADP-ribosylate AHR and reduce its activity and half-life^{86, 87}.

Except for those genetic or epigenetic regulations, the modulation of the endogenous ligand FICZ can be another sort of regulation, as certain chemicals (e.g., quercetin, resveratrol, and curcumin) can repress CYP1-mediated degradation of endogenous FICZ, which can activate AHR in an indirect manner^{88, 89}. Collectively, the AHR reactivation process is complex and during which multiple factors can independently or cooperatively cause variations. Especially, when investigating DLCs, the ligand- and species-specific effects through and on the AHR should be carefully considered.

4. Diversity of AHR ligands and ligand-specific effects

4.1 Overview of AHR ligands

In environmental science, evaluating the toxicity and exploring the molecular mechanism of AHR-active ligands, especially contaminants, are of great interest. AHR pathway signaling is an important theoretical basis for developing receptor-based toxicity evaluation systems for environmental pollutants. Multiple *in vitro*, *in vivo*, and *in silico* methods have been developed to identify potential AHR ligands (agonistic or antagonistic)^{60, 90}. These natural or synthetic ligands can be classified into environmental contaminants (e.g., HAHs), marketed/prodrugs (e.g., rifampicin and rifabutin)⁹¹, natural or endogenous metabolites/compounds^{92, 93}, industrial products (e.g., quinoline yellow dyes)⁹⁴, and others. Currently, the number of AHR ligands is increasing and their diverse mechanisms have been continuously identified. For instance, ligands with pharmaceutical effects, which are usually

termed selective AHR modulators, exert their function in a ligand-specific manner via AHR (e.g., for treating cancer or inflammation)⁹⁵⁻⁹⁷. Similarly, for environmental contaminants, ligand-specific effects should be of interest to environmental scientists or toxicologists and thus are also reviewed below.

A recent view has questioned the traditional classification of AHR ligands into ‘agonists’ or ‘antagonists’ and proposes that ‘modulator’ is a more appropriate term⁹⁸. Some new terms have been adopted according to certain demands, including selective AHR modulators (sAHRMs)⁹⁷ and rapidly metabolized ligands (RMAHRLs)⁹⁹. sAHRMs are compounds that bind and activate AHR and then regulate a selected pool of canonical and/or noncanonical target genes, therefore eliciting specific biological effects. Certain sAHRMs can exert beneficial functions without causing dioxin-like toxicity (e.g., 6-MCDF, 3,30-DIM)⁹⁸. RMAHRLs (e.g., IMA-06201 and IMA-06504) are AHR agonists endowed with fast metabolic degradation, and they are devoid of dioxin-like toxicity due to the lack of their harmful bioaccumulation and the short half-life of the activated AHR complex⁹⁸. RMAHRLs may be a subgroup of sAHRMs that have a highly polar physicochemical nature⁹⁸. Currently, the definition of sAHRMs is still ambiguous¹⁰⁰. The metabolic kinetics and the subsequent gene regulation may vary among ligands, including among the emerging DLCs, which are another important group of AHR ligands that have been ubiquitously identified in the environment (usually with persistent nature) and have received increasing focus due to their toxic potential. For instance, the emerging DLC 4,4’-di-CDPS has high bioaccumulation potential in mussel tissues and four metabolites were identified with the S-oxidation representing the dominant metabolic pathway¹⁰¹. However, with respect to metabolism, there is a need for further exploration of the detailed metabolic pathways (including variation among species^{101, 102}) for all of the emerging DLCs. With respect to activity, most dioxins and DLCs have been found to have agonistic effects, while some also have partial or weak agonistic potential^{103, 104}.

4.2 Ligand-specific effects via AHR

Beyond those definitions, true ligand-specific effects should be considered. Numerous pieces of evidence have revealed the ligand-specific effects of AHR, and even when treated using compounds under the same TEQ, their outcome could be distinct from a systems biology or histopathology viewpoint⁴⁶. The possible reasons may lie in the metabolic potential of distinct ligands, as traditional persistent HAHs can continuously activate AHR, while rapidly metabolized ligands (like the RMAHRLs discussed above) cannot^{105, 106}. In line with this finding, Hoffman et al. has reported that persistent ligands tend to elicit great ultrasensitivity and the maximal response, while consumption-based ligands (e.g., indole-3-carbinol, an exogenous ligand identified in cruciferous vegetables, and its metabolite 3,3’-diindolylmethane) seem to produce low-level activation in a graded manner¹⁰⁷.

As a metabolically stable and potent compound, TCDD does not induce AHR to bind the stanniocalcin 2 (Stc2) promoter the same way it binds the CYP1A promoter¹⁰⁸. In contrast, cinnabarinic acid (CA), a proposed endogenous agonist¹⁰⁹, cannot induce AHR to bind the CYP1A promoter¹¹⁰. Among PCB congeners, their intrinsic efficacies span a continuum between full agonism and full antagonism, and a weak agonistic congener yields

less than additive responses in mixtures with potent agonists⁶⁹. Similarly, PCB-11 may act as a partial agonist/antagonist of AHR when co-exposed with the potent agonist PCB-126. However, PCB-11 does not block but exacerbates toxicity when co-exposed with BNF¹⁰³. As another example, the full antagonist CH223191 blocks TCDD but has little inhibitory effect on BNF, PAHs, flavonoids, or indirubin¹¹¹.

