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ARTICLE *in* THE JOURNAL OF STEROID BIOCHEMISTRY AND MOLECULAR BIOLOGY · JANUARY 2012

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## Review

## Therapeutic potential of Liver Receptor Homolog-1 modulators

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## ARTICLE INFO

## Article history:

Received 10 February 2011

Received in revised form

14 November 2011

Accepted 27 December 2011

## Keywords:

Orphan nuclear receptor

NR5A2

LRH-1

## ABSTRACT

Liver Receptor Homolog-1 (LRH-1; NR5A2) belongs to the orphan nuclear receptor superfamily, and plays vital roles in early development, cholesterol homeostasis, steroidogenesis and certain diseases, including cancer. It is expressed in embryonic stem cells, adult liver, intestine, pancreas and ovary. It binds to DNA as a monomer and is regulated by various ligand-dependent and -independent mechanisms. Recent work identified synthetic ligands for LRH-1; such compounds may yield useful therapeutics for a range of pathologic conditions associated with aberrant expression and activity of LRH-1.

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## 1. Introduction

Nuclear receptors (NRs) comprise a large superfamily of mammalian transcription factors that are essential in embryonic development, differentiation, metabolism and cell death [1–3].

NRs mediate cellular signals to the nucleus by directly interacting with DNA sequences known as hormone response elements (HREs) [3,4]. Unlike most NRs, orphan NRs regulate transcription independent of known ligands. Orphan receptors play a diverse and important biological role in development and adult physiology [1,5–7].

Liver Receptor Homolog-1 (LRH-1; NR5A2; FTZ-F1; FTF; CPF) is one such orphan nuclear receptor that plays vital roles in early development and is important for bile acid synthesis, cholesterol metabolism and steroidogenesis in the adult [8–14] (see Fig. 1).

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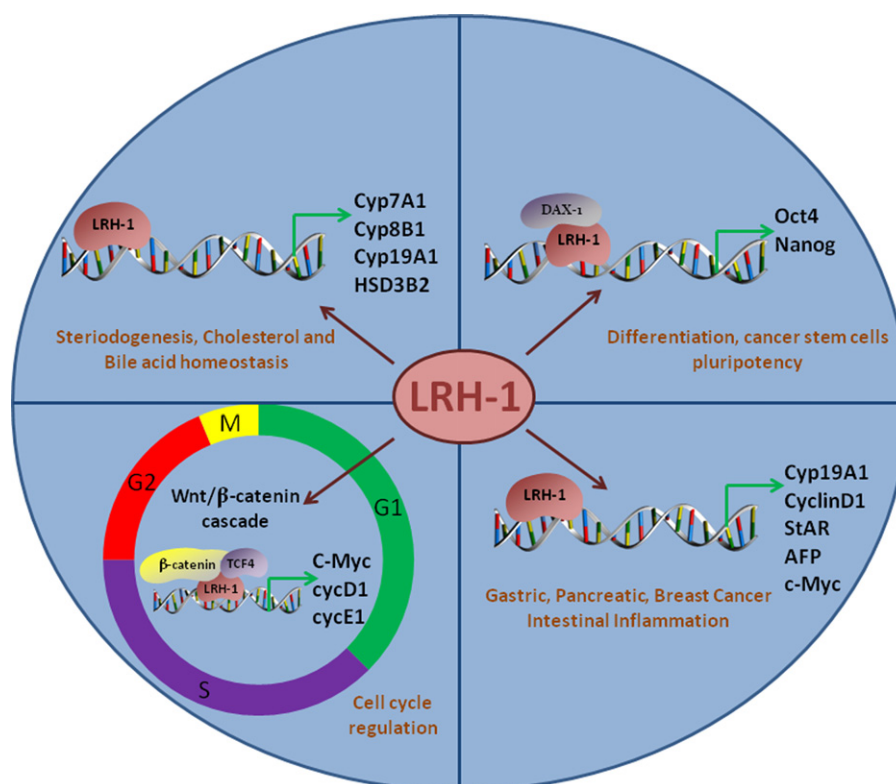


Fig. 1. Physiological actions of LRH-1.

LRH-1 and its mammalian homolog Steroidogenic Factor-1 (SF-1) binds to DNA as monomers to nuclear receptor half site sequences [1,15,16]. As LRH-1 is constitutively active [8], its regulation of function occurs via interactions of co-activators and co-repressors [17–19]. Furthermore, interactions with other orphan receptors including small heterodimer partner (SHP) [9,20–24] and dosage sensitive sex reversal-adrenal hypoplasia congenital gene on the X chromosome, gene 1 (DAX-1) cause the repression of LRH-1 transcriptional activity [25,26]. Ligands identified for LRH-1 and its homologue, SF-1 include small drug-like molecules [8] and endogenous phospholipids [27–30]. With its wide implication for disease progression in various organs, this review will focus on the therapeutic potential of LRH-1 modulators.

