

# CHOLESTEROL AND OXYSTEROLS AS SIGNAL MOLECULES IN HUMAN PATHOPHYSIOLOGY AND CANCER: IMPLICATIONS FOR NEW THERAPEUTIC STRATEGIES

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PUBLISHED IN: Frontiers in Endocrinology





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ISSN 1664-8714

ISBN 978-2-88963-278-7

DOI 10.3389/978-2-88963-278-7

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# CHOLESTEROL AND OXYSTEROLS AS SIGNAL MOLECULES IN HUMAN PATHOPHYSIOLOGY AND CANCER: IMPLICATIONS FOR NEW THERAPEUTIC STRATEGIES

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**Citation:** Pezzi, V., Sirianni, R., Umetani, M., eds. (2019). Cholesterol and Oxysterols as Signal Molecules in Human Pathophysiology and Cancer: Implications for New Therapeutic Strategies. Lausanne: Frontiers Media SA.  
doi: 10.3389/978-2-88963-278-7

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# Editorial: Cholesterol and Oxysterols as Signal Molecules in Human Pathophysiology and Cancer: Implications for New Therapeutic Strategies

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**Keywords:** cholesterol (chol), oxysterol, cancer, signal molecules, nuclear receptor (NR)

## Editorial on the Research Topic

### Cholesterol and Oxysterols as Signal Molecules in Human Pathophysiology and Cancer: Implications for New Therapeutic Strategies

## OPEN ACCESS

### Edited and reviewed by:

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University of Bristol, United Kingdom

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### Specialty section:

This article was submitted to  
Cancer Endocrinology,  
a section of the journal  
Frontiers in Endocrinology

**Received:** 17 September 2019

**Accepted:** 10 October 2019

**Published:** 23 October 2019

### Citation:

Sirianni R, Umetani M and Pezzi V  
(2019) Editorial: Cholesterol and  
Oxysterols as Signal Molecules in  
Human Pathophysiology and Cancer:  
Implications for New Therapeutic  
Strategies. *Front. Endocrinol.* 10:732.  
doi: 10.3389/fendo.2019.00732

Cholesterol (Chol) is a lipid essential for membrane biogenesis and functionality, cell proliferation, and cell differentiation (1), however its “popularity” comes from hypercholesterolemia, a main risk factor for cardiovascular disease, neurodegeneration, inflammatory bowel disease, and cancer (2, 3). Chol can be the precursor of steroid hormones, bile acids, and other sterol metabolites responsible for a number of specific effects on human physiology (4). Among Chol metabolites, increasing attention is drawn by the family of oxidation products termed oxysterols that have been recently recognized as ligands for nuclear receptors involved in the regulation of cell viability and metabolism (5). Effects promoted by these Chol oxidation products appear to be dependent on their concentration, cell specific, dynamic condition of the cellular and tissue environment (6). For these reasons, the knowledge of molecular mechanisms that regulate the balance of Chol and oxysterol metabolism in different tissues is of crucial importance for understanding the occurrence of several diseases including cancer.

This collection is focused on the role of Chol and/or oxysterols as signaling molecules whose alteration can determine the onset or progression of pathologies. Consequently, modulation of sterol homeostasis represent a promising therapeutic strategy. Yamauchi and Rogers in this collection reviewed the connection between sterol metabolism and atherosclerosis as well as cancers. Their paper focuses on several drugs including those currently used in clinic (i.e., statins to block Chol synthesis and enhance LDL uptake) and those targeting sterol metabolism in preclinical and clinical studies (i.e., drugs targeting SREBPs and SREBP regulators, LXR, ABC transporters, ACAT, and sterol hydroxylases). Chol-free reconstituted or synthetic HDL (sHDL) represent a new reasonable strategy for delivering chemotherapeutic drugs to cancer cells. HDL receptor (Scavenger receptor type B-I; SR-BI), is highly expressed in endocrine cancers, notably due to the high demand for Chol by cancer cells. Binding sHDL loaded with a chemotherapeutic will deplete Chol while assuring specificity for cancer cells. This attractive approach is reviewed by Morin et al. suggesting the application of sHDLs as endocrine cancer therapeutics.

Patients suffering from hyperlipidemia or metabolic syndrome clearly evidence a link between male reproductive function and Chol homeostasis. Sèdes et al. in this collection highlighted molecular mechanisms involving nuclear receptors LXRs and FXR $\alpha$  and their sterol ligands important for testicular function. Drugs targeting these nuclear receptors could be used in the clinic either to treat male infertility or as new approach for male contraception.

Another interesting aspect is evidenced by Oguro reviewing in this collection recent advances in our understanding of the roles of Chol and its metabolites as signaling molecules in the regulation of hematopoiesis and hematologic malignancies. In particular, Chol metabolism to steroids and oxysterols promotes hematologic cancers, and statins that inhibit *de novo* Chol synthesis have cytotoxic effects in malignant hematopoietic cells.

The therapeutic potential of statins for the treatment of solid cancer has been reviewed in this collection by Chimento et al. Statins prevent cancer growth and metastasis by interfering with Chol activities which include signal molecules on membrane rafts, substrate for steroids, oxysterols, and Vitamin D3 synthesis, ligand for estrogen-related receptor alpha (ERR $\alpha$ ). This last aspect that proposes Chol as an endogenous ERR $\alpha$  agonist has been reviewed in depth by Casaburi et al. In several cancer cells, the expression and the activity of ERR $\alpha$ , together with its cofactors (PGC-1  $\alpha/\beta$ ), is further influenced by oncogenic signals and can thus be re-directed to induce metabolic programs favoring tumor growth and progression (7). Based on these considerations, the use of therapeutic strategies aimed to reduce Chol levels, such as statins or drugs targeting the SREBP metabolic pathways, could be a promising option to counteract metabolic rewiring in cancer cells where ERR $\alpha$  plays a pivotal role. Another relevant signal molecule binding nuclear receptors and involved in cancer progression is the oxysterol 27-hydroxycholesterol (27HC). 27HC is an abundant Chol metabolite in the human

circulation and promotes breast cancer cell proliferation (8, 9). Hiramitsu et al. in this collection clearly describe how this oxysterol promotes also lung cancer cell proliferation through Estrogen Receptor  $\beta$ /PI3K-Akt signaling. Thus, lowering 27HC levels may lead to a novel approach for the treatment of lung cancer. Oxysterols are also involved in the pathology of three major gastrointestinal cancer (hepatocellular carcinoma, pancreatic, and colon cancer). Kovac et al. in this collection suggest an interesting theory on the circadian clock effects on gastrointestinal carcinogenesis by regulating lipid metabolism and beyond. With this in mind, classical therapies (statins) to modulate Chol in gastrointestinal cancers, must be administered at a proper time and for a proper duration (chronotherapy) for successful therapies.

In conclusion, from this collection it emerges that regulation of sterol homeostasis is a complex network of transcription factors, protein modifiers, sterol transporters/carriers, sterol sensors dysregulated in various pathological settings such as atherosclerosis, cancers, and neurodegenerative diseases. In this context Chol and oxysterol as signal molecules are an appealing target to counteract these pathologies. New strategies aimed to modulate their levels and actions in different tissues are worth to be developed.

## AUTHOR CONTRIBUTIONS

RS, MU, and VP contributed conception and design of the study. All authors contributed to manuscript revision, read, and approved the submitted version.

## FUNDING

MU was supported by National Institutes of Health grant HL127037. VP and RS were supported by grants from Associazione Italiana per la Ricerca sul Cancro (AIRC) project no. IG20122 and IG15230.

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**Conflict of Interest:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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# Cholesterol: A Gatekeeper of Male Fertility?

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Cholesterol is essential for mammalian cell functions and integrity. It is an important structural component maintaining the permeability and fluidity of the cell membrane. The balance between synthesis and catabolism of cholesterol should be tightly regulated to ensure normal cellular processes. Male reproductive function has been demonstrated to be dependent on cholesterol homeostasis. Here we review data highlighting the impacts of cholesterol homeostasis on male fertility and the molecular mechanisms implicated through the signaling pathways of some nuclear receptors.

**Keywords:** cholesterol, fertility, testis, spermatozoa, nuclear receptors

## OPEN ACCESS

### Edited by:

Vincenzo Pezzi,  
University of Calabria, Italy

### Reviewed by:

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### Specialty section:

This article was submitted to  
Cancer Endocrinology,  
a section of the journal  
Frontiers in Endocrinology

**Received:** 16 March 2018

**Accepted:** 19 June 2018

**Published:** 19 July 2018

### Citation:

Sèdes L, Thirouard L, Maqdasy S,  
Garcia M, Caira F, Lobaccaro J-MA,  
Beaudoin C and Volle DH (2018)  
Cholesterol: A Gatekeeper of Male  
Fertility? *Front. Endocrinol.* 9:369.  
doi: 10.3389/fendo.2018.00369

Infertility is a major public health issue defined by the World Health Organization as the inability of a couple to conceive a child after 1 year of unprotected regular sex. About 15% of couples worldwide are reported to be infertile (1); and male disorders are diagnosed in 30–50% of cases (2). Azoospermia is one of the most severe case of infertility; which is defined by the total absence of spermatozoa in the ejaculate and affects more than 20% of infertile men (3).

Male infertility can be divided into two categories: abnormalities of excretory origin, which define a defect of sperm delivery in the genital tract and abnormalities of secretory origin, which correspond an alteration of the production of the spermatozoa by the testis. The aetiologies of testicular lesions involve multiple genetic, environmental and/or behavioral factors. However, in 30% of cases, male fertility disorders remain unexplained (4). It is therefore necessary to better understand the physiology of the testis in order to identify the causes of infertility that are still idiopathic.

Male reproductive function has been demonstrated to be highly dependent on cholesterol homeostasis. Indeed, cholesterol is the precursor of steroid synthesis which is crucial for normal sperm production (5–7). Moreover, many experimental and clinical data have highlighted the importance of lipid metabolism in the control of testicular physiology and male fertility (8). As example, the depletion of cholesterol in plasma and tissues in a mouse model deficient for the gene encoding 24-dehydrocholesterol reductase (*Dhcr24*) leads to mouse infertility (9).

## CHOLESTEROL HOMEOSTASIS

Cholesterol is essential for mammalian cell functions and integrity. It is an important structural component maintaining the permeability and fluidity of the cell membrane. Within the cells, the cholesterol homeostasis is tightly regulated to ensure normal cellular processes. Cholesterol homeostasis is strictly regulated at the cellular level.

Cholesterol is also a precursor for steroid hormones synthesis such as bile acids and vitamin D. Oxidized derivatives of cholesterol, known as oxysterols, are also implicated in numerous biological processes.

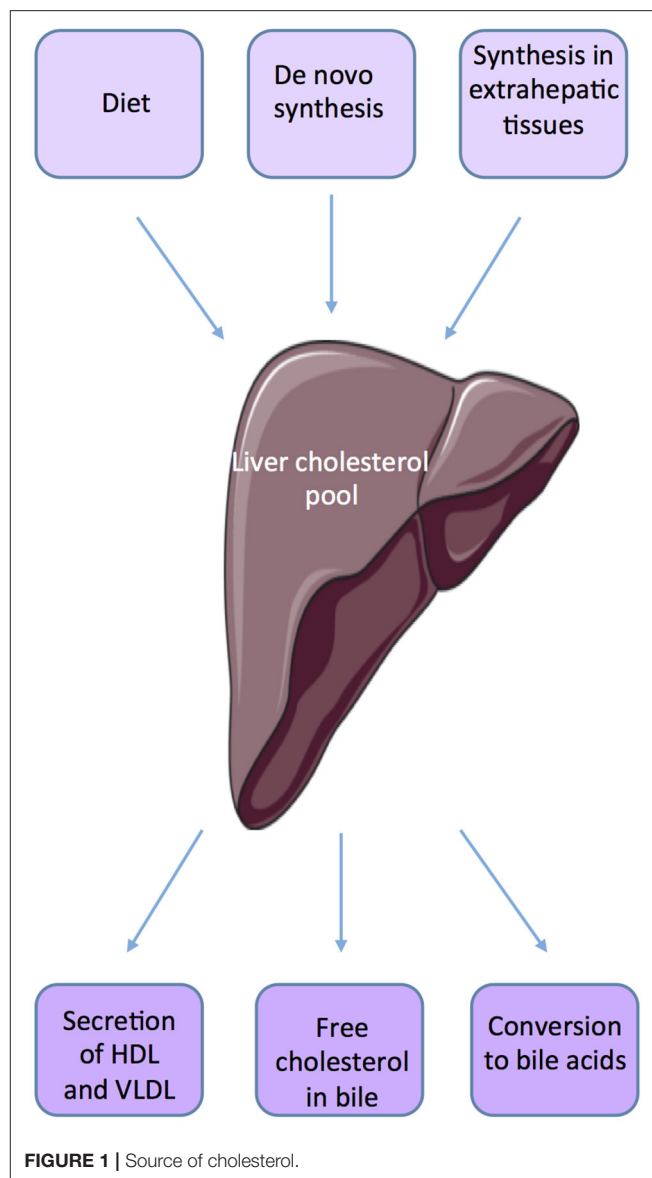


The main source of cholesterol is food. Dietary cholesterol is first routed from the small intestine to the liver, and then redistributed to the requesting organs. Cholesterol is uptake from lipoproteins; the Scavenger receptor B type 1 (SR-B1) is the cell surface high-density lipoprotein (HDL) receptor that mediates HDL-cholesterol ester (HDL-CE) uptake. Next to this, less than half of the cholesterol originates from *de novo* synthesis. Cholesterol synthesis is a multi-step enzymatic process. Synthesis of cholesterol begins from the acetyl-CoA, which is transported from the mitochondria to the cytosol. A series of reactions give rise to Hydroxy-methylglutaryl-CoA (HMG-CoA), which is then converted to mevalonate by HMG-CoA reductase. Finally, multi-steps will then give rise to cholesterol.

The cellular efflux of cholesterol is essential to maintain the homeostasis, as cells in peripheral organs do not express genes involved in the catabolism of cholesterol. The efflux of cholesterol requires acceptors such as HDL. There is either a simple diffusion (aqueous diffusion pathway) or a facilitated one through SR-B1 pathway. There could also be active process *via* members of the ATP-binding cassette (ABC) family transporters such as ABCA1 and ABCG1.

Within the body, the liver plays an important role in maintaining cholesterol homeostasis by regulating absorption and synthesis to prevent over accumulation in the plasma and tissues (10, 11) (**Figure 1**). The small intestine is also an important actor of *de novo* synthesis of cholesterol, bile synthesis, and absorption and fecal excretion. Molecular mechanisms involved have been quite well defined in the organs such as liver, adipose tissue, and intestine (12). The cross talks between liver and intestine illustrate the complex mechanisms involved in the regulation of cholesterol homeostasis through the involvement of several factors such as SREBP-2 (sterol regulatory element-binding protein), LXR (Liver X receptor, NR1H2, NR1H3), and FXR $\alpha$  (Farnesoid X receptor, NR1H4). Many studies suggest that SREBP and LXRs work in a coordinated manner to maintain cholesterol homeostasis (11, 13). SREBP2 up-regulates the expression of genes involved in the biosynthesis and uptake of cholesterol when cholesterol level is low.

LXR $\alpha$  and LXR $\beta$  are ligand-activated nuclear receptors; which are critical for the elimination of excess cholesterol. LXR $\alpha$  is primarily expressed in macrophages, intestine, liver, adipose, and kidney, whereas LXR $\beta$  is more ubiquitous (14). The major endogenous LXRs agonists that have been identified are oxysterols [20(S)-, 22(R)-, 24(S)-, 25-, 27-hydroxycholesterol; 24(S), 25-epoxycholesterol] and cholesterol biosynthetic intermediates [desmosterol, follicular fluid meiosis-activating sterol (FF-MAS), or testis meiosis-activating sterol (T-MAS)] (15, 16). Two synthetic LXR $\alpha/\beta$  agonists were developed and have been used widely such as T0901317 and GW3965 (17). The physiologically most important oxysterols are generated in cells by mitochondrial or endoplasmic reticulum cholesterol hydroxylases belonging to the cytochrome P450 family (CYP46A1, CH25H, CYP27A1 CYP3A4, and CYP7A1). Several natural compounds derived from plants have also been shown to activate (phytosterols, diterpenes...) or inhibit (naringenin) LXRs activity (15). Studies from LXR-knockout mice have demonstrated that LXRs are important in the



control of cholesterol homeostasis. Activation of LXRs protects cells from cholesterol accumulation by suppressing cholesterol biosynthesis, activating the conversion of cholesterol to bile acids in the liver, and decreasing intestinal cholesterol absorption (18, 19). Indeed, LXR $\alpha$ -knockout mice fed with a high-cholesterol diet show accumulation of cholesteryl-esters in the liver (20). LXR $\alpha$  is the prevalent isoform acting as hepatic sensor of cholesterol. While *Lxr $\alpha$*  knock-out mice showed an impaired hepatic function when fed high fat diet, mice lacking *Lxr $\beta$*  are able to resist to the deleterious impact of diet enriched in cholesterol (20, 21).

Cholesterol is the precursor for bile acids (BAs) synthesis within the liver. These molecules are the main constituents of bile and ensure solubilisation and emulsification of fat to help digestion (22). Their synthesis and excretion are major mechanisms of cholesterol catabolism in mammals.



Enzymatic modifications of cholesterol result in the production of primary BAs: cholic acid (CA) and chenodeoxycholic (CDCA) (23). There are two main BA synthesis pathways (24). The «classical» pathway involves CYP7A1 and CYP8B1 enzymes while the «alternative» pathway involves the cholesterol 27-hydroxylase CYP27A1 and 25-hydroxycholesterol 7- $\alpha$ -hydroxylase CYP7B1. Before their excretion, BAs are, in part, conjugated with glycine or taurine in the liver. This leads to the production of tauro-, or glyco-conjugates BAs. Stored in the gallbladder, primary BAs and conjugates are discharged during the meal into the duodenum to facilitate fat digestion. In the ileum, BAs are in part deconjugated and modified to give rise to secondary BAs (25). Deoxycholic acid (DCA) and lithocholic acid (LCA) are derived respectively from CA and CDCA. BAs have been described as signaling molecules that signal through two main receptors: the nuclear Farnesoid X receptor  $\alpha$  (FXR $\alpha$ ; NR1H4) (26–28) and the membrane G protein-coupled bile acid receptor TGR5 (GPBAR1) (24, 29).

In addition, the nuclear receptor FXR $\alpha$  plays important role on cholesterol homeostasis through the regulation of bile acid metabolism in the liver and in the intestine. In the liver, FXR reduces the expression of the genes encoding key enzymes of bile acids biosynthesis pathways: the cholesterol 7 $\alpha$ -hydroxylase (Cytochrome P450 7a1; CYP7A1) and the sterol 12 $\alpha$ -hydroxylase (CYP8B1). In the intestine, FXR $\alpha$  activates the expression of the Fibroblast Growth Factor 19 (FGF19 in human) or FGF15 (mouse) which acts in an endocrine manner on hepatocytes *via* the Fibroblast Growth Factor Receptor 4 (FGFR4) to repress *Cyp7a1* expression (30, 31).

## THE TESTIS, CHOLESTEROL HOMEOSTASIS

The testis produces male gametes, namely spermatozoa. It is composed of a network of seminiferous tubules, separated from each other by the interstitial space. These two compartments define the two major functions of the testis with the production of gametes (exocrine function) and sexual hormone (endocrine function). Leydig cells within the interstitial space provide part of the endocrine function, and the exocrine function takes places within the seminiferous tubules. Their efficiencies are based on the specific actions of the different cell types and their interactions.

The purpose of this special issue is to collect recent acquisition on the role of cholesterol and/or derivatives as signaling molecules, whose alteration can determine the onset or progression of different pathologies. Here, we will highlight the roles of pathways activated by cholesterol and derivatives through nuclear receptors on male fertility disorders.

### The Testicular Endocrine Function

In human and rodents, testosterone is the main type of circulating androgens, which is mainly synthesized by the Leydig cells. Testis also produces small amounts of other hormones such as estrogen and progesterone.

Maintenance of an adequate concentration of intra-testicular testosterone is essential for testicular function, especially for spermatogenesis (32). The hypothalamo-pituitary axis exerts a major control on testicular steroidogenesis. Gonadotropin Releasing Hormone (GnRH) secreted by the hypothalamus, stimulates the synthesis and release of Luteinizing Hormone (LH) and Follicle Stimulating Hormone (FSH) by the gonadotropic cells of the anterior pituitary (33). The LH acts directly on the Leydig cells to control their steroidogenic activity *via* the activation of the luteinizing hormone/choriogonadotropin receptor, LHCGR. In return, sex steroids exert a negative feedback on their own synthesis. LH is involved in the regulation of steroidogenesis at different levels. LH pathway promotes the activation of cholesterol ester hydroxylase increasing the free cholesterol pool (34) and also promotes the transfer of cholesterol from the outer membrane to the inner membrane of the mitochondria. LH signaling pathway leads to the transcriptional activation of LH target genes such as *Star* (35), *Cyp11a1* (36), and *3 $\beta$ Hsd* (37).

The major role of cholesterol in the endocrine function has been well established, as cholesterol is the precursor of steroids. There are multiple sources of cholesterol that contribute to steroidogenesis such as *de novo* synthesized, (b) stored cholesteryl esters, exogenous lipoprotein-supplied cholesterol as well as plasma membrane-derived cholesterol. The plasma lipoproteins are the main source of steroid synthesis. The homeostasis of the interstitial tissue, mainly in Leydig cells, involved factors of cholesterol homeostasis such as HMG-CoA reductase, HSL, and ACAT (38, 39). Among others, the links between cholesterol and steroid synthesis are highlighted by the control of the SCAP/SREBP pathway, a regulator of cholesterol homeostasis by cAMP the secondary messenger of the LH pathways.

Sex steroid hormones share a common biosynthesis pathway, with cholesterol as unique precursor. Leydig cells are able to *de novo* synthesize cholesterol or can also use stored cholesterol ester to ensure steroidogenesis function (40). A recent study shows that the plasma membrane is one of the richest source of free cholesterol available for acute steroidogenesis (41). The first enzymatic step of steroidogenesis involves the conversion of cholesterol to pregnenolone, which occurs within mitochondria. It requires the transport of cholesterol from the outer mitochondrial membrane to the inner membrane. This limiting step is mainly provided by the Steroidogenic Acute Regulatory protein (STAR) (42). This crucial point has been highlighted by the use of transgenic mouse models. Mice lacking *Star* present gonadal insufficiencies due to steroidogenesis defects associated with lipid accumulation in the interstitial compartment (43). Recently, using a mitochondrial reconstitution assay system, it has been shown that SNARE proteins (Soluble N-ethylmaleimide-sensitive-factor Attachment protein REceptor) are vital components contributing to cholesterol transport within the mitochondria (44). Then, the biosynthesis involves the oxidative cleavage of the side-chain of cholesterol by cholesterol side-chain cleavage enzyme (cytochrome P450<sub>scc</sub>, CYP11A1), a mitochondrial cytochrome P450 oxidase, to give pregnenolone (45). Pregnenolone may be converted to testosterone through two pathways called

Delta 4 ( $\Delta 4$ ) and Delta 5 ( $\Delta 5$ ) (46). The Delta 4 ( $\Delta 4$ ) pathway involves conversion of pregnenolone to progesterone by the action of the enzyme 3 $\beta$ -Hydroxysteroid Dehydrogenase (3 $\beta$ HSD). Progesterone is then metabolized by cytochrome P450 17 $\alpha$ -hydroxylase/17,20 lyase (CYP17A1) in androstenedione, substrate of the 17 $\beta$ -hydroxysteroid dehydrogenase enzyme (17 $\beta$ HSD) for testosterone synthesis. The Delta 5 ( $\Delta 5$ ) pathway is initiated by the CYP17A1 enzyme, that allows the conversion of pregnenolone to dehydroepiandrosterone (DHEA). Then, 17 $\beta$ HSD and 3 $\beta$ HSD enzymes ensure its conversion into androstenediol or androstenedione, and testosterone. The 3 $\beta$ HSD enzyme allows switching from  $\Delta 5$  to  $\Delta 4$  pathway. In primates including humans, the  $\Delta 5$  pathway predominates because CYP17A1 enzyme has a low activity 17, 20 lyase for the conversion of 17 $\alpha$ -hydroxyprogesterone to androstenedione (47, 48). A recent proteomic analysis of murine testis lipid droplets (LDs) revealed that these LDs contained a large number of enzymes involved in metabolism and steroidogenesis. Testicular LDs could be an active organelle functionally involved in steroidogenesis (49).

Androgens exert autocrine action on Leydig cells via the androgen receptor (AR) to control their own synthesis. The AR knockout mice in Leydig cells have decreased plasma testosterone concentrations, despite high rates of LH. This hypo-androgenicity is explained by a defect in the expression of key genes encoding steroidogenic enzymes *Cyp17a1*, *3 $\beta$ hsd*, and *17 $\beta$ hsd*. This was shown to be associated with an arrest of spermatogenesis at the stage of round spermatid causing infertility (50, 51). In humans, mutations on the gene encoding the receptor of androgen AR (*NR3C4*) result in androgen resistance syndrome (52). Estrogen action is also important in regulating testicular function. Estrogen mainly mediated their signal through the activation of two specific estrogen receptors (ER), ER $\alpha$  and ER $\beta$  (53, 54). Estrogen effects on steroidogenesis have been elucidated using mouse model. It has been shown that ER $\alpha$  regulates fetal and neonatal steroidogenesis and ER $\beta$  is implicated in the control of neonatal gametogenesis. *Er $\alpha$*  is expressed in Leydig cells during fetal and neonatal life and its deletion increases testosterone production during fetal life from 13.5 dpc (55). In human, estrogens also play a crucial role in the control of reproductive functions. Studies in patients with inactivating mutations of *ER $\alpha$*  or *CYP19* (aromatase cytochrome P450) suggest a role of estrogens signaling in human male fertility (56). Next to the steroid receptors, it has been shown that numerous nuclear receptors are implicated in the regulation of steroids synthesis. This was recently well reviewed (57, 58). Nuclear receptor family has been described to locally control the expression and activity of enzymes involved in steroidogenesis. Among these, the Steroidogenic Factor 1 (SF-1) and the Liver Receptor Homolog 1 (LRH-1) are positive regulators of hormone steroids synthesis. They stimulate the expression of common target genes such as *Star*, *Cyp11a1*, *Cyp17a1*, and *3 $\beta$ hsd* encoding enzymes of steroidogenesis (59–62). SF-1 and LRH-1 are also involved in the regulation of cholesterol biosynthesis by regulating the expression of *Sr-b1* (scavenger receptor class B type I) gene which provides plasma cholesterol to steroidogenic tissues (63, 64), and the

enzyme Hydroxymethylglutaryl-CoA synthase and reductase (HMG CoA) involved in the biosynthesis of cholesterol (65, 66).

In addition, it has been shown that LXR $\alpha$  is expressed within Leydig cells (8, 67, 68). It was demonstrated that in 2.5-month-old LXR $\alpha$ -deficient mice, testosterone production is significantly lower than in wild type control mice. This was associated with a decrease of the expression of *3 $\beta$ hsd* enzyme (67). Interestingly, LXR agonist T0901317 increased testosterone concentration in wild-type mice in association with an accumulation of StAR at both mRNA and protein levels (67).

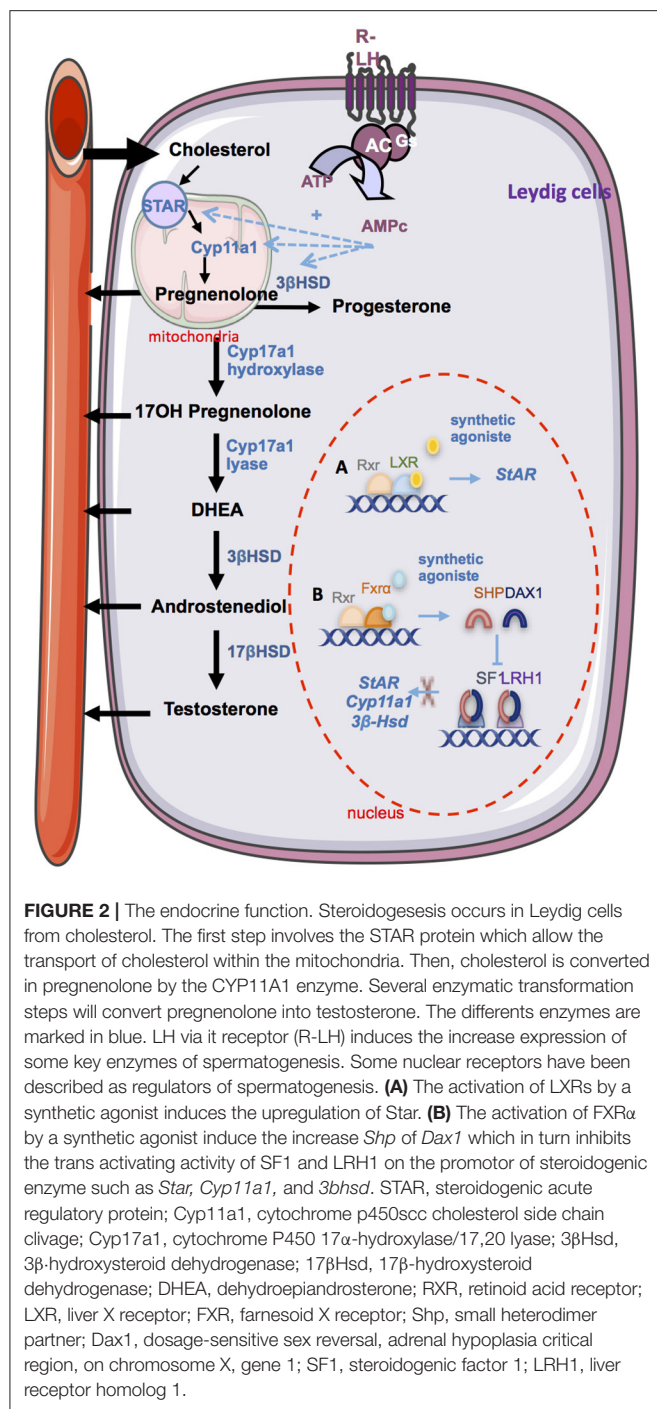
Next to this, a negative regulation of steroid synthesis involving receptors of bile acids has been defined as an important regulator of testicular physiology. BAs receptors, FXR $\alpha$  and TGR5, are expressed within the testis (69, 70) and have been recently shown to be implicated in testis dysfunction (71). Detectable levels of bile acids have been measured in the testis of mice in normal physiological conditions (72) and recently, it was shown that testis expresses key enzymes of BAs synthesis and is able to produce BAs (73).

The bile acids nuclear receptor FXR $\alpha$  is implicated in steroidogenesis regulation. In 2007, the presence of FXR $\alpha$  within mouse Leydig cells was demonstrated for the first time (69). While *Fxr $\alpha$* <sup>-/-</sup> male presented the same plasma testosterone level than control mice, induction of FXR $\alpha$  with a synthetic agonist in wild type mice results in a decrease of androgen production independently of the hypothalamo-pituitary axis. The activation of the FXR $\alpha$  receptor in Leydig cells induces transcription of the gene encoding the orphan nuclear receptors SHP (Small Heterodimer Partner, *Nr0b2*) and DAX-1 (dosage-sensitive sex reversal, adrenal hypoplasia critical region, on chromosome X, gene 1, *Nr0b1*), two orphan nuclear receptors, which are negative regulators of steroidogenic Leydig cells activity. Indeed, SHP AND DAX-1 inhibit the expression of *Lrh1* and *Sf1*. SHP also interacts with LRH1 thereby inhibiting its trans-activating activity. This decreases expressions of genes encoding key enzymes of steroidogenesis and thus leads to lower testosterone levels (69). In that line, through the regulation of the endocrine function, it has been demonstrated that BA-FXR $\alpha$  pathways also regulate male sexual maturation (74). Mice fed a diet supplemented with BAs during pubertal age show increased incidence of infertility. This is associated with altered differentiation and increase apoptosis of germ cells due to lower testosterone levels. This is sustained by the fact that supplementation with testosterone abolished the effect of CA-diet on germ cell apoptosis.

These overall data clearly suggest a complex regulation of testicular steroidogenesis by nuclear receptors whose activities are regulated by cholesterol derivatives such as oxysterols and bile acids (Figure 2).

## The Testicular Exocrine Function

Germ cell differentiation is closely related to somatic Sertoli cells functions, which provide structural and nutritional supports (Figure 3).

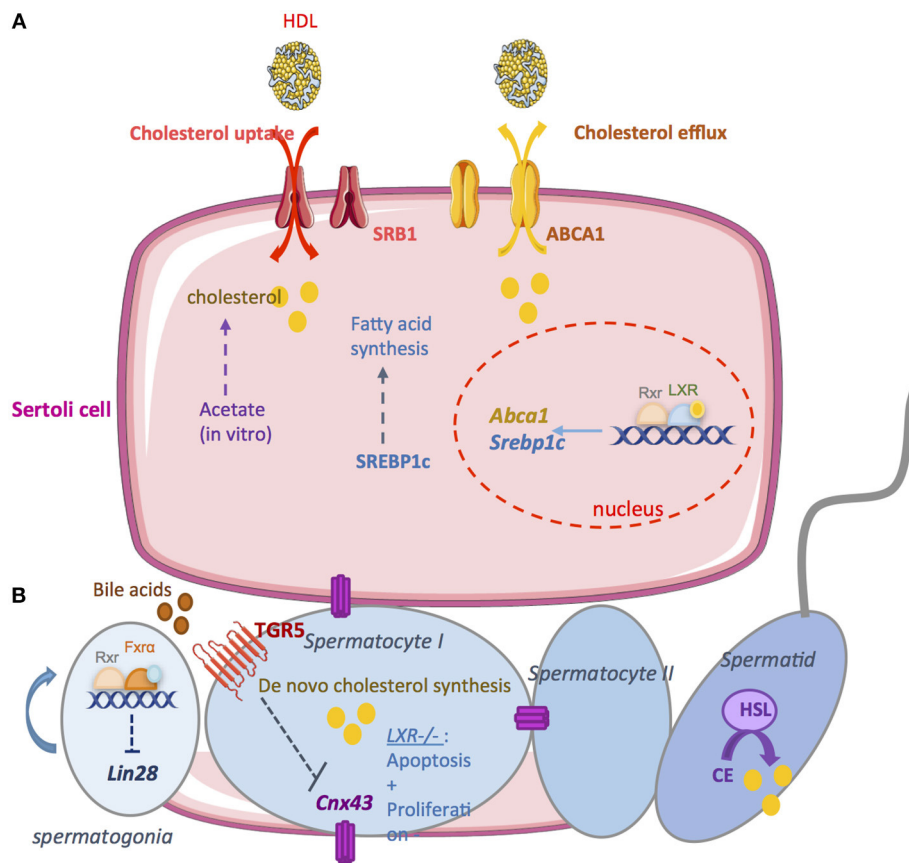


## The Sertoli Cells

One primary function of Sertoli cells is to set up the blood testis barrier (BTB) at puberty under the action of androgens, retinoids and thyroid hormones (75–77). The BTB is composed of specialized junctions established between adjacent Sertoli cells near the basement membrane of seminiferous tubules. That defines Sertoli cells polarity giving them different structural and functional poles. The BTB divides the seminiferous tubules in basal and apical compartments. Self-renewal and differentiation

of spermatogonia as well as progression to the stage pre-leptotene spermatocyte I occur in the basal compartment. The two meiotic divisions and post-meiotic steps take place in the apical compartment. The BTB regulates and restricts the passage of nutritional substances, vital molecules, and toxic compounds in the apical compartment of the seminiferous tubules. BTB also defines an immune privileged environment. It isolates many antigens present on the surface of post-meiotic germ cells from the systemic circulation thus preventing the emergence of the corresponding antibodies and autoimmune diseases leading to infertility (78). Sertoli cells also participate to the secretion of components of the extracellular matrix necessary to maintain the integrity of the seminiferous epithelium and intercellular junctions (79). In addition, they synthesize proteases and protease inhibitors contributing to the dynamic of junction complexes allowing the migration of germ cells (80). Sertoli cells provide a set of essential nutrients for germ cells survival and differentiation, including amino acids, carbohydrates, lipids and vitamins (80). Sertoli cells are able to metabolize glucose into pyruvate and lactate (81) which is the preferential energy substrate for post-meiotic germ cells to support their metabolic activity. Sertoli cells secrete numerous growth factors modulating the proliferation and/or differentiation of germ cells (82). In addition Sertoli cells secrete several transport proteins that will ensure the passage of metal ions (Transferrin) (83) or hormone (androgen-binding protein, retinoid binding protein) (84) through the BTB for the metabolic requirement of the post-meiotic germ cells.

Sertoli cells provide large amounts of lipids used for spermatogenesis. *In vitro*, it has been demonstrated that Sertoli cells are able to synthesize cholesterol from acetate (85). However, this *de novo* synthesis is not a sufficient source of cholesterol to ensure spermatogenesis *in vivo*. Therefore, it is necessary to import cholesterol from the blood circulation. In rodent, it has been demonstrated that high density lipoprotein (HDL) is the primary source of cholesterol used by Sertoli cells (86). The high-density lipoprotein transporter SR-B1 is essential to import cholesterol from blood. SR-B1 is an integral membrane glycoprotein expressed in Leydig and Sertoli cells (87, 88). This transporter facilitates the uptake of HDL. It has been demonstrated that the overexpression of SR-B1 is associated with an increase of esterified cholesterol in Sertoli cells (89). SR-B1 is also implicated in the phagocytosis of apoptotic germ cells. This may also increase cholesterol levels in Sertoli cells (90). Another important point is the elimination of cholesterol overflow. Cholesterol is esterified and stored in lipid droplets to limit toxicity. Sertoli cells maintain cholesterol homeostasis through reverse cholesterol transport. This reverse transport primarily relies on the cholesterol transporter ATP-binding cassette A1 (ABCA1) (91). Genetic mutations in *ABCA1* lead to the absence of HDL in the plasma and the accumulation of esterified cholesterol in tissues, increasing the incidence of atherosclerosis (92). ABCA1 is highly expressed in the testis and it was observed that within the seminiferous tubules, ABCA1 is more expressed in Sertoli cells (91). Authors demonstrated that TM4 Sertoli cells lacking *Abca1* or primary Sertoli cells cultured from *Abca1*<sup>-/-</sup> mice fail to efflux cholesterol. *In vivo*, *Abca1*<sup>-/-</sup>



**FIGURE 3 |** The exocrine function. **(A)** A large amount of lipids used for spermatogenesis are provided by Sertoli cells. *In vitro*, it has been demonstrated that Sertoli cells are able to synthesize cholesterol from acetate. Therefore, it is necessary to import cholesterol from the blood circulation. high density lipoprotein (HDL) is the primary source of cholesterol used by Sertoli cells. SRB1 facilitates the uptake of HDL within mitochondria. Sertoli cells maintain cholesterol homeostasis through reverse cholesterol transport which relies on the cholesterol transporter ATP-binding cassette A1 (ABCA1). LXR/RXR heterodimers increase the cellular cholesterol content by enhancing the levels of SREBP-1c and decrease cholesterol levels by increasing ABCA1 expression. **(B)** Germ cells are able to produce cholesterol *de novo*. Cholesterol *de novo* synthesis was increased during the development of pachytene, leptotene, and zygotene stages of spermatocyte I. During the latest steps, the hormone sensitive lipase (HSL) mediates the hydrolysis of cholesterol esters. The bile acids nuclear receptor FXRα regulate germ cell physiology. FXRα inhibits the expression of the pluripotency marker Lin28. FXR<sup>-/-</sup> mice present an increase number of undifferentiated spermatogonia that induce an increase number of spermatozoa. The G coupled bile acids receptor TGR5 also regulates germ cell physiology. Activation of TGR5 by Bile acids in spermatocytes decrease Cnx43 expression inducing the rupture of blood testis barrier. Nuclear receptor for oxysterols LXRs are also important regulators of germ cells physiology. In LXR<sup>-/-</sup> mice, germ cells apoptosis increase while there is a decrease in the proliferation rate. This could explain the complete loss of germ cells in these mice leading to infertility.

mice present lipid accumulation in Sertoli. At 6 months, intra-testicular testosterone levels and sperm counts are significantly reduced in *Abca1*<sup>-/-</sup> mice compared with controls. Thereby, the fertility of *Abca1*<sup>-/-</sup> mice is reduced across their reproductive lifespans. These results indicate that ABCA1 play important role to Sertoli cells function and male fertility.

