Clinical Relevance of the Constitutive Androstan Receptor

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ABSTRACT

Constitutive androstan receptor (CAR) (NR1I3), a xenobiotic receptor, has long been considered a master mediator of drug disposition and detoxification. Accumulating evidence indicates that CAR also participates in various physiologic and pathophysiologic pathways regulating the homeostasis of glucose, lipid, and bile acids, and contributing to cell proliferation, tissue regeneration and repair, as well as cancer development. The expression and activity of CAR can be regulated by various factors, including small molecular modulators, CAR interaction with other transcription factors, and naturally occurring genetic variants. Given that the influence of CAR has extended beyond the realm of drug metabolism and disposition and has expanded into a potential modulator of human diseases, growing efforts have centered on understanding its clinical relevance and impact on human pathophysiology. This review highlights the current information available regarding the contribution of CAR to various metabolic disorders and cancers and ponders the possible challenges that might arise from pursuing CAR as a potential therapeutic target for these diseases.

SIGNIFICANCE STATEMENT

The growing importance of the constitutive androstan receptor (CAR) in glucose and lipid metabolism as well as its potential implication in cell proliferation emphasizes a need to keenly understand the biological function and clinical impact of CAR. This minireview captures the clinical relevance of CAR by highlighting its role in metabolic disorders and cancer development.

Introduction

The constitutive androstan receptor (CAR) (NR1I3), a member of the nuclear receptor superfamily, plays key regulatory functions in many aspects of physiology and development as it exerts ligand-activated transcriptional regulation (Qatanani and Moore, 2005; Negishi, 2017). Originally defined as an orphan nuclear receptor without a clear biologic function, CAR has been well accepted as a master xenosensor of xenobiotic metabolism and disposition (Timsit and Negishi, 2007). Outside the canonical pathway of CAR, mounting evidence suggests CAR may impact various physiologic and pathophysiologic situations through modulation of energy homeostasis, cell proliferation, and tumor development.

Traditionally, CAR is known for its modulation in hepatic detoxification of xenobiotic and endobiotic chemicals, such as bile acids, bilirubin, and numerous clinically used drugs, where it induces the expression of drug-metabolizing enzymes (DMEs) and transporters (Wang and LeCluyse, 2003; Timsit and Negishi, 2007; Mackowiak et al., 2018). Consistent with its role in xenobiotic disposition, CAR is highly expressed in the liver and small intestine (Bookout et al., 2006; Yan et al., 2015). Upon activation, cytosolic CAR translocates to the nucleus, where it heterodimerizes with retinoid X receptor and binds to the xenobiotic responsive element, initiating the expression of target genes (Honkakoski and Negishi, 1997; Honkakoski et al., 1998). As a classic nuclear receptor, CAR consists of a common N-terminal activation function 1 ligand-independent domain, a conserved DNA-binding domain, and a C-terminal ligand binding domain (LBD) (Banerjee et al., 2015). Interestingly, activation of CAR involves both the ligand-dependent (direct) mechanism and a ligand-independent (indirect) mechanism requiring dephosphorylation of CAR mediated by protein phosphatase 2A (Yoshinari et al., 2003; Yang and Wang, 2014). The relatively large LBD of CAR further expands the scope of structurally
diverse molecules as CAR modulators, influencing metabolism, disposition, and detoxification of xenobiotic and endobiotic molecules (Ekins et al., 2009).

Research thus far has clearly recognized that CAR plays a major regulatory function in xenobiotic metabolism and disposition, dictating drug safety and potential drug-drug interactions (DDIs). Its later identified effects on energy homeostasis, cell proliferation, and tissue regeneration hold significant clinical importance (Fig. 1). This review aims to discuss the clinical relevance of CAR, highlighting its contribution in modulating various disease states, such as metabolic disorders and cancers, thereby, emphasizing CAR as a promising therapeutic target to correct metabolic perturbations.

**CAR in Glucose and Lipid Homeostasis**

The role of CAR in energy homeostasis was initially acknowledged when activation of CAR in mice by phenobarbital (PB), a prototypical CAR activator, downregulated a set of genes responsible for gluconeogenesis, fatty acid, and cholesterol biosynthesis (Ueda et al., 2002). Subsequent studies reveal that CAR, in combination with other transcription factors, such as the forkhead box protein O1 (FOXO1), peroxisome proliferator-activated receptor γ (PPARγ), and peroxisome proliferator-activated receptor-γ coactivator 1α (PGC1α), repress the expression of phosphoenolpyruvate carboxykinase 1 (PEPCK1) and glucose-6-phosphatase (G6Pase) in gluconeogenesis (Kachaylo et al., 2012); sterol regulatory element-binding protein (SREBP) 1c, acetyl-CoA carboxylase 1, fatty acid synthase, and steroyl-CoA desaturase-1 for lipid synthesis (Du et al., 2008); as well as carnitine palmitoyltransferase Iα and cytosolic Acyl-CoA thioesterase for β-oxidation (Maglich et al., 2009). Here, we focus on recent advances in the role of CAR in energy homeostasis through glucose and lipid metabolism and highlight the therapeutic potential for treating diseases, such as obesity and type 2 diabetes (T2D).