## 2. LRH-1: structure

The human gene encoding LRH-1 spans more than 150 kb of chromosome 1q32.11 and has eight exons. LRH-1 binding is dictated by the Ftz-F1 box and it binds as a monomer to the extended half site YCAAGG YCR (where Y is any pyrimidine and R is any purine), the recognition motif for the NR5A subfamily of nuclear receptors [8,16,31,32]. The ligand binding domain (LBD) of most NRs consists of twelve  $\alpha$ -helical regions, folded into a three-layered, anti-parallel helical sandwich with a conserved  $\beta$ -turn between H5 and H6 [8]. The LBD also contains a pocket to which a ligand binds causing a reversible conformational change. This repositions H12 allowing for co-activator recruitment [8,32]. However, in orphan receptors, the key to constitutive activation may lie in the N-terminal region of the LBD. This is strongly conserved amongst orphan receptors and shares limited sequence amongst other nuclear receptors [8]. The presence of an additional structure pertaining to an extension of an H2 layer may provide an explanation of the stabilised conformation, by stabilising H12 which

contains the C-terminal activation helix (AF-2) [8]. The folding over of the AF-2 region allows the LBD to be held in an active conformation without the need for a ligand.

## 3. Established roles of LRH-1: cholesterol metabolism

A key biological function of LRH-1 is the regulation of cholesterol metabolism via its effect on bile acid homeostasis. LRH-1 regulates enterohepatic development and function via the expression of key genes involved in the regulation of bile acid synthesis, cholesterol homeostasis and transport (Table 1) [8,10,15,20,33–38]. LRH-1 activates gene transcription of the rate-limiting enzyme in bile acid biosynthesis, cytochrome P450 family 7A1 or Cholesterol 7  $\alpha$ -hydroxylase (Cyp7A1) [20,33,39,40]. In humans, the loss of function of Cyp7A1 results in a decrease in bile acid excretion and an increase in hepatic and serum cholesterol levels [41]. However, LRH-1  $\pm$  heterozygous mice have elevated CYP7A1 and CYP8B1 mRNA levels [42]. This may be due to a dominant effect of LRH-1 on Cyp7A1 and Cyp8B1 transcription. Interestingly, hepatocytes and intestinal epithelium (IE) specific LRH-1 knockout mice showed no overt abnormalities [43]. Furthermore, LRH-1 deficiency in the IE, had no effect on Cyp7A1 levels. This discrepancy in observations may be due to the minor role LRH-1 plays in Cyp7A1 regulation, or there might be an alternative redundant factor regulating Cyp7A1 in the absence of LRH-1 [43]. Further work need to be undertaken in determining the role of LRH-1 in the feedback mechanism of bile acid synthesis. In contrast to Cyp7A1, Cyp8B1 levels were significantly decreased with LRH-1 deficiency, consistent with previous findings.

LRH-1 positively regulates expression of other enzymes and transporters involved in reverse transport of cholesterol and bile acid synthesis pathways. These genes which contain the LRH-1 response element (nuclear receptor half site) in their promoters

include cytochrome P450 family 8B1 (Cyp8B1) or Sterol 12 $\alpha$  hydroxylase, multidrug resistance protein 3 (MRP3), cholesteryl ester transfer protein (CETP), scavenger receptor class B type I (SR-BI), mouse apical sodium-dependent bile acid transporter (ASBT) and human Apolipoprotein A1 (ApoA1) [8,20,33,34,37,44,38,45]. These findings are consistent with the selective knockout of LRH-1 in hepatocytes where expression of these targets were significantly ablated [43]. By activating gene expression, LRH-1 impacts various functions outlined. Increase in ApoA1 allows the initiation of high density lipoprotein (HDL) biosynthesis and for ApoA1 to act as an acceptor of cholesterol and phospholipids effluxed from peripheral tissues. Up regulation of SR-BI receptors allows the transfer of mature HDL particles from plasma into hepatocytes [46]. CETP transfers the cholesteryl esters from plasma HDL into Apolipoprotein B-containing triglyceride-rich very low density lipoproteins (VLDL). These VLDL particles are acted upon by lipoprotein lipase and the fatty acids are taken up by the adipose and skeletal muscle. The cholesterol-rich remnants are then taken up by the liver [37,47].

Within hepatocytes, cholesterol and cholesteryl esters are converted to bile acids by Cyp7A1 and Cyp8B1 for secretion out of the liver in bile. Furthermore MRP3 and ASBT are involved in bile acid recycling, indicating that LRH-1 is important for bile acid homeostasis [44,48]. Major subsets of LRH-1 gene targets are involved in the transfer of cholesterol to the liver and subsequent elimination into bile acids, and in bile acid synthesis, highlighting the importance of LRH-1 in cholesterol metabolism [41].