Regarding the cellular signaling, it has been demonstrated that LXRβ is expressed in Sertoli cells. The *Lxrβ*<sup>-/-</sup> knockout mice are fertile with few observed defects (57, 67). However, these mice present cholesteryl ester accumulation in the Sertoli cells. This is associated with a decrease of germ cell proliferation rate. Interestingly, it was shown that men with azoospermia present a significant decrease of *Lxrβ* expression within the testis associated with fewer proliferating germ cells (93). Mice deficient for both LXRs isoforms present progressive

testicular degeneration associated with germ cell depletion. *Lxrα*<sup>-/-</sup>; *Lxrβ*<sup>-/-</sup> are reported to be infertile by 7–9 months of age (67, 68). As in *Lxrβ*<sup>-/-</sup> mice, lipid accumulation in Sertoli cells appears to be the earliest phenotype of *Lxrα*<sup>-/-</sup>; *Lxrβ*<sup>-/-</sup> mice. A recent study further investigate the roles of LXRβ in Sertoli cells by generating a mouse model that re-expresses *Lxrβ* only in Sertoli cells in the *Lxrα*<sup>-/-</sup>; *Lxrβ*<sup>-/-</sup> mice (94). Authors showed that this *Lxrβ* re-expression is fundamental for Sertoli cells to maintain functional BTB and to sustain the germ cell pool. As expected, *Lxrβ* re-expression restored lipid homeostasis in Sertoli cells and regulates the endocrine function of Leydig cells. However, these mice are infertile with spermatogenesis defects. Furthermore, it was also demonstrated that wild-type animals exposed to the synthetic LXR agonist T0901317, within diet, exhibited increased levels of the LXR target genes sterol



regulatory element-binding protein-1c (SREBP-1c) and ABCA1 (14, 95). Another study comforts the previous results in MSC-1 cells treated with T0901317 where ABCA1 levels were also increased (68).

These data clearly demonstrate the main roles of LXRs in the regulation lipid homeostasis of Sertoli cell and thus male fertility.

### The Germ Cell Lineage

Spermatogenesis is a highly coordinated process leading to the production of male haploid gametes differentiated from diploid germ stem cells. Spermatogenesis begins with a proliferative phase with the differentiation of type A spermatogonia located in contact with the basement membrane of the seminiferous tubules. A<sub>s</sub> (A single) spermatogonia possess the ability to renew the population of undifferentiated germ cells. Spermatogonia can also enter in the differentiation process. Then spermatogonia engaged in meiosis, the diploid spermatocyte gives rise to haploid cells called secondary spermatocyte or spermatocyte II and then round spermatids. Meiosis step is followed by spermiogenesis; which is the terminal process of spermatogenesis differentiation. The spermatids nucleus will be reorganized leading to chromatin compaction (96). Firstly the majority of histones is replaced by small basic transition proteins (TNP1 and TNP2). Secondly, transition proteins will be replaced by specific testis nuclear protein, protamines (PRM1 and PRM2) (97) to protect the genome from physical and chemical attack.

There is an intimate association between cholesterol metabolism and fertility during spermatogenesis. Cholesterol is required for the mass production of germ cells during spermatogenesis. A study determined that cholesterol *de novo* synthesis was increased during the development of pachytene, leptotene, and zygotene stages (98), which was associated with increased diameter and surface area of germ cells. In later stages, the rate of cholesterol synthesis tends to decrease and remains low throughout the following phases of spermatogenesis. During the last steps of spermatogenesis the Hormone-sensitive lipase (HSL) is known to mediate the hydrolysis of cholesterol esters. It has been shown that the HSL is localized in elongating spermatids and spermatozoa. The most striking phenotype of *Hsl*<sup>-/-</sup> mice is male sterility caused by oligospermia (99). *Hsl*<sup>-/-</sup> mice were found to accumulate diacylglycerols and cholesterol esters in the testis. A recent study further investigate *Hsl*<sup>-/-</sup> mice testis. Authors showed that spermatogenesis is arrested just before spermiogenesis elongation step (100). An important pathway of lipid metabolism must be lost in *Hsl*<sup>-/-</sup> testes causing an arrest of cell differentiation.

Like any animal cell, spermatozoa have a lipid bilayer plasma membrane. The proportion of the different constituents gives to the spermatic plasma membrane unique properties. The spermatic membrane has been shown to be rich in polyunsaturated fatty acids (PUFAs) important for ensuring the viability and mobility of the spermatozoon (101–103). The high proportion of PUFA also seems to play an important role in the process of membrane fusion between spermatozoon and oocyte. Indeed, PUFAs contribute to flexibility and

membrane fluidity (104, 105). The high proportion of PUFA, especially docosahexaenoic acid (DHA) in humans, is important for fertility. Indeed, one study showed a decrease in PUFAs and an increase in saturated fatty acids (SFA) in spermatozoa of asthenozoospermic men compared to sperm of normozoospermic men (106). Another study also found a negative correlation between body mass index and DHA and a positive correlation between DHA and normal sperm parameters (107). Sterols are the second major components of the plasma membrane. Cholesterol is the most abundant sterol found in the spermatic membrane of many species (102). Spermatozoa are enriched in cholesterol within the seminiferous tubules. Indeed, in the spermatocyte stage, the germ cells are able to synthesize *de novo* cholesterol to allow the increase of their membrane surface (98). Sertoli cells also participate in this process by providing to sperm cells *de novo* synthesized cholesterol or derived from the bloodstream (85, 89). More recently, the presence of oxidized cholesterol derivatives has been described in several species including mice (108). These oxysterols could influence the membrane fluidity (109). The spermatic membrane is also composed of complex lipids such as phospholipids (PL) and sphingolipids (77, 85). The lipid composition of spermatozoa is of great importance during capacitation in the female genital tract and also in membrane fusion events during fertilization. After spermiation, the lipid composition of the spermatic membrane is not definitive and will undergo many modifications during the epididymal transit and the capacitation process. Lipids largely influence post-testicular maturation of spermatozoa. During the epididymal transit, the lipid composition of the gamete is strongly reshuffled (110–112). These modifications influence the membrane dynamics in order to confer greater membrane fluidity. These lipid rearrangements are finely regulated. The epididymis produces lipid vesicles allowing protein transfer to spermatozoa. Finally, capacitation is a stage of post-testicular maturation partly regulated by the lipid composition of the spermatic membrane (113). Therefore, regulation of the lipid profile of gametes is essential for maintaining male fertility. It has recently been shown that the lipid composition of spermatozoa varies according to the dietary intake of lipids (114), demonstrating a direct correlation between diet and gamete composition.

Mammalian spermatozoa are specialized and polarized cells, with one specific function which is the fertilization of the female oocyte. This fertilizing capacity is acquired during a multistep process after spermiation called post testicular maturation. Spermatozoa maturation starts during its epididymal transit and ends in the female genital tract. The maturation of spermatozoa remains the major function of the epididymis. Epididymal maturation is essential for the acquisition of fertilizing power but is also essential to ensure normal embryonic development (115). Epididymal maturation consists of morphological, functional, and biochemical changes.

Regarding the signaling pathways involved, the LXR signaling pathways control implicated in the regulation of spermatogenesis (67). Spermatogenesis results from a balance between cell

proliferation, cell differentiation, and cell death. Proliferation and apoptosis are respectively altered in *Lxr $\beta$ <sup>-/-</sup>* and *Lxr $\alpha$ <sup>-/-</sup>* mice, whereas these mice did not show any fertility troubles. In the *Lxr $\beta$ <sup>-/-</sup>* mice the lower proliferation rate was compensated by a decreased apoptosis rate and in *Lxr $\alpha$ <sup>-/-</sup>* mice the higher apoptosis level was associated with an increased proliferation rate. The lack of both LXRs led to a dramatic decline in proliferation and increase in apoptosis. This could explain the complete loss of germ cells in these mice and thus infertility. Recently, the implication of LXRs in the physiopathology of defective spermatogenesis in non-obstructive azoospermia (NOA) patients was investigated (93). Indeed, abnormalities observed in NOA patients look like those observed in *Lxr<sup>-/-</sup>* mice. It has been shown that *Lxr* mRNA levels were decreased in NOA specimens and positively correlated with germ cell number. As expected, authors showed a decreased level of *Idol* (Inducible Degradator of the LDL receptor) and *Srebp1c* (Sterol regulatory element-binding protein 1), which are LXR target genes.

Next to this, a recent study has shown that the G coupled bile acids receptor TGR5 was expressed within the testis (70). It has been shown that BA-TGR5 signaling pathways alter testicular epithelium integrity leading to adult male fertility disorders (72). Indeed, after 4 months of dietary cholic acid (CA) supplementation, 25% of male mice were sterile and in fertile ones a 20% decrease of pups per litter was reported. Male exposed to BAs presented lower spermatozoa in the tail of the epididymis explaining the fertility defect. Interestingly, authors showed that *Tgr5<sup>-/-</sup>* mice were preserved of the CA deleterious effects on the testis. At the molecular level, BAs exposure induced a repression of cell-cell interactions network through the down-regulation of N-cadherin as well as connexin 43 (CX43) expression. This leads to germ cell sloughing, rupture of the BTB and then spermatids apoptosis. In humans, a reduction in the expression of CX43 was shown to be associated with the degree of spermatogenesis defect (116–118).

Recently, it has been shown that bile acids nuclear receptor FXR $\alpha$  regulates germ cell physiology (73). Authors showed that FXR $\alpha$  plays a role in the establishment and maintenance of the undifferentiated germ cell pool that in turn influences male fertility. *Fxr $\alpha$ <sup>-/-</sup>* males present an extended fertility with aging. In *Fxr $\alpha$ <sup>-/-</sup>* males, the maintenance of fertility capacities results from a higher number of undifferentiated germ cells during aging associated with high spermatozoa production. FXR $\alpha$  regulates the expression of several pluripotency factors within the germ cell lineage. *In vitro* approaches show that FXR $\alpha$  controls the expression of the pluripotency marker Lin28 in the germ cells.

## Obesity and Male Fertility

In the last decades infertility has become a global public health issue affecting 15% of all reproductive couples. It has been estimated that 70 million couples worldwide experience subfertility or infertility (119). Male factors are responsible for ~25% of cases of infertility (2). Currently, the etiology of low semen quality is poorly understood. Many physiological, environmental and genetic factors have been implicated (120).

Metabolic syndrome (MetS) is a group of risk factors such as high blood pressure, high blood sugar, unhealthy cholesterol levels, and abdominal fat. The association between MetS and male hypogonadism is well established and reviewed (121). Cross-sectional studies have found that between 20 and 64% of obese men have low total testosterone levels (122). A number of studies also show that low testosterone is associated with insulin resistance and an increased risk for diabetes mellitus and MetS in men. Testosterone supplementation seems to be beneficial on inflammation, muscle mass, lipid profile, sexual function, and improves comorbidities of obesity, MetS, or cardiovascular disease in males (121).

Evidence from human studies indicates that male obesity and components of the diet could play an important role in the deregulation of spermatogenesis, sperm maturation, or fertilizing ability. Obese or overweight men could present a decrease sperm quantity, quality, and motility (123, 124). A study showed differences between obese and lean patients regarding the acrosome reaction (125). Sperm acrosome reaction is impaired in obese men associated with altered circulating levels of estradiol and sperm cholesterol content. Obese men can also present an increase sperm DNA damage or lower embryo implantation rate (122, 126). The majority of studies in humans focuses on the impact of obesity on male fertility and do not take into account the plasma lipid profile. It is reported that 65% of infertile men show hypercholesterolemia and/or triglyceridemia (127). The impact of dyslipidemia on male fertility remains controversial. Even if cholesterol and lipid homeostasis is essential for male fecundity (57, 128), a recent study reported that hypercholesterolemia is not associated with sperm concentration or motility in men (129). It has also been shown that there is no correlation between sperm concentration and serum total cholesterol or triglyceride in human (130).

Some animal studies revealed that high cholesterol diet can impair fertility and lower sperm quality. Rabbit fed a High fat diet (HFD) is an experimental model of metabolic syndrome (MetS) that closely similar to the human syndrome (131–133). This model has been characterized by hyperglycaemia, hypercholesterolemia, hypertension, hypogonadotropic hypogonadism, penile alterations (131, 132, 134) or nonalcoholic steatohepatitis. This model is very useful to study the deleterious impact of MetS symptoms such as hypercholesterolemia on male fertility. It has been demonstrated that supplementation with testosterone (131, 132) with the FXR $\alpha$  agonist the obeticholic acid (133, 134) normalize several MetS symptoms including HFD-induced penile alterations. These animals presented abnormal sperm morphology, decreased sperm number and declined percentage of motile sperm or acrosome reaction (134–136, 138, 139). It has been shown that administration of tamoxifen, used in the treatment of idiopathic male infertility to HFD rabbits partially restored sperm motility, but further decreased morphology and increased spontaneous acrosome reaction (136). It has also been shown that hypercholesterolemic rabbits present lower testicular efficiency related to both a decrease in spermatogonial cells and an increase in germ cell apoptosis (137). On the other hand,



spermiogenesis, which is the last step of spermatogenesis, was also affected in these animals. In post-meiotic germ cells from hyper-cholesterolemic rabbits, abnormal development of acrosome, nucleus, and inaccurate tail implantation were associated with actin- $\alpha$ -tubulin-GM1 sphingolipid altered distribution. It was recently shown in rabbits that a cholesterol-enriched diet increased lipid deposition in the seminiferous tubules and disrupted the BTB (138). Total protein levels of the tight-junction protein 1 (ZO-1) and occludin and their distribution patterns were markedly affected, impairing fertility.

A similar study has demonstrated a disruption of BTB in mice exposed to High Fat Diet (HFD) (139). It has been reported that male rodents exposed to HFD present a decreased number of motile spermatozoa associated with a decline of fertilization rates (140–142). Intracellular reactive oxygen species (ROS) and sperm DNA damage were elevated in the HFD group compared with controls that could explain the decrease sperm motility (141). It has been demonstrated that HFD induces a decrease in testosterone production associated with a decrease level of steroidogenic enzyme (143, 144). A recent study suggests that the increase of autophagy process could be a cause of fertility defects induced by HFD (145). Authors demonstrate that inhibiting autophagy with chloroquine improves the decreased fertility of HFD male mice. Furthermore, the excessive activation of autophagy was also observed in sperm samples from obese, sub-fertile male patients.

In addition, some studies were interested in the impact of paternal or maternal exposure to HFD on male offspring (146, 147). It has been shown that preconception exposure of fathers to HFD impairs the motility of spermatozoa of male offspring, despite their control diet consumption (146). Feeding females with a HFD through pregnancy and lactation induces a decrease on LH and testosterone levels in male offspring (147). If translatable to human health, these studies suggest that reproductive defects may be amplified throughout generations because of calorie dense diet.

Interestingly, in the last decade, it has been proposed that derivatives of bile acids (BAs) could be interesting molecules for the treatment of metabolic diseases such as diabetes or obesity. Regarding the links between BA signaling pathways and male testicular physiology (72–74), a study has investigated the consequences of a long term exposure to molecules that activate BA signaling pathways to treat obesity. For that purpose, mice were fed HFD to induce obesity and concomitantly treat with BAs (148). Even if BAs improves abnormalities induced by the HFD such as body weight, glycemia, or lipidic profiles, co-exposure of HFD and BAs leads to a higher level of infertility. This was associated with altered germ cell proliferation, default of endocrine function and abnormalities in cell-cell interactions within the seminiferous tubule.

## CONCLUSIONS

Male fertility disorders represent serious health problem and in 30% of the cases the cause remains unknown. Understanding

the various pathologic mechanisms causing male infertility represents an active area of research. As reviewed here, cholesterol homeostasis is crucial for testicular functions such as steroidogenesis, Sertoli cells function, or germ cell differentiation. Thus, altered concentrations of plasma cholesterol can affect the reproductive function leading to male infertility. This link between lipid homeostasis and male fertility disorders is clearly evident in patients suffering from hyperlipidemia or metabolic syndrome. Lipid-lowering drugs could probably ameliorate some reproductive symptoms. However, epidemiological data are currently scarce and controversial.

All these data could help in proposing new molecular markers to diagnose cases of infertility or to define whether the results obtained on the incriminated nuclear receptors LXR $\alpha$  and FXR $\alpha$  which can be modulated by ligands can lead to concepts transferable to the clinic either to develop new strategies to treat infertile men or new approached for male contraception. Such perspectives will require the development of testicular-specific LXR or FXR modulators to treat testicular disorders and therefore male disorders without causing their impacts that may lead to metabolic disorders.

In the opposite way, modulating some of these receptors through the use of agonist or antagonist molecules would improve the symptoms of metabolic syndrome diseases. However, it has been shown in mice that modulating nuclear receptors signaling induce deleterious effects on testicular physiology leading to infertility. In that line, as molecules modulating the BA receptor signaling pathways have been proposed to treat metabolic diseases, it will be important to define the molecular mechanisms involved in the deleterious impact of BAs on testis physiology. Such studies will be essential to define how to pharmacologically or genetically modulate bile acid receptors to treat metabolic disorders while minimizing impacts on male reproductive functions. In addition, the identification of the crosstalk between increased BA levels and metabolic diseases on fertility capacities of male mice should be a mechanism explaining rare clinical situations of infertility following bariatric surgical approach in some obese men.

It will be interesting in the future to identify at the clinical levels, using biopsies of patients suffering from liver disorders (cholestasis, hepatitis...), the potential involvement of bile acid signaling pathways in the human regulation of male fertility. According to previous published data, it will be necessary to analyse both BA levels as well as the BA pool composition. Indeed, it appears that secondary BA, namely DCA, is the one whose levels are inversely correlated with fertility. Such analyses on human cohort will be useful to define if BA levels or pool composition might be a useful biomarker linking liver disorders and male infertility; or even if BA could be markers of idiopathic infertility.

In the recent decades, assisted medical procreation (AMP) has been importantly developed to overpass the fertility disorders. Next to *In vitro* fecundation, important efforts have been done in order to develop approach of *in vitro* production of germ cells from spermatogonial stem cells. This strategy is important to propose AMP to azoospermic men. The recent data regarding the role of FXR $\alpha$  in the establishment of the

pool of undifferentiated spermatogonia, suggest that FXRalpha modulators might be useful in such approaches to increase the rate and efficiency to produce male gametes.

## AUTHOR CONTRIBUTIONS

LS, LT, SM, MG, FC, JML, CB and DV have participated to the writing of this review.

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## FUNDING

This work was funded by Inserm, CNRS, Clermont Université, Ligue contre le Cancer (Comité Puy de Dôme to DV), Nouveau Chercheur Auvergne (#R12087CC to DV), and Plan Cancer—Cancer-Environnement InCa/Inserm (C14012CS to DV). DV's team received support by the French government IDEX-ISITE initiative 16-IDEX-0001 (CAP 20-25).

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**Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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OPEN ACCESS

**Edited by:**

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**Specialty section:**

This article was submitted to  
Cancer Endocrinology,  
a section of the journal  
Frontiers in Endocrinology

**Received:** 23 May 2018

**Accepted:** 30 July 2018

**Published:** 23 August 2018

**Citation:**

Hiramitsu S, Ishikawa T, Lee W-R,  
Khan T, Crumley C, Khwaja N,  
Zamanian F, Asghari A, Sen M,  
Zhang Y, Hawse JR, Minna JD and  
Umetani M (2018) Estrogen Receptor  
Beta-Mediated Modulation of Lung  
Cancer Cell Proliferation by  
27-Hydroxycholesterol.  
Front. Endocrinol. 9:470.  
doi: 10.3389/fendo.2018.00470

# Estrogen Receptor Beta-Mediated Modulation of Lung Cancer Cell Proliferation by 27-Hydroxycholesterol

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27-hydroxycholesterol (27HC) is an abundant cholesterol metabolite in human circulation and promotes breast cancer cell proliferation. Although lung is one of the organs that contain high levels of 27HC, the role of 27HC in lung is unknown. In this study, we found that 27HC promotes lung cancer cell proliferation in an estrogen receptor  $\beta$  (ER $\beta$ )-dependent manner. The expression of 27HC-generating enzyme CYP27A1 is higher in lung cancer cells than in normal lung cells. Treatment with 27HC increased cell proliferation in ER $\beta$ -positive lung cancer cells, but not in ER $\alpha$ -positive or ER-negative cells. The effect on cell proliferation is specific to 27HC and another oxysterol, 25-hydroxycholesterol that has a similar oxysterol structure with 27HC. Moreover, among ligands for nuclear receptors tested, only estrogen had the proliferative effect, and the effect by 27HC and estrogen was inhibited by ER $\beta$ -specific, but not ER $\alpha$ -specific, inhibitors. In addition, the effect by 27HC was not affected by membrane-bound estrogen receptor GPR30. Interestingly, despite the high expression of CYP27A1, endogenously produced 27HC was not the major contributor of the 27HC-induced cell proliferation. Using kinase inhibitors, we found that the effect by 27HC was mediated by the PI3K-Akt signaling pathway. These results suggest that 27HC promotes lung cancer cell proliferation via ER $\beta$  and PI3K-Akt signaling. Thus, lowering 27HC levels may lead to a novel approach for the treatment of lung cancer.

**Keywords:** lung cancer, estrogen receptor, ER $\beta$ , 27-hydroxycholesterol, cholesterol metabolites

## INTRODUCTION

Lung cancer is the leading cause of cancer deaths in men and women in the United States (1), and there is accumulating evidence that estrogen is a major driver of lung cancer (2). In addition, the proportional occurrence of histological lung carcinoma subtypes differs between men and women. While squamous cell carcinoma is the most common subtype in men, adenocarcinoma



is the most common subtype in women (1, 3). Estrogen receptors, ER $\alpha$  and ER $\beta$ , are members of the nuclear receptor family, and are present both in normal lung tissue and lung tumors with ER $\beta$  as a dominant isoform (4–6). Large-scale randomized and observational studies showed that women who used hormone replacement therapy (HRT) including estrogen have a higher risk of adenocarcinoma than women who did not use HRT, and that risk of lung cancer was associated with chronic use of HRT (7). In contrast, breast cancer patients who received anti-estrogen treatment had significantly lower subsequent lung cancer mortality (8). Studies using genetically modified mice showed that both male and female lungs are highly estrogen-responsive (9, 10). Mice deficient in ER $\beta$  exhibited significant lung dysfunction both in males and females, indicating the importance of ER $\beta$  in the maintenance of lung function (11). Estrogens also stimulate growth and progression of lung tumors, and local production of estrogen in lung tissues by aromatase could affect lung tumor progression in ER(+) malignancies in men and women (12, 13). ER also interacts with epidermal growth factor receptors (EGFRs), and the combination of EGFR tyrosine kinase inhibitors and ER antagonists gives maximal inhibition of tumor cell proliferation *in vitro* and also anti-tumor activity in mouse tumor xenograft models *in vivo* (14, 15). Taken together, estrogen and ERs play important roles in lung cancer pathogenesis and treatment.

Oxysterols are metabolites of cholesterol that are produced in the liver and other peripheral tissues as a means to eliminate cholesterol (16). The most abundant circulating oxysterol is 27-hydroxycholesterol (27HC), and serum concentrations of 27HC correlate well with that of cholesterol. The levels of 27HC also rise progressively with age. The enzyme that generates 27HC, sterol 27-hydroxylase (CYP27A1), is primarily expressed in the liver, but also in peripheral tissues to a lesser extent (17). Using cell-based and *in vitro* assays, we discovered that 27HC is a competitive ER antagonist in the cardiovascular system (18). We further found that 27HC binds directly to ER $\alpha$  ( $K_i = 1.32 \mu\text{M}$ ) and ER $\beta$  ( $K_i = 0.42 \mu\text{M}$ ) in their ligand binding pockets, and it inhibits both transcriptional and non-transcriptional estrogen-dependent production of nitric oxide by vascular cells. In mice, elevated 27HC levels decreased ER-dependent expression of vascular nitric oxide synthase and repressed carotid artery reendothelialization after vascular injury. In addition to the anti-estrogenic effects of 27HC in vascular cells, we identified pro-estrogenic actions of 27HC in hepatoma HepG2 and colon cancer Caco-2 cells (18). Combinatorial peptide phage display revealed that 27HC induces a unique active conformation of ER $\alpha$  (19). In contrast to estrogens that have various levels of agonistic activity in all tissues, selective ER modulators (SERMs) are compounds that act as agonists or antagonists depending on the target genes and tissues (16). Although many compounds have been identified as SERMs, all of them were synthetic compounds. Thus, 27HC is the first identified endogenously produced SERM, and has important biological actions *in vitro* and *in vivo*.

In breast cancer, in which ER $\alpha$  is classically involved in the development and progression of many tumors, paradoxically, post-menopausal women with decreased estrogen production

are particularly at increased risk of ER-positive breast cancer. This risk occurs at a time when circulating estrogen levels are declining, and endocrine-based therapies against ER-positive breast cancer employing synthetic SERMs or aromatase inhibition are often ineffective or acquire resistance, suggesting other important unknown ER-mediated mechanisms (20). Once we identified 27HC as a novel endogenous SERM and that its abundance increases with age, we tested its potential actions on ER-positive breast cancer cells, and found that 27HC up-regulated ER $\alpha$  target gene expression and increased cell proliferation (19). Also in mice, 27HC promoted tumor growth and metastasis to the lung in an orthotopic breast tumor xenograft model (21). In humans, we found that elevated levels of 27HC in tumors, which are correlated with reduced expression of the 27HC-catabolizing enzyme oxysterol 7 $\alpha$ -hydroxylase (CYP7B1), are associated with poorer patient survival (22). Even when age, tumor size, nodal status, and perioperative therapy are taken into consideration, low expression of CYP7B1 continues to be associated with poor overall outcome. Thus, 27HC is a non-estrogen, locally-modulated, non-aromatized ER ligand that stimulates ER-positive breast tumor growth, and, most importantly, it is abundant in the microenvironment of tumors in women.

In the present study, we investigated how 27HC impacts lung cancer cell proliferation through its modulation of the ER-mediated action. We found that ER $\beta$  expression is higher in lung cancer cells than in normal lung cells, and also that 27HC promotes ER $\beta$  (+) lung cancer cell proliferation. Although lung cancer cells have elevated gene expression of 27HC-producing enzyme CYP27A1, endogenously produced 27HC was not the major factor involved in the 27HC-induced cell proliferation. We sought to determine the underlying mechanism, and found that the PI3K-Akt pathway is involved in the effect by 27HC on lung cancer cell proliferation.

## MATERIALS AND METHODS

### Materials

27HC was purchased from Avanti Polar Lipids. T0901317 (T1317) was purchased from Cayman Chemical. 1,3-bis (4-hydroxyphenyl)-4-methyl-5-[4-(2-piperidinylethoxy)phenol]-1H-pyrazole dihydrochloride (MPP), 4-[2-phenyl-5,7-bis(trifluoromethyl)pyrazolo[1,5-a]pyrimidin-3-yl]phenol (PHTPP), G1, G15, and iressa were purchased from Tocris Bioscience. Cholestane-3 $\beta$ ,5 $\alpha$ ,6 $\beta$ -triol and 5 $\alpha$ -hydroxy-6-ketocholesterol were purchased from Steraloids. 17 $\beta$ -estradiol (E $_2$ ), GW3965 (GW), 4 $\beta$ -hydroxycholesterol, 7-ketocholesterol, 22(R)-hydroxycholesterol, 24(S)-hydroxycholesterol, 25-hydroxycholesterol, cholesterol 5 $\alpha$ ,6 $\alpha$ -epoxide, cholesterol 5 $\beta$ ,6 $\beta$ -epoxide, cholesterol, progesterone, 5 $\alpha$ -dihydrotestosterone (DHT), dexamethasone, cortisone, Wy-14643, GW501516, troglitazone, EGF, insulin-like growth factor (IGF), vascular endothelial growth factor (VEGF), PD0325901, U0126, SB203580, LY294002, and clotrimazole were purchased from Sigma-Aldrich.

## Gene Expression Analyses and Assessments of Gene Expression

Expression profiling of *ERα*, *ERβ*, *CYP27A1*, and *CYP7B1* was part of a larger study (Gene Expression Omnibus DataSets accession number GSE32036) that has been previously published (23, 24). Raw data was background corrected with RMA, Log2 transformed, and summarized by medianpolish. Differently expressed genes were called using the LIMMA package and *p*-values were corrected for multiple testing with the Benjamini-Hochberg procedure. The expression heatmap was generated in R and ontology enrichment was performed in HOMER. *CYP27A1*, *CYP7B1*, *ERα*, and *ERβ* transcript abundance were further evaluated by quantitative RT-qPCR (25). Primer sequences used for RT-qPCR are listed in **Supplemental Table 1**.

## Cell Culture Assays

MCF-7 (ATCC), A549 (ATCC), Lewis lung carcinoma (LLC, ATCC), H1395, and H596 cells were maintained in RPMI 1640 medium containing 5% FBS. Cell proliferation was assessed by quantifying <sup>3</sup>H-thymidine incorporation (22). Cells were maintained in phenol red-free DMEM containing 5% charcoal-stripped FBS for 72 h. Cells were then passed into 24-well plates at a density of 100,000 cells per ml in media containing 5% charcoal-stripped FBS, and 24 h later they were treated with compounds for 24 h, during which <sup>3</sup>H-thymidine incorporation was quantified. To provide a complementary approach in H1395 cells, in selected studies cell proliferation was quantified by cell number using FluoroReporter Blue Fluorometric dsDNA Quantitation kit (Thermo Fisher Scientific). To evaluate the involvement of *ERβ* in the 27HC-induced lung cancer cell proliferation, LLC cells were transfected with an *ERβ*-expression plasmid using Lipofectamine 2000 and used for the cell proliferation assay. To specifically evaluate the impact of silencing of *CYP27A1* or *CYP7B1* on the modulation of lung cancer cell proliferation, their expression was knocked down using dsRNA targeting human *CYP27A1* (TF313602, OliGene Technologies), *CYP7B1* (Dharmacon), or control dsRNA. H1395 cells were transfected with 50 nM RNA as described previously (25) and cell proliferation responses to vehicle or 27HC were evaluated from 48 to 72 h post-transfection.

## Immunoblot Analyses

ER protein abundance was assessed by immunoblot analysis using antibodies against *ERα* (ab75635, Abcam), *ERβ* (26), and GAPDH (G8796, Sigma-Aldrich) as a control. Phosphorylation of ERK1/2, p38 MAPK, and Akt proteins were assessed by immunoblot with their phosphorylated protein-specific antibodies (Cell Signaling), and their total protein abundance was also assessed.

## Statistical Analysis

All data are expressed as mean ± SEM. Two-tailed Student's *t*-test or ANOVA was used to assess differences between two groups or among more than two groups, respectively, with Newman-Keuls *post-hoc* testing following ANOVA. *P*-values <0.05 were considered significant.

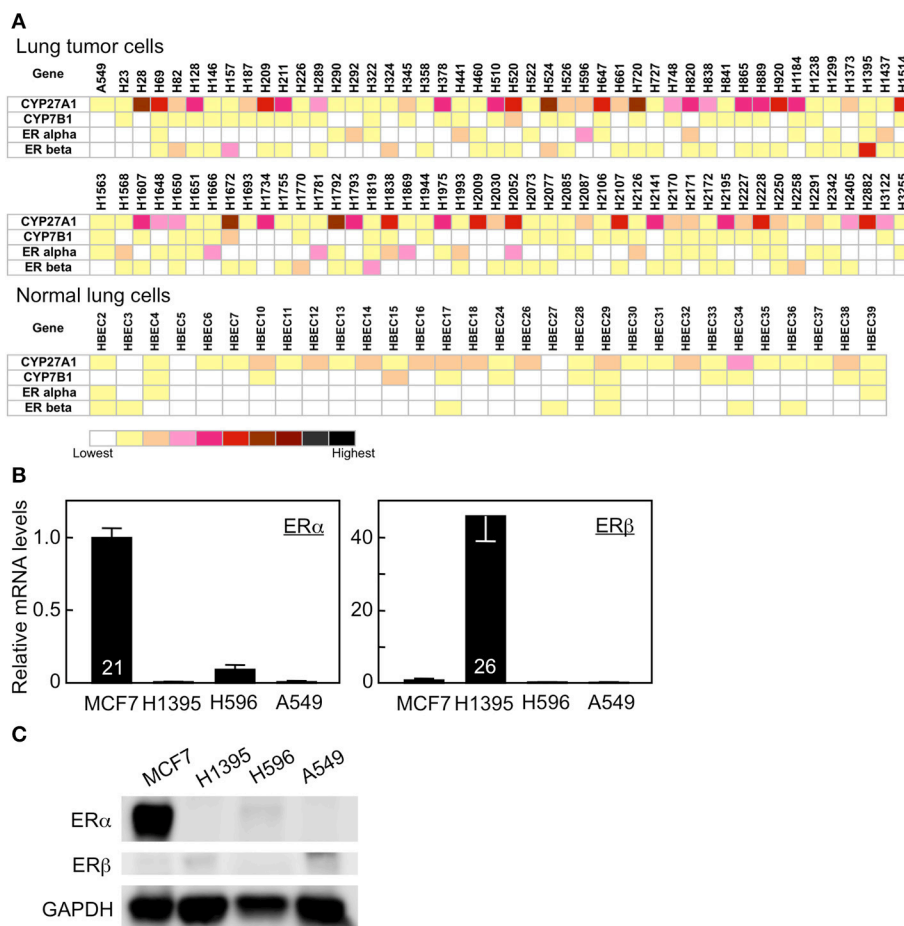
## RESULTS

### Gene Expression of ER in Lung Cancer Cell Lines

To evaluate possible actions of 27HC in lung cancer pathogenesis, we determined the expression levels of *CYP27A1*, *CYP7B1*, *ERα*, and *ERβ* in a variety of lung cancer and normal lung cell lines. Ninety-one human lung tumor cell lines and 30 human normal bronchial epithelial cell lines from the Lung Cancer Program at UT Southwestern Medical Center were analyzed. With relative levels of expression represented as log<sub>2</sub> (signal) in the heat diagram, mRNAs for *CYP27A1* were detectable at varying levels with clear difference among the different cell types (**Figure 1A**). Thirty-one tumor cell lines showed moderate to high expression of 27HC-generating enzyme *CYP27A1* while none of the normal cell line showed moderate to high *CYP27A1* expression. The log<sub>2</sub> *CYP27A1* expression ratio of tumor vs. normal lung cells is 0.87 (*P* < 0.001). The mRNA expression for *ERβ* was also higher in tumor cells than normal lung cells (log<sub>2</sub> ratio 0.28, *P* = 0.004). There were also varying levels of mRNA expression for *CYP7B1* and *ERα* transcripts, although there is no significant difference between tumor vs. normal lung cells. We further validated the microarray data and also compared the mRNA expression levels in high *ERβ* expressed H1395, high *ERα* expressed H596, and *ER*-negative A549 cells with those in breast cancer MCF-7 cells by qRT-PCR analysis. As expected, MCF-7 cells have high mRNA expression of *ERα*. Consistent with the microarray results (**Figure 1A**), H1395 and H596 cells have high expression of *ERβ* and *ERα*, respectively (**Figure 1B**). The protein expression of *ERα* and *ERβ* was also confirmed in MCF-7 and H1395 cells, respectively (**Figure 1C**). The mRNA expression of *CYP27A1* and *CYP7B1* varied among cell lines, and the gene expression of aromatase, which converts testosterone to estrogen, was not observed in the cells tested (**Supplemental Figure 1** and data not shown). These results suggest that the molecular machinery necessary to synthesize and metabolize 27HC is found in lung cancer cells, and local 27HC production and *ERβ* mRNA expression are higher in lung tumor cells than normal lung cells.

### 27HC Promotes H1395 Lung Cancer Cell Proliferation

Next, we evaluated whether 27HC has cell proliferative effects in lung cancer cells. We selected H1395 and H596 lung adenocarcinoma cells, which express high levels of *ERβ* and *ERα*, respectively and also A549 cells which have no expression of *ER* (**Figure 1**). 27HC and E<sub>2</sub> induced cell proliferation of H1395, but not H596 or A549 cells (**Figure 2A**), suggesting that the effect by 27HC is *ERβ*-dependent. The proliferative effects of 27HC are also dose-dependent (**Figure 2B**) and specific to the 27HC structure, but not to general oxysterols. Among other oxysterols tested, only 27HC, and 25-hydroxycholesterol were able to induce cell proliferation in this model (**Figure 2C**). 25-Hydroxycholesterol has a similar oxysterol structure as 27HC and also acts as an *ER* ligand. We could not see any promoting effect on the cell proliferation by 4β-Hydroxycholesterol, 7-keto-cholesterol, 22(R)-hydroxycholesterol, 24(S)-hydroxycholesterol, cholesterol



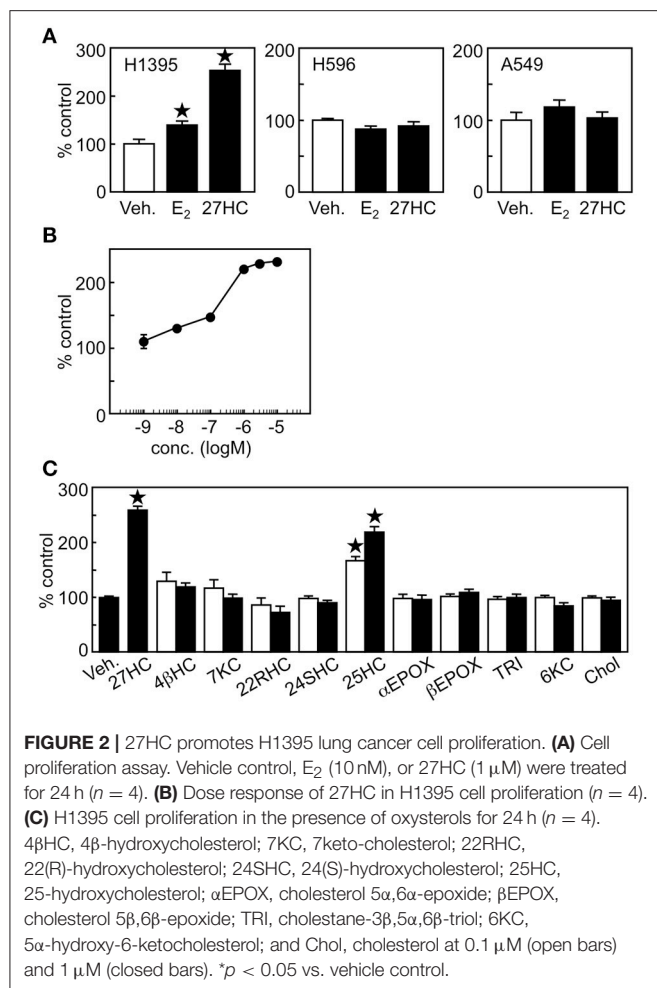
**FIGURE 1 |** Gene expression in human lung tumor and normal bronchial epithelial cells. **(A)** Gene expression profile of *CYP27A1*, *CYP7B1*, *ERα*, and *ERβ*. **(B)** qRT-PCR analysis of *ERα*, and *ERβ* in MCF7, H1395, H596, and A549 cancer cells ( $n = 6-7$ ). Cycle time of the highest expressing group for each gene is indicated inside its corresponding bar. **(C)** Immunoblots of *ERα*, *ERβ*, and GAPDH proteins.

5 $\alpha$ ,6 $\alpha$ -epoxide, cholesterol 5 $\beta$ ,6 $\beta$ -epoxide, cholestane-3 $\beta$ ,5 $\alpha$ ,6 $\beta$ -triol, and 5 $\alpha$ -hydroxy-6-ketocholesterol, which are reported to stimulate breast cancer cell proliferation (27). These results indicate that 27HC promotes H1395 lung cancer cell proliferation and that the effect is specific to 27HC and 25-hydroxycholesterol.

## Effects of 27HC on Lung Cancer Cell Proliferation Are ER $\beta$ -Specific

To examine whether the effect of 27HC on lung cancer cell proliferation was ER $\beta$ -specific, ligands for other nuclear receptors were tested on H1395 cells. Ligands for liver X receptor (LXR, T1317, GW), progesterone receptor (progesterone), androgen receptor (5 $\alpha$ -dihydrotestosterone), glucocorticoid receptor (dexamethasone), mineralocorticoid receptor (cortisone), or  $\alpha$  (Wy-14643),  $\delta$  (GW501516), and  $\gamma$  (troglitazone) isoforms of PPAR in the concentrations known to activate their receptors (18) did not induce growth promoting effects in H1395 cells (Figure 3A). Together with the results in Figure 2C that 22(R)-hydroxycholesterol and

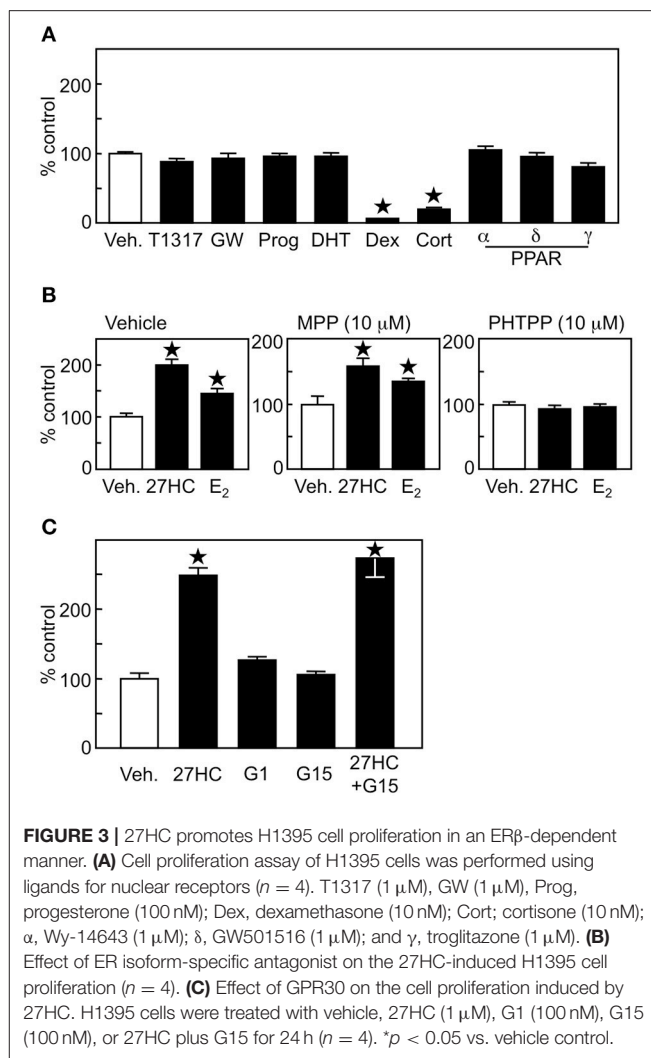
24(S)-hydroxycholesterol, which also act as ligands for LXR and retinoic acid related orphan receptors (RORs), respectively (28, 29), did not show any promoting effect on the H1395 cell proliferation, these results indicate that the effect by 27HC is not LXR-, PR-, AR-, MR-, GR-, PPAR-, or ROR-dependent. Next, we used ER isoform-specific inhibitors. The effect by 27HC and E<sub>2</sub> was inhibited by the ER $\beta$ -specific inhibitor PHTPP, but not by the ER $\alpha$ -specific inhibitor MPP (Figure 3B). To confirm the importance of ER $\beta$  in the 27HC-mediated lung cancer cell proliferation, we compared the effect by 27HC on LLC cells, which are ER-negative, and LLC cells that overexpress ER $\beta$  following transfection with an ER $\beta$  expression plasmid. 27HC and E<sub>2</sub> induced cell proliferation of LLC cells that expressed ER $\beta$ , but had no effect on parental LLC cells (Supplemental Figure 2), further indicating that the effect by 27HC on lung cancer cell proliferation is ER $\beta$ -dependent. In addition to classical ER, estrogen can also activate the G protein-coupled receptor GPR30 (6). Thus, the involvement of GPR30 in the H1395 cell proliferation was tested using its agonist G1 and antagonist G15. Neither of these GPR30 ligands affected H1395 cell



proliferation and G15 did not abrogate the inducing effects of 27HC (Figure 3C), indicating that GPR30 is not involved in the 27HC-induced H1395 cell proliferation. These results indicate that 27HC promotes lung cancer cell proliferation via ERβ.