**CAR in Glucose Metabolism.** PEPCK1 and G6Pase are two critical gluconeogenic enzymes that catalyze the formation of phosphoenolpyruvate and dephosphorylation of glucose-6-phosphate, respectively. The fact that PB treatment of rat hepatocytes led to marked decrease of glucose production via inhibition of PEPCK1 was realized several years prior to the cloning of CAR (Argaud et al., 1991). Moreover, the use of PB as an adjuvant therapy to sulfonyl urea regimen resulted in an increase in glucose metabolic clearance rate and insulin sensitivity index ultimately leading to a decrease in fasting blood glucose levels (Sotaniemi et al., 1983; Lahtela et al., 1985). Later, a microarray analysis on cDNA obtained from wild-type (WT) and CAR-knockout (−/−/−) mouse liver samples confirmed, for the first time, that the repressive effect of PB on gluconeogenic genes, such as PEPCK1, G6Pase, and insulin-like growth factor-binding protein 1 containing an insulin response sequence (IRS), was a CAR-dependent event (Ueda et al., 2002). In the absence of insulin, FOXO1 directly binds to IRS, triggering the transcription of various gluconeogenic genes, thereby, resulting in increased blood glucose levels (Hall et al., 2000; Schmoll et al., 2000). On the other hand, insulin phosphorylates FOXO1 via the phosphoinositide 3-kinase/protein kinase B-mediated pathway and reduces the binding of FOXO1 to IRS. Employing a combination of yeast two-hybrid screening, glutathione

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**Clinical Relevance of CAR**

**Xenobiotic Metabolism**

Without activation, CAR is maintained in the cytoplasm of hepatocytes, forming a protein complex with heat shock protein 90 (HSP90) and cytoplasmic CAR retention protein (CCRPR). Upon activation, CAR is dephosphorylated by protein phosphatase 2A (PP2A) and translocated into the nucleus. Once in the nucleus, CAR (A) forms a heterodimer with retinoid X receptor (RXR) and binds to the xenobiotic responsive enhancer module in the upstream region of different target genes, resulting in transcription of genes encoding DME, such as CYP2B6, UGT1A1, and SULT1A1; (B) competes with transcription factors, such as FOXO1 and HNF4α, for binding to the promoters of their target genes, including PEPCK1 and G6Pase, repressing energy homeostasis; and (C) interacts with YAP, Gad45β, and β-catenin, which are associated with cell proliferation and apoptosis.

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**Energy Homeostasis**

**Liver Cancer and Cell Proliferation**

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**Fig. 1.** The diverse biologic function of CAR. Without activation, CAR is maintained in the cytoplasm of hepatocytes, forming a protein complex with heat shock protein 90 (HSP90) and cytoplasmic CAR retention protein (CCRPR). Upon activation, CAR is dephosphorylated by protein phosphatase 2A (PP2A) and translocated into the nucleus. Once in the nucleus, CAR (A) forms a heterodimer with retinoid X receptor (RXR) and binds to the xenobiotic responsive enhancer module in the upstream region of different target genes, resulting in transcription of genes encoding DME, such as CYP2B6, UGT1A1, and SULT1A1; (B) competes with transcription factors, such as FOXO1 and HNF4α, for binding to the promoters of their target genes, including PEPCK1 and G6Pase, repressing energy homeostasis; and (C) interacts with YAP, Gad45β, and β-catenin, which are associated with cell proliferation and apoptosis.
S-transferase pull down, chromatin immunoprecipitation, and animal experiments, Kodama et al. found that CAR and FOXO1 can reciprocally coregulate their respective target genes through crosstalk, where FOXO1-mediated transcription of gluconeogenic genes can be downregulated by CAR acting as a corepressor (Kodama et al., 2004). Hepatic nuclear factor-4z (HNF-4z), an energy sensor, regulates the expression of numerous hepatic genes involved in cholesterol, lipid, and glucose metabolism (Gonzalez, 2008; Yin et al., 2011; Huang et al., 2020). Activation of CAR by 4-{(4R,6R)-4,6-diphenyl-1,3-dioxan-2-yl}-NN-dimethylamidoline significantly reduced fasting blood glucose levels in rats fed high-fat diets (HFDs) via the suppression of PEPCK and G6Pase expression (Yarushkin et al., 2013). Chromatin immunoprecipitation assays further revealed that 4-{(4R,6R)-4,6-diphenyl-1,3-dioxan-2-yl}-NN-dimethylamidoline–activated CAR inhibits HNF-4z transactivation through competition with HNF-4z for the direct repeat (DR)-1 motif in the promoters of these gluconeogenic genes (Yarushkin et al., 2013). This mechanism resembles CAR-mediated repression of CYP7A1 expression through the competition between CAR and HNF-4z to the DR-1 binding and CYP7A1 transcription (Miao et al., 2006). From an epigenetic perspective, Gao et al. demonstrated that CAR could recruit Cullin 1 E3 ligase-promoting ubiquitination of PGC1z, thus suppressing PGC1z from being recruited to the proximal promoters of PEPCK1 and G6Pase (Gao et al., 2015). Moreover, studies in human primary hepatocytes (HPHs) further confirm the repressive effect of human constitutive androstane receptor (hCAR) activation on these gluconeogenic genes (Lynch et al., 2014). Additionally, genome-wide analysis of hCAR transcriptome in WT and hCAR−/− HepaRG cells revealed that the expression of numerous genes associated with energy metabolism was altered when challenged with prototypical hCAR activators, such as 6-(4-chlorophenyl)imidazo[2,1-b][1,3]thiazole-5-carbaldehyde-O-(3,4-dichlorobenzyl)oxime (CITC) and PB (Li et al., 2015). However, HepaRG cells, which overexpressed CAR that were grown with modified conditions such as high oxygen, medium perfusion, reduced substrate stiffness, and three-dimensional conformation, displayed a switch from glycolysis to oxidative phosphorylation by decreasing glucose consumption, which overall improved mitochondrial energy metabolism compared with monolayer HepaRG cells (van der Mark et al., 2020).