#### 4. Emerging roles of LRH-1 in disease

##### 4.1. Embryonic stem cells: pluripotency and differentiation

LRH-1 is a critical factor in early embryonic development, and LRH-1 null mice die at embryonic day 6.5–7.5 with features typical of visceral endoderm dysfunction [42]. One of the key factors essential for maintaining pluripotency in embryonic stem cells (ESCs), Oct4 is regulated by LRH-1 [49,50]. Its role in Oct4 regulation is confirmed with the loss of Oct4 expression in the absence of LRH-1 [49]. In addition to Oct4, LRH-1 is known to regulate other factors required to maintain pluripotency [51,52].

A recent report suggests that LRH-1 regulates Oct4 and Nanog induction and its expression is regulated via the Wnt signalling pathway, via binding of  $\beta$ -catenin to activate an embryonic-specific LRH-1 promoter [50] thus identifying a new pathway for the regulation of self renewal in ESC.

Somatic cells can be reprogrammed to induced pluripotent stem cells (iPSCs) with the introduction of Oct4, Sox2 Klf4, and c-Myc [53]. Of these factors, Oct4 cannot be replaced by other factors to allow for the generation of iPSC from somatic cells [54]. A study entailing a screen of nuclear receptors for their ability to enhance reprogramming efficiency led to the discovery that LRH-1, and to a lesser extent SF-1 could replace Oct4 in the reprogramming of mouse embryonic fibroblasts to iPSCs further indicating its vital role in the regulation of Oct4 and maintaining pluripotency [49,55].

A point mutation within the LRH-1 LBD (A368M) that interferes with the binding of endogenous phospholipids [56] did not abrogate its reprogramming capacity, suggesting that phospholipid binding is not essential for this function. However, since LRH-1 is constitutively active, and its activity appears to be regulated primarily by binding of protein co-regulators (see below), further studies into looking at the exact function of phospholipids in terms of regulating LRH-1 function are required. The possibility remains that pharmacological modulation of co regulator interactions could impact LRH-1 function in stem cells.

Recent work suggests that a transcriptional partner of LRH-1 to activate Oct4 expression is DAX-1. DAX-1 is abundant in ESCs and it plays a role in maintaining pluripotency [57]. DAX-1 expression is controlled by LRH-1 and Nanog [58]. In mouse ESC, DAX-1 interaction with LRH-1 does not inhibit but rather activates Oct4 gene transcription [46]. This is thought to be due to the interaction of steroid receptor RNA activator (SRA) with DAX-1 to allow an activation function [59]. This interaction of LRH-1 with DAX-1 is evidence of importance of co-regulator interaction in the modulation of LRH-1 activity. It also raises the possibility that co-regulator interaction allows for tissue specific LRH-1 functions.

##### 4.2. Ovarian function: steroidogenesis and luteinisation

LRH-1 is expressed at relatively high levels in the ovary, with highest expression in granulosa cells and corpora lutea, with no expression observed in theca cells [60]. Although SF-1 is also present in the ovary its expression is lower in LRH-1 expressing cells and highest in the theca [60]. The two nuclear receptors are differentially regulated, SF-1 mRNA and protein increased in granulosa cells by estradiol, whereas LRH-1 expression was increased by FSH in granulosa cells and by prolactin in luteal cells [63]. Both receptors have been shown to regulate ovarian steroid synthesis although the relative roles of each are still unclear, since they both share common target genes including aromatase, steroidogenic acute regulatory protein (StAR), 3 $\beta$ -hydroxysteroid dehydrogenase (HSD3B2) and inhibin  $\alpha$  subunit [61–65]. Recent work has

**Table 1**  
LRH-1 target genes and functions.

	Target genes	Organ/tissue	Function
Embryonic	AFP-1, Prox1, HNF3 $\beta$ , HNF4 $\alpha$ , HNF1 $\alpha$	Liver	Early enterohepatic development [34,42,110,111]
	Oct4	ES cells	Early embryonic development [49,55]
Adult	CYP19A1	Preadipocytes	Steroidogenesis [14,22,75,23]
	APOA1, SR-B1, CETP, SHP	Liver	Cholesterol transport [46,112]
	CYP7A1, CYP8B1, CEL, MRP3	Liver	Bile acid homeostasis [8,20,34,44]
	ABST Cyclin D1, TCF4/ $\beta$ -catenin	Intestine	Bile acid homeostasis [37]
			Intestinal epithelium renewal [69]
	CYP11A1, CYP19, HSD3B2	Ovary	Ovary steroidogenesis [8,65]
	SR-BI		Cholesterol transport [8]
	LH $\beta$	Gonadotrope	Normal reproductive function [113]
Disease	Cyclin E1, TCF4, $\beta$ -catenin	Intestine	Gastric cancer [69,95]
			Intestinal inflammation [69,72]
			Pancreatic cancer [89]
			Tumour progression and carcinogenesis
	CYP19A1, Cyclin D1, StAR, AFP	Breast	Pancreatic cancer [89]
	C-Myc	Pancreas	Pancreatic cancer [89]

suggested that LRH-1 preferentially regulates progesterone over oestrogen production [12,66,67]. Consistent with this, granulosa cell-specific LRH-1 null mice exhibit anovulation due to failure of cumulus expansion, luteinisation, and follicular rupture [68]. Loss of LRH-1 in granulosa cells also impaired progesterone synthesis due to reduced expression of StAR and cytochrome P450 side-chain cleavage (P450<sub>scc</sub>). Interestingly aromatase expression was unaltered. This dramatic phenotype highlights the potential of LRH-1 antagonists as novel contraceptives, since loss of LRH-1 inhibits both ovulation and luteinisation [68].