## Exogenous 27HC Is the Major Effector on ERβ (+) Lung Cancer Cell Proliferation

Since lung tumor cells have higher expression of 27HC-generating CYP27A1 (Figure 1A), it is plausible that endogenous 27HC production affects ERβ (+) lung cancer cell proliferation. To examine the involvement of endogenous 27HC production in H1395 cell proliferation, we introduced shRNA against CYP27A1 into H1395 cells and generated clones A3 and D2. The shRNA decreased the expression of CYP27A1 significantly in two clones, A3 and D2 (Figure 4A); however, the cell proliferation was not altered in the presence of control or shRNA against CYP27A1 (Figure 4B). In a similar fashion, siRNA mediated suppression of CYP7B1, #32 and #33, significantly decreased CYP7B1 mRNA levels in H1395 cells (Figure 4C) but did not alter cell proliferation relative to control siRNA cells (Figure 4D). We further confirmed our findings using clotrimazole, an inhibitor of P450 enzymes to which both CYP27A1 and CYP7B1 belong,

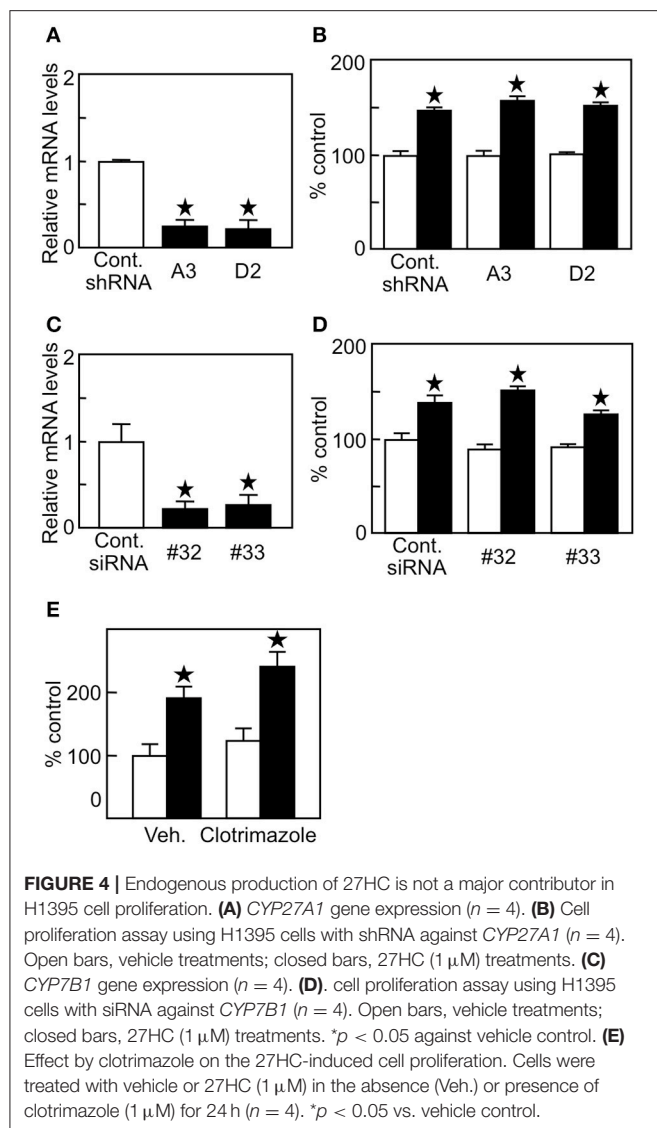


and the treatment of H1395 cells at 1 μM did not alter cell proliferation (Figure 4E). These results indicate that although lung cancer cells have high 27HC-generating enzyme expression, endogenous 27HC is not the major effector of ERβ (+) lung cancer cell proliferation.

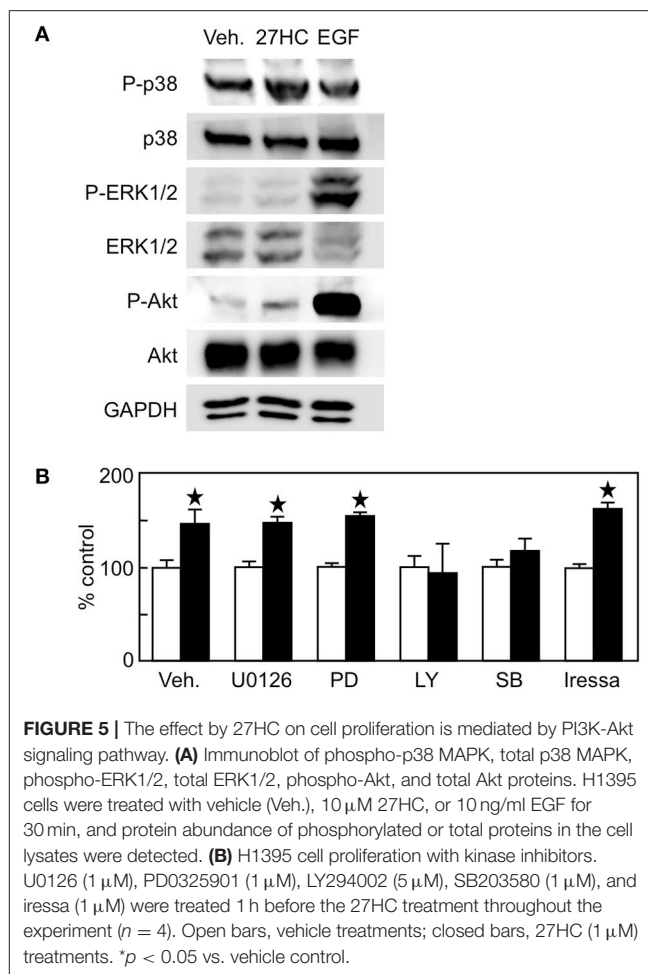
## 27HC Promotes Cell Proliferation Through the PI3K-Akt Pathway

In addition to its action as a transcription factor, ER has an action as an extranuclear signaling molecule involving various kinase pathways such as PI3K-Akt and MEK-MAPK pathways. In non-small cell lung cancer, ER activation leads to the induction of the p44/p42 MAPK signaling pathway, which is considered to be an extranuclear action of ER (14). In addition, ER interacts with EGF receptor and activate tyrosine kinase signaling in breast cancer (15), and EGF, but not IGF or VEGF, promotes H1395 cell proliferation (Supplemental Figure 3A). To examine whether 27HC is capable of eliciting extranuclear effects, we performed immunoblot analysis using H1395 cell extracts. EGF stimulated the phosphorylation of p38 MAPK,





ERK1/2, and Akt in H1395 cells (**Figure 5A**). The treatment of 27HC also phosphorylated p38 MAPK and Akt, but not ERK1/2. Next, we performed cell proliferation assays in combination with kinase inhibitors. These inhibitors suppressed basal cell growth (**Supplemental Figure 3C**). The effect by 27HC was not inhibited by MEK/MAPK inhibitors PD0325901 or U0126 (**Figure 5B**). In contrast, the effect by 27HC was suppressed in the presence of the PI3K inhibitor LY294002. Interestingly, another p38MAPK inhibitor SB203580, which also inhibits Akt, suppressed the effect of 27HC. To examine the involvement of the EGFR signaling pathway in the ER $\beta$ -mediated 27HC effect on cell proliferation, EGFR inhibitor Iressa was also used. Iressa at 1  $\mu$ M, which completely blocked the cell proliferation induced by EGF (**Supplemental Figure 3B**), did not alter the effects of 27HC (**Figure 5B**). These results suggest that 27HC promotes H1395 cell proliferation through the activation of PI3K-Akt signaling pathway in ER $\beta$  (+) lung cancer cells.



## DISCUSSION

Although it is still controversial whether plasma cholesterol levels correlate with lung cancer risks, and also whether higher body mass index (BMI) is protective or harmful to lung cancer depends on cancer types, sex, and treatments (30–32), statins that lower cholesterol levels reduce the risk and mortality of lung cancer in human (33, 34), suggesting that lowering cholesterol levels, which also lowers 27HC levels, has a beneficial effect against lung cancer. Nevertheless, the precise mechanism of how cholesterol affects lung cancer pathogenesis, especially in relation with estrogen receptor status, still remains unknown. In addition, among many risk factors that may contribute to lung cancer incidence or mortality, endocrine factors including estrogen are critical modulators of lung cancer development and progression, and there is accumulating evidence that ER $\beta$  expression in conjunction with aromatase expression predicts survival in non-small cell lung cancer both in men and women (35, 36). Despite the poorly understood role of cholesterol in lung cancer pathogenesis, lung tissue has abundant levels of 27HC over a range of concentrations relevant to the modulation of ER function (18, 37). Additionally, protein expression of *CYP27A1* is higher in lung tissues from chronic obstructive

pulmonary disease patients than normal lung tissues (38). With the gene expression results showing that 27HC production and ER $\beta$  expression is higher in lung tumor cells than in normal lung cells (**Figure 1**), we determined if 27HC modifies lung cancer cell proliferation, and found that 27HC promotes cell proliferation of lung cancer cells that express ER $\beta$ . Although some reports suggested that 27HC is a weak agonist for LXR (39), 27HC does not activate LXR in the vascular system and in liver (18). The effect of 27HC on H1395 cells was ER $\beta$ -specific, and other nuclear receptor ligands tested did not show proliferation-inducing effects (**Figure 3**). The effect of 27HC was observed not only in H1395 cells, but also in LLC cells that are transfected with ER $\beta$  (**Supplemental Figure 1**), indicating the effect of 27HC is not H1395 cell-specific. Recently, a report indicated that 27HC acts as a negative modulator of ER $\beta$  (40). In our study, both 27HC and E<sub>2</sub> promoted H1395 cell proliferation. Considering estrogen always activates ER, 27HC likely has an ER $\beta$ -mediated, pro-estrogenic function in lung cancer cells. Since 27HC shows both agonistic and antagonistic effects on ER $\alpha$  function depending on target organs in our previous studies (16), it is possible that 27HC may also function as both an agonist and antagonist for ER $\beta$  in a cell/tissue type specific manner.

Interestingly, although the expression of *CYP27A1* is higher in lung cancer cells than in normal lung cells (**Figure 1**), endogenously produced 27HC did not alter lung cancer cell proliferation in this study (**Figure 4**). The production of 27HC in lung cancer cells was not determined in this study, however, there is accumulating evidence that *CYP27A1* mRNA expression correlates with its protein expression and enzymatic activity, and also that *CYP27A1* expression correlates with the levels of its product 27HC in various types of cells and also *in vivo* (41–43). In addition, to our knowledge, there is no other enzyme than *CYP27A1* known to endogenously produce 27HC in mammals. Thus, it is reasonable to assume that higher *CYP27A1* expression reflects higher 27HC production in lung cancer cells, and also there are reports showing effective *CYP27A1* knockdown and consequent decrease of its protein expression (44, 45). In breast cancer, resident macrophages are important for generating and providing 27HC to the microenvironment (21). In addition to the key involvement of ER $\beta$  in lung tumor cells, ER activation by 27HC in surrounding stromal cells may also contribute importantly to oncogenesis, such as the regulation of host immunity by estrogen, which is observed in breast tumor models (46). Other possibilities include that the experimental condition in this study was not suitable for detecting the subtle differences caused by endogenously produced 27HC, and also that there are some effects by endogenous 27HC other than those that we examined. Further study will examine the role of endogenously

produced 27HC in lung cancer cells and the major source of 27HC involved in lung cancer cell proliferation.

In this study, we found that the effect of 27HC is stronger than that of E<sub>2</sub>, even with superphysiological doses of E<sub>2</sub> (**Figure 2** and data not shown). Mechanistic studies indicated that the effect of 27HC is mediated not by EGFR or MAPK, but by the PI3K-Akt signaling pathway (**Figure 5**). We could not find evidence that 27HC acts on pathways other than ER; however, there is still a possibility that 27HC acts on unknown pathways, if any, in addition to the ER signaling pathway. The PI3K-Akt signaling pathway is involved in lung cancer progression (47), and 27HC acts on the cardiovascular system through the activation of PI3K-Akt signaling pathway (48). Further investigation on how 27HC affects the PI3K-Akt signaling pathway are necessary to clarify the role of PI3K-Akt signaling on lung cancer progression.

The novel nature of 27HC modulation of ER $\beta$  that we show in this study has revealed a theoretical concept that links cholesterol metabolism with lung cancer progression and treatment failure. Such studies will further our understanding of lung tumor pathogenesis and will further indicate the efficacy of 27HC-directed therapeutic interventions for the treatment of this deadly disease.

## AUTHOR CONTRIBUTIONS

SH, TI, and MU designed the experiments. JM provided cell lines. SH, TI, W-RL, TK, CC, NK, FZ, and AA performed the experiments and acquired the data. SH, TI, MS, YZ, JH, JM, and MU analyzed and interpreted the results, and MU wrote the manuscript.

## FUNDING

This work was supported by National Institutes of Health grants P03DK079328 (MU) and UH CNRCS Startup Fund (MU).

## ACKNOWLEDGMENTS

We thank Drs. Philip Shaul (UT Southwestern), Jan-Ake Gustafsson (University of Houston) and their lab members, Anders Strom, Surendra Chaurasiya, Shivangi Srivastava (University of Houston), and Kendra Carmon (UT-Health) for their technical help, thoughtful discussions, and suggestions.

## SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fendo.2018.00470/full#supplementary-material>

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**Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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# Cholesterol as an Endogenous $ERR\alpha$ Agonist: A New Perspective to Cancer Treatment

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### Specialty section:

This article was submitted to  
Cancer Endocrinology,  
a section of the journal  
Frontiers in Endocrinology

**Received:** 08 June 2018

**Accepted:** 21 August 2018

**Published:** 11 September 2018

### Citation:

Casaburi I, Chimento A, De Luca A, Nocito M, Sculco S, Avena P, Trotta F, Rago V, Sirianni R and Pezzi V (2018) Cholesterol as an Endogenous  $ERR\alpha$  Agonist: A New Perspective to Cancer Treatment. *Front. Endocrinol.* 9:525. doi: 10.3389/fendo.2018.00525

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The estrogen-related receptors (ERRs) are important members of nuclear receptors which contain three isoforms ( $\alpha$ ,  $\beta$ , and  $\gamma$ ).  $ERR\alpha$  is the best-characterized isoform expressed mainly in high-energy demanding tissues where it preferentially works in association with the peroxisome proliferator-activated receptor- $\gamma$  co-activator 1 $\alpha$  (PGC-1 $\alpha$ ) and PGC-1 $\beta$ .  $ERR\alpha$  together with its cofactors modulates cellular metabolism, supports the growth of rapidly dividing cells, directs metabolic programs required for cell differentiation and maintains cellular energy homeostasis in differentiated cells. In cancer cells, the functional association between  $ERR\alpha$  and PGC-1s is further influenced by oncogenic signals and induces metabolic programs favoring cell growth and proliferation as well as tumor progression. Recently, cholesterol has been identified as a natural  $ERR\alpha$  ligand using a combined biochemical strategy. This new finding highlighted some important physiological aspects related to the use of cholesterol-lowering drugs such as statins and bisphosphonates. Even more meaningful is the link between increased cholesterol levels and certain cancer phenotypes characterized by an overexpressed  $ERR\alpha$  such as mammary, prostatic, and colorectal cancers, where the metabolic adaptation affects many cancer processes. Moreover, high-energy demanding cancer-related processes are strictly related to the cross-talk between tumor cells and some key players of tumor microenvironment, such as tumor-associated macrophage that fuels cancer progression. Some evidence suggests that high cholesterol content and  $ERR\alpha$  activity favor the inflammatory environment by the production of different cytokines. In this review, starting from the most recent observations on the physiological role of the new signaling activated by the natural ligand of  $ERR\alpha$ , we propose a new hypothesis on the suitability to control cholesterol levels as a chance in modulating  $ERR\alpha$  activity in those tumors in which its expression and activity are increased.

**Keywords:**  $ERR\alpha$ , cholesterol, cancer metabolism, breast and prostate cancer, colorectal cancer, adrenocortical carcinoma (ACC), IL-8

## GENERAL CONCEPT

Nuclear receptors (NRs) are a large family of transcription factors that are activated by different signal molecules such as steroids, thyroid hormones, vitamins, retinoic acid, oxysterols, and many other metabolites (1).

A distinct subset of the NRs still remains “orphans” (ONRs) waiting for a defined endogenous ligand. Once activated, NRs together with a multitude of co-factors, drive transcription of genes that control cell proliferation, development, reproduction, and different metabolic phenomena upon which those processes are strictly dependent.

A proper functional control of energy pathways within the cells is supported by the coordination of several transcription factors, including NRs, and associated co-factors. Many members of NR superfamily are involved in these processes since they can activate a specific gene expression network in response to hormonal, nutrient, and metabolite signals coming from distinct physiological (or pathological) conditions (2).

## ERRs Structure

The estrogen-related receptors (ERRs) are important members of the ONRs family, deeply involved in the control of energy homeostasis. The ERR subfamily comprises three isoforms, namely ERR $\alpha$  (NR3B1), ERR $\beta$  (NR3B2), and ERR $\gamma$  (NR3B3).

ERR $\alpha$  (45.5kDa, 423a.a.) and  $\beta$  (56.2kDa, 508a.a.) were first identified by screening human male gonad cDNA library with a probe synthesized based on the DNA-binding domain sequence of estrogen receptor alpha (ER $\alpha$ ) and ERR $\alpha$  cDNA as a probe, respectively (3). The discovery of the third member, ERR $\gamma$  (51.3kDa, 45a.a.), was made 10 years later by a different methodological approach (4, 5). In addition, several splice variants of human ERRs have been identified although their physiological role is still to be discovered (6). Despite their name and sequence homology with ERs, they do not bind natural estrogens. Moreover, although the existence of functional crosstalk between ERRs and ERs cannot be ruled out, especially in breast cancer pathology, a deeper investigation revealed that ERRs, particularly ERR $\alpha$ , and ER $\alpha$  have a distinct genomic signature and functions (7).

As members of the nuclear receptor superfamily, ERRs are characterized by a conserved structural and functional organization consisting of:

- A N-terminal region (A/B domain) that contains a ligand-independent transcriptional activation function domain (AF-1). The AF-1 domain of all three ERR isoforms contains conserved motifs that allow the control of the transcriptional activity by post-translational modification such as phosphorylation and sumoylation. In particular, phosphorylation-dependent sumoylation of ERR $\alpha$  within the NH-terminal domain of ERR $\alpha$  and ERR $\gamma$  negatively affects their transcriptional activity without altering DNA binding with cofactors (8). This mechanism becomes particularly important considering the absence of a specific/natural ligand and the constitutively active conformation of this class of

receptors that make their functions dependent on the presence of coactivators and corepressor proteins (see below);

- A central C domain, also known as DNA binding domain or DBD, a sequence shared by almost all three ERR members. DBD allows the recognition of DNA sites through the TNAAGGTCA sequence also known as ERR responsive elements or ERREs. In the DBD there are two digitally shaped helical structures, called “zinc fingers,” in which a zinc ion is coordinated with 4 cysteines. The P-box (proximal box), placed in the first helical structure, enables the recognition of a specific DNA sequence, while the D-box (distal box), placed in the second structure, is involved in the dimerization process on the DNA sequences. Indeed, ERRs can interact with an ERRE sequence as a monomer, homodimer or as a heterodimer consisting of two distinct ERR isoforms (9–11);
- A region linking C to Ligand Binding Domain (LBD);
- A ligand binding domain or LBD, which adopts a transcriptionally active conformation in the absence of any ligand (12);
- A less conserved C-terminal F region, which is present only in some nuclear receptors, including the ERs.

The sequence analysis of all three receptor isoforms reveals a different sequence homology in their domains: all three members show a high sequence identity in their DBD (93–98%); regarding the LBD, ERR $\alpha$ , and ERR $\beta$  are less related (57%) while that of ERR $\beta$  and ERR $\gamma$  are closer (73% sequence identity). The latter domain exhibits a 63% sequence identity between ERR $\alpha$  and ERR $\gamma$ ; high level of sequence identity in the A/B domain (60%) characterizes ERR $\beta$  and ERR $\gamma$  (13).

According to their discovery, ERR isoforms are more strongly related to estrogen receptors (ER $\alpha$  and  $\beta$ ) than to any other member of the NR superfamily. In particular, the analysis of each individual domain reveals that the DBDs of ERR $\alpha$  and ER $\alpha$  are 70% homologues, but their LBD is only 36% similar, explaining the reasons for the absence of ERR $\alpha$  response to ER ligands (12).

## ERR $\alpha$ : Function, Regulation, and Activity

ERR $\alpha$  discovery determined straightforward questions about its physiological function: ERR $\alpha$  plays a role in embryonic development and its expression level is high in the heart, skeletal muscles, and nervous system. The main physiological role of ERR $\alpha$  is to act as energy sensor to control cellular adaptation to energy demands and to respond to various metabolic stress conditions. Therefore, ERR $\alpha$  is present in high-demand energy tissues, such as muscles and brown adipose tissue. Cells that do not express an activated ERR $\alpha$  cannot produce enough energy at peak demand moments.

In adipose tissue, ERR $\alpha$  promotes the differentiation of mesenchymal stem cells into adipocytes where it regulates energy metabolism. In fact, ERR $\alpha$  increases lipid absorption,  $\beta$ -oxidation, tricarboxylic acid cycle, oxidative phosphorylation, and mitochondrial biogenesis and functions. These metabolic effects are clearly noticeable in all those tissues with high-energy demand including cardiomyocytes and cells of the immune system like macrophages. The prominent role of ERR $\alpha$  in metabolic regulation is underlined by the demonstration



that ERR $\alpha$  gene knockout (ERR $\alpha$ -KO) mice have altered fat absorption and metabolism and are resistant to fat-induced obesity (14). Moreover, these mice are not able to adapt to the cold environment and develop cardiac contraction dysfunction. Stress-induced cardiac hypertrophy in ERR $\alpha$ -KO mice is caused by poor ATP synthesis and reduced phosphocreatine deposition (15).

ERR $\alpha$  influences the differentiation of myocytes, T cells, intestinal epithelial cells and osteoblasts. A study showed that ERR $\alpha$  plays a key role in bone development and metabolism during embryogenesis (16). Its mRNA is expressed in murine bone cells during bone formation by endochondral and intramembranous ossification as well as in primary human osteoblasts. ERR $\alpha$  influences the transcription of the gene coding for osteopontin an essential constituent of the mineralized extracellular bone matrix. In the ERR $\alpha$ -KO mice, the loss of ERR $\alpha$  gene expression modestly increased osteoblastic differentiation and spongy bone mineral density, as well as the differentiation of mesenchymal cells into osteoblasts (17).

The constitutive activity of ERR $\alpha$  is structurally related to the presence of a phenylalanine residue (Phe<sup>328</sup> on helix H3) within its LBD which maintains a conformational arrangement suitable for the interaction with different cofactors (18). ERR $\alpha$  transcriptional activity is dependent on the presence of co-regulatory proteins, which are differentially expressed in various cells and tissues. ERR $\alpha$  preferentially works in association with the peroxisome proliferator-activated receptor- $\gamma$  receptor (PPAR $\gamma$ ) co-activator-1 $\alpha$  (PGC-1 $\alpha$ ) and PGC-1 $\beta$  (18). The functional interaction between ERR $\alpha$  and PGC-1s is highly specific and it is essential for full ERR $\alpha$  receptor activity in most cells. Moreover, ERR $\alpha$  together with PGC-1s integrates many intracellular signals arising from extrinsic/intrinsic metabolic stresses, as well as from growth factors (18).

The activity of ERR $\alpha$  has been examined by the study on the transcriptional co-activators PGC-1 $\alpha$  and PGC-1 $\beta$ , which integrate the signals on nutritional and energetic status and drive expression of genes that control mitochondrial biogenesis, oxidative metabolism, and gluconeogenesis.

The ability of the co-activator PGC-1 $\alpha$  to favor the activation of target genes is based on its recruitment at the level of gene-specific regulatory sites through physical interactions with NRs and other transcription factors. Regarding the NRs, the amphipathic propellers of PGC-1 $\alpha$  bind the hydrophobic region of LBD domain while PGC-1 $\alpha$  has a surface that interacts specifically with ERR $\alpha$ . Moreover, ERR $\alpha$  is a powerful transcriptional activator when PGC-1 $\alpha$  or PGC-1 $\beta$  are introduced into the system. The tight dependency between ERR $\alpha$  and PGC-1s as the result of the high affinity between ERR $\alpha$  and PGC-1s, suggests that ERR $\alpha$  activity is mainly controlled by the interactions with PGC-1 $\alpha$  and  $\beta$ . In addition, PGC-1s are also able to modulate ERR $\alpha$  gene expression (19). Consistent with the ability of PGC-1 co-activators to induce ERR $\alpha$  expression, ERR $\alpha$  mRNA levels are higher in tissues with elevated levels of PGC-1 $\alpha$  and  $\beta$  (19).

Given the predominant role of PGC-1s/ERR $\alpha$  transcriptional complex in controlling cellular metabolism, its involvement in the process of tumorigenesis is evident, considering that

metabolic adaptations is an hallmark of cancer cells (20). Nevertheless, there are still many aspects to be clarified. In normal cells, the activity of the PGC-1s/ERR $\alpha$  axis is directed to increase cellular metabolism, to support the growth of rapidly dividing cells, to control metabolic programs during cell differentiation and to preserve energy homeostasis once differentiated (13). In cancer cells, the PGC-1s/ERR $\alpha$  complex is a direct target of oncogenic signals that affect metabolic programs in order to favor or attenuate cell growth and proliferation (18). Moreover, PGC-1 $\alpha$ -mediated mitochondrial biogenesis and respiration in cancer cells is functionally related to metastatic dissemination (21). Accordingly, PGC-1 $\alpha$  gene suppression, by disabling mitochondrial biogenesis and oxidative phosphorylation, decreases the rate of metastasis (21). These findings are also supported by the observations that:

- ERR $\alpha$  together with its coactivator PGC-1 $\alpha$  binds to the promoter and regulates the expression of vascular endothelial growth factor (VEGF), a master regulator of tumor invasion and angiogenesis (22, 23);
- ERR $\alpha$  is able to regulate the expression of HIF (hypoxia-inducible factor) in breast cancer cells and to associate with the HIF $\alpha$ / $\beta$  heterodimer to promote its transcriptional activity on genes involved in angiogenesis and cell migration (23, 24).
- ERR $\alpha$  cooperates with HIF to induce the cancer metabolic reprogramming toward the metastatic-promoting glycolytic state (25).
- ERR $\alpha$ , together with its coactivator PGC-1 $\alpha$ , regulates the expression of WNT11, a mechanism involving ERR $\alpha$  in a transcriptional complex with  $\beta$ -catenin (26). In fact, ablation of either ERR $\alpha$  or  $\beta$ -catenin expression decreases the migratory ability of different types of cancer cells. In addition, functional genomic studies have identified further ERR $\alpha$  target genes playing an important role in the process of invasion, migration and tumor vascularization (27).

All these observations highlight the pivotal role of ERR $\alpha$  in many (altered) processes that characterize tumors especially those signaling driving tumor progression and aggressiveness.

## ERR $\alpha$ Agonists

The constitutive activity of ERR $\alpha$  does not exclude the existence of a molecule able to modulate its activity enabling the recruitment of cofactors and playing a critical role in the maintenance of energy homeostasis as well as in disease progression. Recently, several synthetic antagonists have been identified (28–30). Moreover, dietary products, including cholesterol, have been reported as potential agonists (31, 32). Suetsugu and collaborators identified agonists through virtual ligand screening on an ERR $\alpha$  ligand binding model based on the crystalline structure of ERR $\gamma$ -LBD (33). Thus, four ligands, increasing the transcriptional activity of ERR $\alpha$ , have been identified: isoflavones (genistein, daidzein, and biochanin A) and a flavone (trihydroxyflavone) (33). Later, scientists synthesized the potential molecules able to interact with the ligand-domain, guided by ERR $\alpha$  crystalline structure, but they were not able to demonstrate the activity of the agonists (34). Moreover, Peng and collaborators synthesized a series of pyrid (1,2- $\alpha$ ) pyrimidin-4 in

order to produce more powerful ERR $\alpha$  agonists and to confirm the ability to induce the receptor transcriptional activity (35). These compounds have improved glucose and fatty acid uptake from muscle cells (35) and thus, could have a clinical utility for the treatment of metabolic diseases, including metabolic syndrome and diabetes.

## Cholesterol: The First Endogenous ERR $\alpha$ Agonist

Recently, an important study investigated the binding ability of ERR $\alpha$  with endogenous lipids (36). To this aim experiments by using chromatography techniques were performed according to previous approaches validated for the study of PPAR with endogenous lipids from the lipidome. The experimental model used is the mouse brain, selected for the high expression of ERR $\alpha$ . The receptor was expressed, purified, and immobilized onto a resin and then incubated with enriching lipidomes. This experimental approach allowed the identification of a single ion that was significantly enriched by the beads bound to ERR-LBD and this ion was identified as cholesterol. Furthermore, to check the specificity of the interaction between ERR $\alpha$  and cholesterol, authors used targeted LC-MS method to increase the detection sensitivity for the lower-abundance sterols (37). The latter results were in agreement with those from lipidomic experiments. Moreover, in order to verify the specificity of ERR $\alpha$ -LBD-cholesterol interaction, a deeper investigation was performed with a competitive binding assay by using diethylstilbestrol (DES), a synthetic ERR $\alpha$  antagonist, that binds to the lipid-binding pocket of ERR $\alpha$  (38). A further confirmation was obtained by the authors with circular dichroism (CD) spectroscopy tests, where cholesterol, DES and the inverse agonist XCT790, all induced a conformational change in ERR $\alpha$ -LBD, while estradiol did not. These results suggested that Cholesterol-ERR $\alpha$ -LBD binding is more than a simple hydrophobic interaction. In addition, dye-labeled cholesterol derivatives were used and, after fluorescence polarization assay, the results showed that cholesterol binds the ligand-binding pocket of ERR $\alpha$  through its hydroxyl group. These findings indicate that cholesterol could exert a functional control of the ERR $\alpha$  activity (36).

## Cholesterol Regulates ERR $\alpha$ Transcriptional Activity

The demonstration that cholesterol impacts ERR $\alpha$  activity comes from the investigation during the osteocalciogenesis process. It has been revealed that ERR $\alpha$ -KO mice have a decreased bone resorption and high bone mass indicating that ERR $\alpha$  is able to promote osteoclast differentiation and activity. The suppression of the osteoclast functions was achieved by the use of statins and nitrogen-containing bisphosphonates, two drugs able to inhibit cholesterol biosynthesis, by blocking the HMG-CoA reductase and farnesyl diphosphate synthase (FPPS), respectively (39, 40). Interestingly, in the absence of ERR $\alpha$ , osteoclast differentiation was neither enhanced by cholesterol nor suppressed by statins. In addition, pharmacological inhibition with XCT790 prevented the effects of cholesterol on parental osteoclasts differentiation.

All this data strongly supported the ability of cholesterol to promote osteoclastogenesis acting as an ERR $\alpha$  agonist, whereas statins and bisphosphonates suppressed osteoclastogenesis by reducing cholesterol bioavailability.

Moreover, a further demonstration of the ability of cholesterol to modulate the transcriptional activity of ERR $\alpha$  comes out from conventional transactivation assays by using luciferase as the reporter gene. Indeed, the authors decided to modulate cholesterol abundance in the culture medium. To realize this goal, intracellular sterol levels were reduced by: (i) using lipid-free serum, (ii) adding cholesterol bound to hydroxypropyl cyclodextrin, and (iii) adding the hydrophobic statin, lovastatin.

Cyclodextrin and statin, used as a single agent or as combined treatment, were able to reduce ERR $\alpha$  transactivation. Moreover, the addition of exogenous cholesterol to the samples treated with statins and/or cyclodextrin restored the transcriptional activity of the receptor. This data indicated that cholesterol or a downstream sterol, but not a precursor of the cholesterol pathway, affected ERR $\alpha$  activity. An interesting aspect from the results of the research study by Wei et al. (36), is the need for the presence of cofactors to make ERR $\alpha$  functional, even in the presence of an endogenous ligand. In fact, experiments performed with a silenced PGC-1 $\alpha$  gene, revealed that luciferase expression was no longer detectable upon cholesterol treatment even in the presence of ectopic ERR $\alpha$ . These results clearly indicate that cholesterol, and most likely other sterols, affects ERR $\alpha$  function in a PGC-1 $\alpha$ -dependent fashion. The authors demonstrated also that ERR $\alpha$  is able to recruit PGC-1 $\alpha$  and PGC-1 $\beta$  upon cholesterol addition, but upon cholesterol depletion, PGC-1 coactivators are dissociated from ERR $\alpha$ . Specifically, cholesterol enhances the interaction between ERR $\alpha$  and PGC-1 $\beta$  in osteoclast promoting osteoclastogenesis and bone resorption, while promotes ERR $\alpha$  interaction with PGC-1 $\alpha$  in myocytes inducing myogenesis and decreasing statins-induced muscle toxicity.

## Cholesterol-Lowering Drugs Use and Outcome of Cancer Patients

Many experimental evidence strongly suggest that the inhibition of the mevalonate pathway using statin or bisphosphonate drugs has an impact on oncogenic processes such as cell proliferation, tumor progression, and metastatic potential (41). Statins are inhibitors of HMG-CoA reductase, that block the mevalonate pathway progression limiting the accumulation of the final products such as cholesterol, dolichol, isoprenoids, ubiquinone, and isopentenyladenine (42, 43).

Effects of statins on the outcome of patients affected by different types of cancer, including breast (44, 45), prostate (46–48), ovarian (49), lymphoma (50), renal cell carcinoma (51), and colorectal (52, 53) cancer have been examined in the last years. Some of these studies suggests that statins use is associated with longer survival, while others report no benefits. A recent meta-analysis showed that the average effect of statin use is beneficial for overall survival and cancer-specific survival (54). In particular, the study specified that colorectal, prostate, and



breast cancers, the three largest cancer-type subgroups, showed a benefit from statins use (54). Interestingly, these three tumors are characterized by high expression of ERR $\alpha$  that, depending on the particular tumor phenotype, is associated with tumor progression and/or worst prognosis (55, 56).

Statins may exert their anticancer effect through several molecular mechanisms: via lowering protein prenylation, reducing tumor cell proliferation and migration, inhibiting rat sarcoma (Ras) signaling, inducing apoptosis through inhibition of Akt phosphorylation and consequently mammalian target of rapamycin (mTOR) down-regulation and other pleiotropic effects on cellular level (57, 58).

Bisphosphonates, especially nitrogen-containing bisphosphonates (N-BPs), are widely used to preserve bone health in patients with cancer thank to their ability to negatively regulate osteoclast-mediated bone resorption that is closely associated with metastasis in different cancer types (59). N-BPs work by interfering with two enzymes belonging to the mevalonate pathway called farnesyl pyrophosphate synthase (FPPS) and geranylgeranyl pyrophosphate synthase (GGPPS). The inhibition of mevalonate pathway by N-BPs results in the accumulation of isopentenyl pyrophosphate (IPP), which is then converted to a cytotoxic ATP analog called ApppI. This last event together with the N-BPs-induced inhibition of protein prenylation causes osteoclast dysfunction and reduced bone resorption. Similarly to studies on statins, epidemiological data projecting bisphosphonates as antitumor agents are still controversial. Although further studies are needed to better elucidate the antitumor effects of bisphosphonates, the general concept that is drawn from current available data (60) is that bisphosphonates reduce cancer metastatic lesions in non-solid as well as in solid tumors. Indeed, in addition to their clinical use to preserve bone tissue, emerging *in vitro* and clinical studies suggest that N-BPs have direct effects on cancer cells including induction of apoptosis, inhibition of proliferation, adhesion, invasion and angiogenesis (60). Synergism with chemotherapeutics and enhancement of immune surveillance expand the pleiotropic effects exerted by N-BPs in oncology.

A new regulator of cholesterol metabolism is represented by protein convertase subtilisin/kexin type 9 (PCSK9) (61) an enzyme produced by hepatocytes and secreted into the plasma to bind to the LDL receptor resulting in lysosomal degradation of the receptor. Consequently, PCSK9 reduces the expression of LDL receptors on the cell membrane thereby decreasing the clearance of LDL-cholesterol. PCSK9 inhibitors (monoclonal-antibodies) have become very useful in statin intolerant patients or when statin therapy is unable to reduce LDL (61).

PCSK9 is mostly expressed in the liver (62), which is one of the most common sites for metastasis, thus the ability of PCSK9 and cholesterol to favor a pro-metastatic environment was investigated. Clinical studies are very poor (63, 64), while the majority of the results comes from preclinical experimental models: the PCSK9-KO mice and melanoma cells (65). In the presence of a reduced expression of PCSK9, the number of hepatic metastases was significantly lower. By contrast, PCSK9-KO and wild-type mice fed with a high cholesterol diet showed

an increased number of liver metastasis, suggesting a prominent role of cholesterol in tumor-microenvironment interaction. The results obtained on melanoma cells can be extended to other types of cancer.

The identification of cholesterol as ERR $\alpha$  agonist adds a new anticancer mechanism for statins and nitrogen-containing bisphosphonates that could be further investigated to widen the potential therapeutic alternatives in cancers where ERR $\alpha$  is overexpressed. By contrast, the reduction of LDL-R by PCSK9 inhibitors may result in an increased intracellular content of cholesterol within tumor cells that could sustain ERR $\alpha$  activation. Thus, the use of PCSK9 inhibitors in oncology needs further investigations before the preclinical results can be translated into a clinical setting.

## ERR $\alpha$ , Cholesterol, and Inflammatory Markers

Cholesterol has been shown to inhibit the expression of chemokines, such as CXCL9 and CXCL10, in macrophages (66) while statins and bisphosphonates enhance CXCL9 and CXCL10 gene expression in wild-type (WT) but not in ERR $\alpha$ -KO macrophages. A similar mechanism was observed for other inflammatory markers such as IL-1 $\beta$  and MMP9. These data suggest that chemokine-suppressive effects of cholesterol in macrophages is dependent on ERR $\alpha$ , revealing an anti-inflammatory role for the NR in a cholesterol-rich environment.

However, a deeper analysis should be performed on the role of cholesterol as the modulator of inflammatory markers produced by macrophages. In fact, an interesting paper (67) reported an induction of IL-8 (CXCL8) in response to cholesterol loading in macrophages foam cells, one of the hallmarks of atherosclerosis (68–70). It has been observed that cholesterol loading, in addition to affecting its own uptake, induces several effects in macrophages including the alteration of the cellular metabolism (71, 72), the increase of phospholipids synthesis (73), the increase of apolipoprotein E synthesis and secretion (74), and the enhancement of lipoprotein and apoprotein internalization and degradation (75). All these phenomena contribute to different phases in the progression of atherosclerosis.

In the paper by Wang et al. (67), macrophages were incubated with or without acetylated LDL (acLDL) in the presence or in the absence of an acyl-CoA:cholesterol-acyltransferase (ACAT) inhibitor before evaluating changes in chemokines mRNA content, growth factors, interleukins, and adhesion molecules. Among these genes, a significative increase in mRNA level was observed only for IL-8. Specifically, cholesterol intake by macrophages through scavenger receptor-mediated endocytosis of acLDL enhanced IL-8 expression both at transcriptional and post-transcriptional level.

