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# The aryl hydrocarbon receptor repressor – More than a simple feedback inhibitor of AhR signaling: Clues for its role in inflammation and cancer

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## Abstract

The aryl hydrocarbon receptor repressor (AhRR) was first described as a specific competitive repressor of aryl hydrocarbon receptor (AhR) activity based on its ability to dimerize with the AhR nuclear translocator (ARNT) and through direct competition of AhR/ARNT and AhRR/ ARNT complexes for binding to dioxin-responsive elements (DREs). Like AhR, AhRR belongs to the basic Helix-Loop-Helix/Per-ARNT-Sim (bHLH/PAS) protein family but lacks functional ligand-binding and transactivation domains. Transient transfection experiments with ARNT and AhRR mutants examining the inhibitory mechanism of AhRR suggested a more complex mechanism than the simple mechanism of negative feedback through sequestration of ARNT to regulate AhR signaling. Recently, AhRR has been shown to act as a tumor suppressor gene in several types of cancer cells. Furthermore, epidemiological studies have found epigenetic changes and silencing of AhRR associated with exposure to cigarette smoke and cancer development. Additional studies from our laboratories have demonstrated that AhRR represses other signaling pathways including NF- $\kappa$ B and is capable of regulating inflammatory responses. A better understanding of the regulatory mechanisms of AhRR in AhR signaling and adverse outcome pathways leading to deregulated inflammatory responses contributing to tumor promotion and other adverse health effects is expected from future studies. This review article summarizes the characteristics of AhRR as an inhibitor of AhR activity and highlights more recent findings pointing out the role of AhRR in inflammation and tumorigenesis.

#### Keywords

AhR; AhRR; inflammation; cancer; NF-kB; cytokines

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# Introduction

The aryl hydrocarbon receptor (AhR) belongs to the superfamily of basic Helix-Loop-Helix/ Per-ARNT-Sim (bHLH/PAS) proteins and is activated by low molecular weight compounds (1–3). Upon ligand-binding in the cytoplasm, AhR shuttles in the nucleus, dimerizes with AhR nuclear translocator (ARNT) and binds to dioxin-responsive elements (DRE) in the enhancer/promoter of target genes to induce transcription. AhR target genes encode for drug-metabolizing enzymes, such as cytochrome P450 (CYP) 1A1, as well as for proteins controlling cell proliferation, differentiation, and apoptosis (1, 2). In addition, AhR activation is frequently associated with the stimulation of other signal transduction pathways, including epidermal growth factor receptor (EGFR) (4, 5), protein kinase A (PKA) (6, 7), and NF- $\kappa$ B signaling (7, 8).

In 1999, the team of Yoshiaki Fujii-Kuriyama screened a mouse genomic library using an AhR cDNA as hybridization probe, and discovered a novel component of AhR signaling: The AhR repressor (AhRR) (9). Meanwhile, the *Ahrr* gene has been identified in the human (10, 11), rat (12, 13), chicken (14), frog (15), and fish (16–18) genome.

#### AhRR as a feedback regulator of AhR signaling

The N-terminal half of the AhRR protein has high structural similarities with AhR, i.e. it contains the DNA-binding bHLH domain and the PAS-A domain. In contrast, its C-terminal part does neither contain the PAS-B domain nor the Q-rich transactivation domain, indicating that AhRR lacks the established AhR ligand-binding domain and is transcriptionally inactive (9). AhRR expression is regulated by one or more DREs located in the enhancer/promoter sequence of the murine and human *Ahrr* gene (19–21), indicating that the AhR controls the expression of its own repressor protein. Indeed, overexpression experiments revealed that AhRR is capable of inhibiting AhR/ARNT-triggered transactivation of DRE-containing gene promoters by competing with AhR for both dimerization with ARNT and DRE-binding (9, 19) (figure 1). Specifically, after post-translational sumoylation (22) AhRR may recruit co-repressor molecules and histone deacetylases to DRE-containing gene promoters (21, 23, 24). The subsequent condensation of the local chromatin structure hinders a further binding of transcription factors and abrogates transcription of AhR target genes (25).