Taken together, as the initial step, these variations were largely affected by the molecular initiation event (MIE), which mainly depends on the AHR-ligand interactions, of which the ligand binding pose and binding affinity are two of the major determinant aspects.

4.3 Ligand-binding affinity

Ligand-binding affinity is important for predicting the transactivation potential of AHR ligands for structurally similar classes of compounds. Competitive ligand-binding assays are commonly used methods for determining ligand-binding affinity. In a strictly restricted model with TCDD as the ligand to test a series of mutated forms of AHR, ligand-binding affinity shows good correlation with the following step of DNA binding (not transactivation activity)¹⁵. Among distinct ligands or forms of AHR, the situation is more complicated, and a stronger binding affinity does not ensure greater final activity (agonistic or antagonistic). Murray et al. has revealed similar competitive ligand binding profiles for α -NF (IC₅₀ = 25 nM) and DiMNF (IC₅₀ = 21 nM) but proposed that distinct agonist/antagonistic effects on DRE-mediated gene expression are unlikely to result from (or have a certain correlation with) the relative binding affinities^{98, 112}. α -NF acts as a partial agonist that can induce CYP1A target gene expression and elicit DRE probe binding. However, DiMNF inhibits CYP1A expression and lacks DRE-binding capability. Further predictive docking modeling suggests that DiMNF adopts a unique orientation with higher binding energy within the AHR LBD as compared to α -NF, which may enable AHR binding but not subsequent DRE binding¹¹². Accordingly, Some DLCs (i.e., certain PBDE congeners) do bind the AHR with low to moderate affinity but elicit non-detectable (or very weak) DRE binding¹¹³.

5. Toxicity of emerging AHR-active contaminants

5.1 DLCs and toxic potency

It is now clear that a number of ligands can activate AHR but do not elicit dioxin-like toxic effects; therefore, agonists of AHR can be divided into 'toxic' and 'nontoxic' categories, whose effects need to be respectively discussed. Metabolically stable compounds (e.g., TCDD and many HAHs) induce toxic effects, likely attributed to the persistent or sustained activation of AHR, which also suggests the toxic potential of some emerging DLCs with a persistent nature^{98, 114}. Among those toxic ligands, the production, distribution, transformation, and bioaccumulation of dioxins and DL-PCBs remain of great concern. Dioxins and DL-PCBs were included as initial persistent organic pollutants (POPs) in the Stockholm Convention on Persistent Organic Pollutants that need to be eliminated or their formation and release prevented. In 2005, certain congeners of dioxins and DL-PCBs with a persistent nature and direct evidence of exposure to humans were officially reevaluated and assigned a toxicity equivalent factor (TEF)^{2, 115}. The TEF concept includes a series of compounds that meet several criteria, including structural similarity to PCDD/Fs, the

capability to bind and activate AHR, and persistence and bioaccumulation in the food chain ¹¹⁵.

In addition to TEF-included compounds, other compounds with dioxin-like properties still need to be evaluated for inclusion into TEF concept, such as PCB-37, hexachlorobenzene ^{116, 117}, polychlorinated naphthalenes (PCNs) and polybrominated naphthalenes (PBNs) ². According to the notion that DLCs share a similar structure to dioxins and exert their toxicity predominantly through AHR, a series of emerging DLCs (e.g., PHCZs ¹¹⁸ and PCDPSs ¹¹⁹) have been identified in distinct environmental matrices and organisms. Moreover, there are still many compounds that have been predicted to have AHR binding potential by QSAR, suggesting that they may activate/block AHR or exert dioxin-like toxicity ¹²⁰. However, the environmental concentration, bioavailability, toxicity, and potential molecular mechanism of these compounds are largely unknown.

Since many emerging DLCs have been found to elicit effects similar to dioxin at the physiological or molecular level ^{14, 121, 122}, as a simplified method, the TEF concept is rather helpful for providing an estimate of the toxic potency, but cannot provide an assessment of the whole toxicity landscape. For example, non-dioxin-like PCBs have been observed to induce developmental neurotoxicity, although they have not been classified as the most toxic PCBs involved in the TEF concept ¹²³. Recent research has declared that ‘one TEF concept does not fit all’ because there may be differences in the diversity of congener-specific disturbances of biological processes ¹²⁴. Due to these limitations, a thorough investigation of emerging DLCs should be undertaken. As the concept of dioxin-like compounds is relatively large, we focus on PHCZs, PCDPSs, PCNs, polybrominated diphenyl ethers (PBDEs) and analogs in this review.