These observations arouse some deductions concerning the potential positive effect of cholesterol on the expression of the cytokine IL-8, known to be associated with proliferation, angiogenesis, migration, and chemosensitivity of many cancer cells (76). In fact, IL-8 expression has been detected in numerous cancer types, but its value as a cancer biomarker has been poorly investigated, even though it could be relevant for a good

number of malignant diseases such as thyroid cancers where IL-8 represents the most deeply investigated chemokine in thyroid tumor microenvironment (77).

For these reasons, we can speculate that cholesterol through ERR $\alpha$ -dependent signaling regulates production of inflammatory markers in cancer cells as well as in macrophages within tumor microenvironment. Therefore, it seems necessary to delve into this last aspect because ERR $\alpha$  could represent a relevant therapeutic target since this receptor is a key functional factor shared by several oncogenic signals belonging to both tumor cells and microenvironment.

## ERR $\alpha$ , IL-8, and Colorectal Cancer

Starting from the evidence that ERR $\alpha$  is overexpressed in colorectal (CRC) tumor tissues and cell lines, it was demonstrated that ERR $\alpha$  promotes *in vitro* proliferation and migration (78). Moreover, a close correlation between ERR $\alpha$  protein level and activity and the production of IL-8 in CRC has been found (78). Moreover, chemical inhibition of ERR $\alpha$  activity by treating different CRC cell lines with its inverse agonist, XCT-790, significantly decreased the IL-8 mRNA content, without affecting the expression of other chemokines. These results were further confirmed by ERR $\alpha$  specific silencing experiments. On the other hand, IL-8 expression was upregulated in all CRC cell models characterized by ERR $\alpha$  overexpression.

The same authors, investigating the mechanism by which ERR $\alpha$  regulates the expression of IL-8 in CRC cells revealed that XCT-790 treatment or ERR $\alpha$  gene silencing decreased the promoter activity of IL-8. Moreover, the observation that XCT-790 increased IL-8 mRNA degradation, demonstrated that ERR $\alpha$  regulated IL-8 gene transcription and mRNA stability. Importantly, IL-8 gene silencing suppressed CRC cells proliferation and migration similarly to XCT-790, while a pre-treatment with recombinant IL-8 can rescue the inhibitory effects exerted by XCT-790 on cell proliferation and migration. These results clearly suggest that ERR $\alpha$  activity is directly involved in IL-8-induced CRC cells growth and motility.

Several findings indicate that ERR $\alpha$  activity in CRC could be induced by an excess of cholesterol in the tumor microenvironment. In fact, epidemiologic studies indicate that CRC risk is directly associated with a higher consumption of animal fats and inversely correlated with a diet rich in fruits and vegetables (79, 80). Animal fats diet is also associated with an increased risk of developing chronic intestinal inflammation (81). In fact, an excess of intake in fats of animal origin induces the production of oxidized molecules responsible for lipid oxidation processes able to generate different toxic products for the intestinal epithelial barrier function and the production of pro-inflammatory molecules. All these factors contribute to developing a cancer-prone microenvironment.

The existence of a direct correlation between the levels of cholesterol and the production of IL-8 in the macrophage suggests some interesting hypotheses that could represent the rational basis for further studies: (a) the agonistic action of cholesterol on ERR $\alpha$  in CRC cells could favor the recruitment of co-regulators involved in the enhancement of IL-8 gene expression; (b) a similar mechanism could occur also in

macrophages leading the way for new hypotheses on ERR $\alpha$  involvement in the regulation of the inflammatory process within the tumor microenvironment.

## Cholesterol and ERR $\alpha$ in Breast, Prostate, and Adrenocortical Cancer

A new potential therapeutic application in a clinical setting controlling cholesterol levels come out from the observations on the role played by ERR $\alpha$  in breast (BC) and prostate (PC) cancers. In BC, high ERR $\alpha$  expression characterizes tumors with poor prognosis (81). Moreover, ERR $\alpha$  mRNA is positively correlated with the oncogene ERBB2 and AIB1 (82) and inversely correlated with that of ER $\alpha$  and progesterone receptor that are good prognostic factors for the anti-hormonal treatment of breast cancer patients. Indeed, depending on the cellular context, ERR $\alpha$  could act promoting or inhibiting transcription (83). Findings suggested that in ER-negative BC, ERR $\alpha$  compensates for the loss of ER $\alpha$  in addition to triggering the expression of ER $\alpha$ -independent genes since it recognizes estrogen response element (ERE) as is the case for vascular endothelial growth factor (VEGF) promoting BC metastasis (23, 24). By contrast, in ER-positive BC cells, ERR $\alpha$  negatively controls ERE transcription by interacting with corepressor such as RIP1. Alternatively, ERR $\alpha$  could promote BC cells growth by enhancing circulating estrogen production. In fact, it has been found that ERR $\alpha$  could activate steroid sulfotransferase (SULT2A1) that works to maintain high level of peripheral dehydroepiandrosteronesulfate (DHEAS), an important metabolite in estrogen synthesis in adrenal tissues. In addition, it has also been evidenced that SULT2A1 inactivates tamoxifen and raloxifene (84). Thus, high ERR $\alpha$  expression in breast cancer by enhancing SULT2A1 activity could also support breast cancer cell resistance to anti-hormonal therapy (84).

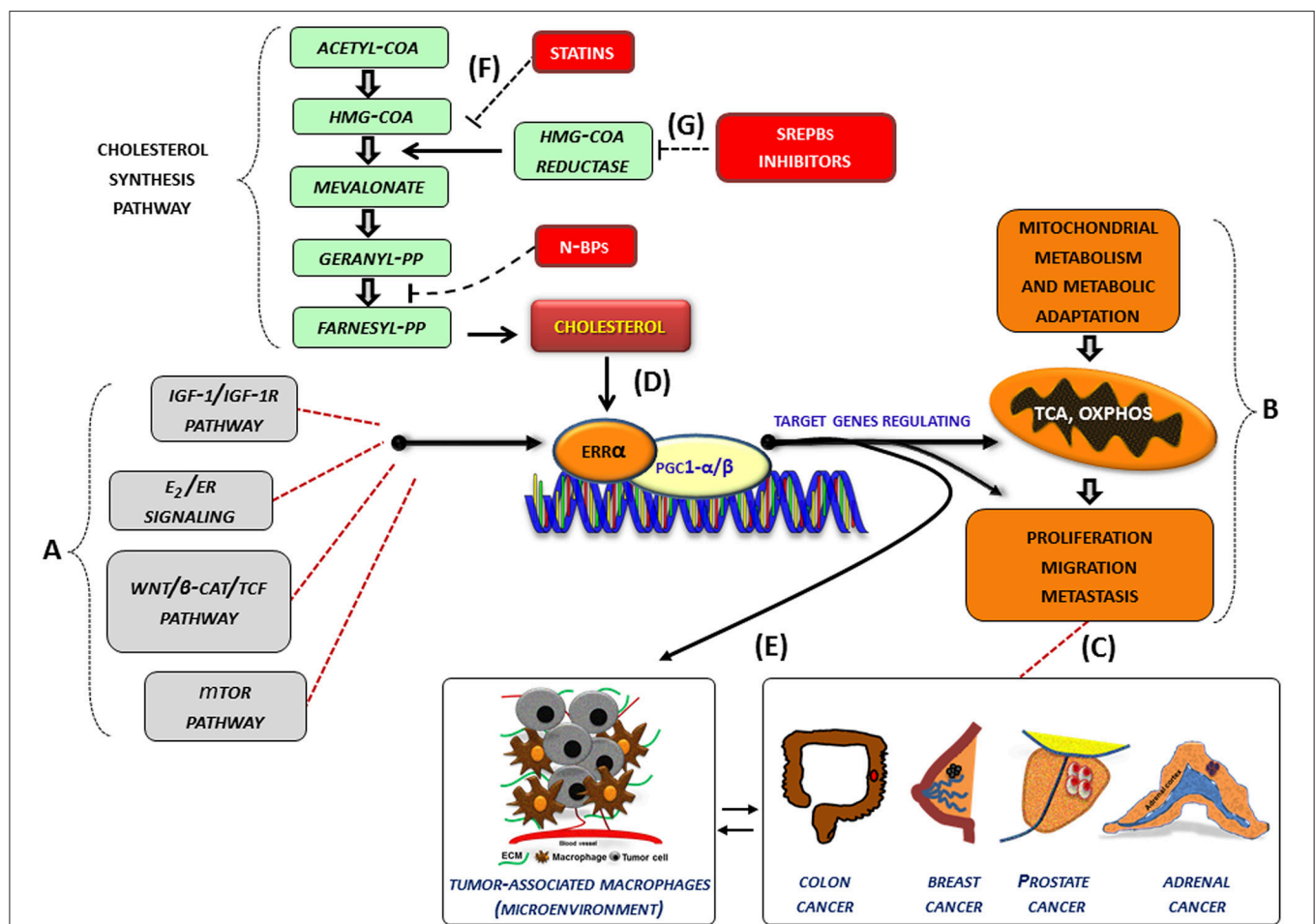
The enhanced expression of ERR $\alpha$  has been found also in prostate cancer (PCa) and PCa cell lines (85). A study indicates a positive correlation between ERR $\alpha$  expression and the Gleason score while results from a preclinical study showed that ERR $\alpha$  can promote the hypoxic growth adaptation of prostate cancer cells by interacting with HIF-1 $\alpha$ . As above explained, ERR $\alpha$  is also expressed in the bone regulating activity of osteoblasts and osteoclasts, that is implicated into the mixed osteolytic and osteoblastic lesions observed in advanced prostate cancer patients (86).

An increased cholesterol biosynthesis, regulated by sterol regulatory element-binding protein-2 (SREBP-2), is a key player in the initiation and progression of PCa where an enhanced stem cell population was observed (87). Moreover, aberrant cholesteryl ester accumulation in lipid droplets exacerbates cancer invasiveness and characterizes high-grade PCa with PTEN loss and consequently, constitutive PI3K/Akt activation promotes metabolic dysregulation where ERR $\alpha$ /PGC-1 $\alpha$ , as already mentioned, play a central role (18). In addition, the cholesterol metabolite, 27-hydroxyl-cholesterol (27-OHC) is now recognized as selective estrogen receptor modulator (SERM) which promotes tumorigenesis in ER-positive BC (88). Higher levels of 27-OHC have been reported in ER $\alpha$ -positive breast cancers with respect to normal breast tissue, along with an

observed reduction in the 27-OHC metabolizing enzyme such as CYP7B1 (89). Results from *in vivo* experiments demonstrated that 27-OHC alone is sufficient to support estrogenic activity in ER-dependent breast cancer cells (89). Accordingly, an increased growth and metastasis of ER-positive tumors were observed in a mouse model of breast cancer fed only with a cholesterol-rich diet (89). The function of cholesterol as an ERR $\alpha$  agonist may provide the molecular basis and mechanistic insight into clinical studies suggesting that drugs able to lower cholesterol levels (i.e., statins) can be used to treat or prevent breast and prostate cancer.

A different tumor phenotype where cholesterol could have positive growing effects, over its physiological role, is the adrenocortical cancer (ACC). ACC is a very rare and aggressive disease with very limited therapeutic options (90). The pathogenesis of ACC involves the integration of molecular

signals and the interplay of different downstream pathways (i.e., IGFII/IGF1R,  $\beta$ -catenin, Wnt, ER $\alpha$ ) (91). Our published results indicate that treatment of ACC cell model with XCT-790, to the purpose of reducing ERR $\alpha$  expression, impaired cancer cell growth, both *in vitro* and *in vivo* (92). Our data well correlate with that reporting an increased ERR $\alpha$  expression in ACC compared to normal adrenal and adenoma (93) underlying the involvement of this metabolic receptor in ACC biology. Indeed, our unpublished results revealed that treatment of H295R cells with statins caused a significant reduction in cell growth and motility. Although these data are still preliminary, they suggest that cholesterol may affect various biological processes in ACC through the modulation of ERR $\alpha$  activity. Therefore, cholesterol lowering-drug could extend the therapeutic opportunity to fight this rare tumor.



**FIGURE 1 |** Role of cholesterol as modulator of ERR $\alpha$  action in cancer. **(A–G)** Schematic representation of how cholesterol, as a new ERR $\alpha$  ligand, can contribute to the complex molecular network consisting in the functional cross-talk between oncogenes and oncogenic pathways (IGF-1/IGF-1R, E<sub>2</sub>/ER,  $\beta$ -catenin/TCF, mTOR) **(A)** that support the overexpression of ERR $\alpha$ . In turn, ERR $\alpha$ , together with its main cofactors (PGC-1 $\alpha$  and PGC-1 $\beta$ ) and activators, such as cholesterol **(D)**, affects cancer cell metabolism promoting proliferation, migration and, metastasis **(B)** of different tumor phenotypes **(C)**. All these bioenergy-consuming functions are strictly related to **(E)** the cross-talk between tumor cells and some key players of the tumor microenvironment, such as macrophages (tumor-associate macrophages). The use of drugs [statins, **(F)**, N-bisphosphonates, N-BPs, SREBPs inhibitors, **(G)**] able to reduce cholesterol levels and ERR $\alpha$  transcriptional activity could widen the therapeutic opportunities for the treatment of different ERR $\alpha$  overexpressing tumors. More details are explained within the text. E<sub>2</sub>, estradiol; ER, estrogen receptor; IGF-1/IGF-1R, insulin-like growth factor-1/insulin-like growth factor-1 receptor; WNT, Wingless-type MMTV integration site family member; TCF, T-cell factor; TOR, mammalian target of rapamycin; N-BPs, nitrogen-containing bisphosphonates.

## CONCLUSION

The ERR $\alpha$  transcriptional activity in normal cells is directed to modulate cellular metabolism, supporting the growth of rapidly dividing cells and to control metabolic programs required for cellular energy homeostasis in differentiated cells and to satisfy energy request during cell differentiation. The recent identification of cholesterol as an endogenous ERR $\alpha$  agonist evidenced that this sterol enhances the interaction between ERR $\alpha$  and PGC-1 $\beta$  in osteoclasts, promoting osteoclastogenesis and bone resorption. Similarly, cholesterol promotes ERR $\alpha$  interaction with PGC-1 $\alpha$  in myocytes inducing myogenesis and decreasing muscle toxicity. The discovery of this new molecular mechanism has elucidated the genesis of two important phenomena with an unexplained mechanism: the statin-induced muscle toxicity and the bisphosphonate suppression of bone resorption.

Moreover, the discovery of cholesterol as an agonist of ERR $\alpha$  demonstrated that this receptor works as a metabolic-sensing nuclear receptor distinguishing it from steroid receptors that respond to an acute and steep rise in hormonal levels. Consequently, ERR $\alpha$  is constitutively active because cholesterol is ubiquitous.

This new mechanism calls fresh thinking about the role of ERR $\alpha$  in cancer cells keeping in mind the key role played by this receptor as modulator of cancer metabolism.

It is well known that the metabolic alterations of lipids, carbohydrates, and proteins are one of the hallmarks of cancers (20). In particular, an increase in the glycolytic rate at the expense of oxidative phosphorylation even in the presence of adequate oxygen concentrations (Warburg effect) (94) allows a rapid adaptation of tumor cells to the continuous metabolic changes that, together with the tumor microenvironment, are the driving forces for cancer survival and its evolution. Given the high interconnection between enzymes that regulate the metabolism and the molecular pathways induced by altered oncogenes, research of the key regulators that behave on metabolic adaptations and proliferative, anti-apoptotic, invasive and metastatic responses, could represent elective targets to break down tumors with a single shot. The ERR $\alpha$  could work for this end due to its location at the intersection of dysregulated metabolism and oncogenic pathways.

In several cancer cells, the expression and the activity of ERR $\alpha$ , together with its cofactors (PGC-1  $\alpha/\beta$ ), is further influenced by oncogenic signals (IGF1-IGF1R pathway, estrogen signaling, Wnt/ $\beta$ -cat/TCF, mTOR pathway) (Figure 1A) and can thus be re-directed to induce metabolic programs (Figure 1B) favoring tumor growth and progression. (Figure 1C). In this context, an increased level of cholesterol, through the new molecular mechanism, supports all tumor-related processes. (Figure 1D). Accordingly, high levels of cholesterol are associated with an increased risk of different type of cancers including breast, prostate (95) and CRC (96).

Although epidemiological data on the correlation between cholesterol and cancer are conflicting, the preclinical results

positively highlight different molecular aspects revealing how oncogenic growth signaling meet the bioenergetics and biosynthetic demands of rapidly proliferating tumor cells. In fact, altered cholesterol pathway in cancer could be reached through different mechanisms. One of the most important is the constitutive activity of the oncogenic PI3K/AKT/mTOR signaling pathway that enhances intracellular cholesterol levels by: (i) inducing cholesterol synthesis through the activation of the transcription factor SREBP (sterol regulatory element binding proteins); (ii) inducing LDL receptor-mediated cholesterol import; (iii) inhibiting ABCA1-mediated cholesterol export. Moreover, high-energy demanding cancer related process are strictly related to the cross-talk between tumor cells and some key players of the tumor microenvironment (TME), such as macrophages (TAM, tumor-associated macrophage), that in turn, fuels cancer progression through the formation of an inflammatory milieu characterized by the production of different cytokines such as IL-1, IL-6, and IL-8 among others. The latter, as above reported, could be a target of ERR $\alpha$  action (Figure 1E). For most solid tumors, infiltration by inflammatory cells such as macrophages is associated with poor prognosis (97, 98).

The links between inflammation and cholesterol are best exemplified by atherosclerosis, but similar mechanisms may also contribute to other metabolic disorders including cancer. It is noteworthy that cholesterol accumulation in TAM triggers the phenotype switch from M1, antitumorigenic, to M2-like macrophage, protumorigenic (99, 100).

Based on these considerations, the use of therapeutic strategy aimed to reduce cholesterol levels, such as statins (Figure 1F) or drugs targeting the SREBP metabolic pathways (Figure 1G), could be a promising option to counteract metabolic rewiring in cancer cells where ERR $\alpha$  plays a pivotal role.

In conclusion, identification of cholesterol as an endogenous ERR $\alpha$  agonist has already elucidated the most likely mechanisms underlying the side-effects induced by statins and bisphosphonate, but at the same time, it gives new perspectives to be further investigated in order to explore new therapeutic options for the treatment of ERR $\alpha$  overexpressing tumors. This alternative approach could bring additional benefits to the treatment of tumors that have already adopted successful therapies, but especially for those tumors, such as ACC, which are characterized by a limited or failed therapeutic choice.

## AUTHOR CONTRIBUTIONS

IC, AC: literature revision and drafting of the article. ADL, MN, SS, PA, FT, and VR: drafting of the article. RS, VP: critical revision of the article and final approval.

## ACKNOWLEDGMENTS

The authors thank the AIRC (Associazione Italiana per la Ricerca sul Cancro, IG2017: Id 20122, PI VP and IG15230, PI RS) for support of their research.



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# Sterol Metabolism and Transport in Atherosclerosis and Cancer

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### Specialty section:

This article was submitted to  
Cancer Endocrinology,  
a section of the journal  
Frontiers in Endocrinology

Received: 23 May 2018

Accepted: 14 August 2018

Published: 19 September 2018

### Citation:

Yamauchi Y and Rogers MA (2018)  
Sterol Metabolism and Transport in  
Atherosclerosis and Cancer.  
Front. Endocrinol. 9:509.  
doi: 10.3389/fendo.2018.00509

Cholesterol is a vital lipid molecule for mammalian cells, regulating fluidity of biological membranes, and serving as an essential constituent of lipid rafts. Mammalian cells acquire cholesterol from extracellular lipoproteins and from *de novo* synthesis. Cholesterol biosynthesis generates various precursor sterols. Cholesterol undergoes metabolic conversion into oxygenated sterols (oxysterols), bile acids, and steroid hormones. Cholesterol intermediates and metabolites have diverse and important cellular functions. A network of molecular machineries including transcription factors, protein modifiers, sterol transporters/carriers, and sterol sensors regulate sterol homeostasis in mammalian cells and tissues. Dysfunction in metabolism and transport of cholesterol, sterol intermediates, and oxysterols occurs in various pathophysiological settings such as atherosclerosis, cancers, and neurodegenerative diseases. Here we review the cholesterol, intermediate sterol, and oxysterol regulatory mechanisms and intracellular transport machineries, and discuss the roles of sterols and sterol metabolism in human diseases.

**Keywords:** ABC transporters, cholesterol, lanosterol, oxysterols, cholesterol efflux, intracellular cholesterol transport, atherosclerosis, cancer

## INTRODUCTION

Sterol biosynthesis is thought to have evolved 2.31 billion years ago (1). In eukaryotes, various complex sterols exist among plants, yeast, and mammals, and a few bacteria are also capable of synthesizing simpler sterols. Cholesterol is a vital lipid molecule for all mammals, and plays diverse and important roles in a number of biological processes, physiology, and disease (2). Mammalian cells can acquire cholesterol from two sources; uptake from extracellular milieu (exogenous source) and *de novo* synthesis (endogenous source). In addition to cholesterol, cells produce a variety of sterols. In the process of cholesterol synthesis, a series of intermediate sterols are generated as cholesterol precursors. Cholesterol is metabolized to cholesteryl ester (CE), oxysterols, bile acids, and steroid hormones. All these non-cholesterol sterols have important physiological functions in cells and in tissues.

Cholesterol is an important constituent of cellular membranes, regulating membrane fluidity and functionality. Cellular cholesterol distribution is highly heterogeneous among organelles [reviewed in (3–5)]. The plasma membrane (PM) contains 60–90% of total cellular cholesterol, which accounts for 25–40 mol% of PM lipids. The endocytic compartments and *trans*-Golgi network (TGN) are also cholesterol-rich organelles; whereas, the endoplasmic reticulum (ER) and the mitochondria contain only ~1% of total cellular cholesterol, which accounts for ~5 mol%

of ER lipids. Cholesterol is an essential constituent of membrane domains known as lipid rafts, which are small domains enriched in cholesterol and sphingolipids [both sphingomyelin (SM) and glycosphingolipids] [reviewed in (6)]. Lipid rafts are involved in key cellular functions like endocytosis, cellular signaling, and cell motility (6). In cells, cholesterol and other sterol molecules move dynamically among organelles to maintain proper distribution.

Aberrant accumulation of unesterified cholesterol in membranes is toxic to cells; therefore, various intrinsic and elaborate systems cooperatively regulate cellular sterol homeostasis. Cellular cholesterol content is tightly controlled by regulating *de novo* synthesis, extracellular uptake, export to extracellular milieu, and metabolic conversion (7, 8). Impairments in sterol homeostasis can cause various congenital and acquired diseases in humans, and pathophysiological conditions can also affect sterol homeostasis (2).

In this review, we provide an up-to-date assessment of the cell-intrinsic regulatory mechanisms for biosynthesis, intracellular transport, and efflux of cholesterol, intermediate sterols, and oxysterols. Additionally, we describe the roles of these sterol molecules in human diseases. This review contains four broad topics; (1) sterol biosynthesis and regulation, (2) intracellular sterol transport, (3) cellular sterol export, and (4) the roles of sterols in human diseases. Finally, we highlight several areas of research where mechanistic clarification is needed for sterol-related disease therapeutic development.

## ROLES OF STEROLS

Cholesterol, intermediate sterols, and oxysterols have various important functions; **Table 1** summarizes some of the functions further described in this review.

### Role of Cholesterol

Cholesterol is a membrane lipid that is indispensable for integrity of biological membranes. It is vital for forming lipid rafts, membrane nano-domains enriched in cholesterol,

and sphingolipids, which play a variety of important roles in mammalian cells (6). Cholesterol can regulate functions of biological membranes including endocytosis, membrane trafficking, and signaling. Cholesterol is the precursor of steroid hormones, bile acids, and oxysterols. In addition, cholesterol modifies select proteins: it is covalently attached to Hedgehog proteins (15) and to smoothened (16), both of which work in concert in Hedgehog signaling, a signaling pathway playing a critical role in embryonic development and tumorigenesis. As described in more detail below, cholesterol partly regulates cholesterol biosynthesis.

### Role of Intermediate Sterols

Sterol intermediates are not just precursors of cholesterol but can also act as biologically active agents. Lanosterol, the first biosynthesized sterol in the cholesterol biosynthetic pathway, can prevent lens protein aggregation and cataracts (9). Lanosterol treatment partially corrects cataracts in animal models. Zhao et al. (9) demonstrated that missense mutations in the lanosterol synthase *LSS* gene cause congenital cataracts. Dihydrolanosterol promotes ubiquitination and degradation of 3-hydroxy-3-methylglutaryl (HMG)-CoA reductase (HMGCR), inactivating cholesterol biosynthesis rapidly (10, 11). 4,4-dimethylcholesta-8,14,24-trien-3 $\beta$ -ol (follicular fluid meiosis-activating sterol, FF-MAS) and 4,4-dimethylcholesta-8,24-dien-3 $\beta$ -ol (testis-MAS, T-MAS) are implicated as meiosis-activating substances in oocyte maturation (12). In addition to cholesterol as described in the following section, desmosterol binds to sterol regulatory element binding protein (SREBP) cleavage activating protein (SCAP), and blocks SREBP activation to regulate cholesterol homeostasis (13). Desmosterol is also known to act as an endogenous ligand for the nuclear receptor liver X receptor (LXR) (14). Defects in enzymes involved in conversion of lanosterol to cholesterol cause severe malformation observed in Smith-Lemli-Optiz syndrome, desmosterolosis, X-linked dominant chondrodysplasia punctate type 2 (CDPX2), CHILD syndrome, Greenberg dysplasia, and Antley-Bixler syndrome (24, 25). In these patients, intermediate sterols accumulate in tissues and plasma.

### Role of Oxysterols

Oxysterols are one of the most potent negative regulators of cholesterol biosynthesis. Side-chain oxysterols including 25-hydroxycholesterol (25-OHC), 27-OHC, and 24(S)-OHC bind INSIG proteins (18), which are ER-resident proteins involved in negative feedback regulation of cholesterol homeostasis. Recent work established virus infection activates conversion of cholesterol to 25-OHC, which inhibits the SREBP pathway and down-regulates cholesterol biosynthesis (20). 25-OHC formation-dependent suppression of cholesterol synthesis plays an important role in viral infection and replication inhibition. In addition, oxysterols act as LXR ligands (19) that induce expression of genes involved in cholesterol efflux, including ATP-binding cassette (ABC) transporters ABCA1 and ABCG1, and apolipoprotein E (apoE) [reviewed in (26)]. Furthermore, recent studies demonstrated that 27-OHC can bind to estrogen receptors and act as an endogenous selective estrogen receptor modulator (SERM) (21). Side-chain oxysterols, but not sterol

**TABLE 1 |** Roles of intermediate sterols, cholesterol, and oxysterols.

Sterols	Biological activities	References
Lanosterol	Inhibition of lens protein aggregation	(9)
Dihydrolanosterol	Stimulation of HMGCR ubiquitination	(10, 11)
FF-MAS	Meiosis activation	(12)
T-MAS	Meiosis activation	(12)
Desmosterol	Binding and regulation of SCAP, LXR ligand	(13, 14)
Cholesterol	Lipid raft formation	(6)
	Binding and regulation of SCAP	(13)
	Modification of Hedgehogs and Smoothened	(15, 16)
7 $\alpha$ -OHC	Major bile acid precursor	(17)
24(S)-OHC	INSIG ligand, LXR ligand	(18, 19)
25-OHC	INSIG ligand, LXR ligand, anti-viral effect	(18–20)
27-OHC	INSIG ligand, LXR ligand, SERM	(18, 19, 21)
7 $\alpha$ ,25-di-OHC	EBI2 ligand	(22, 23)



ring modified oxysterols, show membrane-disordering effects that result in alternations in membrane functions (27).

## STEROL SYNTHESIS AND ITS REGULATION

### Biosynthesis of Intermediate Sterols and Cholesterol

In mammals, virtually all cells are capable of synthesizing cholesterol *de novo*. In humans, the liver is the most active organ in cholesterol synthesis, synthesizing as much as 1 g of cholesterol per day. Biosynthesis of cholesterol from the simple, two-carbon acetyl-CoA is a complex, multi-step process involving over 30 enzymes, and consumes 18 ATP a cholesterol molecule. Cholesterol biosynthesis begins with condensation of acetyl-CoA and acetoacetyl-CoA, which results in formation of HMG-CoA (28). A key rate-limiting enzyme in cholesterol biosynthesis is the ER membrane-bound enzyme HMGCR, which catalyzes reduction of HMG-CoA to mevalonate. This reaction uses NADPH as the reducing agent. Mevalonate is then phosphorylated by mevalonate kinase and phosphomevalonate kinase to yield 5-pyrophosphomevalonate. Subsequent isopentenyl pyrophosphate (IPP) production, a five-carbon (C5) isoprene unit, serves as precursor for all isoprenoids. IPP undergoes isomerization to 3,3-dimethylallyl pyrophosphate (DPP). DPP then condenses with IPP, yielding C10 geranyl pyrophosphate (GPP). Condensation of GPP and IPP produces C15 farnesyl pyrophosphate (FPP). Two molecules of FPP are then condensed and reduced to yield C30 squalene, the final non-sterol precursor of cholesterol. Squalene synthase catalyzes this reaction using NADPH as the reducing agent. Oxidation and cyclization of squalene yield C30 lanosterol, the first sterol in the biosynthetic pathway, via 2,3-epoxysqualene; squalene monooxygenase (also known as squalene epoxidase) that converts squalene to 2,3-epoxysqualene using NADPH and molecular oxygen, and lanosterol synthase then catalyzes the cyclization of 2,3-epoxysqualene to lanosterol.

Lanosterol undergoes extensive modifications en route to the final product, cholesterol (**Figure 1**). Conversion of lanosterol to C27 cholesterol involves at least 18 different enzymatic reactions including removal of the three methyl groups, reduction of the side chain, and rearrangement of the double bonds within sterol rings by consuming NADPH and O<sub>2</sub>. All of the enzymes responsible for converting squalene to cholesterol localize in the ER membrane. Conversion of lanosterol to cholesterol proceeds through either one of two pathways known as Bloch pathway and Kandutsch-Russell pathway (**Figure 1**). Desmosterol and 7-dehydrocholesterol are the final precursors in the Bloch pathway and the Kandutsch-Russell pathway, respectively. The sterol  $\Delta$ 24-reductase, DHCR24, which catalyzes reduction of the side chain at position 24 using NADPH as the reducing agent, is a key branching enzyme for the two pathways. 14 $\alpha$ -methyl group of lanosterol and dihydrolanosterol is first removed by lanosterol 14 $\alpha$ -demethylase (CYP51A1), yielding C29 sterols with two methyl groups at C4 position. The two methyl groups are then sequentially trimmed by a series

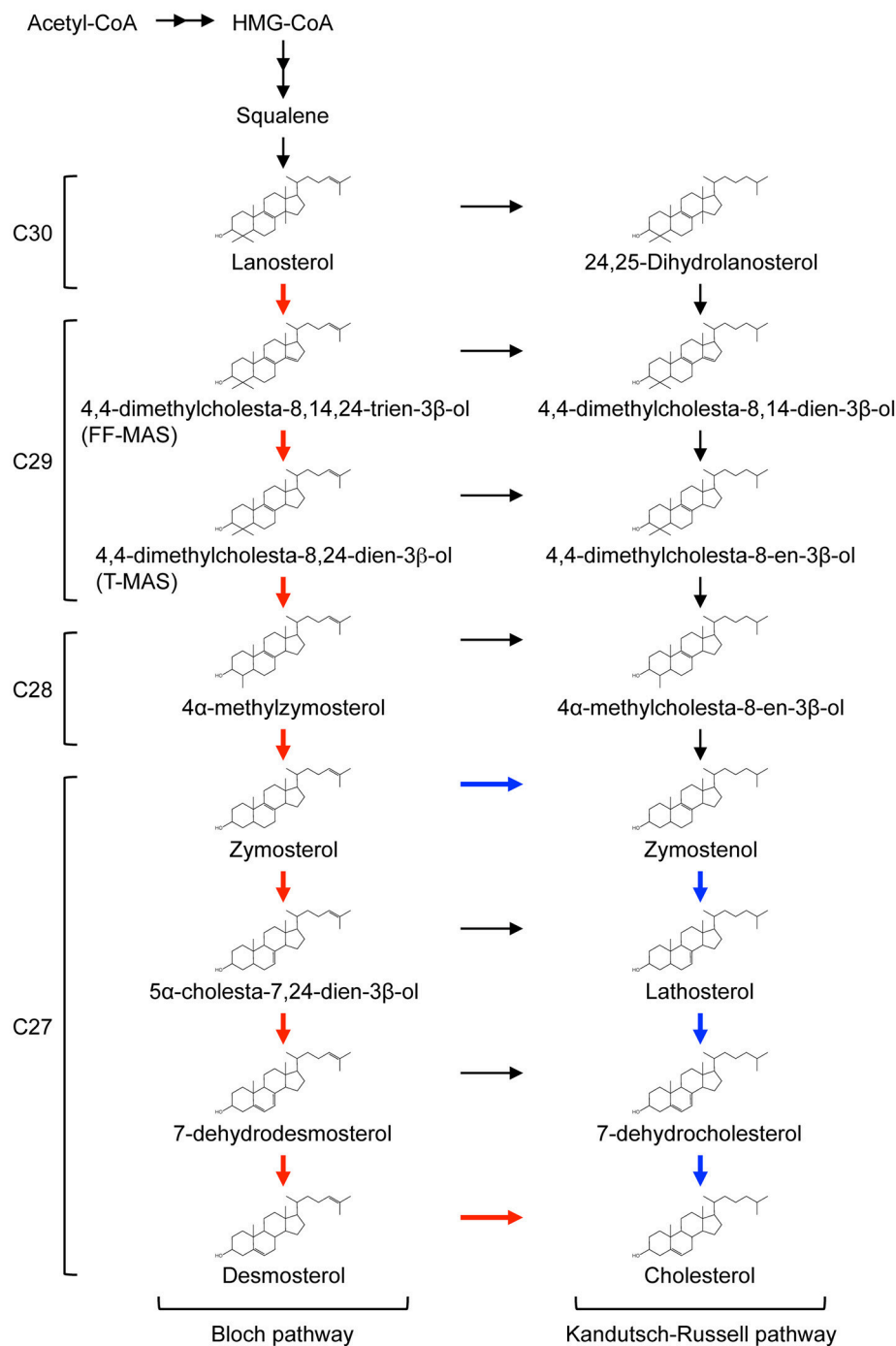
of complex reactions involving three enzymes, methylsterol monooxygenase 1 (encoded by *MSMO1/SC4MOL*), sterol-4 $\alpha$ -carboxylate 3-dehydrogenase (NSDHL), and 3-keto-steroid reductase (HSD17B7), producing C27 zymosterol or zymostenol. Conversion of zymosterol or zymostenol to cholesterol involves rearrangements of the double bonds within the sterol rings. A detailed review describing cholesterol biosynthetic reactions is available (30).

Recent work by Mitsche et al. shows that utilization of the Bloch pathway or Kandutsch-Russell pathway is cell and tissue type-dependent (29). No tissues use canonical Kandutsch-Russell pathway, but instead may use a proposed “modified” Kandutsch-Russell pathway, in which DHCR24 mediates the entry of zymosterol into Kandutsch-Russell pathway (**Figure 1**). In mice, the Bloch pathway mediates 90% or more cholesterol biosynthesis in the testis, spleen, and adrenal, and the modified Kandutsch-Russell pathway is used for more than 70% of cholesterol biosynthesis in the brain, skin, and preputial (29).

### Regulation of Sterol Synthesis

Mammalian cells acquire cholesterol from two sources: endogenous synthesis and uptake from exogenous sources. These two processes are tightly controlled for cellular cholesterol content maintenance by multiple modes of regulation at transcriptional and post-transcriptional levels.

SREBP transcription factors serve as master regulators of cholesterol synthesis [reviewed in (31)]. There are two SREBP genes (*SREBF1* and *SREBF2*) and three SREBP proteins, SREBP-1a, SREBP-1c, and SREBP-2. *SREBF1* encodes SREBP-1a and SREBP-1c through alternative splicing, and *SREBF2* encodes SREBP-2 protein [reviewed in (32)]. SREBP-2 regulates expression of virtually all genes involved in cholesterol synthesis. SREBP-1a regulates both cholesterol and fatty acid synthesis, whereas SREBP-1c participates in the regulation of fatty acid synthesis [reviewed in (32)]. SREBPs are unique, membrane-bound transcription factors. When cellular cholesterol is at sufficient levels, SREBPs locate at the ER as inactive forms by forming a complex with SCAP and INSIG. INSIG1 and INSIG2 are ER resident proteins, and act as retention factors of the SCAP-SREBP complex in the ER. INSIG proteins are stabilized by side-chain oxysterols including 25-OHC and 27-OHC through direct interaction with the oxysterols (18). Upon cellular cholesterol reduction, the SCAP-SREBP complex is transported to the Golgi via the COP-II pathway, and SREBPs are sequentially cleaved by two proteases, Site-1 protease (S1P) and Site-2 protease (S2P), to liberate the transcriptionally active domain from membranes. SCAP possesses a sterol-sensing domain (SSD) and can bind cholesterol. Cholesterol binding to SCAP leads to a conformational change, which prevents the SCAP-SREBP complex from its incorporation into the COP-II vesicles (13, 33). Moreover, small changes in ER cholesterol levels regulate this translocation: SCAP-SREBP-2 complex leaves the ER for the Golgi when the ER cholesterol concentration is below 5% of total ER lipids (34). In addition, polyunsaturated fatty acids regulate proteolytic processing of SREBP-1, but not SREBP-2 (35).



**FIGURE 1 |** Cholesterol biosynthetic pathway. The conversion of lanosterol to cholesterol proceeds through either Bloch pathway (red line) or Kandutsch-Russell pathway. Recently, modified Kandutsch-Russell pathway (blue line) has been proposed (29). See text for more details. The number of carbons in each sterol is presented on the left of the pathway.

In addition to transcriptional regulation, several important enzymes are post-transcriptionally regulated to control cholesterol synthesis. The best-characterized enzyme is HMGCR, an ER-bound protein with eight transmembrane domains and a catalytic domain that projects into the cytosol.

As the rate-limiting cholesterol synthesis enzyme, HMGCR has multiple modes of regulation. In addition to SREBP-dependent transcriptional control, HMGCR is regulated post-transcriptionally. HMGCR is a short-lived protein with a half-life of 1 h when cellular cholesterol is at sufficient levels (36).

HMGCR is degraded by the ubiquitin-proteasome pathway; ubiquitination of HMGCR requires INSIG-1 or-2 (37). INSIG proteins bind not only SCAP but also HMGCR via their SSD (38). INSIG binding to HMGCR facilitates the ubiquitination and degradation. HMGCR ubiquitination is promoted by the intermediate sterol dihydrolanosterol, and the side-chain oxysterols 25-OHC and 27-OHC, but not by cholesterol itself (10, 11, 39). Geranylgeraniol further accelerates degradation of HMGCR in the presence of sterols, but has little effect on the degradation by itself, showing a synergistical effect with sterols (39). Side-chain oxysterols stabilize INSIG proteins that promote HMGCR degradation. Three membrane-bound E3 ligases for HMGCR, gp78 (40), TRC8 (41), and RNF145 (42) have been identified. Importantly, all of these E3 ligases can interact with INSIG-1 and/or INSIG-2 (gp78 binds only INSIG-1), which stimulate HMGCR ubiquitination and degradation. However, involvement of gp78 and TRC8 in sterol-dependent HMGCR degradation may need further clarification since conflicting results have been reported (43). Additionally, another E3 ligase MARCH6 may also be involved in the regulation of HMGCR protein abundance (44).

In addition, phosphorylation regulates enzymatic activity of HMGCR. Serine-872 in human HMGCR (or serine-871 in mouse and hamster HMGCRs) is phosphorylated by AMP kinase (AMPK), a protein serine/threonine kinase regulated by cellular AMP levels (45). This phosphorylation inactivates the enzyme activity. Phosphorylation-dependent inactivation and sterol-dependent degradation are independently regulated to meet cellular demands (46).

In addition to HMGCR, recent studies identified squalene monooxygenase (47) and 7-dehydrocholesterol reductase (48) as enzymes highly regulated at post-transcriptional levels. Both enzymes are rapidly degraded by the ubiquitin-proteasome pathway in response to cholesterol loading (47, 48). The E3 ligase MARCH6 mediates the degradation of squalene monooxygenase (44).

## Esterification and Hydroxylation of Cholesterol

Because cholesterol cannot simply be degraded, excess cholesterol undergoes enzymatic esterification and hydroxylation within cells (**Figure 2**). To prevent toxic accumulation of free cholesterol, excess cholesterol is esterified, and stored in lipid droplets [reviewed in (49)]. This esterification is catalyzed by the ER-resident enzyme acyl-CoA:cholesterol acyltransferase 1 (ACAT1, also known as sterol O-acyltransferase 1, SOAT1), which transfers various long chain fatty acids such as oleic acid to the 3 $\beta$ -position of cholesterol (49). ACAT1 is ubiquitously expressed, while ACAT2, another form of ACAT, is mainly expressed in the intestine (enterocytes) and the liver (hepatocytes). In plasma, lecithin:cholesterol acyltransferase (LCAT) esterifies cholesterol in high-density lipoprotein (HDL). Cholesterol esterification is reversible; cholesteryl ester hydrolase located in the ER converts CE to cholesterol (8, 50), while acid lipase mediates hydrolysis of lysosomal CE derived from low-density lipoprotein (LDL). In addition to cholesterol, oxysterols

(such as 24(S)-OHC, 25-OHC, and 27-OHC), pregnenolone, and phytosterols are substrates of ACAT1 [reviewed in (51)]. Intermediate sterols containing gem-dimethyl moieties at C4 position cannot act as ACAT substrates because the dimethyl moieties sterically hinder the 3 $\beta$ -OH group (52).