In addition, a so-called "transrepression" model was proposed to explain the inhibitory effect of AhRR on AhR transactivation (26). The authors observed that repression of AhRdependent gene expression by AhRR involves the N-terminal part of AhRR and does not involve a competition for ARNT. Also, DRE-binding was not necessary for AhRR's repressive function in this study, but further contributed to it. One hypothesis of the authors is that AhRR represses AhR by competing for limiting co-activator molecules (26). Comparable transrepression models have been proposed for the interaction of AhR with NF- $\kappa$ B RelA (27) and EGFR (28).

Besides the DRE, the human and rodent *Ahrr* genes contain binding sites, which are recognized by NF- $\kappa$ B and zinc-finger transcription factors of the Sp1 family (13, 19–21).

Whereas under inflammatory conditions the NF- $\kappa$ B subunit RelA may cooperate with AhR to induce AhRR expression (19, 29), Sp1-related factors may contribute to basal AhRR expression (21). In addition, nuclear factor erythroid-2-related factor-2 (Nrf2) has been recently identified to control AhRR expression in murine kidney tissue by inducing the expression of microRNA-125b (30).

Mammalian AhRR is expressed in nearly all tissues tested so far, but may be restricted to some and not all of the cell populations in a given tissue (9, 31–35). Interestingly, its expression level does not always correlate with CYP1A1 inducibility, indicating that AhRR may affect other signaling pathways and cellular functions.

#### The AhRR as regulator of inflammatory responses

Inflammatory processes contribute to a multitude of pathologies and have emerged as a major factor promoting cancer development (36). A link of environmental exposure with changes of inflammatory mediators and the possible consequences for carcinogenesis has been recently reviewed (37). 2,3,7,8-tetrachlorodibenzo-*p*-dioxin (TCDD) is a potent tumor promoter that exerts its action via prolonged activation of AhR signaling. Studies on the mechanism of TCDD-induced liver tumor promotion revealed that inflammatory signaling and increased expression of pro-inflammatory cytokines are critical components (38). This hypothesis is also supported by findings showing that the classical AhR signaling pathway does not completely explain the toxic or carcinogenic action of dioxins. In contrast, there is evidence indicating that CYP1A1 and CYP1A2 provide protection from dioxin-induced acute hepatotoxicity and inflammation (39). On the other hand, the deficiency of CYP1A1 protected male mice from TCDD-induced wasting and lethality (40).

Increased levels of AhR as well as constitutively active AhR have been found in tumors and various cancer cell-lines (41–44). The enhanced expression of AhR in cancer may be triggered by NF- $\kappa$ B and STAT3 (45, 46), which could explain the positive correlation of AhR expression with an inflammatory status and inflammatory-dependent tumor development. These findings may provide a possible mechanism connecting anti-inflammatory responses of AhRR with its tumor-suppressive properties. In fact, we have created AhRR-overexpressing transgenic mice (AhRR Tg), which have significantly reduced inflammatory and acute toxic responses to TCDD compared to wild-type (wt) mice (47).

Recent studies, including our own report, revealed that the AhR is involved in immunity and bacterial lipopolysaccharide (LPS)-mediated responses *in vivo* (48–51). Studies on the basic mechanism of LPS tolerance found that it is mediated by the sustained silencing of a set of acute pro-inflammatory genes (52, 53). This paradigm is well-established as an effective means to help animals as well as humans survive serious infections accompanied with severe systemic inflammation. The importance of IL-1 $\beta$  in mediating LPS shock has been demonstrated using knockout (ko) mice that lack IL-1 $\beta$ -converting enzyme and are unable to produce active IL-1 $\beta$  and are resistant to LPS shock (54). This is particularly important since a recent report shows a reduced susceptibility towards LPS shock in AhRR-reporter and AhRR<sup>-/-</sup> mice (55). The authors found that AhRR is highly expressed in immune cells of barrier organs, and has a major impact on the regulation of inflammatory responses. AhRR