#### 4.3. Colon cancer and inflammation

Recent evidence indicates a role of LRH-1 in colon cancer development and progression. LRH-1 is highly expressed in intestinal crypts where it is involved in the control of cell proliferation and renewal [69]. Botrugno et al. have demonstrated that LRH-1 promotes intestinal cell proliferation by stimulating the expression of the G<sub>1</sub> cyclins D1 and E1 [69]. In these cells, LRH-1 co-activates  $\beta$ -catenin/Tcf4 to induce cyclin D1 and c-Myc expression, and also binds directly to the cyclin E1 promoter to promote transcription in synergy with  $\beta$ -catenin [69]. Consistent with this, haplo-insufficiency of LRH-1 markedly protects against tumour development in both genetic (*Apc<sup>Min/+</sup>*) and chemical (azoxymethane) induced models of intestinal cancer [70]. Alterations in LRH-1 expression and localisation are also seen in human colon cancer, with increased LRH-1 expression observed in surface epithelial cells that are normally LRH-1 negative and non-proliferative [70]. However, the lack of significant proliferative

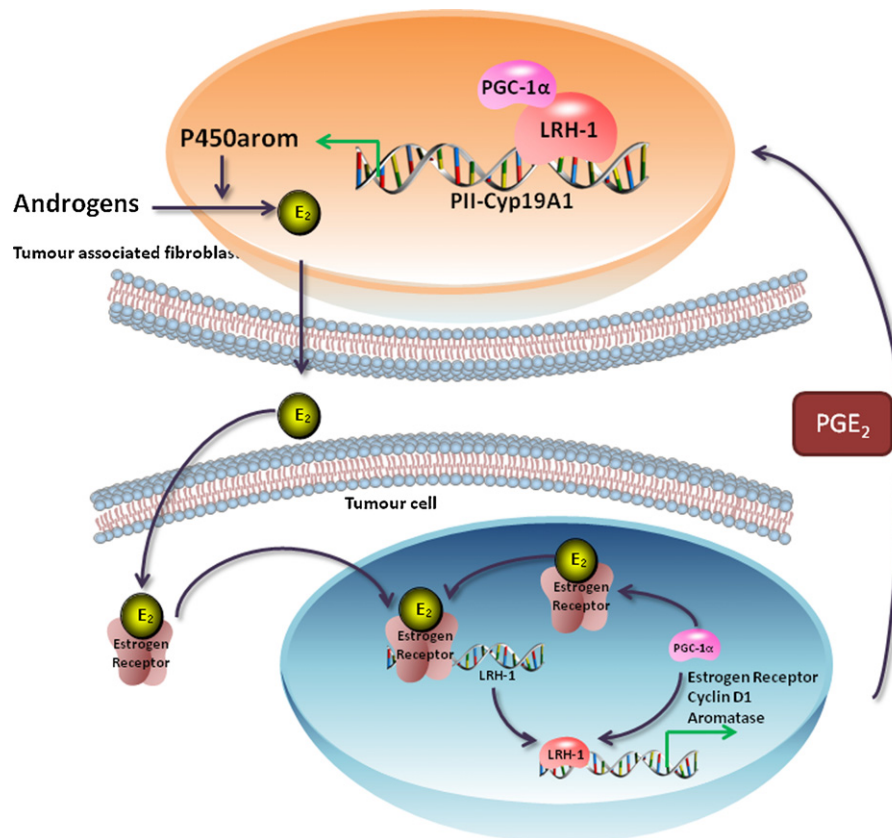
phenotype in intestinal specific LRH-1 knock-out mice [41] raises questions as to the role of endogenous LRH-1 in vivo.

LRH-1 also plays an important role in glucocorticoid synthesis within the intestine by inducing expression of steroidogenic enzymes (cholesterol side chain cleavage enzyme and 11 $\beta$ -hydroxylase that catalyse the first and last steps in glucocorticoid formation, respectively) in intestinal epithelial cell lines [71]. This is likely of physiological relevance since haplo-insufficiency of LRH-1 in mice reduced expression of these enzymes and glucocorticoid synthesis in response to immunological stress [71]. Similar effects were seen in mice with an inducible intestinal epithelial deletion of LRH-1 [72]. Consistent with these findings, expression of both LRH-1 and its steroidogenic target genes were reduced in patients with Crohn's disease and ulcerative colitis [72].