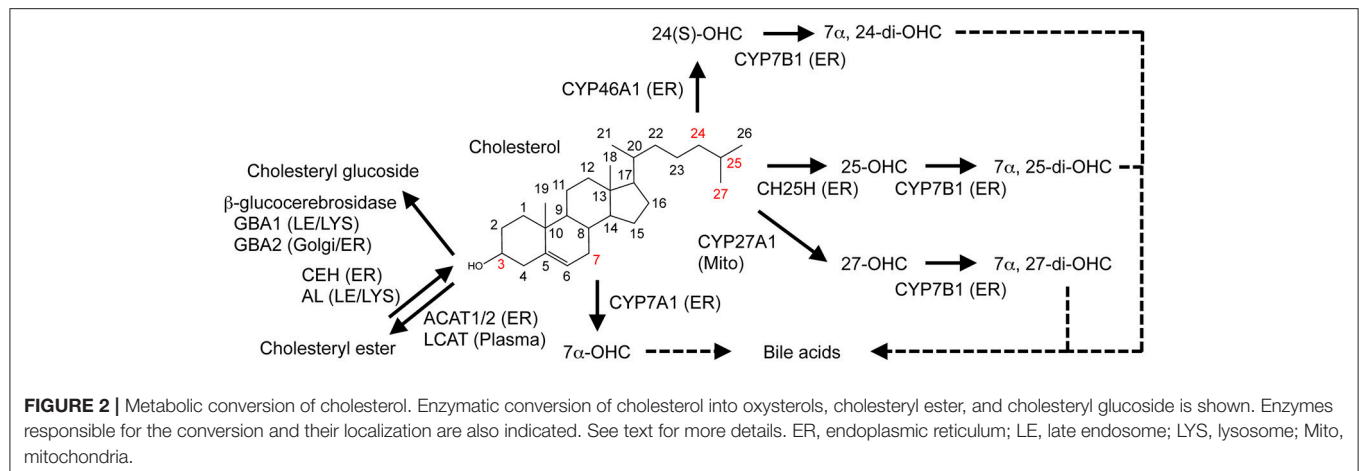
Enzymatic and non-enzymatic processes oxidize cholesterol [reviewed in (53)]. It is converted to oxysterols by the addition of one or more hydroxyl groups, keto groups, or epoxy groups. Side-chain oxysterols act as a potent negative regulator of cholesterol biosynthesis. Recent studies showed that cholesterol can also be glucosylated by  $\beta$ -glucocerebrosidase (GBA1 and GBA2), forming  $\beta$ -cholesteryl glucoside (**Figure 2**) in response to heat shock [reviewed in (54)]. In this review, we focus on the enzymatic production of the cholesterol metabolites, oxysterols, and discuss the roles of several major oxysterols and related enzymes. In mammals, many enzymes mediate cholesterol hydroxylation [reviewed in (53)]. With one exception, cholesterol 25-hydroxylase CH25H, cholesterol hydroxylases belong to the cytochrome P450 family. CH25H is a member of proteins that use diiron-oxygen as a cofactor (55). Hydroxylation of cholesterol occurs on its side-chain and/or on its steroid B ring. Here we review several major oxysterols that play important roles in human health and diseases.

25-OHC is biosynthesized from cholesterol via CH25H, a membrane-bound enzyme localized to the ER orienting the catalytic domain to the ER lumen. 25-OHC is also enzymatically synthesized by cholesterol 27-hydroxylase (CYP27A1) and cytochrome P450 3A4 (CYP3A4) and can be generated by free radical oxidation (53). 25-OHC can be metabolized by CYP7B1 (25-hydroxycholesterol 7 $\alpha$ -hydroxylase), an enzyme that adds an OH-group to the steroid ring (at C7 position) in the ER, generating 7 $\alpha$ , 25-dihydroxycholesterol (7 $\alpha$ ,25-di-OHC), a bile acid precursor (17) as well as a ligand for the G-protein-coupled receptor EBI2 (22, 23).

27-OHC is generated via cholesterol 27-hydroxylase (CYP27A1), which resides in the mitochondria. CYP27A1 can also convert cholesterol to 25-OHC. PM cholesterol is transported to the mitochondria where it serves as a major substrate for this hydroxylase (56). 27-OHC is the most abundant oxysterol in the plasma. CYP27A1 is expressed in many tissues including the liver, lung, and small intestine. Like 25-OHC, 27-OHC is further hydroxylated by CYP7B1 at the C7 position in the ER, forming 7 $\alpha$ , 27-di-OHC that serves as a bile acid precursor (17).

Cholesterol 24-hydroxylase (CYP46A1) catalyzes biosynthesis of 24(S)-OHC [reviewed in (57)]. This enzyme is highly expressed in the brain, particularly in neurons. In the human brain, 24(S)-OHC is present at high concentration (up to 15 ng/mg wet weight) (58). Excess cholesterol in the brain is converted to 24(S)-OHC, which is then released into the plasma across the blood-brain barrier. Thus the conversion of cholesterol to 24(S)-OHC is an important step for eliminating excess cholesterol from the brain [reviewed in (57, 59)].

Hydroxylation of the cholesterol C7 position is catalyzed by CYP7A1 (cholesterol 7 $\alpha$ -monooxygenase or cholesterol 7 $\alpha$ -hydroxylase), which is almost exclusively expressed in the liver. CYP7A1 produces 7 $\alpha$ -OHC, the major precursor of bile acids,



and is a rate-limiting enzyme for synthesizing bile acids [reviewed in (17)].

## Regulation of Oxysterol Synthesis

Although much less is known about regulation of oxysterol synthesis, a growing body of evidence has shown that enzymes involved in hydroxylation of cholesterol is also subjected to tight regulation. Expression of CH25H is highly transcriptionally regulated. In macrophages and hepatocytes, virus infection leads to upregulation of CH25H mRNA levels and to marked increases in 25-OHC (60–63). Furthermore, lipopolysaccharide (component of gram-negative bacteria) induces its expression through toll-like receptor 4 in macrophages (64, 65). Signal transducer and activator of transcription factor 1 (STAT1), a transcription factor activated by type I interferon signaling, induces Ch25h mRNA expression (61). The resultant product 25-OHC has an anti-viral role by suppressing virus infection and replication.

CYP27A1 expression is not associated with cellular cholesterol levels in macrophages, but its expression is transcriptionally regulated by several nuclear hormone receptors. In human macrophages, retinoid X receptor (RXR) and peroxisome proliferator-activated receptor- $\gamma$  (PPAR $\gamma$ ) cooperatively induce expression of CYP27A1 mRNA (66). In HepG2 or Huh7 human hepatoblastoma cells, CYP27A1 expression is increased by glucocorticoids, growth hormone, and insulin-like growth factor 1, and decreased by cholic acid and thyroid hormones (67, 68). In human intestinal Caco2 cells (a colon adenocarcinoma cell line) but not in human hepatocytes, pregnane X receptor (PXR) induces CYP27A1 expression (69). Collectively, CYP27A1 expression is differentially regulated in a cell type-dependent manner.

Expression of CYP7A1, the rate-limiting enzyme of bile acid synthesis, is positively regulated by cholesterol and negatively by bile acids in the liver. Several nuclear receptors including LXR $\alpha$ , farnesoid X receptor (FXR), small heterodimer protein (SHP-1), and liver receptor homolog-1 (LRH-1) cooperatively control CYP7A1 transcription (70, 71). Upon an increase in intake of dietary cholesterol, LXR $\alpha$  activates CYP7A1 gene expression and facilitates bile acid synthesis for excretion in

rodents (72). LXR does not activate CYP7A1 expression in humans due to lack of an LXR response element in the human CYP7A1 promoter (73, 74). For transcriptional repression, FXR binds bile acids, inducing the expression of SHP-1, a nuclear receptor with promoter-specific repressor activity that suppresses CYP7A1 expression by inhibiting LRH-1, a nuclear receptor that positively regulates CYP7A1 expression in humans and rodents (70, 71).

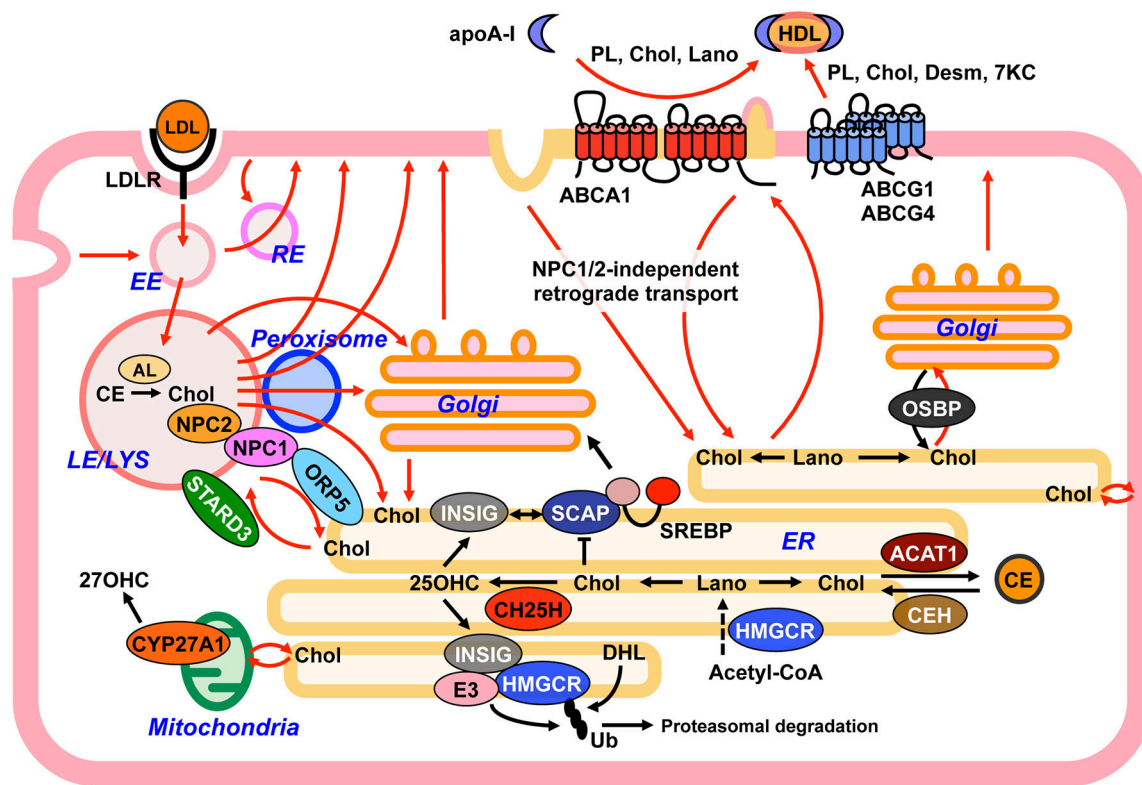
## INTRACELLULAR STEROL TRANSPORT AND CHOLESTEROL HOMEOSTASIS

Cholesterol moves dynamically within a cell (Figure 3), with this movement being essential to control cellular cholesterol homeostasis and to regulate heterogeneous cholesterol distribution among organelles (7, 8). The PM contains most of the cellular cholesterol. Cholesterol is also abundant in the endocytic compartments and the *trans*-Golgi network (TGN). In contrast, the ER and the mitochondria contain only 1% (or less) of total cellular cholesterol. How mammalian cells maintain uneven cholesterol distribution among organelles remains largely unknown. Differences in lipid compositions of each organelle may affect cholesterol-lipid interaction in membranes, allowing for organelle-specific cholesterol contents (4). As sterol is a highly hydrophobic substance, its transport between organelles, probably even within an organelle, requires transport carriers. Both vesicular (membrane-based) and non-vesicular (protein-based) transport are involved in intracellular transport of sterols.

## Sterol Transport Proteins With Sterol Binding Ability

Several proteins directly interact with sterols and transport them within cells. In patients with Niemann-Pick type C (NPC) disease, a lysosomal storage disorder with fatal neurodegeneration, either NPC1 or NPC2 protein is defective (75). Defects in NPC1 or NPC2 cause the aberrant accumulation of unesterified cholesterol and sphingolipids in the late endosome (LE) and the lysosome (LYS) (75). NPC1 and NPC2 both locate to the LE/LYS, but their localization within the organelles is





**FIGURE 3 |** Model depicting intracellular sterol movement. Within cells, sterols dynamically move among organelles (red lines) to maintain cholesterol homeostasis. See text for more details. 7KC, 7-ketocholesterol; 25OHC, 25-hydroxycholesterol; 27OHC, 27-hydroxycholesterol; AL, acid lipase; CE, cholesteryl ester; Chol, cholesterol; Desm, desmosterol; DHL, dihydrolanosterol; EE, early endosome; ER, endoplasmic reticulum; Lano, lanosterol; LE, late endosome; LYS, lysosome; PL, phospholipid; RE, recycling endosome; Ub, ubiquitin.

different: NPC1 has multiple transmembrane domains and localizes to LE/LYS membranes, while NPC2 is a soluble protein and localizes to the lumen. Both NPC1 and NPC2 can directly bind cholesterol, and cooperatively contribute to exporting cholesterol from the LE/LYS as described below.

Oxysterol-binding protein (OSBP) and OSBP-related proteins (ORPs) constitute a family of proteins that have the ability to bind sterol and other lipids [reviewed in (76, 77)]. In humans, 12 members, OSBP and ORP1-11, belong to this family, producing 16 different proteins through alternative splicing. In yeast, there are seven OSBP/ORP proteins, Osh1-7. The OSBP-related domain (ORD that consists of a hydrophobic pocket) is conserved in all OSBP/ORP proteins. Only two members, ORP5 and ORP8 contain transmembrane domain at their C-terminal region. Other functionally important domains found in most, but not all OSBP/ORPs include a pleckstrin homology (PH) domain and a FFAT (diphenyl alanine in an acidic tract) domain. OSBP was originally found as a protein that has high affinity to 25-OHC, in 1980s (78). Recent studies demonstrated that OSBP transports cholesterol (79, 80). A growing body of evidence [reviewed in (77)] has revealed that OSBP/ORPs transport not only sterols but also other lipids including phosphatidylserine and phosphatidylinositol 4-phosphate at membrane contact sites (MCSs), which are

proximal regions of two organelle membranes, through non-vesicular process.

Other sterol transport proteins belong to steroidogenic acute regulatory (StAR) protein-related lipid transfer (START) domain family, which consists of 15 members, STARD1-15 [reviewed in (81)]. The START domain forms a hydrophobic cavity that can accommodate one lipid molecule. STARD proteins also mediate non-vesicular lipid transport, and some of these proteins can bind sterols.

## Anterograde Transport of Cholesterol and Intermediate Sterols

The enzymes responsible for converting squalene to cholesterol are all located at the ER, indicating that intermediate sterols and cholesterol are synthesized in this organelle. Upon synthesis, cholesterol leaves the ER, and rapidly reaches the PM with a half-time of 10–20 min (82, 83). In addition to cholesterol, cells contain small but significant amounts of intermediate sterols as cholesterol precursors. A significant portion of intermediate sterols including lanosterol (C30 sterol), dimethylsterols (C29 sterols), monomethylsterols (C28 sterols), zymosterol (C27 sterol), and desmosterol (C27 sterol) is transported to the PM immediately after synthesis but prior to conversion to cholesterol (84–87). The ER-to-PM anterograde sterol transport is not

impaired in NPC cells (87), indicating that an NPC1/NPC2-independent pathway transports sterols from the ER to the PM. Involvement of OSBP in the anterograde sterol transport has been recently suggested (79). Upon binding to 25-OHC, OSBP translocates to the Golgi apparatus from cytoplasm (88). Recent findings show that OSBP counter-exchanges cholesterol in the ER and phosphatidylinositol 4-phosphate (PI4P) in the Golgi (80). On the other hand, an earlier study showed that there are Golgi-dependent and Golgi-independent routes that transport newly synthesized cholesterol from the ER to the PM, and that the Golgi-independent route plays a major role in this anterograde transport (83). How much newly synthesized cholesterol relies on OSBP for reaching the PM is unknown. Additionally unknown and of interest is whether OSBP can transfer intermediate sterols from the ER to the Golgi. In addition to OSBP, several other proteins including ORP2 (89) and sterol carrier protein-2 (90) are suggested to participate in the anterograde transport; however, this involvement needs further investigation.

### Active Cholesterol Hypothesis, Sterol Sensing, and Sterol Homeostasis

At the PM, cholesterol forms stoichiometric complexes with phospholipids, particularly with SM and glycerophospholipids containing long saturated acyl chains (91). Cholesterol pools that exceed the binding capacity of phospholipids could become more chemically active and more mobile. This mobile cholesterol is recognized as “active” cholesterol, and is expected to act as regulatory cholesterol for cellular cholesterol homeostasis (92). The ER contains a series of sterol sensing proteins. For storage, excess cellular cholesterol is esterified by the ER resident enzyme ACAT1 (49). ACAT1 enzymatic activity is stimulated by cholesterol and oxysterols. As described above, SREBP activation depends on the transport of SCAP-SREBP complex from the ER to the Golgi via COPII pathway. This transport is sensitive to ER cholesterol levels (34). A novel ER sterol sensing protein was recently identified; nuclear factor erythroid 2 related factor-1 (Nrf1, also known as Nfe2L1) is an ER-membrane bound transcription factor, which is cleaved near its N-terminus to be released from the ER. Through its ability to bind cholesterol, cholesterol blocks the cleavage and translocation of Nrf1 to the nucleus, and enhances LXR target gene expression including *Abca1* and *Abcg1* as a means to respond to excess cellular cholesterol (93). Thus, delivering active cholesterol to the ER is considered an essential step to sense and respond to excess cellular cholesterol (94, 95). Retrograde sterol transport from the PM to the ER involves both vesicular and non-vesicular transport. Here we describe the current understanding of these two transport processes and the proteins involved.

### Retrograde Sterol Transport

Cells can acquire exogenous cholesterol from lipoproteins. The best-characterized, major lipoprotein uptake process is LDL receptor (LDLR)-mediated internalization of LDL (**Figure 3**). LDL contains a large amount of cholesterol in an esterified form. LDL is first bound at the cell surface by LDLR, and internalized by endocytosis (96). LDLR-mediated endocytosis is classified as clathrin-mediated endocytosis (CME). CE in LDL is hydrolyzed

by acid lipase (**Figure 2**) in endocytic compartments, yielding free cholesterol (97). Endogenously synthesized cholesterol and a portion of intermediate sterols are also internalized from the PM and reach the LE/LYS (87, 98). Egress of free cholesterol from the LE/LYS requires the two cholesterol-binding proteins, NPC1 and NPC2. NPC1 is a large membrane-bound protein with 10 transmembrane domains (TMDs), whereas NPC2 is relatively small, 154-amino acid protein localized to luminal side of the LE/LYS. NPC1 has a cholesterol-binding pocket in its N-terminal luminal side (99). NPC1 also contains a SSD. Although whether the SSD is also able to directly bind cholesterol is not known, mutations within this domain lose cholesterol-transporting and cholesterol-binding activities (100). A potential model by which NPC1 and NPC2 act in concert to export cholesterol from the LE/LYS has been proposed (99, 101). In this “hand-off” model, at luminal side of the LE/LYS, NPC2 binds cholesterol and transfers it to the N-terminal, luminal cholesterol-binding domain of NPC1. Cholesterol is then incorporated into late endosomal/lysosomal membranes, and moves to various organelles including the ER, TGN (102), PM, mitochondria (103), and peroxisome (104) in a manner dependent of NPC1 and NPC2. In response to LDL uptake, delays in SREBP inactivation and in cholesterol re-esterification by ACAT1 both at the ER are observed in NPC cells. In addition, deficiency in either NPC1 or NPC2 impairs the conversion of LDL-derived cholesterol to 25-OHC at the ER and 27-OHC at the mitochondria (103). LDL-derived cholesterol also reaches the PM in a manner dependent on NPC1/NPC2 activity and becomes available for ABCA1-dependent release (105). As such, NPC1/NPC2 proteins play a crucial role in redistribution of internalized cholesterol from the LE/LYS to other organelles.

Both vesicular and non-vesicular transport processes participate in cholesterol transport from the LE/LYS to other organelles. Vesicular cholesterol transport to the ER involves several TGN-specific SNARE proteins including syntaxin 6, syntaxin 16, and VAMP4, indicating that LDL-derived cholesterol is at least partially delivered to the TGN from the LE/LYS before arriving at the ER (102). Transport of LDL-derived cholesterol from the LE/LYS to the PM is mediated by Rab8-dependent vesicular trafficking (106). Non-vesicular cholesterol transport is at least partly mediated by MCS. At the LE/LYS-ER MCS, ORP5 binds to NPC1, and transport cholesterol from the LE/LYS to the ER (107). On the other hand, at the same MCS, STARD3 mediates cholesterol transport from the ER to the LE/LYS (108). Chu et al. found that significant amounts of cholesterol in the LE/LYS are transported to peroxisomes through LE/LYS-peroxisome MCS, which precedes its arrival at the ER and PM (104). The LE/LYS physically interacts with peroxisomes, and the MCS formation is mediated by synaptotagmin VII at the LE/LYS and PI(4,5)P<sub>2</sub> at peroxisomes (104). Unknown cytosolic factors are suggested to facilitate cholesterol movement from the LE/LYS to peroxisomes (104).

Retrograde sterol transport from the PM to the ER is an important element of sterol sensing at the ER (95). Aside from NPC1/NPC2-dependent pathway, recent works show that mammalian cells utilize a PM-to-ER sterol trafficking route that does not require NPC proteins (87, 109). The nature

of this NPC1/NPC2-independent sterol transport is not well understood, but it has been suggested that both vesicular and non-vesicular mechanisms participate in it. ER membranes are partly elongated to proximal regions of the PM and form the MCSs where non-vesicular lipid transport can occur. The ORP proteins ORP1S and ORP2 are implicated in the PM-to-ER cholesterol transport through a non-vesicular pathway (110). Other studies show that STARD4 mediates cholesterol transport from the PM to the endocytic recycling compartments and to the ER (111). In addition to a non-vesicular process, involvement of endocytic sterol internalization is also proposed as a mechanism for the delivery of PM sterol to the ER (87, 94). Inhibition of clathrin-independent endocytosis (CIE), but not CME, significantly impairs PM-to-ER transport of cholesterol and intermediate sterols (87, 94). This CIE is suggested to require dynamin, a GTPase that plays a key role in scission of endocytic structure from the PM. Importantly, blocking dynamin activity results in a marked increase in SREBP-2 processing and in a reduction in esterification of PM cholesterol, indicating a decrease in ER cholesterol levels (94).

ABCA1, which plays an essential role in HDL formation (discussed in more detail in the following section), mediates transport of phospholipids and sterols. Although ABCA1 transports lipids to apoA-I for formation of HDL, its activity is independent of availability of lipid acceptors such as apoA-I (112, 113). In absence of a lipid acceptor, ABCA1 deficiency represses retrograde cholesterol transport (94), causes accumulation of cholesterol in the PM (94, 114), and impairs internalization of cholera toxin B subunit, a marker of CIE (94). It is therefore plausible that ABCA1 contributes to the regulation of PM lipid composition and functionality of PM through its lipid transport activity. How and whether lipid compositions of the PM are modulated by ABCA1 and other lipid transporters, and whether this affects PM functionality as well as non-vesicular sterol transport are important issues yet to be determined.

Select tissues including the liver and steroidogenic tissues also acquire cholesterol from plasma HDL for biliary secretion and steroidogenesis, respectively (115). Scavenger receptor class B type I (SR-BI) serves as a HDL receptor, and mediates the selective uptake of HDL-cholesterol (both CE and free cholesterol) (116). In contrast to the endocytic internalization of LDL, SR-BI-mediated uptake does not involve lysosomal degradation of HDL. How HDL-cholesterol is internalized and transported into cell interior through SR-BI remain to be clarified (117).

### Intracellular Transport of Oxysterols

Oxysterols are synthesized in the ER and mitochondria depending on hydroxylase localization. Oxysterols play various roles in different organelles. Oxysterols bind LXR, and regulate the transcription of LXR target genes in the nucleus. At the ER, side-chain oxysterols bind INSIGs, leading to their stabilization (18), and also become ACAT1 substrates (51). At the PM, oxysterols can affect membrane organization (27). Oxysterols are also released from cells (118). Furthermore, several proteins with sterol transporting activity, including OSBP (78) and NPC1 (119) have the ability to bind oxysterols. Together these findings

strongly suggest that, like cholesterol, oxysterol distribution is tightly regulated. However, little is known about intracellular transport of oxysterols due to their extremely low cellular contents (~0.1% of cholesterol), in addition to difficulties in their handling.

Recent work developed an intrinsically fluorescent oxysterol, 25-hydroxycholestatrienol (25-HCTL) that mimics 25-OHC (120). 25-HCTL is a hydroxylated derivative of cholestatrienol (CTL), a fluorescent cholesterol analog without fluorophore that may affect the physical properties of cholesterol. Both 25-HCTL and CTL contain two additional double bonds at the steroid B and C rings, thereby exhibiting intrinsic fluorescence with excitation max at 325 nm. When cells are incubated with 25-HCTL in the presence of LDL, 25-HCTL enters cells via LDLR-mediated endocytosis, and is transported to the LE/LYS. Like cholesterol, egress of 25-HCTL from the intracellular compartments requires functional NPC1 protein (120), which is consistent with 25-OHC-binding ability of NPC1 protein (119). Furthermore, 25-HCTL can be transported to the ER, and is also redistributed to the PM and the recycling endosome (120). It remains to be determined how endogenously synthesized oxysterols are transported from the sites where they are synthesized: the ER and mitochondria.

## STEROL EXPORT TO EXTRACELLULAR MILIEU

Because mammalian cells cannot break down the sterol backbone, and conversion of cholesterol into bile acids is restricted to only the liver, efflux of excess cholesterol and other sterols from cells is crucial for cellular cholesterol homeostasis. Cholesterol can be removed from cells by two processes; active export and passive diffusion. Passive diffusion largely depends on a cholesterol gradient between the cell surface and cholesterol acceptors such as HDL. Active export is energy-dependent and involves several ABC transporter proteins that use ATP as driving force.

### ABC Transporters

The human genome encodes 48 ABC transporters, classified into seven subfamilies, ABCA-G families (121). ABC transporters bind and hydrolyze ATP for energy-dependent transport of chemically diverse substrates across biological membranes. The substrates vary greatly for the various ABC transporters. Studies have revealed that several ABC transporters play a role in exporting cellular sterols including cholesterol, intermediate sterols, oxysterols, and phytosterols (122), as described in further detail in this review.

### ABCA1 and HDL Assembly

It was first reported in 1991 by Hara and Yokoyama (123) that interaction of lipid-free apoA-I with macrophages resulted in formation of HDL with cellular phospholipids and cholesterol. It was subsequently demonstrated that fibroblasts isolated from patients with Tangier disease, a severe HDL deficiency, lack the apoA-I-mediated phospholipid and cholesterol release and HDL formation (124). In 1999, ABCA1 was identified as the gene



mutated in Tangier disease patients (125–127). These reports and numerous other studies established that ABCA1 plays an essential role in the release of cellular phospholipids and cholesterol and in the assembly of nascent HDL [reviewed in (128)]. Further studies with conditional *Abca1* knockout mice revealed that liver ABCA1 and intestinal ABCA1 contribute to produce 70–80 and 30% of total plasma HDL, respectively (129, 130). The physiological acceptor for phospholipids and cholesterol is apoA-I, a major HDL apolipoprotein. HDL is a key lipoprotein that transports excess cholesterol from peripheral tissues to the liver where cholesterol is converted to bile acids for excretion. This cholesterol transport system is often referred to as “reverse cholesterol transport.” Because Tangier disease patients largely lack serum HDL, they exhibit accumulation of cholesterol (both unesterified and esterified cholesterol) in peripheral tissues and have increased risk of cardiovascular disease (131–133).

How does ABCA1 mediate HDL formation? ABCA1 localizes to both the PM and the endocytic compartments. ABCA1 that resides in the PM mediates the assembly of nascent HDL (134), while ABCA1 internalized into the endocytic compartments is subjected to degradation or recycles back to the PM (135). ABCA1 creates membrane deformation sites at the PM, where apoA-I binds (136). This could be related with the finding that overexpression of ABCA1 disrupts lipid rafts (137). In contrast, ABCA1 deficiency increases lipid rafts and cholesterol contents in the PM (94, 114, 138). ApoA-I can directly bind to ABCA1, and this interaction plays a role in ABCA1-dependent lipid release and HDL formation; therefore, lipid compositions of nascent HDL may reflect those of membrane domains where ABCA1 mediates HDL assembly. A study using recombinant ABCA1 reconstituted in liposomes shows that ABCA1 can export phosphatidylcholine (PC), phosphatidylserine (PS), and SM (139). Cholesterol reduces ATPase activity of ABCA1 (112, 139), suggesting that cholesterol may not be a direct substrate of this transporter. These *in vitro* observations are consistent with a cell-based study showing that ABCA1 primarily mediates phospholipid release to apoA-I. Recent work showed that ABCA1 also flops and releases phosphatidylinositol (4,5) bis-phosphate (PIP2) (140). Increases in cell surface PIP2 levels enhances apoA-I binding to cell surface and ABCA1-dependent HDL biogenesis (140). In certain cell models, ABCA1 primarily releases phospholipids and can generate cholesterol-poor nascent HDL particles (141). ABCA1-dependent cholesterol release can thus uncouple phospholipid release and HDL formation. Although the mechanisms by which ABCA1 mediates cholesterol incorporation into nascent HDL remain obscure, cholesterol availability for ABCA1-dependent HDL formation is dependent on cellular cholesterol pool sizes regulated by ACAT1 (142). In cholesterol-loaded macrophages, autophagy-dependent lysosomal degradation of lipid droplets, called lipophagy, hydrolyzes lipid droplet-associated CE by lysosomal acid lipase, generating free cholesterol available for ABCA1-dependent HDL assembly (143).

Our recent work determined sterol specificity of ABCA1-mediated sterol release (144). We showed that in addition to cholesterol, ABCA1 preferentially releases intermediate sterols with extra methyl groups including lanosterol, which

accounts for very minor quantity of cellular sterol (0.1% or less of cellular total cholesterol) and its half-life is <1 h in cells. Lanosterol and other methylated intermediate sterols synthesized at the ER are immediately delivered to the PM (87). Therefore it is postulated that these minor sterols become constituents of certain PM domains where ABCA1 preferentially release these sterols along with cholesterol and phospholipid for HDL formation (144). There are significant structural differences between lanosterol and cholesterol, and lanosterol has the ability to induce membrane curvature formation in model membranes (145). Whether lanosterol affects membrane structure/organization in living cells remains to be investigated. In the absence of acceptors, lanosterol and other intermediate sterols immediately leave the PM domains and are transported back to the ER for cholesterol synthesis (87). ABCA1 participates in this retrograde transport (94). ABCA1 deficiency thus associates with accumulation of cholesterol and other sterols in the PM of various cell types including macrophages and fibroblasts (94, 114). In addition to endogenously synthesized sterols, LE/LYS-derived cholesterol is a significant source for ABCA1-dependent HDL formation (105, 146).

Recently, the structure of human ABCA1 in digitonin micelles but not in phospholipid bilayer was determined by cryoelectron microscopy (cryo-EM) (147). The structure reveals that an elongated hydrophobic tunnel is present within the two large extracellular domains. Whether this hydrophobic tunnel serves as a route for delivering lipids to apoA-I needs further investigation. Although the molecular mechanisms by which ABCA1 transports lipid and mediates HDL biogenesis remain obscure, the cryo-EM structure supports that structure-based studies of ABCA1 can provide further insights into its function and HDL assembly.

## Regulation of ABCA1

ABCA1 expression is tightly regulated at transcriptional and post-transcriptional levels. LXR serves as major transcription factor that activate *ABCA1* gene expression (148, 149). Oxysterols and intermediate sterols, including desmosterol, activate LXR and induce ABCA1 expression (14, 148). LXR forms a heterodimer with another nuclear receptor, RXR. 9-*cis* retinoic acid, an RXR ligand, also induces ABCA1 expression (148). Recent studies found that many microRNAs (miRNAs), such as miR-33a/b and miR-148 are involved in *ABCA1* gene expression [reviewed in (150)]. These miRNAs suppress *ABCA1* gene expression and reduce plasma HDL levels in mice and non-human primates (151–153). MiR-33a and miR-33b are encoded by introns of *SREBF2* and *SREBF1* genes, respectively (151, 152).

ABCA1 protein is a short-live protein with half-life of about 1–2 h (154, 155). ABCA1 is degraded by the calcium-dependent cysteine protease, calpain (154, 156), and in proteasomes or in the LYS through ABCA1 ubiquitination by an unknown ubiquitin ligase (157–159). Unsaturated fatty acids accelerate ABCA1 degradation (160). Free cholesterol loading enhances the ubiquitination and degradation of ABCA1 (158, 161). Importantly, in addition to its lipid acceptor function, apoA-I has an ability to protect ABCA1 from calpain-mediated degradation, thereby



increasing cell surface ABCA1 and further inducing lipid release (154, 156). It has been suggested that the ABCA1-apoA-I interaction at the cell surface leads ABCA1 to recycle back to the PM from the endocytic compartments (135) through a Rab8-dependent trafficking pathway (162). It would be interesting to determine whether the interaction between ABCA1 and apoA-I causes modifications of ABCA1 before endocytic internalization, to prevent its degradation.

ABCA1 has several important motifs/domains that modulate its stability. It has been demonstrated that the PDZ domain located in the C-terminal cytosolic region binds to several proteins including  $\alpha$ 1-syntrophin and  $\beta$ 1-syntrophin (155, 163). Interaction of these two proteins with ABCA1 leads to its stabilization. LXR $\beta$  also binds to the C-terminal region of ABCA1 and stabilizes ABCA1 (164). The cytosolic region between the two transmembrane domains contains the PEST sequence that plays an important role in calpain-mediated degradation (154). Near the PEST sequence, ABCA1 contains calmodulin binding site. Calmodulin binding to ABCA1 inhibits ABCA1 degradation (165).

Several protein kinases including protein kinase A (PKA), PKC, and Janus kinase 2 (JAK2) modulate ABCA1 activity and stability. PKA phosphorylates ABCA1 and modulates its lipid efflux activity (166, 167). PKC, activated by apoA-I-cell interaction or by apoA-I-dependent lipid removal, is involved in the stability of ABCA1 (168, 169). JAK2 is activated by apoA-I and modulates ABCA1 activity without affecting its stability (170, 171). Other factors regulating ABCA1 protein activity and/or stability are reviewed elsewhere (172).

## ABCG1 and ABCG4

In addition to ABCA1, the ABCG subfamily proteins ABCG1 and ABCG4 are well-recognized members of ABC transporters that facilitate cholesterol efflux to HDL (173). ABCG transporters are half-transporters that contain one nucleotide-binding domain in the N-terminal region. ABCG1 and ABCG4 transporters form either homodimer or heterodimer to function as an active transporter. ABCG1 is expressed in numerous tissues. ABCG1 localizes to both the PM and the endocytic compartments when overexpressed (174, 175). At physiological expression levels, however, this transporter largely resides in the intracellular compartments and acts as intracellular cholesterol transporter (176). Regardless of its localization, deficiency of ABCG1 impairs cholesterol efflux to HDL in macrophages (177). Importantly, ABCG1 also exports 7-ketocholesterol, an oxysterol abundant in oxidized LDL and atherosclerotic lesions, to HDL, whereas ABCA1 does not (118). Because 7-KC can induce apoptosis in macrophages, ABCG1-mediated 7-KC efflux to HDL protects macrophages from its cytotoxicity (118). Furthermore, in addition to sterols, ABCG1 preferentially exports SM over PC (174). While how ABCG1 mediates efflux of sterols and phospholipids is poorly characterized, its ATPase activity is stimulated by cholesterol and SM *in vitro* (178). These findings suggest that the activities of ABCA1 and ABCG1 are differentially regulated. ABCA1 and ABCG1 cooperatively promote cholesterol export pathway, and as

such act synergistically to prevent cholesterol accumulation in macrophages (179).

ABCG4 is highly expressed in the brain (180). ABCG1 and ABCG4 are expressed in both neurons and astrocytes. Both of these transporters have the ability to export cholesterol as well as the intermediate sterol desmosterol to HDL (180). Deficiency in ABCG1 and/or ABCG4 results in the accumulation of intermediate sterols including lanosterol, desmosterol, and lathosterol, but not cholesterol, in mouse brains, with greater accumulation in double knockout mice (180). In ABCG1/ABCG4 double knockout mice, 27-OHC but not 24(S)-OHC is also accumulated in the brain (180).

## ABCG5 and ABCG8

ABCG5 and ABCG8 form a heterodimer as an active transporter and are expressed in the apical membranes of enterocytes and hepatocytes. In the small intestine, ABCG5/G8 promote efflux of cholesterol and plant sterols absorbed through NPC1 like 1 (NPC1L1), to the lumen, thus limiting the absorption of dietary sterols (181). In the liver, the heterodimer exports cholesterol and phytosterols into the bile, thus enhancing sterol excretion from the body (182). Deficiency in either one the two transporters causes  $\beta$ -sitosterolemia, which is characterized by the robust accumulation of dietary sterols in plasma and tissues (183, 184). This accumulation is caused by increased intestinal absorption and decreased biliary excretion, and individuals with  $\beta$ -sitosterolemia develop premature atherosclerosis [reviewed in (185)].

## Other ABC Transporters With Potential Sterol Exporting Activity

ABCA7, a close homolog of ABCA1, is highly expressed in the brain, lung, spleen, and adrenal in mice. ABCA7 is associated with Alzheimer's disease [reviewed in (186)]. The exact functions of ABCA7 are largely unknown, but it is capable of exporting lipids (phospholipid and cholesterol) to extracellular apoA-I and generates HDL-like particles when overexpressed in mammalian cells (187, 188). The ability of ABCA7 to export cholesterol is much less compared to that of ABCA1 (189). Consistent with the cell-based studies, an *in vitro* reconstitution assay shows that ABCA7 exports PS and PC with preference for PS (139). Although ABCA7 has similar lipid transporting functions as ABCA1, it plays a minimum, if any, role in lipid efflux and HDL formation in macrophages and in mice (190). At physiological expression levels, ABCA7 is mainly intracellular localized in resting macrophages, and following stimulation with apoptotic cells, ABCA7 translocates to the PM and plays a role in phagocytosis (191).

Additional ABCA family proteins are involved in cholesterol efflux. ABCA8 facilitates cholesterol efflux to apoA-I and modulates HDL-cholesterol levels (192). In humans, mutations in this gene are associated with low HDL-cholesterol levels (192). In addition, ABCA12 also regulates cholesterol efflux (193). It has been reported that ABCA12 interacts with ABCA1 and regulates its stability in macrophages, thereby modulating ABCA1-dependent lipid release (193). ABCA12 was originally identified as a protein defective in one of the most severe

skin disorders, Harlequin ichthyosis that is characterized by severe skin barrier defects and by abnormal keratinocyte lamellar granules (194). It is suggested that ABCA12 is involved in the transport of glucosylceramide in the lamellar granules (194). Unlike other ABC transporters described above, ABCA2 attenuates cholesterol efflux to extracellular cholesterol acceptors through poorly characterized pathway (195).

Certain ABCB family proteins also exhibit cholesterol transport activities. ABCB1 (also known as multidrug resistant protein 1, MDR1, or P-glycoprotein) translocates cholesterol from the inner leaflet to the outer leaflet of the PM (196). ABCB4 (also known as MDR3 in humans or MDR3 in mice), is expressed on the apical canalicular membranes of hepatocytes and exports PC and cholesterol to bile acids, as such ABCB4 along with ABCG5/ABCG8 contributes to biliary cholesterol excretion (197).

## Passive Diffusion

Cholesterol can be removed from cells through passive diffusion, which is driven by a cholesterol gradient between cell surface and acceptors [reviewed in (198, 199)], with HDL serving as the major cholesterol acceptor. LCAT has phospholipase A2 and acyltransferase activities; LCAT transfers an acyl-chain from PC to 3-OH position of cholesterol, resulting in the formation of CE. LCAT-mediated cholesterol esterification plays a role in HDL maturation (200). Cholesterol esterification by LCAT in HDL causes the expansion of the cores in HDL particles and the reduction of free cholesterol at HDL surface, further facilitating net cholesterol efflux from cells to HDL. Serum albumin acts as a shuttle to facilitate passive cholesterol efflux from cells (199). Although the HDL receptor SR-BI is known to enhance cholesterol efflux from cells to HDL, SR-BI-mediated cholesterol efflux may not contribute to net cholesterol removal from cells, as it mediates bidirectional transport of cholesterol between the cell surface and HDL [reviewed in (115)]. As previously described, SR-BI rather plays an important role in selective uptake of HDL-cholesterol in the liver and steroidogenic tissues (115).