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prevents excessive IL-1 $\beta$  production in bone-marrow derived macrophages. This is consistent with a reduced expression of IL-1 $\beta$  found in tissues from TCDD-treated AhRR Tg mice (47). In contrast to the antagonizing effect of AhRR in response to LPS, AhR and AhRR seem to cooperate dampening intestinal inflammation (55). Similar to AhRdeficiency (56–58), AhRR<sup>-/-</sup> mice exhibited an enhanced susceptibility to dextran sodium sulfate-induced colitis. In contrast to AhR, whose expression in intestinal epithelial cells is important to maintain proper barrier functions (59), AhRR contributes to the maintenance of colonic intraepithelial lymphocytes and prevents excessive production of IL-1 $\beta$  and differentiation of Th17/Tc17 cells. Moreover, AhRR enhances  $\gamma$ -interferon production by effector T cells in the inflamed gut (55). These findings underscore that AhR and AhRR are expressed in a cell- and tissue-specific manner and may affect different target cells. Future studies with AhRR Tg and AhRR-reporter mice for instance may provide further insight into the role that AhRR plays in various inflammatory responses.

# The AhRR in cancer biology

AhR is overexpressed and/or over-activated in various solid cancers (41-43), in which it may drive proliferation, apoptosis resistance, extracellular matrix degradation, and immunosuppression (60-66). Thus, AhR's opponent may exhibit tumor-suppressive properties as depicted in figure 2. Indeed, the human *Ahrr* gene is located on the short arm of chromosome 5 (5p15.3), a region which is frequently deleted in various tumors (67-72), indicating the presence of a tumor suppressor gene. Frank Cuttitta and his team observed a very low AhRR expression rate in several human cancer biopsies, which was due to hypermethylation of the AhRR promoter (73). These cancers include colon, lung, esophagus and stomach tumors (73), and, interestingly, AhR is abundantly expressed in these cancer types (74–78). A low AhRR expression level that correlated with poor prognosis was also found in gastric adenocarcinomas (79). In human colorectal cancer tissue, AhRR expression correlated with CD40/CD40L signaling and histological grade. Subsequent experiments in colon cancer cell-lines revealed that CD40L treatment increases AhRR expression, resulting in a more pronounced inhibition of tumor cell growth and induction of apoptosis, respectively (80). Like other members of the tumor necrosis factor (TNF) receptor family, CD40 activation induces nuclear translocation and DNA-binding of RelB/p50 (81), which may contribute to proper anti-tumor immune responses (82), for instance in colorectal cancer (83). However, whether the CD40-dependent induction of AhRR is triggered by noncanonical NF-KB signaling remains to be elucidated. Alternatively, AhRR expression may be induced by constitutive AhR activation via CD40L. Allan and Sherr demonstrated that CD40L upregulates AhR mRNA and protein levels in B cells leading to nuclear translocation of AhR and induction of CYP1A1 in the absence of exogenous ligands (84).

*In vitro* analyses of several human tumor cell-lines further underscored a tumor-suppressive function of AhRR (table 1). For example, RNAi-mediated AhRR-silencing in human lung carcinoma cells enhanced proliferation, apoptosis resistance, motility, and invasive growth (73). Transplantation of AhRR-silenced tumor cells into immune compromised mice resulted in an enhanced growth and a pronounced angiogenic potential of the tumors (73). AhRR overexpression inhibited anchorage-dependent and –independent growth as well as the angiogenic potential of lung cancer cells (73), and abrogated proliferation and AhR-

mediated anti-apoptosis in breast cancer cells (85–87) (table 1). Overexpressed AhRR was clearly capable of overcoming the anti-apoptotic effect of TCDD-activated AhR in those cells. Moreover, a recent study with AhRR<sup>-/-</sup> mice showed a lower number of apoptotic cells in liver of LPS-treated mice (55), confirming the role of AhRR to resolve an anti-apoptotic response *in vivo*.