Utilizing genetically modified animals, Dong et al. reported that hexokinase, an enzyme required for catalyzing the initial irreversible step in glycolysis, is upregulated twofold in the liver of leptin-deficient mice, but not in leptin-deficient, CAR−−/− double knockout mice administered 1,4-bis[2-(3,5-dichloropyridyl)] benzene (TCPOBOP), a mouse CAR agonist (Dong et al., 2009). Likewise, activation of CAR also enhanced the expression of phosphogluconate dehydrogenase (PGD), a rate-limiting enzyme in the pentose phosphate pathway. Transient transfection assays further illustrated that the proximal promoters of both the hexokinase and PGD genes can be transactivated by CAR (Dong et al., 2009). Recently, results obtained from NMR and liquid chromatography with tandem mass spectrometry-based metabolomics in WT and CAR−−/− mice showed that activation of CAR by TCPOBOP reduced the level of glucose while increasing the abundance of fatty acids, lactate, and ketone bodies in the blood. This metabolic phenotype is correlated with significant downregulation of key gluconeogenic genes and the upregulation of genes in glucose utilization pathways in the liver (Chen et al., 2019). Notably, the expression of glucokinase, an enzyme that converts glucose to glucose-6-phosphate in glycolysis, was nearly doubled when CAR was activated after treatment with TCPOBOP for 48 hours. Consistent with previous findings, this study supports an increase in glucose utilization by regulating the pentose phosphate pathway in TCPOBOP-treated WT mice indicated by the rise of PGD transcript levels and uridine diphosphate-glucose (Dong et al., 2009; Chen et al., 2019). In another report, Yarushkin et al. demonstrated that after a long-term TCPOBOP treatment (8 weeks), a collection of key glycolytic genes including Gck, Gpi1, Pfk1, Aldoa, Pgk1, and Pklr are upregulated 2- to 6-fold in mouse liver (Yarushkin et al., 2016). In parallel to increases in mRNA expression, the hepatic levels of different glycolytic intermediates, namely glucose-6-phosphate and pyruvate, were each elevated 1.5-fold. Thereby, these studies suggest that CAR activation could potentially boost glucose metabolism while having a simultaneously repressive effect on gluconeogenesis.

Irisin is a hormone modified from fibronectin type III domain-containing protein 5 (FNDC5) through proteolytic processing and is expressed in skeletal muscles, liver, heart, and adipose tissue (Perakakis et al., 2017). Serum irisin levels detected in patients with T2D are low (Choi et al., 2013; Liu et al., 2013). Mo et al. showed that FNDC5 is a direct CAR transcriptional target and activation of CAR leads to hepatic induction of FNDC5 and subsequent elevation of the circulating irisin levels in mice (Mo et al., 2016). Thus, this research offers an alternative route by which CAR activation can influence energy homeostasis and glucose metabolism.