## STEROLS AND HUMAN DISEASES

Cholesterol, sterol intermediates, and oxysterols play diverse and important roles in the body, in addition to contributing to various human diseases including cancer, cardiovascular disease, neurodegenerative disorders such as Alzheimer's disease and infection. This review focuses on discussing the connection between sterol metabolism and atherosclerosis as well as cancers. For a detailed discussion between cholesterol metabolism and neurodegenerative diseases, a recent review by Chang et al. (201) is available. Detailed reviews on the roles of sterols in immune responses are available elsewhere (20, 202). Pathophysiological roles of SREBPs in various human diseases are extensively discussed by Shimano and Sato (203).

## Sterols and Atherosclerosis

Cholesterol along with inflammation regulation are major therapeutic targets for atherosclerosis, a condition in which

plaque buildup in the artery wall can lead to a multitude of vascular complications, including heart attack and stroke. Large-scale trials have demonstrated the effectiveness of HMGCR inhibitors, statins, but have also shown residual risk with many statin-taking patients suffering from cardiovascular events (204). Further LDL cholesterol lowering by combining statin with the Niemann-Pick C1-like 1 intestinal cholesterol absorption inhibitor, ezetimibe provides modest benefit (205). Monoclonal antibody inhibition of proprotein convertase subtilisin-kexin type 9 (PCSK9), which reduces LDL cholesterol by about 60% via reducing LDL receptor degradation, improves clinical outcomes in patients with cardiovascular disease (206). While outcomes are not known, inhibition of the lipoprotein lipase inhibitor, angiopoietin-like 3 reduces circulating cholesterol, notably in homozygous familial hypercholesterolemia patients that only have limited responses to statin and PCSK9 therapies, and who typically require arduous LDL apheresis treatment (207). Supporting a key role of SR-BI-mediated HDL-cholesterol uptake in human reverse cholesterol transport, a loss-of-function variant (P376L) in SR-BI was recently identified in people with extremely high HDL cholesterol that also have increased risk of coronary heart disease (208). Much is known about the impact of reducing cholesterol in cardiovascular disease; however, less is known about the contributions of sterol metabolites to atherosclerosis that may provide insight into novel risk factors and therapies to target residual cardiovascular risk.

Macrophage lipid accumulation leads to foam cell formation and inflammation, contributing to atherosclerosis (209). In macrophages, the cholesterol precursor desmosterol exhibits several beneficial properties including inhibiting expression of cholesterol biosynthesis and proinflammatory genes, along with induction of LXR genes and cholesterol efflux (210). LXR-deficiency in mice exacerbates atherosclerosis disease pathology, and LXR activation generally reduces cell and animal model pathology through a variety of mechanisms [reviewed in (211)]; however, LXR activation can also have an accompanying unacceptable side effect of raising liver triglyceride synthesis (212).

Oxysterols are associated with nearly every atherosclerosis-contributing pathway, as such they present a promising area of future therapeutic research. Oxidized forms of cholesterol produced by LDL oxidation exhibit pro-atherosclerotic properties [reviewed in (213, 214)]. Like cholesterol, oxysterols can be stored as fatty acid esters [reviewed in (51)]. In mice, ACAT1 small molecule inhibition (215), genetic knockout (216), and macrophage-specific deletion (217) reduce atherosclerosis pathology. Additionally, ACAT1 was recently associated as a causal modifier variant explaining strain differences in mouse atherosclerosis pathology (218); although a cardiovascular benefit of ACAT inhibition has not been demonstrated in human ACAT inhibitor trials (219).

Oxysterols can regulate atherosclerosis-related pathologies, but the extent to which oxysterols drive atherosclerosis is unclear. Multi-omics mapping of oxysterols and associated genes and proteins in healthy and diseased tissue could clarify the complex roles of these lipids in cardiovascular disease. In primary mouse macrophages, 22-OHC, 24-OHC, and the sterol

24, 25 epoxycholesterol repress activation of the inflammation-related factor, inducible nitric oxide synthase, while also inducing ABCA1 expression, and 25-OHC and 27-OHC activate ABCA1 but do not repress inducible nitric oxide synthase (220). On top of plaque formation, calcification is frequently observed in atherosclerosis, and may contribute to plaque rupture (221). In bovine aortic and mouse smooth muscle cells, 25-OHC stimulates mineralization pathways leading to vascular calcification, including through LXR-independent mechanisms (222, 223). 27-OHC is increased in human atherosclerotic arteries and functions in macrophage cholesterol elimination (224); however, the role of 27-OHC in atherosclerosis is complex. Elevated 27-OHC via deletion of CYP7B1 that metabolizes 27-OHC promotes atherosclerosis via a proinflammatory process involving estrogen receptor alpha in apoE-deficient mice (225). Knockout of *Cyp27A1* in apolipoprotein E-deficient mice revealed a gene dose effect with a 10-fold reduction in atherosclerosis severity observed in double knockout mice, and *Cyp27A1* heterozygosity leads to accelerated atherosclerosis (226). Cerebrotendinous xanthomatosis develops in the absence of CYP27A1 in humans, while mice lacking CYP27A1 do not develop xanthomas. Further complicating matters are that loss of 27-hydroxylase may have athero-protective effects including increased cholesterol degradation, in addition to pro-atherogenic effects, such as reduced cholesterol efflux, and the balance of this may vary between patients (227). Raising a confounding factor, sex-specific effects in bile acids are observed in CYP27A1 overexpressing mice (227).

## Sterol Metabolism and Cancer

Altered metabolism is a hallmark of cancer cells, with a major metabolic alteration being elevated glucose uptake and glycolysis (228). In addition to this “glycolytic phenotype,” biosynthesis of lipids (including cholesterol), which are essential building blocks of cell membranes, is increased in cancer cells to support proliferation (229). Elevated lipogenesis is referred to as “lipogenic phenotype.” In human melanomas, increased expression of various cholesterol biosynthetic genes is found in more than 60% of patients (230). SREBPs serve as master drivers for lipogenic phenotype of cancer cells. Activation of SREBPs and/or upregulation of SREBP-target gene expression is observed in a wide variety of human cancers including glioblastoma (231), prostate cancer (232), breast cancer (233), melanoma (230, 234), and is often associated with poor prognosis/survival. Cholesterol is an indispensable component of lipid rafts, which serve as platforms for various oncogenic signals including Akt activation, and therefore cholesterol synthesis in cancer cells links to the integrity of these membrane domains. SREBPs are activated by PI3K-Akt-mTORC1 signaling (235, 236), which is hyperactivated in human cancers. Consequently, a positive feedback loop between PI3K-Akt-mTORC1 signaling and SREBP-dependent lipogenesis is formed to sustain malignant properties of cancer cells (234, 237). Several mechanisms are involved in the activation of SREBP by PI3K-Akt-mTORC1 signaling: (1) Phosphorylation of SREBP-1 mature form by the protein kinase GSK3 $\beta$  results in ubiquitination by the ubiquitin ligase Fbw7, leading to the proteasomal degradation of the mature form (238).

Independently of mTORC1, Akt phosphorylates and inactivates GSK3 $\beta$ , thereby increasing SREBP transcriptional activity. (2) PI3K-Akt-mTORC1 axis regulates processing of both SREBP-1 and SREBP-2 (234). mTOR phosphorylates cytosolic CREB regulated transcription coactivator 2 (CRTC2) and attenuates its inhibitory effect on COPII-dependent transport of SREBP-1 from the ER to the Golgi, which facilitates SREBP-1 processing (239), and this pathway is at least partly involved in PI3K-Akt-mTORC1 regulation of SREBP processing. Whether this axis also regulates SREBP-2 processing is unknown at present. In addition, the mTOR-CRTC2 axis could be involved in general COP-II transport. Additional mechanisms may also participate in SREBP processing as the protein kinase S6K also regulates SREBP processing downstream of mTORC1 (240). (3) mTORC1 phosphorylates lipin1 and regulates nuclear entry of SREBP mature form through an unknown mechanism (241). While cholesterol plays crucial roles in malignant properties of cancer cells, whether blocking cholesterol biosynthesis by statins, HMGCR inhibitor, reduce the risk of cancer onset or mortality is controversial at present; the statin effects could be dependent on types of cancer (242–244). To plausibly explain this, inhibiting HMGCR increases LDL uptake through upregulation of LDLR expression, which could enable cancer cells to acquire sufficient amounts of cholesterol. LDL levels are much higher in humans than mice. Therefore, inhibiting SREBP could be a more direct target to treat a broad range of cancers.

An aberrant accumulation of CE in lipid droplets via ACAT1 is found in prostate (245) and pancreatic cancer tissues (246). Pharmacological or genetic ACAT1 inhibition attenuates cancer cell proliferation and invasive activity *in vitro* and tumor growth and metastasis in xenograft models (245, 246). Blocking ACAT1 causes an increase in free cholesterol at the ER, which inactivates SREBP-1 but not SREBP-2, reducing cholesterol synthesis and uptake (245). Increased ER free cholesterol levels may induce ER stress and cancer cell apoptosis (246). Furthermore, ACAT inhibition blocks activation of Akt partly through a reduction of cellular arachidonic acid (245), and reduced SREBP activity and cholesterol biosynthesis could also impair the integrity of lipid rafts and suppress Akt activity. Therefore, ACAT1 is an attractive therapeutic target for certain types of cancer where large accumulations of CE are observed.

Cancer immunotherapy targeting PD-1 expressed on T cells or PD-L1 expressed on cancer cells is clinically used. In these therapies, CD8<sup>+</sup> T cell activity is crucial for successful achievement. Recent work by Yang et al. (247) showed that blocking ACAT1 activates T cells; ACAT blockage increases PM cholesterol levels and enhances T-cell receptor clustering and signaling, which in turn potentiates effector function and proliferation of these cells to suppress tumor growth in mice. Inhibiting ACAT1 further improved anti-tumor efficacy of anti-PD1 antibody (247). Given the additional suppressive effects of ACAT1 inhibitor on malignant properties of cancer cells, ACAT1 blockage thus has dual beneficial effects in cancer therapy. However, proliferation of CD8<sup>+</sup> T cell depends upon SREBPs and cholesterol biosynthesis (248), creating difficulties in targeting SREBP pathway to combat cancer. Developing specific drug delivery systems could overcome this barrier.



## Oxysterols and Cancer

Serum cholesterol levels are positively correlated with serum 27-OHC, the most abundant oxysterol (213). Hypercholesterolemia is a risk factor of breast cancer, and 27-OHC is involved in the pathophysiology of human breast cancer (249). Expression of CYP27A1, which converts cholesterol to 27-OHC is positively correlated to tumor grade in human breast cancer (250). In aggressive tumor tissues, high CYP27A1 expression was found in both tumor cells and tumor-associated macrophages (TAMs) (250). 27-OHC administration increases the growth of human breast cancers, and CYP27A1 inhibition suppresses tumor growth in xenograft models (250, 251). Further, abrogation of Cyp7B1, which catalyzes the conversion of 27-OHC to  $7\alpha$ , 27-di-OHC resulting in 27-OHC accumulation in plasma and tumor tissues, accelerates tumor growth in a mouse estrogen receptor-positive mammary adenocarcinoma model (250). Reduced expression of CYP7B1 is correlated with estrogen receptor-positive breast cancer aggressiveness (251). 27-OHC exerts pro-tumor effects on breast cancer cells by acting as an estrogen receptor agonist (as a SERM). Additionally, 27-OHC promotes metastases of not only estrogen receptor-positive and -negative breast cancer cells but also of melanoma, lung cancer cells, and pancreatic cancer cells (252). The pro-metastatic roles of 27-OHC depend partly on LXR activity of tumor cells (250) and on immune cells within tumor microenvironment (252). 27-OHC affects several types of immune cells, increasing the number of polymorphonuclear-neutrophils and  $\gamma\delta$ -T cells, and decreasing CD8<sup>+</sup> T cells (252).

In contrast to breast cancer, CYP27A1 expression is negatively associated with aggressiveness of prostate cancer; patients whose tumors express higher CYP27A1 mRNA exhibit lower tumor grade and longer disease-free survival (253). 27-OHC suppresses growth of human prostate cancer cells at least partially by inactivating SREBP-2 pathway (253).

## Sterol Transporters and Cancer

Lipid transport proteins can modulate malignant properties of cancer cells. ABCA1 has an anti-cancer activity dependent on lipid transport activity (254). ABCA1 expression levels are inversely correlated with tumor aggressiveness in prostate cancer. The ABCA1 gene promoter is hypermethylated in the tissues of prostate cancer, suppressing its expression (255). ABCA1 deficiency causes an increase in mitochondrial cholesterol content, which promotes survival of cancer cells (254).

Studies using LXR agonists showed that activation of LXR reduces cellular cholesterol content in glioblastoma cells through increased cholesterol export and decreased cholesterol uptake, which suppresses the growth of glioblastoma cells *in vitro* and in xenograft models (256, 257). LXR agonists also suppress metastases of melanoma and prolong animal survival, at least partially through LXR $\beta$ -dependent upregulation of apoE expression, in several *in vivo* models (258). Furthermore, accumulation of endogenous  $4\alpha$ -monomethylsterols by genetic manipulation leads to LXR activation and inhibits tumorigenesis in a mouse model (259).

Several ABCA family transporters associate with overall survival of serous ovarian cancer patients. Patients with high

expression of ABCA1, ABCA6, ABCA8, or ABCA9 in primary tumors exhibit reduced survival (260). Furthermore, combined expression of ABCA1, ABCA5, and either ABCA8 or ABCA9 leads to poorer survival (260). In this cancer type, ABCA1 seems to have an opposite effect on malignancy by unknown mechanisms. The roles of ABCA5, ABCA8, and ABCA9 are not well-understood.

Independently of LXR/RXR-mediated transcription, ABCA1 expression is regulated by cell density in A431 human epidermal carcinoma cells (261). In cells at low density, focal adhesion kinase (FAK) inactivates the transcription factors Foxo3 and TAL1, resulting in suppression of ABCA1 expression. In contrast, at high density, FAK activity is suppressed, and ABCA1 expression is upregulated (261). Cell density-dependent ABCA1 expression regulates PM lipid compositions (261); cells expressing ABCA1 at high levels contain less cholesterol and ganglioside in the PM compared to those expressing ABCA1 at low levels (94, 114, 261). ABCA1 modulates trans-bilayer distribution of cholesterol at the PM (262). Collectively, in addition to a well-known role in HDL biogenesis, ABCA1 acts to fine-tune membrane lipid compositions to modulate PM functionality that may alter cancer cell phenotypes in a cell type-dependent manner.

Macrophage ABCA1 and ABCG1 also play roles in tumor growth. Deficiency in either ABCA1 or ABCG1 in macrophages attenuates tumor growth in xenograft models (263, 264). Deletion of these genes in macrophages converts the tumor-promoting M2 phenotype to the anti-tumor M1 phenotype TAMs within the tumor microenvironment (263, 264).

Additional lipid/sterol transporter is also involved in human cancer. Higher expression of ORP5, an ER membrane anchored ORP, associates with poor prognosis of patients with pancreatic cancer (265). ORP5 expression levels are positively correlated with cell proliferation and invasive activity. Of mechanistic interest, ORP5 interacts with mTOR, and enhances mTORC1 activity (266).

## CONCLUDING REMARKS

Cells are highly compartmentalized at both the cellular and organelle levels. Cholesterol, oxysterols, and intermediate sterols move dynamically in cells with correct cellular distribution, being paramount to regulating cellular functions. Cellular sterol transport must be spatiotemporally regulated; however, the mechanisms of this are not fully understood. Compared to cholesterol, much less is known about the transport of oxysterols and intermediate sterols. Additionally, elucidating sterol metabolism and transport mechanisms in disease via pathophysiologically relevant models, such as patient-derived iPSC cell systems and organoid culture, could help identify novel therapies for human diseases. State-of-the-art technologies including genome editing, imaging, and multi-omics may provide new insights into how cells handle sterols in physiological and pathophysiological conditions.

Experimental evidence demonstrates that sterols and sterol metabolism play crucial roles in various aspects of human



diseases, not only in atherosclerosis and cancer, but also those not reviewed here, including Alzheimer's disease and other neurodegenerative disorders, and infection among others. Sterol metabolism is an attractive target in disease treatment. Several drugs targeting sterol metabolism are clinically used to treat patients currently, including statins to block cholesterol synthesis and enhance LDL uptake, Ezetimibe to block NPC1L1-mediated absorption of dietary cholesterol, and the anti-PCSK9 monoclonal antibodies (Evolocumab and Alirocumab) to block LDLR degradation and reduce plasma LDL. New potential therapeutic target molecules include SREBPs and SREBP regulators, LXR, ABC transporters, ACAT, and sterol hydroxylases, as a growing number of preclinical and clinical studies targeting these molecules are ongoing. Given the importance of target localization, development of novel drug delivery systems to address associated issues will also be key.

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## AUTHOR CONTRIBUTIONS

YY designed and wrote the article. MR contributed to writing and revising the article. Both authors approved the final version.

## ACKNOWLEDGMENTS

We thank Dr. Ta-Yuan Chang (Geisel School of Medicine at Dartmouth, USA) and Dr. Ryuichiro Sato (University of Tokyo, Japan) for discussion and critical reading of this manuscript. YY is supported by AMED-CREST Grant 18gm0910008h0103 from Japan Agency for the Medical Research and Development (AMED) and by KAKENHI Grant 16K08618 from Japan Society for Promotion of Sciences. MR is supported by an NIH fellowship.

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**Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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# HDL in Endocrine Carcinomas: Biomarker, Drug Carrier, and Potential Therapeutic

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## OPEN ACCESS

### Edited by:

Vincenzo Pezzi,  
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### Specialty section:

This article was submitted to  
Cancer Endocrinology,  
a section of the journal  
Frontiers in Endocrinology

**Received:** 22 September 2018

**Accepted:** 12 November 2018

**Published:** 30 November 2018

### Citation:

Morin EE, Li X-A and Schwendeman A  
(2018) HDL in Endocrine Carcinomas:  
Biomarker, Drug Carrier, and Potential  
Therapeutic. *Front. Endocrinol.* 9:715.  
doi: 10.3389/fendo.2018.00715

High-density lipoprotein (HDL) have long been studied for their protective role against cardiovascular diseases, however recently relationship between HDL and cancer came into focus. Several epidemiological studies have shown an inverse correlation between HDL-cholesterol (HDL-C) and cancer risk, and some have even implied that HDL-C can be used as a predictive measure for survival prognosis in for specific sub-population of certain types of cancer. HDL itself is an endogenous nanoparticle capable of removing excess cholesterol from the periphery and returning it to the liver for excretion. One of the main receptors for HDL, scavenger receptor type B-I (SR-BI), is highly upregulated in endocrine cancers, notably due to the high demand for cholesterol by cancer cells. Thus, the potential to exploit administration of cholesterol-free reconstituted or synthetic HDL (sHDL) to deplete cholesterol in endocrine cancer cell and stunt their growth of use chemotherapeutic drug loaded sHDL to target payload delivery to cancer cell has become increasingly attractive. This review focuses on the role of HDL and HDL-C in cancer and application of sHDLs as endocrine cancer therapeutics.

**Keywords:** High-density lipoprotein (HDL), Apolipoprotein A-I (ApoA-I), endocrine cancer, cholesterol, cancer therapy

## INTRODUCTION

Endocrine cancers are defined as those affecting the hormone secreting tissues of our body, including cancers of the adrenal, thyroid, parathyroid, prostate, pancreatic, and reproductive tissues. A rare subset of endocrine cancers, called neuroendocrine tumors (NETs), are neoplasms originating in endocrine tissue that migrate to form hormone-secreting tumors in other organs of the body, including intestine, lung, and pancreas (1). While specific molecular signatures may vary among the different types of endocrine cancers, they all share a common modality which is essential for tumor cell proliferation and overall survival: a high demand for cholesterol (2–4).

Cholesterol is a precursor molecule for steroid synthesis and bile acid production, making it essential for hormone production by endocrine tissue (5). Cholesterol is also an important component of cellular membranes, offering structure and rigidity to the plasma membrane as well as clustering with sphingolipids and glycerophospholipids to form highly-stable membrane microdomains or “lipid rafts” that host a number of proteins and lipids involved in key cell signaling pathways (6). In cancer, rapid cellular division is needed for the growth and survival of the tumor. Hence, a large demand for cholesterol is needed to facilitate the rapid formation of new membranes (3). Endocrine cancers in particular, display an even higher demand for cholesterol due to increased hormone and steroid production by these cells (7, 8).

A hydrophobic molecule, cholesterol has very poor aqueous solubility and thus is transported throughout the body by lipoproteins. Under normal conditions, HDL is a key participant in the reverse cholesterol transport (RCT) pathway, a process by which excess cholesterol from peripheral tissue is taken up by HDL and transported back to the liver for secretion in the bile or for redistribution to endocrine tissue for steroid production. Historically, HDL-C has been the focus of lipid metabolism modulating therapeutics for cardiovascular diseases, as high HDL-C or “the good cholesterol” and low LDL-C “bad cholesterol” have been well established as markers of cardiovascular health. Specifically, nascent HDL has the ability to reduce the burden of atherosclerosis by depleting foam-cell macrophages of their cholesterol and reducing inflammation and oxidation in the surrounding atheroma environment (9, 10). In this review, we will summarize what is known about the association between HDL-C levels and cancer and examine the utility of reconstituted or synthetic HDL as a potential therapeutic and drug delivery vehicle for endocrine cancers.

## HDL-C IN CANCER

HDL is an endogenous, nanosized particle composed of apolipoproteins, and lipids (11). Naturally, these particles range in shape, size, density, and charge depending on their lipid composition, protein cargo, and degree of maturation (11). The main protein component of HDL, apolipoprotein A-I (ApoA-I), is initially synthesized in the liver where it is subsequently secreted into the circulation. Once secreted, ApoA-I picks up a small amount of lipid to form pre- $\beta$  HDL particles. These nascent, cholesterol-poor discs can then further interact with cholesterol-rich cells of the periphery to take up and deliver that cholesterol back to the liver where it is taken up via scavenger receptor type B-I (SR-BI) for secretion or further processing. Once picked up by HDL, cholesterol is esterified by lecithin:acyl cholesterol transferase (LCAT) to form cholesterol ester. Cholesterol ester is then buried within HDL's hydrophobic lipid core, inducing the maturation and formation of larger, spherical HDL particles. Spherical HDL particles contain not only ApoA-I, but also ApoE, which facilitates the growing load of CE into the hydrophobic core since ApoA-I can only facilitate a limited amount of CE in the HDL core. ApoE is also useful in that it is a substrate for low-density lipoprotein receptor (LDLR) and can deliver HDL cargo to hepatic LDLR for biliary excretion or to endocrine tissue expressing LDLR or SR-BI for use in steroid production (12, 13).

HDL is highly heterogeneous and is present in a variety of different forms depending on its size, shape, density, and lipid/protein composition. This is a result of HDL remodeling, which is a continuous process involving several endogenous enzymes (14). Put simply, HDL can be continually and reversibly recycled between lipid-poor apoA1, discoidal HDL, and small/large/larger spherical HDLs. These subsets of HDL are classified into two groups, HDL<sub>2</sub> and HDL<sub>3</sub>, based on their densities (11, 15). HDL<sub>2</sub> is lipid-rich and less dense

(1.063–1.125 g/mL) than its HDL<sub>3</sub> counterpart, which is dense (1.125–1.21 g/mL) protein-rich in comparison (11). Both HDL<sub>2</sub> and HDL<sub>3</sub> can be further divided into 2 and 3 subclasses, respectively, based on their size; HDL<sub>3</sub> ranges in size from roughly 7–9 nm in diameter while HDL<sub>2</sub> ranges from about 9–12 nm (11). To further complicate things, HDL can also be classified according to its surface charge and shape. Spherical, more neutral HDL particles are classified as  $\alpha$ -HDL, while nascent, discoidal HDL particles, known as  $\beta$ -HDL, are poorly lipidated and more negative in overall charge.

In addition to the existing variety of subpopulations in healthy individuals, HDL particle makeup can vary significantly among patients of different disease states (16). Particularly, recent studies have identified changes in the diverse proteome of HDL particles in the various disease states (17, 18). While ApoA-I is the main protein in HDL, other proteins including ApoA-II, ApoC, paraoxanase (PON), ApoM, and serum amyloid A (SAA) have been identified and can be altered under disease conditions (19–21). The lipid composition of HDL particles can also vary with disease (22), and chronic changes in the HDL lipidome have been attributed to the high inflammatory state of various diseases, including the presence of lysophosphatidic acid (LPA), a phospholipid implicated in the progression of several endocrine cancers (23–25). Under such conditions, including atherosclerosis and lupus, HDL isolated from patients is said to be dysfunctional or proinflammatory, and its abilities to carry out cholesterol efflux and exert anti-inflammatory properties are lost (26–31). Similarly, studies have shown that HDL can promote breast cancer metastasis, which is attributed to the alterations in HDL's lipid and protein compositions under inflammatory and oxidative conditions (32, 33).

## Epidemiology

A number of observational studies and retrospective study analyses have shown that plasma HDL-C and ApoA-I levels are significantly reduced in cancer patients, including those with breast, ovarian, colon, prostate, and pancreatic carcinomas (34–50). These studies are summarized in **Table 1**. A number of studies also sought to investigate the predictive power of HDL-C or ApoA-I levels in subsets of cancers and found that, when combined with other traditional cancer biomarkers cancer antigen 125 (CA125) and transthyretin (TTR), either ApoA-I or HDL-C levels significantly increased the power of these panels to predict patient prognosis (52, 54–58). In some cases, however, there were no significant associations between HDL-C, ApoA-I, and cancer risk (51). This is likely due to differences in study design and evaluation as well as the methods used to quantify HDL-C and ApoA-I. For example, direct measurements of HDL-C are generally performed by mass precipitation and can be confounded by the presence of ApoE and other proteins. Other methods directly measure HDL particles via size and charge separation using density gradient ultracentrifugation, gel filtration, high performance liquid chromatography (HPLC), and nuclear magnetic resonance (NMR) among others. Each of these techniques has its drawbacks, and is generally bias toward one or more subpopulation of HDL or risks chemical modification of

**TABLE 1** | Clinical relationships between HDL-C and endocrine cancers.

Cancer	Study design	Major findings	References
Breast	<ul style="list-style-type: none"> <li>Preoperative serum lipid profile (TC, TG, HDL-C, LDL-C, ApoA1, ApoB) and the clinical data were retrospectively collected for 1,044 breast cancer patients undergoing operation</li> <li>Kaplan-Meier method and the Cox proportional hazards regression model were used in analyzing the OS and DFS</li> </ul>	<ul style="list-style-type: none"> <li>Preoperative lower TG and HDL-C level were risk factors of breast cancer patients</li> <li>Decreased HDL-C associated with lower OS rate</li> <li>Decreased TG associated with lower DFS rate</li> </ul>	(49)
Multiple	<ul style="list-style-type: none"> <li>Twenty-six studies including 24,655 individuals identified via PubMed and EMBASE</li> <li>Meta-analysis to investigate the prognostic significance of serum blood TC, TG, HDL-C, and LDL-C for cancer</li> </ul>	<ul style="list-style-type: none"> <li>Patients with higher HDL-C had a 37% reduced risk of death compared with lower HDL-C</li> <li>DFS patients with higher HDL-C level had the risk of disease relapse reduced by 35% compared with patients with lower levels.</li> </ul>	(50)
Breast	<ul style="list-style-type: none"> <li>Examined the possible association of low HDL-C with incidence of breast cancer using data from the Atherosclerosis Risk in Communities Study (ARIC) cohort</li> <li>Among 7,575 female members of the ARIC cohort, 359 cases of incident breast cancer were ascertained during the follow-up from 1987 through 2000</li> </ul>	<ul style="list-style-type: none"> <li>No association of low baseline HDL-cholesterol (&lt;50 mg/dL) with incident breast cancer in the total sample and a modest association among women who were pre-menopausal at baseline. No association was observed among women who were post-menopausal at baseline</li> <li>Low HDL-cholesterol among pre-menopausal women may be a marker of increased breast cancer risk</li> </ul>	(51)
Multiple	<ul style="list-style-type: none"> <li>Assess the relationships of TC, TG, HDL-C, ApoA, ApoB-100, Lp(a) with risk of common cancer forms, and total cancer mortality in comparison to incidence and mortality of CVD</li> <li>Case-cohort sample out of the prospective EPIC-Heidelberg study, including a random subcohort (<math>n = 2,739</math>), and cases of cancer (<math>n = 1,632</math>), cancer mortality (<math>n = 761</math>), CVD (<math>n = 1,070</math>), and CVD mortality (<math>n = 381</math>).</li> </ul>	<ul style="list-style-type: none"> <li>High TC, HDL-C, ApoA, and Lp(a) levels were associated with a reduction in total cancer mortality</li> <li>High levels of apoB-100 and TG were inversely associated, and high HDL-C levels were positively associated with breast cancer risk</li> <li>Higher levels of Lp(a) were associated with an increase in prostate cancer risk</li> </ul>	(48)
Multiple	<ul style="list-style-type: none"> <li>Serum TC, LDL-C, HDL-C, and TG were analyzed in 530 patients with newly diagnosed cancer (97 with hematological malignancies, 92 with tumor of the lung, 108 of the upper digestive system, 103 of colon, 32 of breast, and 98 of the genitourinary system) and in 415 non-cancer subjects</li> </ul>	<ul style="list-style-type: none"> <li>TC, LDL-C, HDL-C, SA, and BMI were significantly lower in cancer than in non-cancer subjects; similar trend for metastatic vs. non-metastatic cancer patients</li> <li>Lowest values of TC, LDL-C, and HDL-C recorded in patients with hematological malignancies</li> <li>Highest values of TC, LDL-C, and HDL-C in patients with breast tumor</li> </ul>	(36)
Renal cell carcinoma	<ul style="list-style-type: none"> <li>Preoperative serum lipid-profile (TC, TG, HDL-C, LDL-C, ApoA-I, and ApoB) were retrospectively performed in 786 patients with RCC</li> </ul>	<ul style="list-style-type: none"> <li>Patients with low ApoA-I (&lt;1.04) had significantly lower OS than the high ApoA-I</li> <li>In the 755 patients with nonmetastasis, the low ApoA-I group was also associated with shortened DFS time compared to the high ApoA-I group</li> </ul>	(47)
Pancreatic	<ul style="list-style-type: none"> <li>Identify and validate new biomarkers in PCa patient serum samples</li> <li>96 serum samples from patients undergoing PCa surgery was compared with sera from 96 healthy volunteers as controls.</li> </ul>	<ul style="list-style-type: none"> <li>Apolipoprotein A-II, transthyretin, and apolipoprotein A-I were identified as markers</li> <li>These identified proteins were decreased at least 2-fold in PCa serum compared with the control group.</li> </ul>	(52)
Multiple	<ul style="list-style-type: none"> <li>A retrospective cohort study of 14,169 men and 23,176 women with type 2 diabetes to investigate the relationship between HDL cholesterol (HDL-C) and cancer risk among type 2 diabetic patients</li> <li>During a mean follow-up period of 6.4 years, 3,711 type 2 diabetic patients had a cancer diagnosis</li> </ul>	<ul style="list-style-type: none"> <li>A significant inverse association between HDL-C and the risk of cancer was found among men and women</li> <li>Suggests an inverse association of HDL-C with cancer risk among men and women with type 2 diabetes, whereas the effect of HDL-C was partially mediated by reverse causation</li> <li>Each 15 mg/dL increase in baseline HDL-C was associated with an 8–10% decreased risk of cancer in men and a 1–7% decreased risk of cancer in women with type 2 diabetes</li> </ul>	(44)
Breast	<ul style="list-style-type: none"> <li>Review and meta-analysis of prospective studies investigating associations between TC, HDL-C, and LDL-C levels and the risk of breast cancer</li> </ul>	<ul style="list-style-type: none"> <li>Evidence of a modest inverse association between TC and more specifically HDL-C and the risk of breast cancer</li> <li>No association observed between LDL-C and the risk of breast cancer</li> </ul>	(45)

(Continued)

TABLE 1 | Continued

Cancer	Study design	Major findings	References
Multiple	<ul style="list-style-type: none"> <li>Evaluated the prospective association of total, breast, colorectal, and lung cancers and cancer mortality with lipid biomarkers in 15,602 female health professionals in the Women's Health Study (aged <math>\geq 45</math> y, free of cardiovascular disease and cancer, and without hormone replacement therapy or lipid-lowering medications at baseline)</li> <li>Included 2,163 incident cancer cases (864 breast, 198 colorectal, and 190 lung cancers) and 647 cancer deaths</li> </ul>	<ul style="list-style-type: none"> <li>Total cancer risk significantly lower for the highest quartile of ApoA-1</li> <li>Significant associations included colorectal and lung cancer risk with HDL cholesterol</li> <li>LDL cholesterol was not significantly associated with risk of total cancer or any site-specific cancers</li> </ul>	(46)
Multiple	<ul style="list-style-type: none"> <li>Prospective examination of the association between TC and cancer incidence among 1,189,719 Korean adults enrolled in the National Health Insurance Corporation</li> <li>Over follow-up, 53,944 men and 24,475 women were diagnosed with a primary cancer</li> </ul>	<ul style="list-style-type: none"> <li>High TC (<math>\geq 240</math> mg/dL) was positively associated with prostate cancer and colon cancer in men and breast cancer in women</li> <li>Higher TC was associated with a lower incidence of liver cancer, stomach cancer, and, in men, lung cancer</li> <li>TC was inversely associated with all-cancer incidence in both men and women</li> <li>TC was associated with the risk of several different cancers, although these relationships differed markedly by cancer site</li> </ul>	(42)
Multiple	<ul style="list-style-type: none"> <li>Examined the relationship between serum HDL-C and risk of overall and site-specific cancers among 29,093 Finnish male smokers in the Alpha-Tocopherol Beta-Carotene (ATBC) study cohort</li> <li>7,545 incident cancers were identified during up to 18 years of follow-up</li> </ul>	<ul style="list-style-type: none"> <li>Higher serum TC inversely associated with cancer risk</li> <li>Greater HDL-C levels associated with decreased risk of cancer of the lung, prostate, liver, and hematopoietic system</li> <li>Largely explained by reverse causation</li> </ul>	(40)
Multiple	<ul style="list-style-type: none"> <li>Systematic analysis of 24 lipid intervention randomized controlled trials (76,265 intervention patients and 69,478 control patients)</li> <li>Examined association between baseline and on-treatment HDL-C levels and cancer risk</li> </ul>	<ul style="list-style-type: none"> <li>Significant inverse association between HDL-C and cancer risk</li> <li>For every 10 mg/dL increase in HDL-C, 28–36% lower risk of developing cancer</li> </ul>	(41)
Ovarian, breast, prostate, colon	<ul style="list-style-type: none"> <li>A five-center case-control study, involving a retrospective sample of 645 serum specimen</li> <li>Serum proteomic expressions were analyzed on 153 patients with invasive epithelial OC, 42 with other OC, 166 with benign pelvic masses, and 142 healthy women</li> <li>Utilized a ProteinChip Biomarker System and SELDI-TOF-MS</li> </ul>	<ul style="list-style-type: none"> <li>Three biomarkers identified as biomarkers for OC: ApoA-1 (<math>\downarrow</math> in cancer); TT (<math>\downarrow</math>); and a cleavage fragment of ITIH4 (<math>\uparrow</math>)</li> </ul>	(53)
Ovarian	<ul style="list-style-type: none"> <li>Serum analysis from 31 healthy individuals and 43 from patients with ovarian tumors</li> <li>Use of micro-LC-MS/MS followed by Western/ELISA to identify five serum protein biomarkers previously reported using SELDI-TOF-MS (54)</li> </ul>	<ul style="list-style-type: none"> <li>TT (<math>\downarrow</math>), beta-hemoglobin (<math>\uparrow</math>), ApoA-1 (<math>\downarrow</math>), and transferrin (<math>\downarrow</math>) in early-stage OC</li> <li>When combined with CA125, biomarkers should significantly improve the detection of early stage ovarian cancer</li> </ul>	(55)
Ovarian	<ul style="list-style-type: none"> <li>Evaluated markers identified by Zhang et al. (53) in an independent study population</li> <li>Sera from 42 women with OC, 65 with benign tumors, and 76 with digestive diseases</li> <li>Measured levels of various posttranslationally forms of TTR, apolipoprotein A1, and CA125 using SELDI-TOF-MS</li> <li>Examined power of markers to discriminate sera from women with ovarian cancer from sera from women with other diseases</li> </ul>	<ul style="list-style-type: none"> <li>Confirmed findings by Zhang et al. (53)</li> <li>ApoA-I and TT levels were lower in disease states compared to controls</li> <li>Markers used alone improved detection of controls with CA125 levels <math>\geq 35</math> units/mL but lost sensitivity for late-stage cases.</li> </ul>	(56)
Ovarian	<ul style="list-style-type: none"> <li>Evaluated multiplexed bead-based immunoassay of OC-associated biomarkers (TTR and ApoA-1, together with CA125) using serum of 61 healthy individuals, 84 patients with benign ovarian disease, and 118 patients with OC</li> </ul>	<ul style="list-style-type: none"> <li>Panel of ApoA-I, TT, and CTAPIII combined with CA125 increased sensitivity for detection of early stage OC</li> <li>Combination of three markers offered maximum separation between non-cancer and stage I/II or all stages of disease</li> </ul>	(57)

(Continued)



TABLE 1 | Continued

Cancer	Study design	Major findings	References
Ovarian	<ul style="list-style-type: none"> <li>Development of multiplexed bead-based immunoassay for detection of known serum biomarkers of cancer (118 OC, 84 benign ovarian disease, 61 healthy controls)</li> </ul>	<ul style="list-style-type: none"> <li>Combination of transthyretin, and ApoA-I with CA125 improved sensitivity and specificity of OC diagnosis</li> </ul>	(58)
Ovarian, breast	<ul style="list-style-type: none"> <li>Measured ApoA-I and GPX3 mRNA levels via qRT-PCR in 121 effusions (101 OC, 20 BC) and 85 solid OC specimens (43 primary carcinomas, 42 metastases)</li> </ul>	<ul style="list-style-type: none"> <li>APOA1 and GPX3 transcript levels were higher in ovarian carcinoma compared with breast carcinoma effusions</li> <li>APOA1 and GPX3 mRNA levels can effectively differentiate ovarian from breast cancer</li> </ul>	(59)
Breast	<ul style="list-style-type: none"> <li>Fasting serum samples analyzed for lipid fatty acid and lipoprotein levels</li> <li>Malignant breast tissue analyzed for hormone receptor binding</li> <li>100 women with breast masses (50 malignant, 50 benign)</li> </ul>	<ul style="list-style-type: none"> <li>Serum lipid and apolipoprotein components of LDL were increased in fibrocystic disease and early stage cancer but decreased in women with early recurrence</li> <li>Ratio of serum ApoA-1/ApoB levels at time of biopsy was the best predictor of cancer recurrence</li> </ul>	(34)
Breast	<ul style="list-style-type: none"> <li>Nested case-control study to examine association between HDL-C and breast cancer risk</li> <li>Serum lipid profiles from 200 age-matched (100 diagnosed before age 50 and 100 at age 50 or older) case-control BC patients</li> </ul>	<ul style="list-style-type: none"> <li>No difference in HDL-C between BC and control samples</li> <li>Pre-menopausal cases had significantly lower HDL-C levels than controls</li> <li>In pre-menopausal cases, each 1 mg/dL increase in HDL-C is associated with a 4% reduction in risk of BC</li> </ul>	(35)
Breast	<ul style="list-style-type: none"> <li>Estimated the relative risk of breast cancer associated with HDL-C levels using serum samples of 38 823 Norwegian women aged 17–54 years at time of entry</li> <li>708 BC cases identified over median follow up time of 17.2 years</li> </ul>	<ul style="list-style-type: none"> <li>Low HDL-C, as part of the metabolic syndrome, is associated with increased postmenopausal BC risk</li> </ul>	(37)
Breast	<ul style="list-style-type: none"> <li>Examined relationship between breast cancer and lipid profiles in Taiwanese women</li> <li>Lipid profiles in fasting serum of 150 BC patients before treatment and 71 healthy controls</li> </ul>	<ul style="list-style-type: none"> <li>BC patients had significantly lower HDL-C and apoA-I, lower apoA-I/apoB ratios, and higher VLDL-C levels than controls</li> <li>Lower ApoA-1 and HDL-C levels associated with higher incidence of BC</li> </ul>	(38)
Breast	<ul style="list-style-type: none"> <li>Nested case-control study from trial containing 4,690 women with extensive mammographic density</li> <li>Examined whether serial measures of serum lipids and lipoproteins were associated with risk of BC</li> <li>Measured lipids in an average of 4.2 blood samples for 279 invasive breast cancer case subjects and 558 matched control subjects</li> </ul>	<ul style="list-style-type: none"> <li>HDL-C and apoA-I were positively associated with BC risk only when HRT was not used</li> </ul>	(60)
Endometrial	<ul style="list-style-type: none"> <li>Case-control study nested within the European Prospective Investigation into Cancer and Nutrition (EPIC)</li> <li>Examined the relation between prediagnostic plasma lipids, lipoproteins, and glucose, metabolic syndrome, and EC risk in 284 women with EC and 546 matched controls</li> </ul>	<ul style="list-style-type: none"> <li>HDL-C levels were inversely correlated with the risk of developing EC</li> <li>Metabolic abnormalities and obesity may act synergistically to increase risk of developing EC</li> </ul>	(39)
Prostate	<ul style="list-style-type: none"> <li>Examined the association between serum lipids and prostate cancer risk</li> <li>A cohort (<math>n = 69,735</math>) of all men aged 35 years or older were selected from the Apolipoprotein MOrtality RiSk (AMORIS),</li> <li>Levels of TG, TC, glucose, LDL-C, HDL-C, ApoB, and ApoA-I were measured at baseline, was database</li> <li>2,008 men developed prostate cancer</li> </ul>	<ul style="list-style-type: none"> <li>ApoA-I and HDL levels were inversely associated with prostate cancer risk</li> <li>Low HDL and ApoA-I as well as increased lipid ratios are related to increased risk of prostate cancer</li> <li>No association between ApoB, LDL, and non-HDL with prostate cancer risk</li> </ul>	(43)

ApoA-I, apolipoprotein A-I; ApoA-II, apolipoprotein A-II; ApoB, apolipoprotein B; BC, breast cancer; CA125, cancer antigen 125; CTAPIII, connective tissue activating protein III; CTC, circulating tumor cells; DFS, disease-free survival; DMFS, distant-metastasis-free survival; EC, endometrial cancer; HDL-C, High-density lipoprotein cholesterol; IMRT, intensity-modulated radiation therapy; ITIH4, inter-trypsin inhibitor heavy chain H4; LDL-C, low-density lipoprotein cholesterol; OC, ovarian cancer; OS, overall survival; PCa, pancreatic cancer; SELDI-TOF-MS, surface-enhanced laser desorption/ionization time-of-flight mass spectrometry; TC, total cholesterol; TF, transferrin; TG, triglycerides; TT, truncated transthyretin; TTR, transthyretin; VLDL-C, very low-density lipoprotein cholesterol.

the particles during sample preparation (61). In addition other confounding factors such as lifestyle factors, co-morbidities, and physiological factors (i.e., pre- vs. post-menopausal women), all contributed to heterogeneity of the results since most of the analyses were done retrospectively using the existing body of publicly available clinical trial data. On the other hand, there are studies describing positive correlations between HDL-C and cancer risk, namely in breast cancers (60). However, given the high heterogeneity in HDL proteome, lipidome, and subclass distribution between patients in different disease settings, it is reasonable that such variability exists between studies. While the verdict is still out on the utility of HDL-C and ApoA-I as predictive biomarkers in cancers, there is clearly a role for HDL in this complex disease which will be discussed in more detail to follow.