5.2 Toxicity of emerging DLCs

5.2.1 Polyhalogenated carbazoles (PHCZs)—PHCZs are a series of halogen-substituted carbazole congeners generated by natural (e.g., forest fires, volcanic eruptions, and enzymatic synthesis) or industrial processes (e.g., electronic devices, dyes, and pharmaceutical industrials). Their occurrence has already been found in various environmental matrices across the globe (e.g., up to 46.3 ng/g dw in sediments; 1.5-15.9 ng/g dw in soil from electronic-waste dismantling regions). As a novel class of environmental contaminants, they are of increasing concern (Table 1). A toxicology study in zebrafish has indicated that certain congeners (27-BCZ and 2367-CCZ) can induce swollen yolk sacs, elongated and unlooped hearts, and pericardial sac edema ¹²⁵. These adverse outcomes are similar to the cardiotoxic effects induced by TCDD and are indicated to be AHR-dependent by knocking down AHR2 ¹²⁵. *In vitro*, many PHCZ congeners show obvious CYP1A1 and 1B1 induction; furthermore, their magnitudes of response are similar to that of TCDD. The *in silico* molecular docking results indicate that certain PHCZ congeners can bind within the LBD utilizing the pose similar to TCDD, which supports the notion that PHCZs can be ligands of AHR and function through AHR ¹⁴. After an initial toxicity screen, certain congeners (27-BCZ and 36-BCZ) with greater toxic potential have been further investigated for other physiological effects (developmental toxicity and cardiotoxicity) as well as to determine their underlying mechanisms, such as epigenetics and

transcriptomic alterations^{27, 126}. Interestingly, most tested PHCZs congeners induced AHR downstream genes (e.g., CYP1A1). However, the differential effects of PHCZs as compared with TCDD is also revealed in that expression of AHRR (a sensitive AHR target gene usually up-regulated by TCDD) is down-regulated by 50% of the tested PHCZs congeners¹²⁷. In addition to their AHR-mediated effects, estrogen receptor (ER)-, glucocorticoid receptor (GR)-, and mineralocorticoid receptor (MR)-based reporter gene assays have revealed the endocrine disruption potential of PHCZs, especially through the ER¹³.

5.2.2 Polychlorinated diphenyl sulfides (PCDPSs)—PCDPSs, produced by incomplete combustion of wastes or other sorts of high-temperature processes¹²⁸, are a series of sulfur analogs of polychlorinated diphenyl ethers (PCDEs) and have dioxin-like toxic potential due to their structural similarity (Table 1). They include 209 congeners, and many of them can be detected in various environmental matrices (e.g., 0.10-6.89 ng/g dw in sediments and 0.18-0.21 ng/L in surface water of Yangtze River)¹¹⁹. Modeling data suggest that PCDPSs have bioaccumulation potential (i.e., most congeners' log *K_{ow}* > 5) and are environmentally persistent with half-lives of 120 days in the air, 6 months in water, and 12 months in soil^{129, 130}. Toxicology studies have shown that PCDPSs can induce adverse effects, including but not limited to producing oxidative stress¹¹⁹, inhibiting antioxidant enzyme activity¹³¹, and inhibiting growth¹³². Some of the toxic effects of PCDPSs are mediated by AHR¹²¹, and transactivation assays estimate that PCDPSs can activate human AHR as well as AHR homologs in avian species (chicken, ring-necked pheasant, and Japanese quail) with distinct potencies, indicating that activation is species-specific¹⁰⁴. As a result, the AHR activation potencies of some PCDPSs are even greater than the WHO-TEFs of OctaCDD, OctaCDF, and most coplanar PCBs¹⁰⁴.

5.2.3 Polybrominated diphenyl ethers (PBDEs) and their metabolites and analogs—PBDEs are a series of chemicals widely used since the 1970s as flame retardants in textiles, paints, furniture, and electronic products (Table 1). Despite the bans issued by regulatory actions, the massive reserves still lead to continuous release at present¹³³. Particularly, in certain e-waste dismantling regions, high-level PBDEs contamination has been reported, prompting additional concern¹³⁴. PBDEs are widely distributed in various environmental matrices, wildlife, and humans¹³⁵, and they and their metabolites can interfere with some endocrine nuclear receptors (e.g., ER¹³⁶, TR¹³⁷, etc.) and influence a variety of physiological processes^{138, 139}. Moreover, some PBDEs and analogs can interact with AHR. Both *in vitro* and *in vivo* assays have revealed that PBDEs and their analogs can induce CYP1A expression or AHR-mediated reporter gene expression^{140, 141}. Certain PBDE congeners have been confirmed to bind to AHR with low to moderate affinity¹¹³. A theoretical investigation has illuminated the potential AHR binding property of PBDEs and indicated that they contact via π - π stacking, and electron polarization may be involved in AHR binding, with Phe289, Phe345, and His285 being structurally required¹⁴². However, the final activity of PBDEs, as indicated by CYP1A expression, EROD, or other reporters, is still not clear. In various cell lines (MCF-7, HepG2, and H4IIE), certain PBDE congeners (BDE47, 77, 99, 100, 153, 154, 183, and 209) lead to no obvious induction of EROD or CYP1A expression. In addition, PBDE congeners exert antagonistic effects when coexposed with the potent agonist TCDD, both by interfering with the AHR interaction and the DNA

binding process¹⁴³. Based on these human and mouse models, the current opinion is that PBDEs possibly bind AHR but do not elicit transactivation^{113, 141, 143}. However, in the zebrafish ZFL cell line, evidence indicates that certain PBDE congeners, such as BDE99, can activate AHR¹⁴⁴. However, the results indicate that the active congener possibly acts as a transient and weak activator. Taken together, results indicate that PBDEs may not be potent activators of AHR in human or rodent models but may be partial weak agonists or antagonists. In addition, their species- or congener-specific effects still need further examination.