Collectively, CAR-mediated repression of gluconeogenic gene expression occurs through multifaceted signaling that includes inhibition of FOXO1 and IRS interaction, competition with other transcription factors, such as HNF-4z for specific DNA motif binding, and through post-translational regulation of the subcellular localization and degradation of PGC1z. These studies firmly establish that CAR activity can regulate gluconeogenesis, glucose uptake, and hepatic glycolysis, implying a potential implication of CAR in T2D therapy. Nevertheless, the majority of research thus far has been conducted in rodent animals; comprehensive investigation in human relevant systems is highly demanded to understand the biologic role that hCAR asserts.

**CAR in Lipid Metabolism.** Lipogenesis includes the process of fatty acid synthesis and subsequent triglyceride generation, occurring predominantly in the liver and adipose tissues. SREBPs are a group of transcription factors known for their regulation of genes involved with cholesterol and fatty acid biosynthesis (Brown and Goldstein, 1997; Bertolino et al., 2019; Osborne, 2000). Insulin-induced gene (Insig)-1, an endoplasmic reticulum membrane protein, is one of the upstream regulators of lipogenesis. It has been reported that both Insig-1 and Insig-2 bind to the SREBP cleavage activating protein, a protein required for transport and subsequent activation of SREBP transcription factors (Brown and Goldstein, 1997; Edwards et al., 2000). Activation of Insigs, however, maintains the SREBP cleavage activating protein-SREBP complex in the endoplasmic reticulum, thus preventing SREBP gene transcription, potentially attenuating fatty acid biosynthesis (Yang et al., 2002).

Early evidence indicated that under HFD feeding, TCPOBOP-mediated activation of CAR noticeably alleviates symptoms of obesity, diabetes, and fatty liver in mice, which is associated with CAR-dependent suppression of SREBP-1c as well as its downstream targets, namely fatty acid synthase and steroyl-CoA desaturase-1 (Dong et al., 2009; Gao et al., 2009). Mechanistically, activation of CAR in mouse liver resulted in the induction and activation of Insig-1, which is associated with decreased activation of SREBP-1 along with a 67% decline of hepatic triglyceride levels (Roth et al., 2008). Further analysis using chromatin immunoprecipitation and in silico genomic analysis identified a DR-4 type response element in the Insig-1 promoter region that responded with high binding affinity to CAR. Importantly, in CAR−−/− mice, PB failed to induce Insig-1 expression and did not significantly change the hepatic triglyceride profile compared with WT mice (Roth et al., 2008). The liver X receptor (LXR) is another sterol sensor that promotes lipogenesis through activation of SREBP-1. A mutual suppressive effect between LXR and CAR was recognized, where activation of CAR compromised the LXR agonist responsive recruitment of
LXR to SREBP-1c and subsequent lipogenic gene expression, decreasing hepatic triglyceride levels (Zhai et al., 2010). Most recently, Cai et al. showed that in a HFD-induced obesity model, TCPOBOP demonstrated a protective effect on body weight gain and ameliorated insulin sensitivity as expected, whereas this effect was markedly reduced in mice without expression of the growth arrest and DNA damage-inducible gene 45β (Gadd45β), a well-recognized antiapoptotic factor, acting as a coactivator for CAR (Cai et al., 2021). Loss of Gadd45β is known to impair the early transcriptional stimulation caused by CAR activation and hepatomegaly (Tian et al., 2011). Although the exact mechanism(s) remains unclear, these studies revealed that CAR requires Gadd45β for mediation of antiobesity and antiadipogenic effects in vivo by influencing the induction of genes associated with hepatic lipogenesis, gluconeogenesis, and adipose inflammation. Interestingly, although the expression of CAR is trivial in most extrahepatic tissues, such as white adipose tissues, knockout of Gadd45β abrogates the mitigation of inflammation in white adipose tissues by TCPOBOP, a probable secondary metabolic benefit in extrahepatic tissues (Cai et al., 2021). Likewise, Xu et al. observed that TCPOBOP-mediated CAR activation reduces the mammary gland weight approximately by 25%, hinders lipid accumulation via inhibiting lipogenesis and gluconeogenesis in the mammary fat pad, and promotes collagen formation and fibrosis in the mammary glands of female mice (Xu et al., 2018). Collectively, these findings suggest that activation of CAR, which is predominantly expressed in the liver, may profoundly influence systematic energy metabolism in extrahepatic tissues.