## Mechanism

Whether decreased levels of HDL-C are a causal or consequential factor to cancer progression is yet to be elucidated, however we are logically drawn to the latter. It is known that cancer cells, in particular prostate, adrenal, and breast cancer cells, highly express the SR-BI on their plasma membrane (62–64). Because of their high-demand for cholesterol, cancer cell upregulation of SR-BI is likely a survival mechanism to increase HDL-C recruitment and, thus, increase cholesterol uptake needed for proliferation and hormone production while consequently decreasing circulating HDL-C. That being said, this argument could also be used to explain why, in some reports, HDL-C is associated with an increased risk of cancer, as it continues to provide additional cholesterol to and fuel the growth of the tumor. Regardless, we can take away several key points from these findings: (i) SR-BI is overexpressed in cancer cells, (ii) HDL-C levels are significantly affected by the presence and development of cancer, and (iii) the high affinity between SR-BI and HDL facilitates the transport of cholesterol to/from HDL and the cancer cell. In addition, HDL is known to have potent antioxidant activity and both endogenous and reconstituted HDL particles were shown to inhibit oxidative-stress induced proliferation of pancreatic cells *in vitro* (65). And although the details of the epidemiology can be disputed, there are clear opportunities for therapeutic intervention by utilizing the HDL/SR-BI axis, of which will be discussed below.

## SYNTHETIC HDL PRODUCTS

As previously mentioned, the main focus of HDL research over the past several decades has been surrounding its role in cardiovascular disease. Because of its role in facilitating RCT, several “HDL mimetics” have been developed and tested clinically in humans for their ability to reduce the burden of atherosclerosis and number of events following an acute coronary event (66–69). These HDL-mimicking particles, termed reconstituted HDL (rHDL) or synthetic HDL (sHDL), are cholesterol-free HDL particles prepared from plasma purified or recombinantly expressed ApoA-I or short synthetic ApoA-I mimetic peptides complexed with phospholipids. Since they

lack cholesterol, these “empty” particles are highly effective in effluxing cholesterol from lipid-laden cells both *in vitro* and *in vivo* (9, 70, 71). In addition to their augmented efflux capacity, these particles offer a natural ability to target SR-BI-expressing cells. When combined, the ability of rHDL/sHDL to deplete cellular cholesterol, target SR-BI expressing cells, along with the biocompatibility of the individual components and proven clinical safety make the application of sHDL for cancer therapy increasingly attractive.

## Clinically Tested sHDL Products

The concept of utilizing sHDL and ApoA-I mimetic peptides as a cholesterol depletion therapy has been around for decades, but focused primarily in the context of cardiovascular diseases. In fact, several sHDL therapies have been developed and tested in various stages of human clinical trials (66, 69, 72). The purpose of such sHDL infusion therapies was to efflux cholesterol and reduce plaque size and vulnerability following an initial coronary event, in order to decrease the occurrence of secondary events. Early sHDL clinical trials utilized lipid-free ApoA-I protein or mimetic peptides, such as ApoA-I milano, D-4F, and L-4F, however it was shown that the naked proteins and peptides themselves had a very short plasma half-life, and their pharmacological effect suffered as a consequence (73, 74). Formulation of peptide or full-length ApoA-I protein with phospholipid, forming sHDL, was shown to markedly improve plasma half-life and thus its overall therapeutic effect (75). Moreover, studies have shown that the phospholipid component of sHDL therapies is a driving determinant of the overall pharmacokinetic and pharmacodynamic effect (71).

Measurable improvements in the pharmacokinetic and pharmacodynamic effects of sHDL therapies has led to their progression from bench to bedside in both early and late stage clinical trials. Such sHDL products include peptide-based sHDLs, including ETC-642 (22A peptide/dipalmitoylphosphatidylcholine/sphingomyelin), and ApoA-I protein based sHDLs, including ETC-216 (recombinant ApoA-I/palmitoylphosphatidylcholine) and CER-001 (recombinant ApoA-I/sphingomyelin/dipalmitoylphosphatidylglycerol), among others. These products were all shown to be safe at high doses of up to 100 mg/kg in humans and possess potent cholesterol efflux abilities (76, 77). More recently CSL-112, reconstituted ApoA-I/soybean phosphatidylcholine, has advanced to a 17,000 patient Phase III clinical trial after showing promising ability to reduce atheroma burden and decrease secondary coronary events in earlier trials (78–80). Given their proven clinical safety and ability to facilitate cholesterol removal, sHDL products could be easily translated for use as cholesterol depleting therapies in cancer.

## sHDL FOR CANCER THERAPY

### Cholesterol Depletion

Given the dependence of endocrine cancers on cholesterol, cholesterol-targeting therapies have gained increasing attention.

**TABLE 2 |** Experimental studies utilizing HDL for endocrine cancer therapy.

Cancer	Treatment	Model	Major findings	References
Ovarian	<ul style="list-style-type: none"> <li>• L-4F peptide or sc-4F ctrl</li> <li>- 10 mg/kg/day S.Q. for 5 wks, starting either the day of ID8 cell injection or 2 wks post-ID8 injection</li> <li>• L-5F peptide</li> <li>- 10 mg/kg/day S.Q. for 5 wks (for S.Q. tumors) or 9 wks (for I.P. tumors)</li> <li>• Compared to buffer treated control mice</li> <li>• D-4F peptide</li> <li>- 300 µg/mL (129.8 µM) in drinking water, starting immediately post-ID8 injection</li> <li>- Compared to normal drinking water</li> </ul>	<ul style="list-style-type: none"> <li>• Female C57BL/6/J mice, 9 wk old</li> <li>• ID8 cells given:</li> <li>- S.Q. (5 wk flank tumor model)</li> <li>- I.P. (9 wk tumor model)</li> </ul>	<ul style="list-style-type: none"> <li>• L-4F:</li> <li>- Smaller flank tumor volumes when given both immediately following or 2 wks post-ID8 injection (5 wk S.Q. tumor model)</li> <li>• L-5F:</li> <li>- Flank tumor size decreased (5 wk S.Q. tumor model)</li> <li>- Number of tumor nodules decreased (9 wk I.P. tumor model)</li> <li>• D-4F:</li> <li>- Smaller flank tumor volume (5 wk S.Q. tumor model)</li> <li>- Fewer number of tumor nodules (9 wk I.P. tumor model)</li> </ul>	(86)
Ovarian	<ul style="list-style-type: none"> <li>• L-5F peptide</li> <li>- 10 mg/kg/day S.Q. for 5 wks, starting immediately after ID8 cell injections</li> </ul>	<ul style="list-style-type: none"> <li>• Female C57BL/6 mice</li> <li>• ID8 cells injected S.Q.</li> </ul>	<ul style="list-style-type: none"> <li>• Decreased the number of perfused vessels within tumors</li> <li>• Decreased size of total vessels within tumor</li> <li>• Decreased VEGF levels in both serum and tumor tissue</li> </ul>	(87)
Ovarian	<ul style="list-style-type: none"> <li>• L-4F peptide</li> <li>- 10 mg/kg/day S.Q. for 3 wks, starting 2 weeks post-ID8 injection</li> <li>- Compared to sc-4F peptide treated mice</li> </ul>	<ul style="list-style-type: none"> <li>• Female C57BL/6 mice, 9 wk old</li> <li>• ID8 cells injected S.Q.</li> </ul>	<ul style="list-style-type: none"> <li>• Decreased expression and activity of HIF-1α in tumors</li> <li>• Reduced the number of vessels and overall angiogenesis within tumors</li> </ul>	(88)
Breast	<ul style="list-style-type: none"> <li>• L-4F peptide</li> <li>• 10 mg/kg S.Q. daily from weaning to 45 days, and 3x per wk until 19 wks of age</li> </ul>	<ul style="list-style-type: none"> <li>• Mammary PyMT transgenic mice</li> </ul>	<ul style="list-style-type: none"> <li>• Significantly increased tumor latency and inhibited tumor development</li> <li>• Decreased plasma levels of oxLDL</li> </ul>	(89)
Pancreatic	<ul style="list-style-type: none"> <li>• L-4F peptide</li> <li>- 10 mg/kg/day I.P. for 1 week, starting immediately post-H7 injection</li> <li>- Compared to sc-4F peptide treated mice</li> </ul>	<ul style="list-style-type: none"> <li>• Female C57BL/6 mice, 6–8 w/o</li> <li>• H7 cells injected directly into pancreas</li> </ul>	<ul style="list-style-type: none"> <li>• Reduced tumor size and weight</li> <li>• Reduced number of inflammatory tumor infiltrating cells, including Th17 and Th1 lymphocytes</li> <li>• Decreased mRNA expression of inflammatory cytokines in tumors</li> <li>• Decreased % of M2 macrophage polarization in tumors</li> </ul>	(90)

D-4F, D-amino acid version of L-4F; I.P., intraperitoneal; L-4F, DWKAFYDKVAEKFEAF; L-5F, DWLKAIFYDKVFEKFEFF; oxLDL, oxidized low-density lipoprotein; PyMT, mammary tumor virus-polyoma middle T-antigen; sc-4F, scrambled-4F peptide; S.Q., subcutaneous; Th1, T-helper cell 1; Th17, T-helper cell 17; VEGF, vascular endothelial growth factor; wk, week.

One approach is to directly deplete cholesterol from cells using cholesterol scavenging therapies. In addition to cholesterol being essential for the formation of new membranes during cell division, it is also vital for the formation of lipid rafts in the plasma membrane. These lipid rafts are rich in cholesterol and sphingolipids and house many proteins and transporters involved in key signaling pathways, including the Akt signaling pathway implicated in the migration, proliferation, and survival of cancer cells (81). By depleting cholesterol from cells, lipid rafts are disrupted and the proteins they house internalized, drastically reducing the cell's ability to carry out its functions and often triggering cell death (4). In cancer cell lines, treatment with cyclodextrins induced marked cell death, and that cells with a higher abundance of lipid rafts were more susceptible to such treatments (82–84). More recently, Taylor et al. showed that HAC15 adrenal carcinoma cells treated with ETC-642, a clinically tested sHDL, displayed

marked reduction in cellular cholesterol levels in addition to inhibition of aldosterone, cortisol, and androstenedione production (85). Thus, the application of cholesterol-depleting therapies, namely sHDL, for endocrine cancer deserves further investigation.

## sHDL Peptides

Several recent studies have investigated the use of HDL-mimetics, including sHDL, ApoA-I protein, and ApoA-I mimetic peptides, for cancer treatment, outlined in **Table 2**. In addition, treatment of cells with both sHDL and chemotherapeutic drugs was able to reduce the overall effective dose (91). Other studies utilizing ApoA-I protein or mimetic peptides L-4F, L-5F, and D-4F have shown that treatment of tumor-bearing mice with either protein or peptide can reduce both tumor volume and angiogenesis in tumor tissues when compared to control mice (87–90, 92–94). For example, in a mouse model of ovarian cancer, Gao et al.

show that L-4F peptide, when administered subcutaneously at 10 mg/kg/day for 3 weeks, could reduce overall angiogenesis and vessel number within the tumor tissue, which was connected to a decrease in expression levels of hypoxia inducible factor-1 $\alpha$  (HIF-1 $\alpha$ ) (88). In a similar study, they also show that L-5F peptide could exert similar anti-angiogenesis effects and led to decreased levels of serum vascular endothelial growth factor (VEGF) (87). In a separate study utilizing a similar ovarian cancer mouse model, Su et. al. demonstrated that both L-4F and L-5F peptides could decrease the overall volume of tumors in both flank and intraperitoneal tumors when given 10 mg/kg/day over the course of 5 or 9 weeks, respectively (86). They postulate that the antitumorigenic effect could be related to peptides' abilities to reduce circulating levels of LPA, and they were found to have significantly greater binding affinity for LPA when compared to full length ApoA-I protein. In a study by Peng et. al. L-4F peptide given at 10 mg/kg/day for 1 week was able to not only reduce size and weight of H7 pancreatic tumors in mice, but also significantly reduce several markers of inflammation within the tissue as well (90).

While the above studies also included extensive screening of ApoA-I and mimetic peptides for viability and anti-proliferative activity in a broad range of cancer cell lines *in vitro*, there are also reports describing the ability of HDL to induce proliferation, migration, and survival in cancer cell cultures (32, 33, 95, 96). Consistent with previously mentioned clinical findings showing a positive association between HDL-C and cancer risk, these studies support the notion that HDL-C may promote the progression of cancer by supplying the tumor cells with their increasing demand for cholesterol. However, a distinction should be made between the epidemiology of HDL and cancer and the utility of HDL in cancer treatment: namely, that the use of HDL in cancer therapy referred to in this review involves the administration of "empty" cholesterol-free particles. These particles are the nascent, discoidal HDL particles with high cholesterol efflux activity as proven both in basic and clinical research. Of course, studies utilizing plasma purified HDLs should be considered differently. Plasma HDLs contain a variety of different components, including signaling lipids responsible for many of HDLs pro-angiogenic and Akt-activating properties (22, 97), and namely cholesterol capable of being delivered to cells (98, 99). While such studies are integral to understanding the role of endogenous HDL in cancer pathogenesis, they should not be confused with therapeutic implications utilizing sHDL or mimetic peptides with a defined molecular makeup and superior cholesterol efflux capacity.

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## Targeted Drug Delivery

Given the very poor solubility of many chemotherapeutic drugs, the hydrophobic lipid core of HDL presents an attractive environment and alternative strategy for delivery and formulation of this class of drugs. Not only is it possible to lower the overall dose of drug given by improving its solubility, but the SR-BI targeting ability of these sHDL nanoparticles affords the additional benefit of site-specific, cytosolic drug delivery to SR-BI over-expressing tumor cells while subsequently reducing systemic toxicity (72, 94, 100). Others have, with varying success, shown anti-tumorigenic by introducing HDL surface modifications to augment the targeting capacity and to extend particle half-life (101). The use of HDL-mimetics for targeted drug delivery has been extensively reviewed elsewhere (72, 102) and is beyond the scope of this review, however, its importance and growing relevance warrant mentioning.

## SUMMARY AND PERSPECTIVE

Decades of epidemiological evidence suggests that, notably -C, plays a role in the incidence and progression of cancer. Whether or not this role is causal or consequential, or whether the risk association is positive or negative under specific conditions is still left for debate. Despite, we know from years of clinical and basic cardiovascular research that is an intimate player in the RCT process and has specific and potent cholesterol efflux ability both *in vitro* and *in vivo*. We also know that cholesterol is a vital resource for cancer cells, which require a constant supply to maintain and facilitate their rapid proliferation and overall survival. Endocrine cancers, in particular, are at an increased demand for cholesterol given their additional need for steroid production making them even more susceptible to cholesterol depletion interventions and targeting by due to upregulation of SR-BI.

## AUTHOR CONTRIBUTIONS

All authors listed have made a substantial, direct and intellectual contribution to the work, and approved it for publication.

## FUNDING

This publication was made possible by Grant Number R01GM113832 (to AS and X-AL) from NIGMS/NIH and NIH T32-HL125242 (EM). Its contents are solely the responsibility of the authors and do not necessarily represent the official views of the NIGMS or NIH.

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**Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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# Cholesterol and Its Metabolites in Tumor Growth: Therapeutic Potential of Statins in Cancer Treatment

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### Specialty section:

This article was submitted to  
Cancer Endocrinology,  
a section of the journal  
Frontiers in Endocrinology

**Received:** 19 September 2018

**Accepted:** 21 December 2018

**Published:** 21 January 2019

### Citation:

Chimento A, Casaburi I, Avena P, Trotta F, De Luca A, Rago V, Pezzi V and Sirianni R (2019) Cholesterol and Its Metabolites in Tumor Growth: Therapeutic Potential of Statins in Cancer Treatment. *Front. Endocrinol.* 9:807. doi: 10.3389/fendo.2018.00807

Cholesterol is essential for cell function and viability. It is a component of the plasma membrane and lipid rafts and is a precursor for bile acids, steroid hormones, and Vitamin D. As a ligand for estrogen-related receptor alpha (ESRRα), cholesterol becomes a signaling molecule. Furthermore, cholesterol-derived oxysterols activate liver X receptors (LXRs) or estrogen receptors (ERs). Several studies performed in cancer cells reveal that cholesterol synthesis is enhanced compared to normal cells. Additionally, high serum cholesterol levels are associated with increased risk for many cancers, but thus far, clinical trials with 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) reductase inhibitors (statins) have had mixed results. Statins inhibit cholesterol synthesis within cells through the inhibition of HMG-CoA reductase, the rate-limiting enzyme in the mevalonate and cholesterol synthetic pathway. Many downstream products of mevalonate have a role in cell proliferation, since they are required for maintenance of membrane integrity; signaling, as some proteins to be active must undergo prenylation; protein synthesis, as isopentenyladenine is an essential substrate for the modification of certain tRNAs; and cell-cycle progression. In this review starting from recent acquired findings on the role that cholesterol and its metabolites fulfill in the contest of cancer cells, we discuss the results of studies focused to investigate the use of statins in order to prevent cancer growth and metastasis.

**Keywords:** cholesterol, statins, cancer treatment, lipid raft, oxysterols, steroids, vitamin D, ERRα

## INTRODUCTION

Cholesterol homeostasis is required for the normal growth of eukaryotic cells. Cholesterol is needed within cell membranes where it regulates membrane fluidity, signaling initiation, and cell adhesion to the extracellular matrix (1). In mammals, cholesterol is a precursor for bile acid and steroid hormone synthesis, cholesterol can be derived from food or synthesized *de novo* by specialized cells. The low-density lipoprotein (LDL) receptor (LDLR) is the primary pathway for removal of cholesterol from the circulation (2) and its activity is accurately controlled by intracellular cholesterol levels (3). The biosynthetic pathway of cholesterol is highly conserved, from yeast to humans. In the mitochondria, citrate, derived from the tricarboxylic acid (TCA) cycle, is converted to acetyl-coenzyme A (acetyl-CoA) beginning cholesterol synthesis. In the endoplasmic reticulum, acetyl-CoA is converted to lanosterol through a cascade of enzymatic reactions known as the mevalonate pathway. This series of reactions is regulated by a rate-limiting step catalyzed by 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase, which converts



HMG-CoA to mevalonate. Downstream products of mevalonate, include cholesterol, ubiquinone, dolichol, and the isoprenoids geranylgeranyl pyrophosphate (GGPP) and farnesyl pyrophosphate (FPP) that bind to several small GTP-binding proteins such as Ras and Rho. Protein prenylation facilitates protein translocation from the cytosol to the membrane, promoting protein-protein and protein-membrane interactions and regulating protein function (4).

Several studies reported that cholesterol plays critical roles in the progression of numerous cancers (5), suggesting how cholesterol accumulation represents another general feature of tumors. HMG-CoA reductase and LDL receptor activities are increased in proliferating cancer cells, causing a rise in cholesterol content and consumption (6, 7). Cholesterol synthesis is under feedback control (8, 9), which is operated at the level of mevalonic acid production (10–12). When exogenous cholesterol is not available, the synthesis of mevalonate is increased in order to maintain levels of cholesterol and isoprenoids. When exogenous cholesterol levels are elevated a negative feedback mechanism inhibits the synthesis of mevalonic acid (10–12), this is particularly true for the liver (9), but in some species (13) for all tissues, blocking the overall *de novo* synthesis of endogenous cholesterol. In malignant cells this feedback mechanism is lost (10).

Statins are cholesterol-lowering drugs, which inhibit the rate-limiting step of conversion of HMG-CoA to mevalonate (14). Statins can be differentiated into two types, based on their solubility: hydrophilic (pravastatin, rosuvastatin) and lipophilic (simvastatin, lovastatin, fluvastatin, atorvastatin) statins. Several reports propose a promising role for statins in cancer treatment (15). Observational studies have tried to evaluate the effect of statins on patients with several cancer types such as prostate (16), colorectal (17, 18), renal cell carcinoma (19), breast (20), ovarian (21), and lymphoma (22). Results are variable, with some studies suggesting longer survival, and others reporting no benefit. Epidemiological evidences are also variable, depending on the cancer particular type as well as on the statin class used (23). Several data suggest that lipophilic statins may be preferable over the hydrophilic ones as anticancer agents (24). Statins anticancer properties could be explained through their pleiotropic effects such as lowering protein prenylation (17), reducing tumor cell proliferation and migration (20, 25), inhibiting Ras signaling (26) inducing apoptosis through inactivation of Akt and down-regulation of mammalian target of rapamycin (mTOR) (27).

Statins can interfere with cholesterol activities, which include:

- signal molecule on membrane rafts;
- substrate for steroids, oxysterols and Vitamin D3 synthesis;
- ligand for estrogen-related receptor alpha (ERR $\alpha$ ).

In this review, we will discuss the results of studies focused on the use of statins to the purpose of interfering with cholesterol activities, in order to prevent cancer growth and metastasis.

## CHOLESTEROL AS SIGNAL MOLECULE ON MEMBRANE RAFTS

Cholesterol can act as a signaling molecule at the membrane rafts (28). It is well established that cholesterol-rich microdomains in the plasma membrane and lipid rafts constitute centers of organization for signal transduction and intracellular transport (29). Rafts are small functional areas of the plasma membrane, rich in sphingolipids and cholesterol. These regions are fluid but more ordered and tightly packed than the surrounding bilayer, because of saturated fatty acids. Rafts and related membrane microdomains, such as caveolae characterized by high caveolin-1 expression, have been proposed to play important roles in sorting of membrane molecules and in signal transduction in animal cells (30). Glycophosphatidylinositol-anchored (GPI-anchored) proteins; doubly acylated proteins, such as tyrosine kinases of the Src family, G $\alpha$  subunits of heterotrimeric G proteins, endothelial nitric oxide synthase (eNOS), and cholesterol-linked and palmitate-anchored proteins are examples of molecules that can be found at membrane rafts (31).

Growth factors signaling are often deregulated in cancer cells. Insulin-like growth factor-I (IGF-I) through its receptor (IGF1R) is one of the most potent natural activators of the phosphatidylinositol 3-kinase (PI3K) and its downstream target Akt, which participate in cell survival pathway. The PI3K/Akt pathway is compartmentalized within plasma membrane raft domains (32). Activated PI3K/Akt control of cell proliferation, apoptosis and tumorigenesis, and aberrant activation of PI3K/Akt pathway contributes to the development and invasiveness of cancer cells (33, 34).

Other studies suggest that, within lipid rafts localize both epidermal growth factor receptor (EGFR) and Human Epidermal growth factor Receptor 2 (HER2) and their signaling events are dependent on cholesterol content of the lipid-rafts (35). Once again, the disruption of the lipid rafts, via depletion of circulating cholesterol levels, interferes with the receptor activation, inhibiting cell growth and development (35–37).

Metastatic events are characterized by cell adhesion decrease and cell migration promotion. Integrins and cell surface glycoproteins such as CD44, have a central role in adhesion mechanisms. CD44 is an adhesion molecule associated with lipid rafts and expressed in several cancers (38, 39). It has been demonstrated that ligand-binding ability of CD44 to hyaluronan, is governed by its cholesterol-dependent localization to cell membrane microdomains (40).

Several cancer cell types, including breast and prostate, have higher membrane cholesterol levels and are richer in membrane rafts (probably as a result of cholesterol accumulation) than their normal counterparts. For this reason, cholesterol-depleting agents are more effective in inducing apoptosis on these cancer cells than on normal cells (41, 42). Rafts/caveolae are rich in various signaling molecules and they have been associated with a number of functions, including cell survival, proliferation, and migration (28, 43).

It has been reported that apoptotic pathways, both extrinsic (death receptor pathway) and intrinsic (mitochondrial), are

associated with lipid rafts because changes in cholesterol content within specific membrane regions regulate apoptotic signaling events (41, 44). Signalings from death receptors Fas receptor (FasR) and TNF-related apoptosis-inducing ligand (TRAIL) receptors 1 and 2 are strictly dependent on translocation into lipid rafts (44, 45). In fact, TRAIL- and Fas-mediated apoptosis is down-regulated by lowering membrane cholesterol in non-small cell lung carcinoma (46) and human Jurkat T leukemia cells (44).

Very recently, disruption of lipid rafts on breast cancer (BC) cell lines MDA-MB231 and MDA-MB468, using the cholesterol depleting agent methyl- $\beta$ -cyclodextrin, resulted in reduced proliferation and migration, induction of apoptosis evidenced by cell shrinkage, membrane blebbing, nuclear condensation, and chromatin cleavage (47). It was already demonstrated for BC, that lipid rafts disruption causes decreased migration and invasion downregulating caveolin-1 along with urokinase-type plasminogen activator receptor (uPAR) and matrix metalloproteinase 9 (MMP-9) (48). In general, proteins identified in cancer lipid rafts include those involved in endocytosis, Src signaling, cytoskeletal remodeling, chaperones, extracellular matrix (ECM) remodeling (49).

## Statins and Lipid Rafts

Based on the importance of cholesterol at the raft/caveola, cholesterol depletion from the plasma membrane would disrupt intracellular signaling triggered by cell surface receptors (50). Statins lower cellular cholesterol content and thus are useful in the analysis of lipid-raft function. However, the effect on raft/caveola formation in cancer cells after statins treatment are not completely defined.

Menter et al. (51), evidenced that simvastatin inhibited the growth of several tumor cell lines with a time-dependent behavior. A significant reduction in cellular cholesterol level were observed after simvastatin treatment, starting at 24 h and up to 72 h. During this time frame, authors observed a reduction in cholesterol content at membrane rafts, caveolin-1 phosphorylation inhibition, disruption of caveolae and loss of membrane integrity. However, cholesterol depletion affected membrane signaling also in caveolin-negative cells (52). Specifically, using the prostate cancer (PCa) cells LNCaP, which do not express caveolin, simvastatin lowered raft cholesterol content, inhibited Akt signaling and induced apoptosis. In addition, using the same cells grown as xenografts, authors demonstrated that elevation of circulating cholesterol using a cholesterol enriched diet, promoted tumor growth and survival, as a consequence of activated Akt signaling via cholesterol-rich lipid rafts (52).

In another study, four head-and-neck squamous cell carcinomas (HNSCCs), four cervical carcinomas, five non small cell lung cancers (NSCLCs), four colon carcinomas, the epidermoid carcinoma cell line A431, and the breast adenocarcinoma MCF-7 were treated with lipophilic lovastatin, which inhibited EGF-induced EGFR autophosphorylation and its downstream signaling cascades (53).

Similarly, another hydrophobic statin, simvastatin caused in A431 cell line anoikis-like apoptosis, characterized by decreased

raft levels, Bcl-xL down-regulation, caspase-3 activation, and Akt inactivation (41).

In PC-3 cells simvastatin treatment down-regulated IGF1R expression (54) and inhibited both basal and IGF-1-induced ERK and Akt activation (55). Raft modulating agents are more effective in cells containing a higher content of lipid rafts. In fact, breast (MCF-7, MDA-MB231) and prostate (PC-3, LNCaP) cancer cell lines were more sensitive to cholesterol depletion-induced cell death than normal breast and prostate cell lines (MCF-10A and PZ-HPV7, respectively) (41).

Garnett et al. examined the effects of M $\beta$ CD and the hydrophilic paravastatin on cholesterol-rich rafts and caveolae and on gene transcription in MDA-MB231 and CaLu-1, lung adenocarcinoma. Both treatments caused a downregulation of genes involved in signal transduction, chemokine and anti-apoptotic pathways. Pravastatin increased expression of caveolin-1, but caveolae density was decreased, because of caveolin-1 inability to properly complex with cholesterol in an altered sterol environment. Similarly, M $\beta$ CD caused an increase in caveolin-1 expression and reduced both rafts and caveolae, however, it had less effects on gene transcription. Indeed, signaling are more profoundly affected by statins than by the cholesterol-sequestering drug, indicating that not only cholesterol but also some intermediates of cholesterol synthesis downstream of mevalonate, play an important role in signaling pathways at the caveolae (56).

It has been reported that primary cells, HEL, SET-2, and UKE-1, derived from myeloproliferative neoplasms (MPNs) patients require mutated Janus kinase 2 (JAK2), responsible for increased growth signaling (57, 58). Simvastatin disrupts lipid raft and has a negative effect on mutated JAK2-dependent signaling. More specifically, in MPNs cells, simvastatin, lovastatin and atorvastatin inhibited mutated JAK2 localization to lipid rafts reducing cell viability, inducing apoptosis and inhibiting colony formation (59). Colony formation assay is considered a 3D cell culture assay where cells grow independently of a substrate (it is also known as anchorage-independent growth). This assay is particularly useful when studying long-term effects of drugs on anchorage-independent growth of cancer cells. Colony formation evaluates the ability of tumor cells, escaped from the primary tumor site, to exit the blood flow and initiate the post-intravasation phases of metastasis. CD44, as adhesion molecule, plays a central role in the progression of metastasis. The modulation of cholesterol either by statin or M $\beta$ CD causes dissociation of CD44 from the lipid rafts (40) suggesting that membrane cholesterol may impact metastasis formation. Similar to the results on CD44 cholesterol depletion triggers the shedding of several molecules involved in cancer cell adhesion, including CD30 (60), L1-CAM (61) and collagen types XVII (62) and XXIII (63).

Activity of Ras-Related C3 Botulinum Toxin Substrate 1 (Rac1), a member of the Rho family of Small GTPase, is dependent upon its localization in membrane rafts and its activation is correlated with invasion and metastasis. Cholangiocarcinoma cells treated with simvastatin lose Rac1 rafts localization, because of decreased total cellular cholesterol and disruption of membrane rafts. In normal human cholangiocytes,

simvastatin reduced cholesterol level, but did not affect Rac1 localization. In addition, simvastatin inhibited cell proliferation but, differently from cancer cells, it did not lead to apoptosis (64).

All these data unequivocally suggest that statins have a direct impact on membrane rafts, reducing signaling transduction and adhesion mechanisms in several cancer cell types, thus interfering with cell proliferation and metastasis.

## CHOLESTEROL AS SUBSTRATE FOR STEROIDS AND OXYSTEROLS SYNTHESIS

Steroid hormones are synthesized from cholesterol in gonads, adrenal cells and placenta (65). The *de novo* synthesis of some steroid hormones occurs also in the nervous system (66, 67), in cardiac tissue (68) and other peripheral sites (69).

Based on their physiological function, steroid hormones are divided into five groups: mineralocorticoids, which act on the kidney to retain sodium; glucocorticoids, involved in the regulation of glucose metabolism; estrogens, which induce female secondary sexual traits; progestins, which are essential for reproduction; and androgens, which induce male secondary sexual characteristics. These classes of hormones contain the cyclopenta-phenanthrene nucleus and arise from reactions catalyzed by enzymes that belong mainly to the family of cytochrome P450 (CYP). They bind to specific steroid hormone receptors, which act as transcription factors. The active hormone/receptor complexes regulate transcription of distinct set of genes in a tissue-specific manner.

Oxysterols represent 27 carbon-atom molecules derived from cholesterol oxidization through enzymatic processes, or by-products of the cholesterol biosynthetic pathway. Considering the shorter biologic half-life when compared to cholesterol, oxysterols can be considered a way to route cholesterol for catabolism. Specific CYP, localized within the mitochondria or endoplasmic reticulum, are responsible for oxysterol synthesis (70, 71). Among them, the most abundant in human serum are 27, 24(S), 7 $\alpha$ , and 4 $\beta$  hydroxycholesterol (HC). The 24(S)HC is synthesized by cholesterol hydroxylase encoded by CYP46A1 in neurons of the central nervous system (72). 7 $\alpha$  and 27HC are synthesized in the liver by CYP7A1 and CYP27A1, and represent, respectively, the first intermediates of classic and acidic bile acid synthetic pathways (73). However, 27HC and its synthesizing enzyme CYP27A1 are found also in other cell types (74). Lastly, 4 $\beta$ HC is generated by CYP3A4, a hepatic drug metabolizing enzyme.

Oxysterols act as ligands of Liver X Receptors (LXR)  $\alpha$  (NR1H3) and  $\beta$  (NR1H2) (75) to regulate transcription of specific genes. LXR $\alpha$  is expressed primarily in liver, intestine, adipose tissue and macrophages (76), and adrenal (77), whereas LXR $\beta$  is expressed in many cell types (78).

LXR $\alpha$  is also involved in the regulation of the adenosine triphosphate-binding cassette (ABC) proteins A1 and G1, cholesterol transporters involved in the flux of cholesterol from enterocytes and macrophages, respectively (79–82). LXRs also seem to have a role in the regulation of human cholesterol ester transfer protein (CETP), which translocates cholesterol esters

between lipoproteins (83). Either steroid hormones or oxysterols activate proliferative and metastatic pathways in cancer cells.

## Steroid Dependent-Cancer Growth and Progression

It is well known that estrogens exert their biological effects interacting with two members of the nuclear receptor (NR) family, estrogen receptor  $\alpha$  (ER $\alpha$ ) or estrogen receptor  $\beta$  (ER $\beta$ ) (84) and with a G-protein coupled receptor namely GPER (85). All three receptors can act at the cell membrane to activate signaling transduction pathways that ultimately regulate gene expression (rapid signaling). Additionally, ER $\alpha$  and ER $\beta$  can bind promoter regions of target genes, modulating their transcription (nuclear action). They directly bind DNA at estrogen response elements (EREs) located within promoters of estrogen-regulated target genes. Alternatively, they indirectly bind DNA through the interaction with transcription factors (TFs) that directly bind gene promoters. These TFs are stimulating protein 1 (Sp1) (86), activator protein (AP)-1 (87), nuclear factor- $\kappa$ B (NF- $\kappa$ B) (88). The oncogenic role of estrogens is well characterized in carcinomas of hormone-sensitive tissues including breast, prostate, endometrium and ovary, as well as in non-classical estrogen target tissues such as, adrenal, colon, and lung (89).

Genes involved in cell survival and proliferation and regulated by ERs, through direct or indirect binding to DNA, include myelocytomatosis viral oncogene homolog (MYC), cyclin D1 (CCND1), member RAS oncogene family 17 (RAB17), eukaryotic translation initiation factor 3 subunit A (EIF3A), and tumor protein D52-like 1 (TPD52L1) (90–92). Additionally, membrane ERs engage a functional crosstalk with growth factor receptors, including epidermal growth factor receptor (EGFR), insulin receptor (IR), insulin-like growth factor receptor (IGFR). Growth factor signaling can activate ER $\alpha$  in a ligand independent fashion through phosphorylation, and at the same time, estrogens can regulate IGF signaling (93). Treatment of ER $\alpha$  positive BC with selective estrogen receptor modulators (SERMs) such as tamoxifen, often leads to resistance. EGFR and/or IGFR are critical for the resistance to endocrine therapies (94). Additionally, transactivation of EGFR has been observed in MCF7 breast cancer cells via tamoxifen-dependent activation of GPER (95). The use of tamoxifen on patients with initial GPER-positive tumors increased GPER protein expression, and survival of these BC patients was markedly reduced (95).

Currently, a hot topic in the field of BC research is the definition of the role of androgens and the androgen receptor (AR), with studies revealing both tumor promotion and inhibition (96–98). Expression of AR is associated with favorable prognosis depending on the BC subtype and on whether ER is expressed or not (99, 100). Recently, dihydroxytestosterone (DHT) bound to AR has been shown to directly mediate epigenetic modifications of the chromatin, regulating expression of target genes (101). AR binds to ARE on target genes and, with the help of Lysine-specific demethylase 1A (LSD1), regulates histone modifications, demethylation by LSD1 at H3K4 of the E-cadherin promoter represses gene expression; similarly, LSD1 demethylation at H3K9 activates vimentin gene expression.

Importantly, LSD1 is crucial for epithelial to mesenchymal transition (EMT) induction in several cancer cells (102, 103).

Prostate cancer relies on distinct proliferative pathways, including the PI3K and RAS/RAF pathways downstream of membrane AR activation; dysregulation of these pathways in both early and late stage prostate cancer was demonstrated through genomic profiling (104). In prostate cancer, androgens, testosterone (T), and DHT stimulate proliferation and inhibit apoptosis. Androgen ablation using anti-androgens such as bicalutamide favors cancer regression. This event is related to a lower rate of cell proliferation and to an increased rate of cell death (105). However, many patients do not respond to this therapy and die of recurrent androgen-independent prostate cancer (AIPC), characterized by a high metastatic rate. A crosstalk between androgen-sensitive PCa cells, androgen-independent PCa cells, and PCa-derived stromal cells has been very recently highlighted (106). Adrenal dehydroepiandrosterone (DHEA) is metabolized to DHT in androgen-independent PCa cells (AR negative cells, AR-) as well as in stromal cells. DHT is able to activate AR in androgen sensitive PCa cells (AR positive cells, AR+). Crosstalk among these cells may increase the migration and invasion potential of androgen independent PCa cells via EMT, evidenced by induction of N-cadherin, Snail and vimentin (106). GPER seems to have a role in tumor growth and progression of triple negative breast cancers (TNBC), tumors that lack expression for ER $\alpha$ , progesterone receptor (PR) and HER2 (107, 108). AR directly binds to GPER promoter and treatment with DHT decreases its transcription, possibly by competitively blocking the binding of positive regulators of GPER transcription (109). This reduced GPER expression following DHT treatment, is associated with increased tumor growth (110). Indeed, GPER role in TNBC is still controversial, with some studies indicating GPER involvement in increased tumor growth and worse overall survival (OS) (108) and some others a positive correlation between GPER and OS (111).

Estrogens exert carcinogenic effects on the prostatic epithelium. Combination of estradiol with low-doses of testosterone increased the incidence of prostate carcinomas in a rat model of PCa (112). Similar effects were observed in a mouse model of PCa. When ER $\alpha$  was knocked out in those mice, chronic treatment with testosterone combined with estradiol was unable to induce PCa. Additionally, mice had reduced PCa incidence when aromatase was knocked out. All together these data indicate that autocrine-produced estradiol working through ER $\alpha$  is determinant in PCa development (113). In agreement with animal studies, in the human prostatic epithelium ER $\alpha$  is overexpressed during the malignant transformation, supporting its role as an oncogene (114). On the contrary, ER $\beta$  is considered a tumor suppressor; in fact, its expression is decreased or lost in about 40% of PCa (115).

Inhibitory functions of GPER activation in prostate cancers has been demonstrated both *in vitro* and *in vivo* (116).

## Statins and Steroid Production

Statins, by decreasing cholesterol synthesis, will also affect the production of steroid hormones. Most steroid hormones are produced by the gonads and adrenal cortex from cholesterol,

which is uptaken from the circulating LDL and HDL (117, 118). Since steroidogenesis requires an efficient intracellular pool of cholesterol, by reducing its synthesis, statin therapy could affect steroid production. Cortisol is a steroid hormone produced by the adrenal gland, is mainly released at times of stress, but in normal conditions, its production has a circadian rhythm (119). The effects of statin treatment on cortisol synthesis or cortisol levels were evaluated in several studies, that, however, did not demonstrate any significant effect of statins on cortisol levels (120, 121). An increase in plasma cortisol concentrations was highlighted by a recent meta-analysis study of data from seven randomized controlled trials with various statins (122). In general, the study demonstrated a higher impact of lipophilic statins (atorvastatin, lovastatin, and simvastatin), when compared to hydrophilic statins (pravastatin and rosuvastatin) (123). The increase in cortisol after statin treatment might explain the previously demonstrated anti-inflammatory effects of these drugs. The precise mechanism underlying the rise in cortisol after statin use is not known. Studies evaluating the effect on hypothalamic-pituitary system or adrenal cortex itself should be performed to explain the mechanism activated by statins and responsible for the increase in cortisol levels. Based on the observation that only lipophilic statins, which have a greater non-hepatic distribution, affect cortisol levels, it can be speculated that statins have a direct effect on the adrenal gland. Enhancement of LDL-receptor expression, following the inhibition of adrenal HMG-CoA reductase, is responsible for increased cholesterol uptake allowing higher substrate availability for cortisol production. The effect of statins on the expression of steroidogenic enzymes involved in cortisol production is unknown.