#### 4.4. Breast cancer

In human breast adipose, LRH-1 is expressed in low levels, localising specifically in the stromal fraction [13]. However in breast cancer, LRH-1 expression is high and localised both in tumour epithelial cells and intra-tumoural stroma [73,74]. High expression is observed in primary invasive breast carcinoma and ductal carcinoma in situ [74]. Although the effects of LRH-1 in breast cancer are not fully understood, evidence suggests that its roles are tightly integrated with the oestrogen signalling pathway (Fig. 2).

One of the first identified target genes of LRH-1 in breast adipose stromal cells is *CYP19A1* [13,14,75], encoding for cytochrome P450 family 19A1 or aromatase. Aromatase is a critical enzyme required for the conversion of androgens to oestrogens. After menopause,



**Fig. 2.** LRH-1 actions in a breast cancer cell. LRH-1 activates aromatase transcription in cancer associated adipose fibroblasts leading to increased oestrogen synthesis, thus promoting tumour growth. The oestrogen receptor (ER $\alpha$ ) activates LRH-1 expression in malignant epithelial cells. LRH-1 in turn further up regulates ER $\alpha$  and aromatase expression. Cyclin D1 a known target gene is also up regulated by LRH-1. LRH-1 is positively regulated by co-activator PGC-1 $\alpha$ , leading to the activation of target genes such as ER $\alpha$  and aromatase. Therefore through its involvement in ER $\alpha$  expression and co-regulators and repressors also act on the ER, suggesting that the LRH-1 signalling pathway is tightly linked with the oestrogen signalling pathway.



when the risk of developing oestrogen-dependent breast cancer is greatest, local aromatase expression in adipose tissue represents the major source of oestrogen in women (as well as in men). Aromatase activity is regulated primarily by transcription of the *CYP19A1* gene via tissue specific promoters [76–78]. By activating *CYP19A1* transcription, LRH-1 most likely regulates the availability of mitogenic oestrogen for tumour growth [14]. In the tumour context, the aberrant expression of LRH-1 allows the activation of the gonadal-specific aromatase promoter (promoter II). LRH-1 expression in adipose stromal cells is positively regulated by breast tumour derived factors such as prostaglandin  $E_2$  [75]. In addition to stromal cells, aromatase is present in breast cancer epithelium [79], and its expression also regulated by LRH-1 in breast cancer epithelial cells [80].

A second level of cross-talk is evident in that expression of LRH is itself regulated by oestrogen in breast cancer cells. Annicotte et al. reported that the human LRH-1 promoter contains a near-perfect palindromic oestrogen response element (ERE) [74], to which ER $\alpha$  binds to stimulate promoter activity. This is consistent with the observed correlation between LRH-1 mRNA levels and ER $\alpha$  status in a variety of breast cancer cell lines [74], as well as the known positive association between LRH-1 positivity and ER $\alpha$  status in primary human breast carcinoma [11,81]. Knockdown of LRH-1 expression with siRNA in MCF-7 cells inhibits the proliferative effect of oestrogen [74], suggesting that the mitogenic effects of oestrogen may be mediated, in part, via LRH-1.

Furthermore LRH-1 regulates expression of ER $\alpha$  in breast cancer cells; siRNA knockdown of LRH-1 in MCF-7 cells inhibits expression of both ER $\alpha$ , and of ER $\alpha$  target genes such as pS2, whereas transfection of LRH-1 into these cells stimulates ER $\alpha$  expression [81]. This effect is mediated by LRH-1 binding directly to the major ER $\alpha$  promoter used in breast cancer cells [81]. Therefore, LRH-1 both regulates, and is regulated by ER $\alpha$  in addition to regulating the synthesis of its ligand.

Although the above evidence indicates that LRH-1 induces proliferation by stimulating oestrogen signalling, LRH-1 also has oestrogen independent effects on breast cancer cells. siRNA-mediated knockdown of LRH-1 inhibited breast cancer cell motility, invasion and colony formation in both ER +ve MCF-7 and ER –ve MDA-MB-231, as well as the non-tumorigenic MCF-10A mammary epithelial cell line [82]. Over-expression of LRH-1 (in the absence of oestrogen) produced the opposite effects.

In addition, over-expression of LRH-1 resulted in the post-translation cleavage of mature 120 kDa E-Cadherin to its inactive 97 kDa form. This effect may be mediated by matrix metalloproteases (MMPs) since LRH-1 was also shown to induce MMP9 mRNA expression in MCF-7 cells [82], consistent with the known role of LRH-1 as a regulator of MMP9 expression in the ovary [68]. LRH-1 was also shown to influence actin remodelling in breast cancer cell lines [82] which, taken with its effects on E-Cadherin and MMP9, may suggest a role for LRH-1 in promoting epithelial to mesenchymal transition (EMT). Given that LRH-1 has well-characterised roles in mouse and human embryonic stem cells [49,83–85], and that breast cancer stem cells possess many of the characteristics of cells undergoing EMT [86,87], the potential role of LRH-1 in promoting EMT is an intriguing possibility that merits further investigation.