In MCF7 breast cancer cells, an inhibitory effect of AhRR on the transcriptional activity of estrogen receptor-a. (ERa.), which was probably due to a direct protein-protein interaction, was observed (88). Interestingly, some of the ERa target genes whose expression was repressed by AhRR, such as pS2 and cathepsin D, have been previously reported to be down-regulated in TCDD-exposed MCF7 cells (89–91). Further analyses revealed that the repression of ERa target gene expression occurred in an AhR-dependent but ARNT-independent manner (91), suggesting that AhR and AhRR may directly cooperate to inhibit ERa-dependent transcription. Notably, a physical interaction between AhR and AhRR has been observed in ectopic overexpression experiments (92).

The above mentioned changes in angiogenesis and invasion (73) may be also explained by a potential crosstalk with the other binding partner of ARNT, hypoxia-inducible factor-1a. (HIF-1a.). The HIF-1a/ARNT complex is activated by low oxygen concentrations or oncogenic signal transduction (e.g. overactive RAS) to enable angiogenesis and ensure oxygen and nutrient supply in fast growing tumors (93). HIF-1 is also important for tissue invasion and metastasis of tumor cells and thus is a key player in cancer progression (93). Interestingly, Mark Hahn and co-workers have identified a splice variant of AhRR that lacks exon 8 and is pre-dominantly expressed in human cells and tissues (92). Overexpression experiments revealed that this AhRR variant is capable of inhibiting HIF-1-dependent transcription (92). Although further research is needed, these observations already mark AhRR as a potentially very attractive target molecule for cancer therapy.

In soft tissue angiofibroma, a histologically distinctive benign mesenchymal neoplasm of unknown cellular origin, a chromosomal rearrangement between chromosomes 5 (5p15) and 8 (8q13) resulted in the creation of a fusion protein between AhRR and nuclear receptor co-activator-2 (NCOA2) (94). The N-terminal part of the chimeric protein consists of the AhRR protein and thus harbors all domains necessary for DRE-binding. The C-terminal AhRR domain, lacking a Q-rich transactivation domain, is substituted by the NCOA2 protein, producing a fusion protein with two activation domains (94). Global gene expression analyses showing an upregulation of AhR target genes, revealed that the AhRR/NCOA2 fusion protein is able to mimic canonical AhR signaling (94). Although this chimeric AhRR/ NCOA2 protein has so far only been detected in a small number of soft tissue angiofibromas, it is conceivable that an inactivation of AhRR's repressive function through chromosomal rearrangements may also occur in other tumor types.

In context of chemical skin carcinogenesis, however, AhRR may not act as a tumor suppressor. Benzo[*a*]pyrene (BaP) and structurally related PAHs need to undergo CYP1A-mediated oxidations in order to unleash their carcinogenic potential (95). Accordingly, AhR<sup>-/-</sup> mice as well as transgenic mice carrying an epidermis-specific ARNT-deficiency are largely protected against the skin carcinogenicity of BaP (96–98). Thus, one would expect

that AhRR<sup>-/-</sup> mice are more prone to BaP-induced skin cancer. However, a chronic carcinogenesis study on AhRR<sup>+/+</sup> and AhRR<sup>-/-</sup> mice has shown a significantly delayed occurrence of BaP-induced skin tumors in mice that lack AhRR (99). The authors conclude that a shift of CYP1A1-driven metabolism from metabolic activation to detoxification is responsible for this unexpected outcome (99). A comparable shift in toxification/ detoxification was previously discussed with regards to various CYP1-ko strains, exhibiting significantly more DNA adducts after oral BaP exposure than wt littermates (100).

Another observation that may contradict AhRR's tumor-suppressive function is the hypomethylation of the AhRR promoter, which is frequently observed in blood and lung tissue samples from smokers (101–110). These epigenetic modifications are associated with an elevated risk to develop malignancies of the respiratory tract (104, 108, 109) and thus imply a putative role of AhRR in lung carcinogenesis. As previously discussed (106), tobacco smoke is rich in PAHs and may cause an AhR-mediated induction of AhRR gene expression, which requires chromatin relaxation associated with DNA demethylation (111). However, at least three studies found that the alterations in AhRR promoter methylation induced by prenatal maternal smoking may persist in the exposed offspring until adolescence (101, 102, 110).