In contrast to the beneficial effects of CAR on lipid homeostasis, evidence suggests that CAR activation significantly increases total plasma cholesterol as well as hepatic levels of saturated, monounsaturated, and polyunsaturated fatty acids (Darrington et al., 1976; Calandre et al., 1991; Chen et al., 2019). Moreover, clinical trials have determined that the long-term use of antiepileptic drugs, including PB, can precipitate the condition of atherosclerosis (Tan et al., 2009). Activation of CAR was also reported to cause a 50% elevation in blood triglyceride levels by decreasing the expression of PPARα target genes (Maglich et al., 2009). PPARα is a transcriptional regulator of genes associated with peroxisomal and mitochondrial β-oxidation and fatty acid transport, and PPARα ligands, such as fenofibrate and bezafibrate, have been clinically used to lower blood triglyceride levels. Subsequent mechanistic studies revealed that both CAR and PPARα can bind to PGC1α, a coactivator required for PPARα-mediated gene transcription (Shiizu et al., 2020). Through competition, CAR can effectively suppress transcription of PPARα target genes related to lipid metabolism leading to elevation of blood triglyceride levels in mice (Shiizu et al., 2020).

Although the exact reasons for the observed discrepancy of CAR in lipid metabolism remain elusive, information pertaining to the antilipogenic effects of CAR was mostly obtained under metabolic and/or nutritional stresses, such as HFD feeding or caloric restriction. Marmugi et al. demonstrated that TCPOBOP-mediated CAR activation in healthy mice maintained on standard chow markedly increased hepatic triglyceride and cholesterol ester levels in WT but not in CAR−/− mice (Marmugi et al., 2016). Under this physiologic condition, activation of CAR upregulates the expression of patatin-like phospholipase domain-containing protein 3, an emerging marker of liver steatosis, as well as a panel of genes associated with glycolysis and lipogenesis, including Fasn, Elovl6, Scd1, and Gpat (Marmugi et al., 2016). In vitro studies using HPH or hepatoma cells also indicated that activation of hCAR by CITCO or PB upregulates hepatic lipogenic genes (Breuker et al., 2010; Marmugi et al., 2016). Dysregulation of lipid biosynthesis as well as its breakdown can lead to obesity and manifest into several other health concerns, such as T2D, nonalcoholic fatty liver disease, and cardiovascular diseases. Notably, CAR-mediated regulation of fatty acid metabolism involves a complex interplay of dynamic pathways. The metabolic and nutritional stresses to which mice were subjected may attribute significantly to the antilipogenic effects displayed by CAR, hence, not reflecting the true physiologic state. Therefore, depending on the exact nature of the impact of CAR in lipogenesis and in maintaining triglyceride levels, CAR may be considered clinically relevant for treating lipid metabolism disorders in a condition-specific manner.

**CAR in Bile Acid Metabolism.** Bile acids have long been known to function as physiologic detergents, solubilizing circulating cholesterol remnants and fat-soluble vitamins, however accumulation of toxic bile acids in the hepatobiliary system can cause hepatic inflammation, cholestasis, and eventually lead to fibrosis, cirrhosis and even cancers (Narisawa et al., 1974; Radominska et al., 1993). The balance of bile acid synthesis, transport, and detoxification is tightly regulated under physiologic conditions. Consistent with its promiscuous effects on metabolism, CAR is known to modulate numerous genes associated with bile acid homeostasis including CYP3A for bile acid hydroxylation (Staudinger et al., 2001; Xie et al., 2001; Makishima et al., 2002), uridine diphosphate glucuronosyltransferase (UGTs) for the glucuron conjugation (Radominska et al., 1990), sulfotransferases (SULTs) for sulfation, and the canalicular bile acid transporter, multidrug resistance associated protein 2 (Sugatani et al., 2001; Kast et al., 2002; Huang et al., 2003).

Using transgenic mice, Saini et al. showed that CAR-mediated induction of both SULT and 3′-phosphoadenosine-5′-phosphosulfate synthetase 2, an enzyme responsible for generating the co-substrate 3′-phosphoadenosine-5′-phosphosulfate, can confer resistance to bile acid-induced hepatotoxicity (Saini et al., 2004). Sequence analysis identified and characterized an inverted repeat lacking a spacing nucleotide (IR0) in rodent SULT2A gene promoter region that converts CAR-mediated transactivation. Accumulating evidence revealed that activation of CAR is associated with marked reduction of blood levels of bile acid and bilirubin concentrations and can ameliorate cholestasis-induced liver dysfunction, inflammation, and oxidative stress (Guo et al., 2003; Zhang et al., 2004; Stedman et al., 2005; Gabbia et al., 2018). Importantly, both primary and secondary bile acids can function as signaling molecules that modulate the activity of many transcription factors including CAR (Fiorucci et al., 2010). Moreover, through cross-talk and competitive binding to the response elements, CAR represses FXR-mediated transcription of CYP7A1, a rate-limiting enzyme converting cholesterol to bile acids in the liver, whereas FXR exerts suppressive effect on CAR-induced multi-drug associated protein 4 expression and basolateral bile acid transport (Miao et al., 2006; Renga et al., 2011).

Collectively, understanding the interplay between bile acids and CAR and defining the role of CAR in bile acid homeostasis would eventually benefit the identification of new molecules as therapeutic choices for cholestatic liver diseases.