For PBDE metabolites and analogs such as OH-PBDEs and MeO-PBDEs, the situation is quite different, and more obvious AHR activity can be observed. In the H4IIE cell-based transactivation assay, many PBDE analogs are capable of activating AHR and eliciting 5.0% to 101.8% of the TCDD response, with potencies ranging from 7.35×10^{-12} to 4.00×10^{-4} . It has also been found, by comparing 6-HO-BDE-47, 5-Cl-6-HO-BDE-47, 6-HO-BDE-137, and 5-Cl-6-MeO-BDE-47, that slight alterations in the PBDE analog structure can alter the activation potency¹⁴¹. Generally, HO-PBDEs can induce greater dioxin-like activity than their corresponding MeO-PBDEs¹⁴¹. Moreover, these analogs specifically induce various adverse effects at both the molecular and physiological levels (e.g., endocrine disruption¹⁴⁵ and developmental disruption¹³⁸).

5.2.4 Polychlorinated naphthalenes (PCNs)—PCNs (Table 1), including up to 75 congeners, were listed in Annexes A and C to the Stockholm Convention on Persistent Organic Pollutants in 2015. The most toxic congeners of all known PCNs are hexachloronaphthalenes (e.g., PCN66 and PCN70) as determined by the DR-CALUX assay¹⁴⁶. PCNs were once largely used but are now banned in most countries due to their structural and potential toxicity similarity to dioxins¹⁴⁷. AHR activation by PCNs is an important mode of action. A recent screen revealed that 31 out of 42 tested PCN congeners have dioxin-like activity, and their relative potencies range from 1.2×10^{-7} to 0.0051, which are equal to or higher than WHO-TEFs of some PCBs¹⁴⁶. Similar to other DLCs, PCNs can induce multiple effects not limited to activating AHR/inducing CYP1A, including hepatotoxicity, neurotoxicity¹⁴⁸, and endocrine disturbances¹⁴⁹. Due to their legacy and unintentional generation by technical formulations, impurities in PCBs, and release from thermal processes, a recent determination of their presence in human food and human milk indicates health risks to humans¹⁵⁰. The data have indicated that PCNs have potential health impacts; although their cancer risk to infants is not significant, the noncarcinogenic adverse health effects of PCNs should not be neglected¹⁵⁰. As once there was no sufficient exposure data for PCNs on humans in the early days of their use, PCNs were not included in the TEF concept². However, presently, an increasing number of human samples¹⁵⁰ as well as food¹⁴⁷ and environmental¹⁵¹ sources of exposure data have been published, pointing out their toxic potential and the need for further research.

6. Evaluation of AHR activation/AHR-mediated toxicity

For environmental scientists, the AHR pathway is vital both for toxicity evaluation and mechanism exploration. The prototypical biomarker CYP1A, for the most part, can be used as an indicator of AHR activation but does not always indicate toxic potential¹⁵². The

toxicity of some DLCs has gradually been revealed, but in contrast to traditional dioxins and DL-PCBs, research on emerging DLCs is insufficient. Most scientific data are related to toxicity quantification using molecular endpoints or phenotypic effects. However, AHR, as a mediator of DLC toxicity, has many transactivation stages and mechanistic complexity (e.g., species-, ligand-, and tissue-specific variations), which prevent researchers from simply obtaining unified data for all situations. Therefore, to comprehensively understand traditional/emerging DLCs and evaluate their toxicity, many bioassays have been developed as described below.

6.1 Species-specific AHR evaluation

Generally, in research, AHR and its downstream effects mainly refer to those in human or rodent models, since their AHR pathways are relatively well characterized. However, certain metazoan species in which AHR genes have been identified may not be equally sensitive to dioxins and DLCs according to both theoretical speculation and experimental observations. The reasons for the difference in sensitivity could lie in the aspects of AHR sequence differences, the number of homologs, and AHR subform properties (e.g., expression level, predominance, and sensitivity) within or among species (Figure 2)^{1, 42}. All these aspects can interfere with the results of toxicity evaluation of dioxins/DLCs and should be considered when performing ecotoxicology research on various species. Regarding emerging DLCs, most toxic studies are performed by evaluating certain biomarkers using human or mouse models. As AHR largely accounts for the sensitivity of a species to DLCs, functional characterization of AHRs from distinct species would provide evidence for evaluating the potential toxicity of DLCs on a certain species¹⁵³. Species-specific evaluation includes traditional exposure experiments conducted *in vivo* or cloning and then artificially expressing a certain AHR *in vitro* and performing biochemical assays, such as those described for evaluating the effects of PCDDs on AHRs of various species¹⁰⁴.

6.2 Ligand-AHR interaction

Since ligand binding is the initial step of AHR activation and leads to subsequent downstream effects, examining the interaction of a potential ligand with AHR is an important aspect of toxicity evaluation. Using a saturation binding assay, ligand-AHR interaction can be assessed directly, including examining the binding properties of radiolabeled ligands (e.g., TCDD³, 2-azido-3-iodo-7,8-dibromodibenzo-p-dioxin¹⁵⁴, beta-naphthoflavone³², 2-(1'*H*-indole-3'-carbonyl)-thiazole-4-carboxylic acid methyl ester (ITE)¹⁵⁵, or kynurenine¹⁵⁶) or examining whether an uncharacterized AHR is capable of binding one of these ligands^{153, 157–159}. In addition, some indirect methods such as competitive binding assays have been developed to assess the AHR-binding activity of unlabeled ligands, such as described in Murray et al., who used a photoaffinity binding assay^{154, 160} to evaluate the competitive binding of α -naphthoflavone (α -NF) and several derivatives¹¹². For the characterization of the binding properties of kynurenine with AHR, using radioligand-binding assays with mouse liver cytosol from AHR-deficient and AHR-proficient mice, the equilibrium dissociation constant K_d of kynurenine binding to AHR has been determined to be approximately 4 μ M¹⁵⁶. With respect to receptor characterization, numerous AHR homologs (including some mutated homologs) from species across taxa have been functionally characterized^{22, 24, 157, 161, 162}. Interestingly, by comparing the