#### 4.5. Pancreatic cancer

Recent genome-wide association studies have linked mutations in the LRH-1 gene and its up-stream promoter regions with pancreatic cancer [88]. In addition, LRH-1 expression is found to be elevated in human pancreatic ductal adenocarcinomas [89]. In pancreatic cancer cells, LRH-1 also mediates tumour cell proliferation via the up regulation of cyclins D1, E1 and c-Myc. Conversely knockdown of LRH-1 expression resulted in cell cycle arrest but not

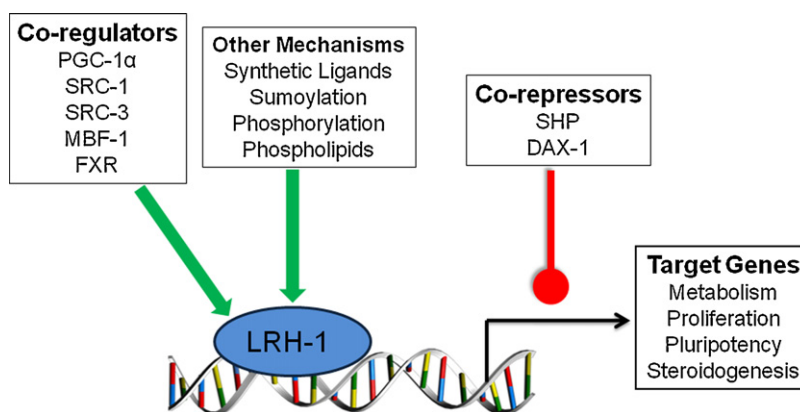
apoptosis in pancreatic cancer cells. This study implicates an important role for LRH-1 in mediating proliferation and differentiation pancreatic ductal adenocarcinomas and therefore a potential therapeutic target for this cancer [89].

#### 4.6. Metabolic disorders

One of the key sites of LRH-1 expression and function is in the hepatocytes where it regulates transcription of genes such as *Cyp7A1*, *Cyp8B1*, encoding enzymes critical in bile acid and cholesterol synthesis; scavenger receptor class B member 1 (SR-B1) important for cholesterol transport and SHP, an LRH-1 co-repressor with known roles in obesity and diabetes [20,46,90]. Whilst these roles in the liver are well characterised, until recently the effect of LRH-1 in metabolic disorders was not well understood. A recent study [91] describes two phosphatidylcholine phospholipids, dilauroyl phosphatidylcholine (DPLC) and diundecanoyl phosphatidylcholine (DUPC) as potent agonists of LRH-1, binding to the ligand binding pocket of the human receptor. This is an extension to previous findings where structural analysis of LRH-1 identified bacterial phospholipids bound in the ligand binding pocket [24,92]. These two lipid ligands, DPLC and DUPC potentially activate NR5A receptors: LRH-1 (human and mouse homologues) and SF-1 (mouse homologue), however, show no effects on other nuclear receptor function. Lee and colleagues hypothesised that the activation of liver-specific activity of LRH-1 would increase bile acid production thereby having a positive metabolic effect in diabetic and obese disease models. In diet induced obese mice, oral administration of DPLC resulted in increased bile acid production, decreased hepatic steatosis and improved glucose utilisation [91]. Additionally in liver specific LRH-1 knockout animals, DPLC treatment did not show any improvement in the high fat diet induced metabolic phenotype. This suggests a direct effect on LRH-1 receptor activity and/or the downstream activation of LRH-1 dependent pathways in regulating insulin sensitivity. Due to the absorption and clearance of these lipid ligands, the primary site of LRH-1 activation appeared to be the liver and SF-1 activity in the adrenal was not affected. This study therefore reveals a novel, LRH-1 dependent phosphatidylcholine pathway that could be targeted for metabolic disorders such as diabetes.

### 5. LRH-1 modulators as a novel therapeutic target

Since its identification in 1996, there is accumulating evidence of LRH-1 as an important regulator of pathways involved in metabolism, steroidogenesis, cancer and regulation of pluripotency. Given its expression and functions in various tumours including invasive breast carcinomas, ductal carcinomas in situ, colon, gastric and pancreatic cancers, the potential impact of LRH-1 modulators as therapeutic targets should be considered. Recent progress with the identification of small molecule agonists [93,94] and phospholipid ligands will eventually lead to the development of sensitive LRH-1 modulators. There appears to be therapeutic benefits for both the activation of LRH-1 (in the liver) where it would be beneficial in the treatment of metabolic disease such as diabetes; and in the inactivation of LRH-1 in tumour cells. Suppression of LRH-1 activity in tumour cells (gastric, pancreatic, intestinal, breast) would potentially have an anti-proliferative effect [70,82,89,95]. As LRH-1 is expressed in inflammatory cells such as lymphocytes [89] and in surrounding breast adipose stromal cells, blocking of LRH-1 function would have additional anti-tumour effects such as down-regulating inflammatory pathways and reducing oestrogen synthesis within the tumour milieu. Given the importance of LRH-1 in metabolism and cancer, the