**The Role of CAR in Cell Proliferation and Cancer Development.** In addition to the role of CAR in energy homeostasis, the impact of CAR on carcinogenesis has been intensely investigated since the initial discovery of PB- and TCPOBOP-mediated liver tumor promotion in mice was validated as a CAR-dependent event (Yamamoto et al., 2004; Huang et al., 2005). Subsequent studies expanded these findings, whereby many rodent CAR activators, such as cyproconazole (Tamura et al., 2015), metofluthrin (Deguchi et al., 2009), triclosan (Yueh et al., 2014), and propiconazole (Currie et al., 2014), exhibit their nongenotoxic tumor-promoting effects by CAR-mediated regulation of liver tumorigenesis (Maeda et al., 2015; Wang et al., 2017).
A growing body of evidence suggests CAR mediates carcinogenesis through a complex interaction of diverse signaling pathways, promoting hepatocyte proliferation, antiapoptosis, and tumorigenesis. In this regard, studies exhibited that the activation of CAR modulates the expression of a plethora of genes involved in proliferative and oncogenic signaling, such as Gadd45α (Columbano et al., 2005), the murine double minute 2 (Huang et al., 2005), c-Myc, and forkhead box protein M1 (Blanco-Bose et al., 2008) family, with sequence similarity 84 member A (Kamino et al., 2011b), tubulin alpha 8 (Kamino et al., 2011a), and cyclin D1 and cyclin dependent kinase 4 (Kazantseva et al., 2013). Interestingly, in addition to its recently realized beneficial effects on CAR-mediated glucose and lipid metabolism, Gadd45α, a well-known antiapoptotic factor, was markedly induced by TCPOBOP in a CAR-dependent manner, whereas this induction was independent of tumor necrosis factor α and nuclear factor kappa B (Columbano et al., 2005). In PB-treated hepatocytes isolated from WT mice, CAR forms a complex with Gadd45α to repress tumor necrosis factor α-induced Jun N-terminal kinase 1 phosphorylation and cell death, which was absent in hepatocytes from Car−/− mice (Yamamoto et al., 2010). The interaction between CAR and Gadd45α can also repress the tumor suppressive p38 Mitogen-activated protein kinases signaling (Hori et al., 2018). Notably, knockdown of Gadd45α does not significantly affect TCPOBOP-stimulated proliferative responses, while largely decreasing the liver/body weight ratio, suggesting loss of Gadd45α may affect CAR-mediated hepatocellular hypertrophy but not hyperplasia (Tian et al., 2011).

Atypical activation of Wnt/β-catenin signaling represents a key mediator in the development of many different cancers, including hepatocellular carcinoma (HCC), and is generally considered a robust driver of cell proliferation; nevertheless, hepatic activation of β-catenin alone does not stimulate liver tumors in mice (Harada et al., 2002). β-catenin was first linked to CAR by Braeuning et al., where liver-specific knock-out of the Ctnnb1 gene (encoding for β-catenin) strongly diminished CAR activation and target gene expression (Braeuning et al., 2009).

Subsequent studies revealed that β-catenin knockout significantly inhibits its CAR agonist-induced hepatocyte proliferation exclusively in male mice (Braeuning et al., 2011). In 2015, Dong et al. uncovered a unique functional synergy between CAR and β-catenin in liver tumorigenesis, where dual activation of CAR and β-catenin results in uncontrollable hepatocyte proliferation and HCC formation (Dong et al., 2015). Consistent with these findings, Aydinlik et al. reported earlier that in diethylnitrosamine plus PB-induced murine liver tumors, more than 80% of them carried an activating β-catenin mutation, which was markedly higher than that of 28% in diethylnitrosamine alone induced tumors (Aydinlik et al., 2001). This bidirectional relationship between β-catenin and CAR dictates the functional requirements of β-catenin signaling on CAR-mediated liver tumor promotion and vice versa (Rignall et al., 2011; Ganzenberg et al., 2013).