LBD of AHR homologs between bird species, the key residues (Val-325 and Ala-381) were found responsible for the reduced activity of tern AHR as compared to the chicken AHR¹⁵³ and, subsequently, to determine differences in activity of AHRs in dozens of other bird species²³. Similarly, by comparing intraspecies AHRs, some ecology-relevant issues have been resolved, such as deciphering the possible mechanism of the PCB tolerance of a certain Atlantic tomcod population in the Hudson River, which largely depends on the key residue loss in the LBD²².

6.3 AHR-DRE binding

During the AHR transactivation process, AHR-DRE binding is a vital variable that can be altered by distinct ligands⁴¹. Using gel retardation assays, 1,2-naphthoquinone (1,2-NQ) and 1,4-naphthoquinone (1,4-NQ) have been examined to determine whether they can directly activate AHR²⁸. To investigate wild-type, artificially mutated, or recombined AHR forms, this assay has been implemented to determine the key structural mechanism underlying AHR activation¹⁵, such as determining the residues that determine ligand efficacy. By testing mutated forms of mouse AHR, the F281A mutant AHR was shown to be constitutively active (ligand-independent) for DNA binding but was less active than wild-type AHR. The K284A mutant AHR has an increased level of DNA binding compared with wild-type AHR, suggesting that K284A may alter the DNA binding mechanism or potency¹⁵. Note that the AHR-DRE binding activity is ligand-specific^{28, 41}. The DNA-binding activity with non-canonical DREs (Section 3.2) needs further investigation.

6.4 Biomarkers or cell-based bioassays

6.4.1 CYP1A and EROD—CYP1A is a widely used biomarker for DLC toxicity evaluation and mechanistic exploration. The expression level of CYP1A along with its catalytic capability (indicated by EROD assay) can be indicators of AHR activation. In most cases of toxic dioxin-like HAHs, a chemical's potency for inducing CYP1A expression parallels its toxic potential, which also serves as the theoretical basis for the TEF concept². However, CYP1A induction should be carefully used when evaluating a potential ligand, as some ligands that induce CYP1A do not have dioxin-like toxicity (e.g., the, RMAHRLs)^{99, 152, 155, 163, 164}. Moreover, after the initial identification of CYP1A induction, a more comprehensive exploration of the tested ligands should be performed, such as performed in exploring PHCZ toxicity¹²⁵.

6.4.2 Reporter gene assays—*In vitro* screening or evaluation is usually the most efficient way to screen candidate compounds and provide initial knowledge about their toxic potential. The reporter gene assay represents a kind of method that meets the demand for toxicity evaluation or screening with the features of low cost, fast response, easy handling, etc.¹⁶⁵ The reporters widely used in AHR evaluation include fluorescent proteins (e.g., GFP, YFP, etc.) and enzymes (e.g., *lacZ* (β -galactosidase), *luxAB* (bacterial luciferase), firefly luciferase, etc.)¹⁶⁶. At present, reporter gene assays, especially luciferase-based assays, are widely used for official screening of food and feed¹⁶⁷ or for the identification and toxicity evaluation of some suspected compounds^{26, 104}. In addition, other alternative methods, such as FRET, fluorescent-conjugated antibodies, and fusion proteins (e.g., AHR-YFP/GFP), can be used for cellular imaging, measuring the degree of AHR activation, examining the AHR-

ARNT interaction, and figuring out the AHR subcellular location/translocation^{168, 169}. To date, these methods are undergoing continuous updates to meet multiple detection demands and improve future research on DLCs.

6.5 In vivo/ex vivo evaluation assays

In vivo/ex vivo methods are another class of tools for evaluating AHR-mediated toxicity and are usually based on wild-type or transgenic models. As implemented in identifying novel DLCs, exposing zebrafish embryos to PHCZs results in phenotypic alterations/toxicity similar to that of TCDD, suggesting that PHCZs function through a similar mechanism to TCDD¹²⁵. By comparing wild-type and AHR-knockout mice or rats exposed to TCDD, many physiological parameters (e.g., bile acid metabolism¹⁷⁰ and B cell responses¹⁷¹) have been observed to be distinctively altered, indicating the role of AHR. While examining the sensitivity of the AHR of an unidentified species, the *ex vivo* exposure method with precision-cut liver slices (PCLS) is direct and rapid and can help to evaluate the AHR sensitivity and gene expression in a certain species, such as in characterizing the Atlantic Cod AHR1a and AHR2a²⁹. To investigate DLCs' influences on various organs/tissues, immunohistochemical imaging of CYP1A expression as well as a type of artificial transgenic reporter would help to identify potential toxicity targets^{140, 172}. By determining molecular and physiological markers, distinct toxic response patterns and tissue-specific patterns can be revealed.