With the exception of PAH-induced cancer (figure 3), the majority of the publications discussed above points to the idea that AhRR is a potent tumor suppressor protein. Its expression level may serve as a prognostic factor with low levels correlating with tumor malignancy. AhRR may inhibit proliferation and increase apoptosis susceptibility of malignant cells, and thus prevent the establishment of a tumor-promoting, pro-inflammatory microenvironment by modulating cytokine responses, and attenuating angiogenic and invasive processes. The underlying molecular mechanisms, however, are enigmatic and probably involve a crosstalk of AhRR with other signal transduction pathways including C/ EBP $\beta$  and NF- $\kappa$ B as recently shown (47). Future studies are needed to address the regulatory mechanisms of AhRR in AhR signaling and adverse outcome pathways based on deregulated inflammatory and/or anti-apoptotic responses contributing to tumor promotion and other adverse health effects.

### Conclusion

While AhRR can effectively block AhR-dependent responses, there are many unanswered questions, including why CYP1A1 is not always suppressed when AhRR is overexpressed (112). The model of "transrepression" as described above may explain, at least partially, this observation. As AhR-driven CYP1A1 gene expression requires transcriptional co-activators, including CBP/p300 and SRC-1 (113–115), cell- or tissue-specific expression patterns of such co-factors could explain the observed discrepancy between AhRR expression and CYP1A1 inducibility.

Previous reports show that AhRR is predominantly located in the nucleus (116), however the effect of AhRR on non-canonical AhR signals (47) suggests the presence and functional activity of AhRR in the cytosol. In this context, it is noteworthy that both the interaction of AhR with HSP90 and XAP2 in the cytosol as well as the repression of AhR by AhRR

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involve the N-terminal domain of AhR (26, 117). Although AhRR does not contain the established AhR ligand-binding domain, it would be important to determine if the nuclear localization of AhRR or dimerization with ARNT can be stimulated by AhR agonists.

Interestingly, the NF-KB member RelB, which may interact with AhR in the non-canonical AhR pathway (118), has been found to interact with ARNT via CD30-mediated NF-κBdependent transcription (119). RelB has been demonstrated to promote cell growth through regulation of p53 stability and retinoblastoma protein activation (120). This mechanism supports recent findings showing that promotion of certain blood cancers (e.g. human multiple myeloma and anaplastic large cell lymphoma) rely on ARNT by antagonizing RelB and p53-dependent cell-cycle arrest and apoptosis (121). Expression of RelB was also shown to be critical for survival of Hodgkin lymphoma (122). Interestingly, a recent meta-analysis found that exposure and increased blood levels of TCDD are significantly associated with the mortality caused by non-Hodgkin's lymphoma (123). Furthermore, our previous reports strongly support the function of AhR to mediate an anti-apoptotic response in human lymphoma cells (124) and the vital role of RelB in AhR-mediated apoptotic resistance in human breast cancer cells (61, 66). Because both, AhRR and RelB, may form heterodimers with ARNT (figure 2), it is essential to understand the possible interaction of AhRR/ARNT with RelB and its consequences in regulation of cellular processes, like cell-cycling and apoptosis. Moreover, it is likely that the dominant role of AhRR in complex with ARNT is via its interaction with RelB and the non-canonical AhR pathway resulting in downregulation of cellular inflammation, suppression of an anti-apoptotic response, and supporting its role as a tumor suppressor gene. Figure 3 summarizes the possible interactions of AhRR with AhR signaling pathways and its consequences in cellular processes and carcinogenesis.

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#### Abbreviations

AhR	aryl hydrocarbon receptor		
AhRR	aryl hydrocarbon receptor repressor		
ARNT	AhR nuclear translocator		
BaP	Benzo[a]pyrene		
СҮР	cytochrome P450		
DREs	dioxin-responsive elements		
EGFR	epidermal growth factor receptor		
bHLH/PAS	Helix-Loop-Helix/Per-ARNT-Sim		

HIF-1a	hypoxia-inducible factor-1a	
LPS	lipopolysaccharide	
NCOA2	nuclear receptor co-activator-2	
Nrf2	nuclear factor erythroid-2-related factor-2	
ГСДД	2,3,7,8-tetrachlorodibenzo-p-dioxin	