**Fig. 3.** LRH-1 activity can be regulated by various mechanisms in a tissue specific manner. Regulation mechanisms include synthetic ligands, post-translational modification, phospholipids. Co-regulators and co-repressors also play a role in regulating LRH-1, which then modulates expression of target genes that are involved in metabolism, proliferation, pluripotency and steroidogenesis.

regulation of its activity could potentially lead to important breakthroughs in treatment of these diseases.

The regulation of LRH-1 function occurs via interaction with intracellular phospholipids, transcriptional co-regulators (CoRs) and post-translational modifications such as phosphorylation and sumoylation (Fig. 3). By considering these modes of regulation, new approaches to block or enhance LRH-1 activity may emerge.

### 5.1. Regulation of LRH-1 activity

#### 5.1.1. Phospholipids as LRH-1 activators

Crystallisation of the LRH-1 ligand binding domain (LBD) (mouse and human isoforms) identified bacterial phospholipids in the ligand binding pocket. Subsequently phospholipids such as phosphatidylcholine, phosphatidylethanolamine and phosphatidylglycerol were shown to bind with human LRH-1 and SF-1 from both mouse and human [24,27,56,92,96] identifying them as endogenous ligands. Functional studies of mouse LRH-1 LBD show that ligands are dispensable for activity [56]. Disruption of the size and shape of the hydrophobic ligand binding pocket does not appear to affect its transcriptional activity. However mutations in the human LRH-1 LBD reduce phospholipid binding, and prevent recruitment of co-activators causing an inhibition of transcriptional activity of LRH-1 [24,96]. In support of this idea is the recent identification of DPLC and DUPC which act as strong LRH-1 activators in vitro and in vivo models [91].

#### 5.1.2. Co-activators of LRH-1

Structurally LRH-1 is permanently held in an active conformation and binds to DNA as a monomer [1,8,15]. LRH-1 activity is primarily regulated by transcriptional co-regulators. LRH-1 can also act as a competence factor by binding to other orphan nuclear receptors and transcriptional complexes to enhance transcription of target genes. Peroxisome proliferator-activated receptor- $\gamma$ -co-activator-1  $\alpha$  (PGC-1 $\alpha$ ) is a key co-activator of LRH-1 in the ovary, facilitating LRH-1 mediated differentiation of granulosa cells into progesterone producing luteal cells [12]. This interaction is blocked by a known repressor of LRH-1 activity, DAX-1 in granulosa cells [12]. Since both DAX-1 and PGC-1 $\alpha$  can bind to LRH-1 [12], this indicates that the binding affinity of DAX-1 for LRH-1 is stronger than PGC-1 $\alpha$  [12]. Furthermore, the interaction between LRH-1 and PGC-1 $\alpha$  is also evident in bile acid homeostasis [9]. However this interaction in the liver is blocked by SHP-1 [9]. Recently a genomic-wide interrogation of hepatic faresoid X nuclear receptor (FXR), revealed that FXR binds to LRH-1, and LRH-1 is required for the FXR mediated activation of SHP, Rdh9, Pcx and Pemt [97].

In human adipose stromal cells, PGC-1 $\alpha$  enhances LRH-1 dependent aromatase promoter II transcription [13]. The p-160 family members steroid receptor co-activators (SRC-1 and SRC-3) also regulate LRH-1 activity [98]. These co-activators contain an LXXLL motif in the receptor interaction domain; short peptide sequences derived from these co-activators are shown to bind LRH-1 LBD [19]. Multi-protein bridging factor (MBF-1) which also interacts with LRH-1 does not possess the LXXLL motif, typical for most co-activators, but interacts with the TATA-binding protein (TBP) [99]. This interaction is either in isolation or through the recruitment of transcription factor IID complex [99].