6.6 Omics-based examination

CYP1A expression is the gold standard for AHR ligand evaluation, for instance, in indicating agonist/antagonist activities and their enhancement or inhibition of AHR-dependent physiological function⁹⁶. CYP1A expression is easy to use but sometimes is not that informative or have a direct relationship with the adverse outcomes. Thus, attempts have been made to use systems biology to gain comprehensive insight into the potential impacts of ligands of interest¹⁷³, which also directly supports the idea that they have the potential to induce ligand-specific effects in addition to just activating AHR¹⁷⁴. By using a novel human reduced transcriptomics (RHT) approach to assess pathway-based profiles of AHR ligands, several ligands' (i.e., TCDD, TCS, and 5-Cl-6-HO-BDE47) toxic mechanisms have been revealed¹⁷⁵. This method provides direct support that the AHR pathway is the major pathway induced by TCDD. For 5-Cl-6-HO-BDE47, the AHR pathway is less sensitively induced than the 'stress response'-related pathway. The authors suspect that 5-Cl-6-HO-BDE47 may initiate multiple biological events as early responses and not just induce AHR activation, which is thought to be a secondary effect¹⁷⁵.

In addition to the above-mentioned methods, other methods, such as *in silico* simulation or biochemical assays (e.g., ELISA), are also helpful for evaluating the AHR activation potential or AHR-relevant parameters. As the protein structure of AHR has not been fully resolved, current simulations are based on homology modeling and need to be further validated by biochemical assays. By virtue of the numerous AHR sequences of distinct species, modeling enables the characterization of the key residues within the LBD of the AHR of interest that interact with potential ligands⁴². With regard to ligands, QSAR models

based on multiple physicochemical parameters can predict the potential binding affinity of suspected compounds and provide factors that influence their binding ¹²⁰.

7. Summary and perspectives

Currently, the elucidation of AHR-related effects, mechanisms, and methods have for the most part been investigated using the classical ligand TCDD. The information obtained provides an important starting point when conducting similar research on other compounds. However, the effects and specific mechanisms of toxicity of emerging DLCs are possibly different from those of TCDD and thus need thorough consideration for chemical-specific variation in the role of AHR in mediating their effects.

For those DLCs, AHR mediation is one of the most fundamental mechanisms. DLCs have diverse toxic effects, which may rely on their corresponding physicochemical properties. Moreover, when considering the AHR, the AHR-ligand interaction (e.g., the binding affinity, binding pose, and structural change of the LBD), DNA recognition and cofactor recruitment are fundamental for the diverse outcomes of DLCs. Although some major motifs or domains of AHR have been defined and preliminarily functionally characterized, the knowledge of AHR is still limited when generating or predicting the potential correlation between AHR structure/sequence and its function or sensitivity. Besides, we also need to investigate AHR holistically, although certain parts of AHR already have ‘widely accepted’ functions, since even subtle changes in AHR or ligands may greatly alter subsequent functions or outcomes.

For these reasons, and the inter-species sequence dissimilarity, the diversity of AHR homologs of distinct species would be of another great interest especially when evaluating the DLC ecotoxicity. However, we currently have limited knowledge and lack a uniform method to clearly specify the sensitivity differences among species to various DLCs. Regarding this aspect, future research may need to focus on developing some new assays that could be easily set up and flexibly extend the usage on cross-species DLC evaluation or even the properties of the candidate AHR itself.

In summary, the current toxicology research on DLCs mostly concerns some basic toxic endpoints and the bioassay-determined potential to elicit certain molecular- or (sometimes) physiological-level effects. Thus, more detailed information on the mechanisms/effects of DLCs on wildlife and humans is expected. As we learn more about these emerging, structurally diverse DLCs, understanding the diversity of AHR-mediated mechanisms involved in their toxicity is both an important and a fascinating area of research. Advances in understanding AHR biology will help advance understanding of the toxicology of these emerging DLCs.

ACKNOWLEDGEMENTS

This work was supported by the National Natural Science Foundation of China (No. 22006049), and the U.S. National Institute of Environmental Health Sciences (NIEHS) (P42ES007381 and R01ES032323).

All the authors wrote and revised this paper. The authors declare no competing financial interests.