The Hippo signaling pathway is a chief regulator of organ size in mammals through the regulation of cell proliferation and apoptosis in coordination with the transcriptional coactivator, Yes-associated protein (YAP), as a prominent downstream mediator (Harvey et al., 2013). YAP has also been identified as a prospective mechanism of CAR-mediated liver hyperplasia, where liver enlargement caused by TCPOBOP was accompanied with increased expression and activation of YAP protein (Kowalik et al., 2011). Moreover, in the diethylnitrosamine plus TCPOBOP HCC model in mice, increased expression of YAP was associated with elevated levels of two YAP target genes, namely alpha-feto-protein and connective tissue growth factor, accompanied by the downregulation of microRNA 375, a known YAP regulator (Kowalik et al., 2011). Recent studies revealed that activation of CAR by TCPOBOP enhanced dephosphorylation and the translocation of YAP from the cytosol to the nucleus where it transcriptionally upregulates cell proliferation (Abe et al., 2018). Alternatively, both knock down of YAP mediated by siRNA and chemical inhibition of YAP/transcriptional enhanced associate domain interaction markedly repressed cell proliferation in a CAR-dependent manner (Abe et al., 2018). Most recently, Gao et al. demonstrated that CAR and YAP proteins directly interact with each other after coimmunoprecipitation, additional experiments found that CAR-mediated liver hepatomegaly, however, was mostly retained in the liver-specific Yap−/− mice (Gao et al., 2021). These findings support the notion that CAR impacts hepatomegaly through complex crosstalk and mediation of multiple signaling pathways with the YAP pathway as one of them.

It should be noted that although a long-term hyperplastic response stimulated by CAR activation could result in liver carcinogenesis, a speedy regenerative response after severe tissue wound is crucial to survival. The regenerative effect of mouse CAR was investigated under extreme (91% liver volume), extended (86% liver volume), and standard (70% liver volume) resections (Tschoor et al., 2016). Although CAR activity impairment was noted in all mice after extended hepatectomy, standard hepatectomy in CAR−/− mice depicts a phenotype similar to the small-for-size syndrome observed in mice that underwent extended resection. After TCPOBOP treatment, pronounced improvement in survival was noted among WT but not CAR−/− mice that received lethal extreme hepatectomy. Mechanistically, the protective effects of TCPOBOP appear to be associated with restoration of the CAR-forkhead box protein M1 axis. Collectively, these data uncover CAR as a critical factor mediating recovery of liver failure from extended tissue loss and injury. Moreover, pharmacological activation of CAR might be sufficient to rescue the liver from such damage.

**CAR in Human Cancer.** In contrast to the well-established tumor-promoting effects of CAR on rodent liver stimulated by PB-like compounds, such a mode of action was regarded to be qualitatively questionable for humans (Elcombe et al., 2014). Although it has been of heightened interest to determine the potential influence of hCAR activation in developing human cancer, information pertaining to the role of hCAR in cancer is relatively scarce (Lake, 2018). Utilizing DNA synthetic activity, Ki67, and proliferating cell nuclear antigen as markers for cell proliferation, previous studies show that PB stimulates murine but not human liver cell proliferation both in vitro in cultured primary hepatocytes and in vivo in WT and human hepatocyte chimeric mice (Parzefall et al., 1991; Yamada et al., 2014). Moreover, epidemiologic studies show that PB does not raise the occurrence of liver cancer in humans, even after a long-term exposure at dose levels (100–300 mg daily for 10 years) challenging what was used in rodent liver carcinogenic studies (Olsen et al., 1989; Lamminpaa et al., 2002).

Notably, although hCAR exhibits several mutual features with its rodent counterparts, such as induction of DME and xenobiotic transporters, significant interspecies differences of CAR in energy homeostasis and cell proliferation have been documented (Lake, 2018; Mackowiak et al., 2018; Wang and LeCluyse, 2003). Structural comparison of classic nuclear receptors from different species revealed >90% sequence conservation in the LBD regions; nevertheless, the LBD sequences of human and mouse CAR share only 71% amino acid homology (Moore et al., 2002; Qatanani and Moore, 2005). Particularly, TCPOBOP, which has been extensively used as a model mouse CAR activator in liver cancer studies, does not active hCAR; whereas, as a prototypical hCAR agonist, CITCO actsives human but not mouse CAR, making the extrapolation of animal data to human challenging (Tzameli et al., 2000; Maglisch et al., 2003). To date, our knowledge regarding the role of hCAR in cancer development is limited and seemingly contradictory.
HepaRG cells, a surrogate of HPH, revealed that disruption of the stimulation. Transcriptome profiling analysis between WT and CAR−/− HepaRG cells, a surrogate of HPH, revealed that disruption of the “quiescent” hCAR is of particular physiologic significance, and subsequent pathway analysis indicated that genes related to cell cycle, cancer biology, and cardiovascular diseases are among the most enriched pathways in CAR−/− HepaRG cells (Li et al., 2015). Meanwhile, analyzing HCC and normal human liver tissue revealed that HCC has increased DNA methylation in the hCAR promoter and lower hCAR expression in comparison with adjacent liver tissues (Tang et al., 2016). Importantly, reduced hCAR expression in HCC is correlated with a worse HCC prognosis (manuscript in preparation).