#### 5.1.3. Co-repressors of LRH-1

Nuclear receptors SHP and DAX-1 act as repressors of many NRs including LRH-1 by inhibiting co-activator binding [35]. The repression of LRH-1 by SHP has been well-defined due to its high interaction with the nuclear receptor [20,31,33]. Like most co-repressors, SHP binds to the AF-2 region of LRH-1 [8]. The LRH-1–SHP interaction occurs via interaction with LRH-1 residues Arg361 and Glu534 which form an atypical charge clamp [24]. Upon SHP interaction, p160 co-activators are competed out for binding to the CoR domain of LRH-1. In addition to the N-terminal receptor interaction domain, SHP includes a C-terminal domain with autonomous repression function [100]. In breast adipose stromal cells and in hepatocytes, SHP represses LRH-1 activity with the blocking of PGC-1 $\alpha$  and LRH-1 interactions [40]. This action in hepatocytes is shown to be mediated via the recruitment of SIRT-1 by SHP [21]. SHP is a well known target gene of LRH-1 and recent reports show a cooperative action with FXR to activate SHP transcription [97]. DAX-1 colocalises with LRH-1 and SF-1 in granulosa cells [12] and in mouse embryonic stem cells [59]. Crystallisation of mouse DAX-1 with LRH-1 LBD indicates that its N-terminus LXXLL-related motifs interact directly with LRH-1 [26,101,102]. It has also been reported that the C-terminus end is essential for DAX-1 mediated repression [103]. DAX-1 binds to the AF-2 domain as a dimer, binding with high affinity in contrast to most repressors which interact via their single LXXLL motif [25]. It is hypothesised that the DAX-1 dimer binds LRH-1 in a “claw-like” fashion, one of the DAX-1 structures extending into the ligand binding pocket. This feature may act as a sensor for ligand binding, and or additional interactions with components of the transcriptional machinery [25,26].

LRH-1 function is also inhibited by the protein inhibitor of activated signal transducer and activator of transcription- $\gamma$  (PIAS $\gamma$ ) [104]. This inhibition occurs due to the competitive binding of PIAS  $\gamma$  on the AF2 domain, which is involved in the binding of co-activator SRC-1. However, the over-expression of SRC-1 could

partially overcome the LRH-1 mediated induction of CYP11A1 [104]. The silencing mediator for retinoid and thyroid receptors (SMRT) is also shown to represses LRH-1 through an indirect mechanism currently unknown [8].

The role of transcriptional CoRs is critical in the modulation of transcription factor activity. In the case of orphan nuclear receptors, co-regulators may well be the most important mode of functional regulation. Evidence of co-localisation and interaction between CoRs and LRH-1 suggest tissue and cell specific modulation of LRH-1 action. Could targeting the disruption of these CoR interactions provide a means to selectively repressing LRH-1 activity? Due to the presence of SHP and DAX-1 in breast cancer [105,106], it is tempting to postulate their roles in repressing LRH-1 in breast cancer cells. However this possibility requires further investigation.

#### 5.1.4. Post-transcriptional regulation of LRH-1

In addition to CoRs, the activity of LRH-1 is modulated by post-translational modification. Phosphorylation of the serine residues 238 and 243 located within the hinge region of LRH-1 via phorbol 12-myristate 13-acetate (PMA), was found to be important for LRH-1 transactivation [107]. Sumoylation of LRH-1 also occurs in the hinge region, allowing for additional control of its activity via regulation of its subcellular localisation [108]. Sumoylated LRH-1 is localised to the transcriptionally inactive nuclear bodies, away from active chromatin. Interestingly, the newly identified phosphatidylcholine agonists of LRH-1, DPLC and DUPC activated LRH-1 mutants lacking phosphorylation sites (S238, 243A) or the sumoylation site (K270R) [91]. The double mutants F342 W and I426 W targeting the ligand binding pocket where not activated by DPLC or DUPC highlighting the importance of the ligand binding pocket in regulating LRH-1 activity.

#### 5.1.5. Synthetic ligands

The identification of synthetic agonists for LRH-1 and SF-1 supports the notion of ligand dependent activity of LRH-1 [93]. GSK8470, a substituted cis-bicyclo[3.3.0]oct-2-ene, was identified as a high affinity ligand for both LRH-1 and SF-1. This molecule led to increased expression of the LRH-1 target gene SHP in liver cells [93]. Modifications to this molecule at 3 different sites also led to the identification of other agonists with varying degree of potency and efficacy. One such molecule, RWJ101 was shown to be selective for LRH-1, however further work is being undertaken to improve its efficiency [94]. Recently an inverse agonist was identified for SF-1; 4-(heptyloxy)phenol (AC-45594) and its analogues were shown to regulate SF-1 activity and subsequently down regulate SF-1 target genes [109]. This molecule had no effect on LRH-1 activity indicating that despite their structural similarities, distinct ligands for LRH-1 and SF-1 could be synthesized.

## 6. Future perspectives

Since LRH-1 is implicated in important cellular functions and plays a role in various diseases, it represents an attractive therapeutic target in infertility, cancer and metabolic disorders. NRs have been targeted by pharmaceutical agents for decades, although the majority of drugs act at the ligand binding pocket to mimic or antagonise endogenous ligands. For orphan receptors, the challenges are greater. Since co-regulators exert profound effects on LRH-1 activity, the possibility of modulating LRH-1: co-regulator interactions should be considered in addition to searching for compounds that bind to the phospholipid/ligand binding pocket. In addition to tissue-specific coregulators, there may be tissue-specific endogenous ligands adding to the complexity of the regulation of orphan nuclear receptors such as LRH-1. Identification of ligands for LRH-1

will not only uncover its true biological roles but provide an avenue for new treatment opportunities for a range of diseases.

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