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interactions rather than by inhibition of the formation or DNA-binding of the AhR/ARNT heterodimer. [PubMed: 18000031]

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# Highlights

- The AhRR as a specific competitive repressor of AhR
- The AhRR represses alternative AhR signaling pathways
- The AhRR regulates inflammatory responses
- The AhRR may act as a tumor suppressor gene



#### Figure 1.

Schematic illustration of the repression of the canonical AhR signaling pathway by AhRR. The ligand-activated AhR translocates into the nucleus, dimerizes with ARNT and binds on DRE sequences in the promoter region of AhR target genes, including CYP1A1 and AhRR. The increased expression of AhRR inhibits AhR activity as a result from the competition with AhR for dimerization with ARNT. Alternatively, the formation of an AhRR/ARNT complex may inhibit AhR function through binding on DRE sequences, which does not involve the competition for dimerization with ARNT. Vogel and Haarmann-Stemmann



#### Figure 2.

Schematic illustration of the interaction of AhRR with the canonical and non-canonical AhR pathways. AhRR represses the canonical AhR pathway including the induction of CYP1A1 *via* competitive binding with ARNT. AhRR may protect from non-canonical AhR-mediated inflammatory responses and inflammation-dependent carcinogenesis via interaction of AhRR with RelB in complex with ARNT and/or AhR. Black double arrows indicate the interaction of AhRR with ARNT and RelB with AhR. The white double arrow indicates the interaction of ARNT with RelB. Abbreviations: Protein kinase A (PKA)



#### Figure 3.

Interactions of AhRR with AhR signaling pathways and possible consequences in carcinogenesis. Abbreviation: CCAAT-enhancer-binding protein (C/EBP), Estrogen receptor (ER), Hypoxia-inducible factor-1 (HIF-1), Retinoblastoma protein (Rb). In red: oncogenic properties; in green: tumor suppressive properties

#### Table 1

Effects of AhRR overexpression and RNAi on cell biological endpoints and gene expression in vitro.

CELL-LINE	MANIPULATION	OUTCOME	REF #
A549 bronchoalveolar carcinoma cells	overexpression of human AhRR	diminished anchorage-dependent and -independent cell growth, reduced angiogenic potential (tube formation)	73
A549 cells	transient RNAi of AhRR	enhanced anchorage-dependent and -independent cell growth	73
BP1 mammary epithelial cells	overexpression of fish AhRR (Fundulus heteroclitus)	reduced constitutive AhR activity; reduced expression of CYP1B1	60
MCF7 breast cancer cells	overexpression of human AhRR	reduced cell proliferation; increased expression of cyclin D1; reduced expression of E2F and cathepsin D	86
MCF7 cells	overexpression of human AhRR	reduced expression of the estrogen-responsive genes pS2, cathepsin D, and complement C3	87
MCF7 cells	transient RNAi of AhRR	no effect on TCDD-induced expression of CYP1A1, CYP1B1, and TCDD- inducible poly (ADP-ribose) polymerase	125
MCF-10AT1 mammary epithelial cells	overexpression of murine AhRR	enhanced susceptibility towards UV-induced apoptosis	87
MCF-10A mammary epithelial cells	stable RNAi targeting AhRR	induced colony formation in soft agar	73
MCF-10F mammary epithelial cells	overexpression of fish AhRR ( <i>F. heteroclitus</i> )	reduced cell proliferation	85
MCF-10F cells	lentiviral overexpression of fish AhRR ( <i>F. heteroclitus</i> )	reduced constitutive AhR activity; reduced expression of CYP1B1	60
HC11 mammary epithelial cells	overexpression of human AhRR	reduced expression of 3-casein	126
HepG2 hepatoma cells	overexpression of human AhRR	reduced expression of the estrogen-responsive genes pS2, cathepsin D, and complement C3	87
Hs578T breast cancer cells	overexpression of fish AhRR ( <i>F. heteroclitus</i> )	reduced constitutive AhR activity; no effect on cell proliferation	127
Hs578T cells	overexpression of fish AhRR (F. heteroclitus)	increased expression of the proto-oncogene c-myc	128