In addition to HCC, CAR expression and activity was examined in other human cancers, such as brain tumors. Brain tumor stem cells (BTSCs) are a key population of tumor cells preserving active proliferation, drug resistance, and recurrence characteristics. Chakraborty et al. demonstrated that CITCO concentration dependently decreased the growth and expansion of CD133(+) BTSCs by inducing cell cycle detention and apoptosis; the anticancer activity of CITCO is accompanied with potent induction of CAR expression in BTSCs but not in normal astrocytes (Chakraborty et al., 2011). The upregulation of CAR by CITCO in the treatment of glioma depicts a potentially novel treatment approach through targeting BTSCs. Nevertheless, given that CITCO is a known agonist of hCAR not necessarily involving the induction of the receptor itself, the exact mechanism underlying this CAR-dependent antineoplastic effect needs be further investigated.

Taken together, mounting evidence suggests that CAR has progressed from a xenobiotic sensor to a signaling molecule that regulates both energy homeostasis and cancer development. Although these findings make CAR an attractive therapeutic target with high clinical relevance, significant species-specific differences between human and rodent CAR, particularly in the context of cancer development and cell proliferation, alarm cautious interpretation and extrapolation of data obtained from animal studies (Fig. 2). Future extensive research is deemed essential to fill these gaps.

**Conclusion**

Over the past two decades, CAR has been known for its involvement in drug metabolism and disposition influencing the pharmacokinetic and toxicological profiles of numerous xenobiotics, including environmental chemicals and clinically used drugs, as well as key endobiotics, such as bile acids and bilirubin. Thus, activation of CAR is associated with potential DDI leading to clinically detrimental or beneficial consequences. For instance, neonatal jaundice and Gilbert’s syndrome, characterized by unconjugated hyperbilirubinemia, can be effectively treated by PB via CAR-mediated induction of UGT1A1, the principal enzyme responsible for the conjugation and clearance of bilirubin (Rossi et al., 2005; Sugatani et al., 2005). In another case, CAR-mediated induction of CYP2B6, which bioactivates the chemotherapeutic prodrug, cyclophosphamide, has been assessed as a potentially attractive approach for cancer treatment (Wang et al., 2013; Hedrich et al., 2016; Kurian et al., 2020). Although of significant clinical relevance, the topics related to the function of CAR in drug metabolism and DDI has been extensively reviewed previously (Willson and Kliwer, 2002; Wang and LeCluyse, 2003; Qatanani and Moore, 2005; Molnar et al., 2013), thus is not a focus of the current minireview.

Unlike typical nuclear receptors that require ligand-dependent activation, CAR activity can be stimulated through various pathways without direct ligand-binding. Emerging evidence indicates CAR has evolved into a signaling molecule that can exhibit functions beyond classic gene

![Fig. 2. Species-specific effects of CAR on energy metabolism and cancer development. Schematic illustration of the effects of mouse and human CAR on energy homeostasis and cancer development. It is widely accepted that activation of mouse CAR inhibits hepatic gluconeogenesis and lipogenesis under nutritional challenge. Mouse CAR activation has also been established as a mode of action for hepatocyte proliferation and liver tumorigenesis induced by PB-like compounds. In the case of human CAR, limited data thus far indicate that hCAR activation represses hepatic gluconeogenesis with uncertain effects on lipogenesis. Activation of hCAR does not increase hepatocyte proliferation, and the expression of hCAR appears to be negatively related to HCC prognosis.](image-url)
transcriptional regulation. The coordination between CAR and other nuclear receptors further complicates the ability to assess the unique role of CAR in certain physiologic processes. For instance, CAR and its sister receptor, PXR, share numerous target genes and small molecular modulators. Many so-called “selective hCAR modulators,” such as CITCO and CIP-101D (CAR inhibitor not PXR activator 1) also activate hPXR (Jeske et al., 2017). In the case of PB, although a CAR activator across multiple species, it also activates human but not mouse PXR. To precisely target and untangle the pathophysiologic influence of CAR, better small-molecule compounds and advanced physiologically relevant models need to be developed to overcome some of these challenges.

Beyond the realm of drug metabolism and disposition, mounting evidence suggests that CAR plays a key role in the modulation of gluconeogenesis, lipogenesis, and bile acid regulation and can influence cell proliferation, tumorigenesis, and inflammation. The pivotal contribution of CAR to these processes may impact the development and treatment of T2D, obesity, and cancers. Nevertheless, the obvious species-specific differences of CAR in energy metabolism and cancer development drastically hinders the interpretation and clinical application of current findings that are predominantly obtained from animal studies. Specifically, current findings strongly support the notion that CAR-mediated mechanisms of action for liver tumor development in rodents is irrelevant or opposite from humans. This knowledge gap has motivated a shift in the research focus and warrants more comprehensive studies to fully appreciate the clinical impact of hCAR in diseases and drug efficacy.

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Authorship Contributions

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Wrote or contributed to the writing of the manuscript: Stern, Kurian, Wang.

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