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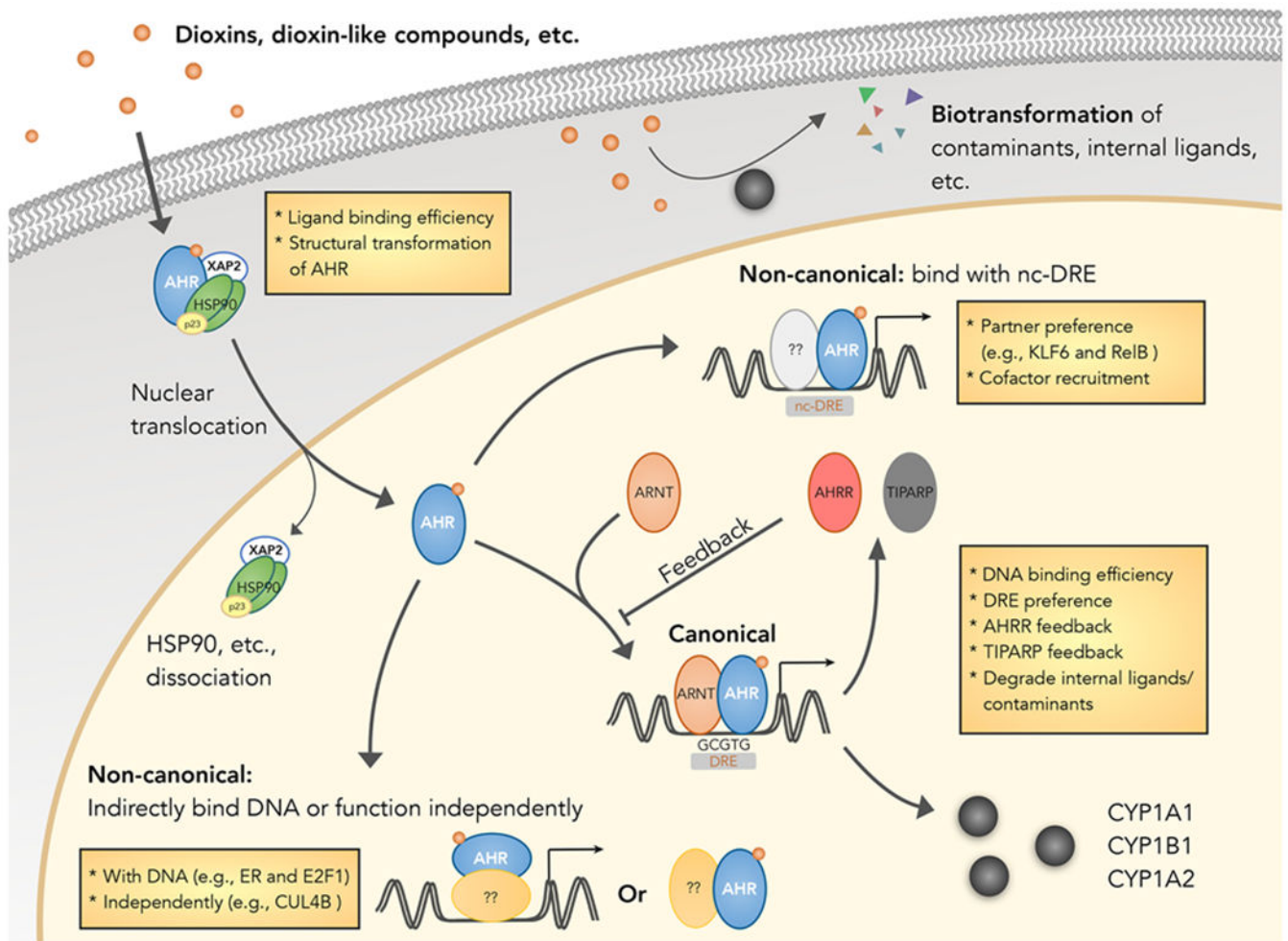


Figure 1. Mechanisms of ligand-dependent AHR activation and AHR-mediated activities with the key influencing factors marked in the boxes. Once potent ligands (including dioxins and DLCs) enter the cell, they bind AHR to induce AHR nuclear translocation, partner dissociation, and the canonical response of AHR-DRE association as well as target gene expression. Alternatively, AHR can exert non-canonical signaling by indirectly binding DNA or functioning with other proteins.

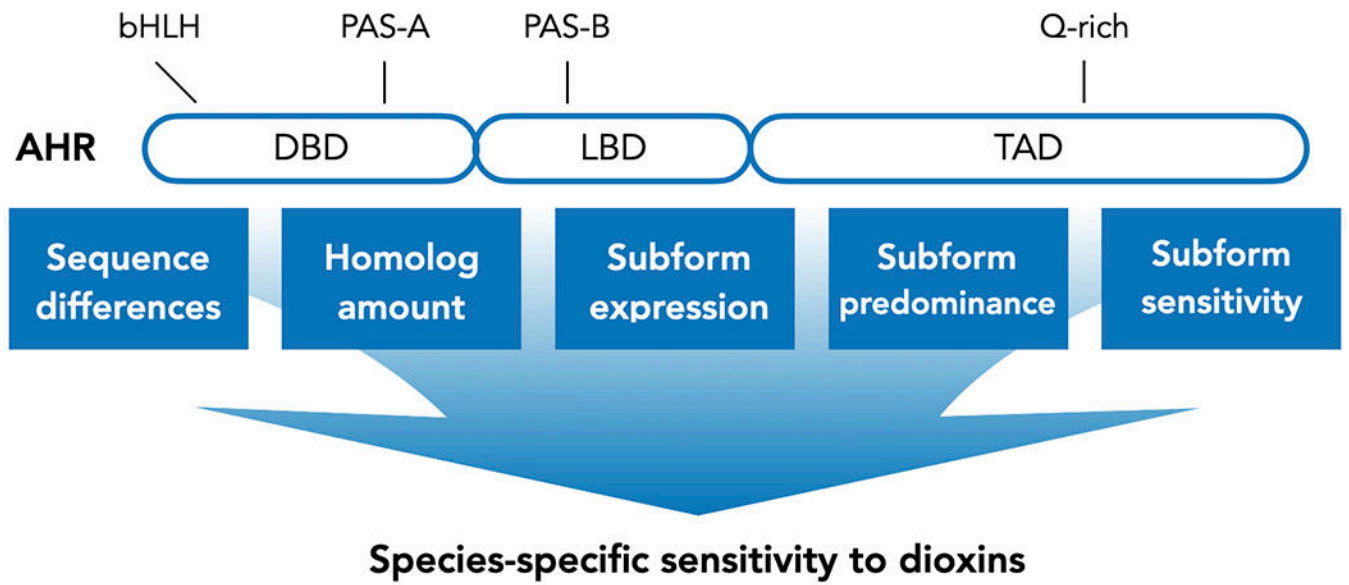
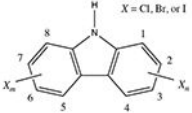
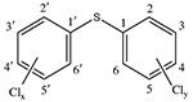
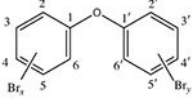
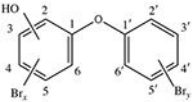
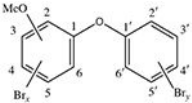
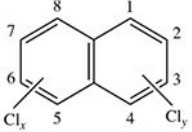


Figure 2.

Key factors that affect species-specific sensitivity to dioxins and DLCs, including the sequence differences of AHRs, the number of homologs in different species and properties of subforms (expression abundance, functional predominance, and sensitivity).

Table 1.

Structure, potency, and toxicity of the DLCs of PHCZs, PCDPs, PBDEs (and analogs), and PCNs.

Compounds	Structure	Potency and toxicity	
		Potency relative to TCDD	In vivo/vitro toxicity
PHCZs		1.3×10^{-5} to 6.6×10^{-4} (human <i>CYP1A1</i>) ⁴⁵ 1.3×10^{-4} to 9.7×10^{-3} (human <i>CYP1B1</i>) ⁴⁵ NE to 2×10^{-2} (CBG 2.8D cells) ¹⁴	cardiotoxicity (zebrafish) ¹²⁵ endocrine disturbance (zebrafish) ¹³ oxidative damage and apoptosis (zebrafish embryo) ¹⁷⁶ inhibited tube formation (HUVECs) ¹²⁶
PCDPs		NE to 7.4×10^{-4} (chicken AHR) ¹⁰⁴ NE to 1.5×10^{-2} (pheasant AHR) ¹⁰⁴ NE to 2.1×10^{-1} (quail AHR) ¹⁰⁴	induce ROS and genotoxicity (HepG2 cells) ¹²¹ notochord kinks and twists (zebrafish) ¹⁷⁷ hepatic oxidative stress (mouse) ¹⁷⁸ alter antioxidant enzymes (goldfish) ¹³¹ growth inhibition (<i>Scenedesmus obliquus</i>) ¹³²
PBDEs		No statistically significant induction of CYP1A (monkey hepatocytes) ¹⁷⁹ inhibit TCDD-induced EROD activity (primary cultured carp hepatocytes) ¹⁸¹ BDE-99 as a transient AHR agonist (ZFL cells)	promote proinflammatory protein (zebrafish) ¹⁸⁰ malformation (zebrafish embryo) ¹⁸² life-long behavioral alterations (zebrafish) ¹⁸³ bind and activate ERR γ (HeLa cells) ¹⁸⁴
OH-PBDEs		NE to 7.8×10^{-4} (chicken AHR) ¹⁸⁵ NE to 1.1×10^{-2} (pheasant AHR) ¹⁸⁵ NE to 1.7×10^{-1} (quail AHR) ¹⁸⁵ 7.35×10^{-12} to 4×10^{-4} (H4IIE- <i>luc</i>) ¹⁴¹	affect early life development (zebrafish) ¹³⁸ estrogenic effects via GPER (SKBR3 cells) ¹⁸⁶ inhibit human placental aromatase activity ¹⁸⁷ disrupt oxidative phosphorylation (zebrafish larvae) ¹⁸⁸
MeO-PBDEs		NE to 1.7×10^{-4} (chicken AHR) ¹⁸⁵ NE to 3.7×10^{-3} (pheasant AHR) ¹⁸⁵ NE to 6.4×10^{-2} (quail AHR) ¹⁸⁵ 2.23×10^{-8} to 6.48×10^{-5} (H4IIE- <i>luc</i>) ¹⁴¹	depressive effect on feeding behavior (<i>Daphnia magna</i>) ¹⁸⁹ phytotoxicity (Maize) ¹⁹⁰ endocrine disruption (CHO cells) ¹³⁷
PCNs		3.6×10^{-10} to 2.6×10^{-3} (H4IIE-EROD) ¹⁹¹ 1.0×10^{-8} to 2.2×10^{-8} (H4IIE- <i>luc</i>) ¹⁹¹ 1.6×10^{-7} to 3.1×10^{-3} (PLHC-1 cells) ¹⁹¹ 1.5×10^{-4} to 4.0×10^{-3} (H4IIE- <i>luc</i>) ¹⁹⁵	androgenic effects (ovarian follicles) ¹⁹² embryo- and fetotoxic effects (rats) ¹⁹³ accelerate spermatogenesis (rat) ¹⁹⁴ disturb GABA metabolism (rat brain) ¹⁹⁶

NE: not estimated

* Note that the potency ranges listed here are determined by the original research using some of the selected congeners but not all.