A systematic review and meta-analysis of randomized controlled trials demonstrated that among 501 hypercholesterolemic men statins lowered testosterone; similarly, testosterone was reduced in a trial of 368 young women with polycystic ovary syndrome (PCOS) (124).

The direct effect of statins on HMG-CoA reductase in tumor cells is responsible for decreased substrate availability, lowering estrogens and androgens production that drive BC and PCa respectively. Recently, it has been found that statins and dehydroepiandrosterone sulfate (DHEAS) compete for the same transporter, SLCO2B1. Statin administration competitively reduces uptake of DHEAS and consequently tumor cell proliferation of PCa cell lines. The authors demonstrated that statin use at the time of androgen deprivation therapy initiation was associated with delayed tumor progression (125).

In physiological conditions, the prostate is not a steroidogenic site; but steroids, particularly testis-derived testosterone and DHT, regulate its function. In the context of a tumor, prostatic cells become capable of autonomous steroidogenesis (126). Evaluation of statin effects on the expression of steroidogenic enzymes in PC3 cells, demonstrated no effects on steroidogenic acute regulatory protein (StAR), cytochrome P450 family 11 subfamily A member 1 (CYP11A1), cytochrome P450 family 17 subfamily A member 1 (CYP17A1), hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 (HSD3B2),



steroid 5  $\alpha$ -reductase 2 (SRD5A2), and aldo-keto reductase family 1 member C2 (AKR1C2). Conversely, the expression of 17 $\beta$ -hydroxysteroid dehydrogenase type 5 (AKR1C3) was increased and 3 $\beta$ -hydroxysteroid dehydrogenase 1 (HSD3B1) was decreased. These changes in gene expression are responsible for the increase in DHT and T observed following simvastatin treatment (55).

All these studies suggest that steroidogenic tissues are potential sites for statins effect. On the adrenal gland there is no clear modulation of cortisol production, with only lipophilic statins having a direct effect on the adrenal and increasing cortisol synthesis. On the testis and PCOS statins reduce T production. In the context of tumors, there are discording data, reporting both decrease and increase in T production.

## Oxysterols Dependent-Cancer Growth and Progression

Epidemiological studies evidenced that high levels of dietary cholesterol would increase the risk of BC in postmenopausal women and the risk of cancers of the stomach, colon, rectum, pancreas, lung, kidney, bladder and non-Hodgkin lymphoma (127). This is probably due to increased oxysterol production which parallels hypercholesterolemia. Elevated concentrations of oxysterols have been associated with colon (128), lung (129), breast (130, 131), skin (132), prostate (133), and bile duct (134) cancers.

Among oxysterols, 27HC is synthesized by CYP27A1, which has a broad substrate specificity and is present in most tissues and not only in the liver. However, 27HC is not an efficient activator of human LXRs (75), instead has been identified to bind ERs (135). 27HC, binds the ER $\alpha$  on epithelial cells of the mammary gland and promotes BC growth (130, 131), while binding LXR $\alpha$  increases metastasis in the MMTV-PyMT mouse model of BC. Similarly, 25HC enhances cell proliferation of a breast cancer cell line via the activation of ER $\alpha$  target genes (136). Both 25HC and 27HC increased the transcription of ER target genes in long-term estrogen deprived BC cell lines, suggesting that these oxysterols replace estrogens and activate ER-mediated gene expression. This event can explain a mechanism involved in the development of resistance to aromatase inhibitors (137). Interestingly, BC patients treated with aromatase inhibitors had significantly increased plasma levels of 27HC and moderately increased levels of 25HC after 28 days of treatment (138), supporting a potential role of 25HC and 27HC level in patient outcome.

More recently, effects of 27HC have been studied in both androgen-responsive LNCaP (AR+) cells and androgen-irresponsive PC3 (AR-) prostate cancer cells. Both cell types increased proliferation in response to the oxysterol binding to ER $\beta$  (133).

Oxysterol-binding protein (OSBP) (139) and OSBP-related proteins (ORPs) were originally isolated because of their ability to bind oxysterols, and later cholesterol (140). They comprise a 12-member mammalian gene family, characterized by a conserved OSBP homology domain (OHD) that binds

sterols and lipids, as well as the pleckstrin homology (PH) domain and two phenylalanines in an acidic tract (FFAT) motif that mediate interaction with organelle membranes. Upon binding to cholesterol, OSBP promotes ERK (extracellular signal regulated kinase) activity and hence cellular proliferation (140). Among them ORP4, also known as OSBP2, is expressed constitutively in brain, heart and testis, where is expressed as three variants, ORP4L, ORP4M, and ORP4S. Recently, cell growth regulatory activity has been evidenced for ORP4 (141). ORP4 binds sterols and phosphatidylinositol 4-phosphate (PI4P), and binding activity is required for ORP4 to promote cell proliferation and survival (141). Silencing of all ORP4 variants (ORP4L, ORP4M, ORP4S) in HEK293 and HeLa cells inhibited cell proliferation and promoted growth arrest without inducing cell death (141). ORP4L promoted proliferation of three different cervical carcinoma cell lines. (142). ORP4 has been identified as high-affinity cellular receptor for a group of natural products named ORPphilins that potentially inhibit the growth of human cancer cell lines (143). Administration of 25HC, a high-affinity ligand for ORP4, suppressed ORPphilin activity.

## Statins and Oxysterols Production

A recent phase II clinical trial aimed to investigate effects of statins on BC growth related to a reduction in 27HC levels. Patients were treated with 80 mg/day of atorvastatin to investigate the impact of statin treatment on serum 27HC and on tumor-specific CYP27A1 expression. Atorvastatin exhibited an anti-proliferative effect evidenced by changes in Ki67 index, which did not significantly correlate with changes in either serum 27HC or changes in intratumoral CYP27A1 protein expression. Collectively these data indicate that the anti-proliferative responses to statin treatment do not depend on 27HC reduction (144).

However, 27HC can still affect proliferation of BC resistant to aromatase inhibitors (AI). It has been suggested that AI-resistant tumors can still proliferate in response to 27HC, which similarly to E2 activates ERs (131). In fact, despite lower estrogen levels, aromatase inhibitors resistant tumors have extensive ER $\alpha$  binding to target genes. This is due to ER $\alpha$  activation by 27HC synthesized consequently to stable up-regulation of the entire cholesterol biosynthetic pathways, including genes involved in 27HC biosynthesis. Statins, reducing cholesterol, reduce 27HC, and decrease ER $\alpha$  binding to DNA, abrogating cell invasion (145).

Statin treatments do not seem to have any beneficial effect on the rate of appearance of prostate cancer, but definitively has an effect on the incidence of advanced PCa (146–148). Moreover, in the PC3 prostate cancer cell line, statins prevent the cell migration potential therefore reducing the formation of metastatic prostate colonies; however, the mechanism relies on inhibition of prenylated proteins, not on inhibition of oxysterol formation (149).

These observations suggest that the reduction of oxysterol production by statins treatment could have effect on specific tumors preventing cell migration and invasion.

## CHOLESTEROL AS SUBSTRATE FOR VITAMIN D SYNTHESIS

Cholesterol is the precursor molecule for vitamin D. There are two major isoforms of vitamin D: vitamin D<sub>2</sub> (ergocalciferol), and vitamin D<sub>3</sub> (cholecalciferol) (150, 151). UVB radiations are needed to synthesize Vitamin D<sub>2</sub> from ergosterol in plants, yeasts, and fungi and can be ingested from a diet containing food products of plant origin. In humans, vitamin D<sub>3</sub> is synthesized from 7-dehydrocholesterol by UVB radiation in the epidermis of skin and can also be derived from the diet containing food products of animal origin.

Vitamin D is a prohormone that undergoes two-step metabolism in the liver by CYP27A1 to produce the 25(OH)D (calcidiol) and in the kidney by CYP27B1 to produce the biologically active metabolite 1 $\alpha$ ,25(OH)<sub>2</sub>D<sub>3</sub> (calcitriol) which binds to the vitamin D receptor (VDR) regulating expression of diverse genes (152). CYP27B1 is also expressed in multiple extra-renal sites, including cancer cells (153). Thus, calcitriol can function in an endocrine (systemic) or autocrine manner when it is locally synthesized. Serum level of 30 to 50 ng/mL is normal for healthy people. Vitamin D deficiency and insufficiency is defined as serum 25-hydroxyvitamin D [25(OH)D] levels <20 and 21 to 29 ng/mL, respectively.

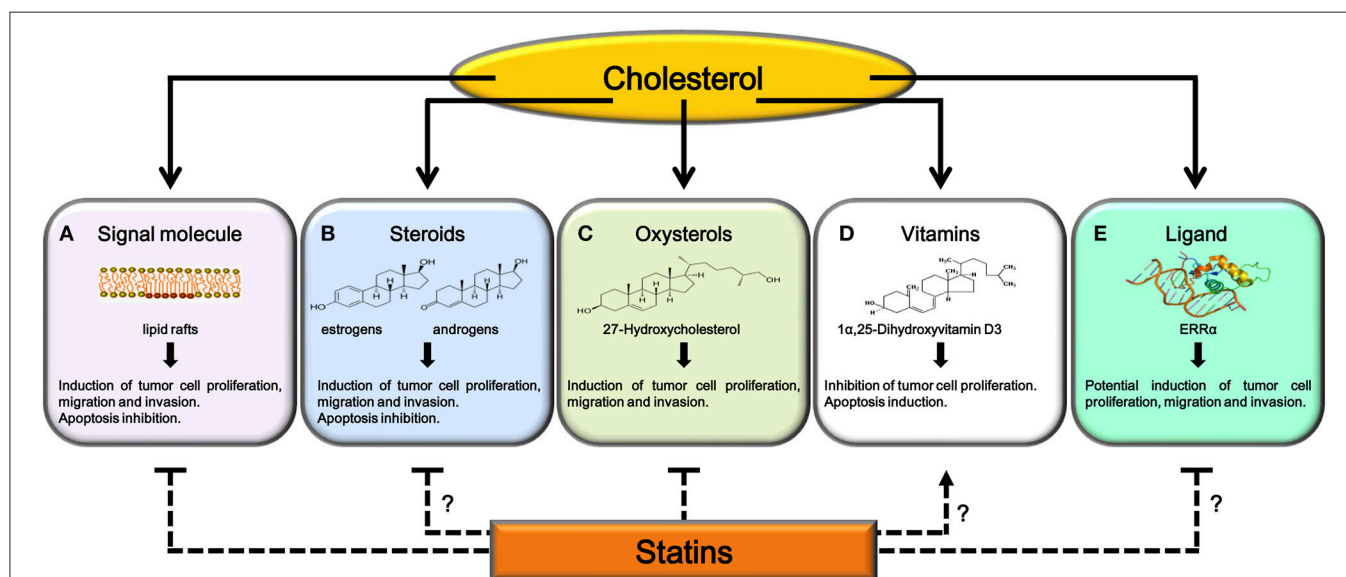
Recent studies have revealed that vitamin D can also be metabolized and activated through a CYP11A1-driven non-canonical metabolic pathway (154). The products of CYP11A1, such as 20(OH)D and its hydroxy-metabolites, produce differentiation, have anti-proliferative and anti-inflammatory effects in skin cells comparable or superior to calcitriol (155). Low vitamin D levels increase cancer risk, as evidenced by

epidemiological, preclinical and cellular studies (154, 156). In particular, many *in vitro* studies, performed in several malignant cell lines, showed that the anti-cancer activity of this molecule is related to the inhibition of proliferation and angiogenesis and induction of apoptosis (157).

Epidemiological studies showed that serum levels of 25(OH)D adversely correlate with prostate cancer risk (158). In men living at high latitude, as in Scandinavia, 25(OH)D blood serum levels are below 16 ng/mL and the incidence of prostate cancer is high (159). It was observed that 1 $\alpha$ ,25(OH)<sub>2</sub>D<sub>3</sub> inhibited proliferation and stimulated apoptosis of VDR-positive prostate cancer cells and, interestingly had an anti-inflammatory effect toward this subtype of prostate tumors (160).

In BC cells 1 $\alpha$ ,25(OH)<sub>2</sub>D<sub>3</sub> caused cell cycle arrest, by interfering with cyclin-dependent kinases activity (161). Additionally, apoptosis can be activated by reducing bcl-2 and up-regulating p53 levels (162). Cell proliferation can be inhibited by 1 $\alpha$ ,25(OH)<sub>2</sub>D<sub>3</sub>, interfering with ER function. Specifically, 1 $\alpha$ ,25(OH)<sub>2</sub>D<sub>3</sub> and its analogs down-regulate the expression of ER $\alpha$ , which in turn reduced estrogen-dependent activation of mitogenic signal (163). Another action of 1 $\alpha$ ,25(OH)<sub>2</sub>D<sub>3</sub> against breast cancer cells is the down-regulation of aromatase expression (164).

Proliferation of colon cancer cells was inhibited by 1 $\alpha$ ,25(OH)<sub>2</sub>D<sub>3</sub> and its analogs, that caused a cell cycle arrest at the G0/G1 phase. This was consequent to enhanced expression of p21 and p27, two cyclin-dependent kinase inhibitors, and to reduced expression of cyclin D1 and cyclin E (165). In addition, following colon cancer cells treatment with 1 $\alpha$ ,25(OH)<sub>2</sub>D<sub>3</sub>, genes with a pro-apoptotic function were increased, while those anti-apoptotic were downregulated (166). It was observed that



**FIGURE 1 |** Potential mechanisms explaining antitumoral effects of statins. Cholesterol, after its utilization as signaling molecule (A), as substrate for steroids (B), oxysterols (C), and 1 $\alpha$ ,25(OH)<sub>2</sub>D<sub>3</sub> synthesis (D) or as ligand for ERR $\alpha$  (E), regulates tumor growth and progression. Statins, inhibiting cholesterol synthesis, interfere with (A) and (C). Further studies are needed to confirm statins ability to: reduce production of steroid hormones involved in cancer progression (B), increase serum or intratumor 1 $\alpha$ ,25(OH)<sub>2</sub>D<sub>3</sub> levels (D) or interfere with ERR $\alpha$  activity (E).

in differentiated human colon tumors CYP27B1 expression is enhanced compared to untransformed colon mucosa. It was observed a parallel increase of VDR and CYP27B1 mRNA during early tumor progression. This suggests that  $1\alpha,25(\text{OH})_2\text{D}_3$  synthesized in colonocytes and bound to its receptor could exert its anti-mitotic function in both an autocrine and a paracrine fashion to prevent intestinal tumor formation and progression during early phases of colon tumorigenesis. In fact, in high-grade undifferentiated tumors, expression of CYP27B1 is decreased (167). However, other reports did not find a rise in CYP27B1 expression in tumors, possibly because there was not a distinction for the biological grade of the tumor (168). With a very similar pattern of expression, when compared with normal colon mucosa, VDR expression is increased in early stages of tumorigenesis, but declines in late-stage tumors (169–171). Alternatively,  $1\alpha,25(\text{OH})_2\text{D}_3$  produced during early phases of transformation could interact with other receptors such as thyroid receptors (TR) (172) and induce cell proliferation. In fact, the expression of TR $\beta$ 1 was found associated with polypoid growth and with higher histological grade and advanced stage (173). To confirm a protective role for  $1\alpha,25(\text{OH})_2\text{D}_3$ , CYP24A1, the degrading enzyme, has enhanced expression in the majority of colon adenocarcinomas, keeping low  $1\alpha,25(\text{OH})_2\text{D}_3$  levels (174). Adrenocortical cancers express VDR, its activation by slightly supra-physiological concentrations of  $1\alpha,25(\text{OH})_2\text{D}_3$  has a moderate anti-proliferative effect, that is related to cell cycle arrest, promoting accumulation of cells in G1 phase, without inducing apoptosis. Additionally, VDR activation decreases cortisol, aldosterone, and DHEA-S production (175).

A very recent study demonstrated no impact of statin therapy on plasma vitamin D levels (176). However, a meta-analysis report indicated opposite data, with statins causing an increase in vitamin D serum levels (177), this effect was observed with lovastatin (178), simvastatin (179), atorvastatin (180), and especially rosuvastatin (181, 182). If further confirmed, these data might help explaining the anti-neoplastic effect exerted by statins on colon cancer (183–185). Currently, there are no studies investigating the effects of statins on intratumor vitamin D synthesis despite vitamin D can act in an autocrine manner to regulate cancer growth. For these reasons further studies on specific tumor are necessary to establish a direct effect of vitamin D on cell tumor proliferation and consequently if statins could induce anti-tumoral effects modulating intra-tumoral vitamin D levels.

## CHOLESTEROL AS ESTROGEN-RELATED RECEPTOR ALPHA (ERR $\alpha$ ) LIGAND

The Estrogen-related receptor (ERR) family is known to comprise three members [ERR $\alpha$  (NR3B1), ERR $\beta$  (NR3B2), and ERR $\gamma$  (NR3B3)] (186). ERR $\alpha$  is ubiquitously expressed in adult tissues; ERR $\beta$  is detected at low levels in the liver, skeletal muscle, stomach, heart, and kidney; ERR $\gamma$  is widely expressed and can be detected in brain, lung, bone marrow, adrenal and thyroid glands, trachea and spinal cord. The ERRs, like most NRs, are organized in functional domains

for ligand (LBD) and DNA binding (DBD), in addition to an activation function 1 (AF-1) involved in cofactors binding. ER $\alpha$  and ERR $\alpha$  LBD share only 37% amino acid homology, indicating low affinity for common ligands, and in fact estradiol fails in activating ERR $\alpha$  (186). While ERR $\beta$  and ERR $\gamma$  are still orphan receptors since their natural ligands have not been identified, ERR $\alpha$  is an adopted orphan receptor, for which ligand has been identified to be cholesterol (187). This finding implies cholesterol involvement in mitochondrial metabolism and biogenesis. In fact, ERR $\alpha$  regulates the expression of a broad range of genes driving mitochondrial biogenesis, the tricarboxylic acid (TCA) cycle, and substrate oxidation.

ERR monomers preferentially recognize the consensus site referred to as the ERR-response element (ERRE). ERR $\alpha$  and ER $\alpha$  share 68% amino acid identity in the DBD, indicating that the two receptors can potentially regulate common genes. Indeed ERR dimers can bind to the ERE, and ER $\alpha$  dimers can also recognize ERRE sites (188). ER $\alpha$  and the ERRs compete for common coactivators such as steroid receptor coactivator (SRC) proteins in transfected cells (189). In addition, another coactivator, the small heterodimer partner (SHP), a coregulator of ER, interacts with all members of the ERR family inhibiting their transcriptional activity. Thus, ERRs and ERs have the potential to differentially regulate common target genes.

ERR $\alpha$  transcriptional activity in normal cells has important roles in cellular metabolism, this is particularly relevant in rapidly dividing cells such as tumor cells. Cholesterol interaction with ERR $\alpha$  (187) allows recruitment of coactivators PGC1 $\alpha/\beta$  and increases ERR $\alpha$  transcriptional activity. ERR $\alpha$  interaction with PGC1 $\alpha$  favors osteoclastogenesis (190) and bone reabsorption in osteoclasts, myogenesis (191) and decreases muscle toxicity in myocytes (187). Differently from other nuclear receptors, ERR $\alpha$  is constitutively active because cholesterol is ubiquitous, meaning that it does not require any spike in ligand concentration, as is the case for steroid hormone receptors. ERR $\alpha$  antagonists have been found to induce cancer cell death (192, 193), inhibit tumor growth (194) and improve insulin sensitivity and glucose tolerance (195).

The use of statins or drugs targeting the SREBP metabolic pathways could be a promising option to counteract ERR $\alpha$ -dependent metabolic rearrangement. Identification of cholesterol as ERR $\alpha$  ligand is relatively new, so far no studies have investigated statins effects on ERR $\alpha$  activity in tumor cells. However, the discovery of cholesterol as ERR $\alpha$  ligand has elucidated the mechanism behind statin-induced muscle toxicity (187).

## CONCLUSIONS

Statins are widely used drugs for their ability to lower cholesterol levels in hypercholesterolemic patients. Their mechanism of action consists in the inhibition of HMG-CoA reductase, the main enzyme involved in cholesterol biosynthesis.

Aim of this review was to discuss the results of studies focused on the use of statins to the purpose of interfering with cholesterol activities, in order to prevent cancer growth and metastasis.

Cholesterol plays an important function as part of membrane rafts where is involved in the modulation of signaling transduction related to cell proliferation and migration (**Figure 1A**). Data discussed herein unequivocally suggest that statins have a direct impact on the function of membrane rafts, inhibiting, in tumor cells, pathways regulating growth, and metastasis. Cholesterol represents a precursor for estrogens and androgens, hormones involved in modulating cell proliferation, migration, invasion and apoptosis in different cancers (**Figure 1B**). Even though steroidogenic tissues are potential sites for statins effects, there are discording data on a direct role for statins in decreasing steroid production in hormone-dependent cancers. Furthermore, using cholesterol as substrate for specific metabolizing enzymes it is also possible to produce oxysterols, such as 27HC, which has been shown to act as an endogenous selective estrogen receptor modulator able to increase cancer growth and metastasis (**Figure 1C**). Data discussed in this review suggest that the reduction of oxysterol production caused by statins could have a strong effect on specific tumors (i.e., breast cancer) preventing cell migration and invasion.

Cholesterol is also precursor of vitamin  $1\alpha,25(\text{OH})_2\text{D}_3$ , which is involved in modulating VDR-responsive genes, encoding for proteins involved in anti-proliferative signaling (**Figure 1D**). However, the analysis of data published in this field suggest that further studies are necessary to establish a direct effect (anti-proliferative or proliferative) of vitamin D on different cell tumors and consequently if statins could induce specific effects modulating intra-tumoral vitamin D levels.

In conclusion, while the anti-tumor effects produced by statins on cholesterol-mediated transduction mechanisms at the membrane raft or on oxysterols synthesis, appear to be a

promising therapeutic strategy, further studies are needed to determine if cholesterol depletion is a valid strategy to limit the effects of steroid hormones on endocrine-dependent tumors. The ability of statins to increase  $1\alpha,25(\text{OH})_2\text{D}_3$  serum levels need to be confirmed, in order to define another antitumor mechanism for these drugs. Recently, the discovery of cholesterol as  $\text{ERR}\alpha$  ligand has elucidated the mechanism behind statin-induced muscle toxicity; however, no studies have investigated statins effects on  $\text{ERR}\alpha$  activity in tumor cells (**Figure 1E**). This last aspect has opened a new field of investigation, in fact, strategies aimed to reduce cholesterol levels, such as the use of statins or drugs targeting SREBP metabolic pathways, could be a promising option to counteract metabolic rewiring in cancer cells where  $\text{ERR}\alpha$  plays a pivotal role.

Preclinical studies support the potential use of statins as anticancer agents. Epidemiological studies indicate that statin use is associated with a reduction in the incidence of some tumor types. The few clinical trials of statins as monotherapy do not provide convincing results; however, in combination therapy with other agents, statins have shown more promising data. Conclusion of clinical trials not yet completed and publication of data from closed trials will provide a wider picture on the effectiveness of this class of drugs as anticancer therapy.

## AUTHOR CONTRIBUTIONS

AC, IC: literature search and drafting of the article. FT, PA, AD, VR: drafting of the article. VP, RS: critical revision of the article and final approval.

## FUNDING

This work was supported by AIRC (Associazione Italiana per la Ricerca sul Cancro), projects n. IG15230 and IG20122.

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**Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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# The Roles of Cholesterol and Its Metabolites in Normal and Malignant Hematopoiesis

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## OPEN ACCESS

### Edited by:

Rosa Sirianni,  
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### Specialty section:

This article was submitted to  
Cancer Endocrinology,  
a section of the journal  
Frontiers in Endocrinology

**Received:** 08 June 2018

**Accepted:** 12 March 2019

**Published:** 02 April 2019

### Citation:

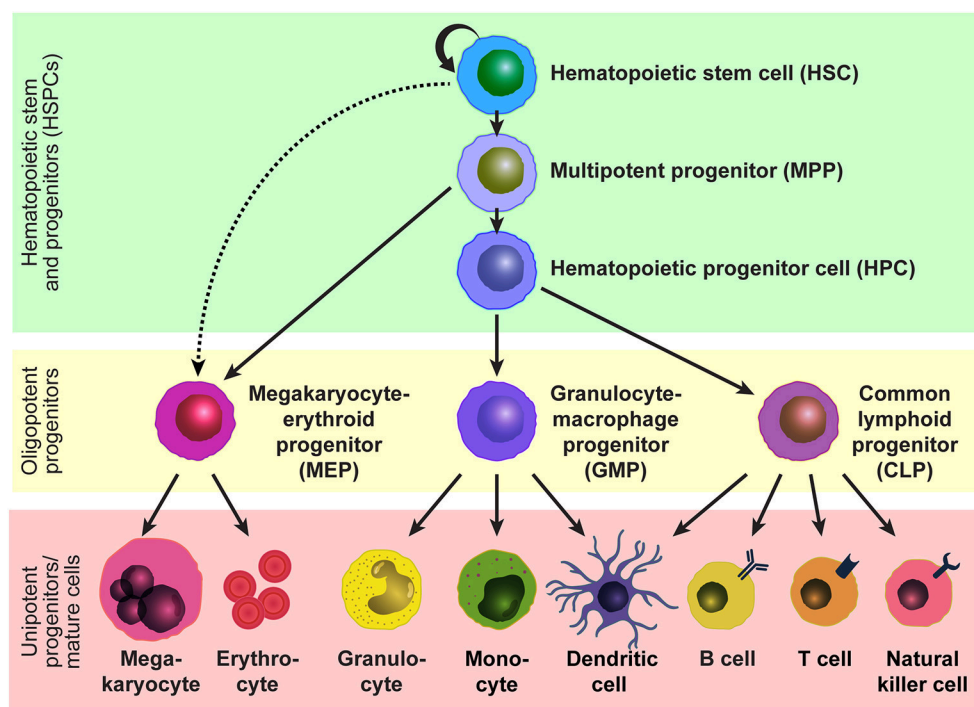
Oguro H (2019) The Roles of  
Cholesterol and Its Metabolites in  
Normal and Malignant Hematopoiesis.  
Front. Endocrinol. 10:204.  
doi: 10.3389/fendo.2019.00204

Hematopoiesis is sustained throughout life by hematopoietic stem cells (HSCs) that are capable of self-renewal and differentiation into hematopoietic progenitor cells (HPCs). There is accumulating evidence that cholesterol homeostasis is an important factor in the regulation of hematopoiesis. Increased cholesterol levels are known to promote proliferation and mobilization of HSCs, while hypercholesterolemia is associated with expansion of myeloid cells in the peripheral blood and links hematopoiesis with cardiovascular disease. Cholesterol is a precursor to steroid hormones, oxysterols, and bile acids. Among steroid hormones,  $17\beta$ -estradiol (E2) induces HSC division and E2-estrogen receptor  $\alpha$  (ER $\alpha$ ) signaling causes sexual dimorphism of HSC division rate. Oxysterols are oxygenated derivatives of cholesterol and key substrates for bile acid synthesis and are considered to be bioactive lipids, and recent studies have begun to reveal their important roles in the hematopoietic and immune systems. 27-Hydroxycholesterol (27HC) acts as an endogenous selective estrogen receptor modulator and induces ER $\alpha$ -dependent HSC mobilization and extramedullary hematopoiesis.  $7\alpha,25$ -dihydroxycholesterol ( $7\alpha,25$ HC) acts as a ligand for Epstein-Barr virus-induced gene 2 (EBI2) and directs migration of B cells in the spleen during the adaptive immune response. Bile acids serve as chemical chaperones and alleviate endoplasmic reticulum stress in HSCs. Cholesterol metabolism is dysregulated in hematologic malignancies, and statins, which inhibit *de novo* cholesterol synthesis, have cytotoxic effects in malignant hematopoietic cells. In this review, recent advances in our understanding of the roles of cholesterol and its metabolites as signaling molecules in the regulation of hematopoiesis and hematologic malignancies are summarized.

**Keywords:** cholesterol, oxysterols, steroids, hematopoietic stem cells, hematopoiesis, hematologic malignancies

## INTRODUCTION

Hematopoietic stem cells (HSCs) sustain blood production throughout life and are the functional units of bone marrow transplantation. HSCs are capable of self-renewal to maintain their pool while producing all mature blood cells through differentiation into multipotent progenitors (MPPs) and subsequent hematopoietic progenitor cells (HPCs) with limited differentiation potentials (**Figure 1**). In adult mice, all HSCs and MPPs fall within the Lineage marker<sup>-</sup>Sca-1<sup>+</sup>c-Kit<sup>+</sup> (LSK) fraction (1–3), which is a heterogeneous population that contains a mixture of hematopoietic stem and progenitor cells (HSPCs), including HSCs, MPPs, and HPCs. HSCs can be further purified by selecting the CD150<sup>+</sup>CD48<sup>-/low</sup> subset (4, 5) or CD34<sup>-/low</sup>Flt3<sup>-</sup> subset (6, 7) of



**FIGURE 1 |** Model of the hematopoietic hierarchy. A hierarchical structure of the adult hematopoietic system based on studies by us and others using mice. HSCs reside at the top of the hierarchy and give rise to MPPs and potentially MEPs. MPPs generate HPCs and MEPs, and HPCs generate GMPs and CLPs. Mature cells are developed from these oligopotent progenitors, MEPs, GMPs, and CLPs, through intermediate progenitors. Some lineage relationships are under debate.

LSK cells. The HSC population is functionally heterogeneous in terms of cell-cycle kinetics, self-renewal capacity, and differentiation potential, and the heterogeneity can be distinguished by additional markers such as CD229 (5) and von Willebrand factor (8). Human HSPCs can be marked by Lineage marker<sup>−</sup>CD38<sup>−</sup>CD34<sup>+</sup> and the HSC population can be further refined by marking the CD45RA<sup>−</sup>CD49f<sup>+</sup> subset of Lineage marker<sup>−</sup>CD38<sup>−</sup>CD34<sup>+</sup> cells (9). HSCs reside in specialized niches which are local tissue microenvironments that support HSC behavior and regulate their function, such as self-renewal, differentiation, and localization, by producing factors that act directly on HSCs (10). In adults, HSCs are quiescent and localize primarily in the bone marrow, and their number is tightly regulated under steady-state conditions, comprising <0.01% of bone marrow cells in mice. In response to acute hematopoietic demands such as blood loss, myeloablation, infection, or pregnancy, HSCs change two aspects of their steady-state behaviors in order to increase production of necessary hematopoietic cells (11–14). First, quiescent HSCs re-enter the cell cycle to proliferate or differentiate through symmetric or asymmetric cell divisions, and second, they mobilize from the bone marrow to extramedullary tissues, such as the spleen, to expand the physical space for hematopoiesis.

In addition to the regulation of HSC behaviors by short-range factors, such as cytokines, cell-surface proteins, extracellular matrix components, oxygen tension, and ion levels, that are generated in their niches, HSCs are also regulated by long-range

systemic signals, such as circulating cytokines, hormones, lipids, and vitamins. Cholesterol is found in the bloodstream and within cells, and is an essential structural component of mammalian plasma membranes and is essential to maintain both membrane structural integrity and to modulate membrane fluidity (15). Cholesterol also serves as a precursor for the biosynthesis of steroid hormones, oxysterols, and bile acids (Figure 2) (16). These cholesterol metabolites have important biological roles as signal transducers and chemical chaperones, and there is accumulating evidence that these metabolites act as systemic signals that regulate normal and malignant hematopoiesis. This review discusses recent advances in understanding the roles of cholesterol and its metabolites in the regulation of hematopoiesis and hematologic malignancies.

## CHOLESTEROL LEVELS AND HEMATOPOIESIS

In the bloodstream, cholesterol is transported within lipoprotein particles, which are organized by apolipoproteins that can be recognized and bound by specific receptors on cell membranes. There are several types of lipoproteins, such as high-density lipoprotein (HDL), low-density lipoprotein (LDL), intermediate-density lipoprotein (IDL), very-low-density lipoprotein (VLDL), and chylomicrons, in order of higher density to lower density. LDL is the major cholesterol carrier in the blood and is





HSPC proliferation. In contrast, infusion with reconstituted HDL reduced the frequency and proliferation rate of HSPCs in the bone marrow, highlighting the opposing effects of LDL and HDL on HSPC proliferation. Scavenger receptor type BI (SR-BI, encoded by *Scarb1* gene) is a HDL receptor, and *Scarb1*<sup>-/-</sup> mice showed increased plasma total cholesterol levels with unchanged plasma concentration of apoA-I, the major protein in HDL (26). Gao et al. reported that *Scarb1*<sup>-/-</sup> mice fed an HFHC diet showed significantly increased the number of HSPCs in the bone marrow, spleen, and peripheral blood, as well as the proliferation of HSPCs as compared to wild-type mice fed an HFHC diet (27). Interestingly, HSPCs in *Scarb1*<sup>-/-</sup> mice fed an HFHC diet displayed increased levels of reactive oxygen species (ROS). Elevation of ROS levels hinders HSC quiescence and self-renewal, and accelerates HSC exhaustion (28). Injection of ROS inhibitor N-acetylcysteine attenuated HSPC expansion and leukocytosis in *Scarb1*<sup>-/-</sup> mice fed an HFHC diet, suggesting a correlation between ROS levels and HSPC proliferation. Tie et al. also reported that *ApoE*-deficiency increased the number and ROS levels of HSPCs, and these were further increased by the HFHC diet (29). They also observed shorter telomere length in HSPCs in *ApoE*<sup>-/-</sup> mice as compared to wild-type mice, suggesting accelerated aging of HSPCs, and this phenotype was reversed by treating *ApoE*<sup>-/-</sup> mice with N-acetylcysteine. These studies clearly indicate increased systemic cholesterol levels promote proliferation and mobilization of HSPCs.

## Cholesterol Efflux Pathways Regulate Proliferation and Mobilization of Mouse Hematopoietic Stem and Progenitor Cells

ABCA1 and ABCG1, adenosine triphosphate-binding cassette transporters, play a key role in promoting active cellular cholesterol efflux (30). Yvan-Charvet et al. reported that *Ldlr*<sup>-/-</sup> mice on an HFHC diet that were transplanted with *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> bone marrow cells showed accelerated atherosclerosis and extensive infiltration of myocardium and spleen with macrophage foam cells as compared to transplantation with wild-type bone marrow cells (31). The same group subsequently reported that *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> mice on a normal diet displayed five-fold increase of HSPCs (including the CD34<sup>+</sup>CD150<sup>+</sup>Flt3<sup>-</sup> highly-pure HSC population) in the bone marrow, as well as the increase in the S/G2/M fraction in HSPCs (32). The overall BrdU incorporation of *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> bone marrow cells was increased *in vitro*, whereas when wild-type bone marrow cells were mixed with *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> bone marrow cells, the overall BrdU incorporation of wild-type bone marrow cells was not increased, suggesting that HSPC proliferation in *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> mice was caused by cell autonomous effects. Interestingly, in their next report, they showed that *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> mice also displayed an increase in HSPCs in the peripheral blood, spleen, and liver, indicating HSPC mobilization and extramedullary hematopoiesis (33). In this study, they performed a competitive bone marrow transplantation experiment by transplanting a mixture of equal numbers of bone marrow cells from wild-type and *Abca1*<sup>-/-</sup>

*Abcg1*<sup>-/-</sup> mice into wild-type recipient mice, and found that HSPC mobilization of both the *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> and wild-type donor cells was induced, suggesting that there is a cell-extrinsic factor that induces HSPC mobilization of wild-type donor cells from *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> donor cells. Plasma levels of granulocyte colony-stimulating factor (G-CSF) were significantly increased in recipients of *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> bone marrow cells and the mobilization of *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> HSPCs was reduced by injection of G-CSF-neutralizing antibody. Interleukin-17 (IL-17) is a potent inducer of G-CSF (34), and the production of IL-17 can be mediated by the secretion of interleukin-23 (IL-23) from splenic phagocytic macrophages and dendritic cells (35). In the recipients of *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> bone marrow cells, plasma G-CSF levels and colony-forming HSPC numbers in the blood were normalized by an IL-17-blocking antibody, and plasma levels of IL-17 and G-CSF, as well as colony-forming HSPCs in the blood, were reduced by administration of IL-23 receptor-neutralizing antibody. Both myeloid cell (including macrophages) -specific and dendritic-cell specific deletion of *Abca1* and *Abcg1* using *lysM-cre*; *Abca1*<sup>fl/fl</sup>; *Abcg1*<sup>fl/fl</sup> mice, and *CD11c-cre*; *Abca1*<sup>fl/fl</sup>; *Abcg1*<sup>fl/fl</sup> mice, respectively, exhibited increased levels of splenic IL-23, plasma IL-17 and G-CSF, and colony-forming HSPCs in the blood, suggesting that IL-23/IL-17/G-CSF signaling is associated with enhanced HSPC mobilization in *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> mice. They further reported that CXCL12 levels and the number of N-Cadherin<sup>+</sup> osteoblasts, one of the CXCL12-expressing cell populations in the bone marrow (36), were decreased in the bone marrow of *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> mice, an effect that might be caused by depletion of bone marrow macrophage populations due to an enhanced IL-23/IL-17/G-CSF signaling axis. Thus, this study supports a step-wise mechanism by which increased intracellular cholesterol levels lead to mobilization of HSCs: (1) increased cholesterol initially promotes secretion of pro-inflammatory cytokines from immune cells, (2) this increases production of G-CSF by bone marrow stromal cells, (3) reducing osteoblast number and osteoblast production of CXCL12, a chemokine which attracts HSCs, and (4) leads to HSC mobilization into the bloodstream. They subsequently reported that *Ldlr*<sup>-/-</sup> recipient mice that received *lysM-cre*; *Abca1*<sup>fl/fl</sup>; *Abcg1*<sup>fl/fl</sup> bone marrow cells and were fed an HFHC diet developed atherosclerosis associated with monocytosis and neutrophilia (37). The authors demonstrated a cell-extrinsic mechanism in which the expression of macrophage colony-stimulating factor (M-CSF) and G-CSF were increased in the spleen, and this might cause monocyte and neutrophil production in the bone marrow.

## Cholesterol Levels and Human Hematopoiesis

Cholesterol homeostasis also affects human hematopoiesis. Crysandt et al. performed a retrospective analysis of a variety of clinical parameters in 83 patients following high-dose cyclophosphamide and G-CSF treatment and found that patients with hypercholesterolemia showed a substantially higher number of harvested CD34<sup>+</sup> HSPCs in the peripheral blood

as compared to normocholesterolemic patients (38). 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) reductase is a rate-limiting enzyme of *de novo* cholesterol synthesis, and statins, as inhibitors of HMG-CoA reductase, prevent the conversion of HMG-CoA to L-mevalonate and inhibit downstream cholesterol biosynthesis (Figure 2). Cimato et al. treated human subjects with different statins, atorvastatin, pravastatin, and rosuvastatin, to vary cholesterol levels and analyzed the number of mobilized CD34<sup>+</sup> HSPCs in the peripheral blood (39). They found a positive correlation between CD34<sup>+</sup> HSPC number and both total and LDL-cholesterol levels. In addition, G-CSF and its upstream regulator IL-17 both correlated positively with LDL-cholesterol levels. Gao et al. studied the correlation between HDL and white blood cell levels in patients with coronary heart disease (27). They found negative correlations between HDL levels and both total white blood cell and neutrophil counts in the peripheral blood, and patients with low HDL-cholesterol had more mobilized Lineage<sup>-</sup>CD34<sup>+</sup>CD38<sup>-</sup>CD45RA<sup>-/low</sup> HSCs in the peripheral blood as compared to the patients with normal HDL-cholesterol. Tolani et al. analyzed data from a clinical trial of rosuvastatin in children with heterozygous familial hypercholesterolemia and found that the children with the lowest HDL-cholesterol levels had higher monocyte counts in the peripheral blood, and there was an inverse correlation between HDL levels and monocyte percentage (40). Thus, increased cholesterol levels induce mobilization of not only mouse HSCs but human HSCs, which suggests that cholesterol level is a factor that should be considered when mobilizing HSCs for clinical transplantation.

## ROLES OF CHOLESTEROL METABOLITES IN HEMATOPOIESIS

### Sex Steroid Hormones

Estrogens and androgens are classically recognized as sex steroid hormones, and progesterone are recognized as a third class of sex steroid hormones. Each of these sex steroid hormones is synthesized from cholesterol, and the first and rate-limiting step of the steroidogenic pathway is the cleavage of the cholesterol side chain by P450<sub>scc</sub> (CYP11A1) to convert into pregnenolone (Figure 2) (41). Estrogens are produced in gonadal and extra-gonadal tissues. In females, 17 $\beta$ -estradiol (E2), a most potent estrogen, is produced primarily by theca and granulosa cells in the ovaries. Androstenedione is generated from cholesterol and is converted into testosterone by aromatase in theca cells, and they are further converted into E2 by aromatase in granulosa cells. Testosterone is the primary androgen secreted from Leydig cells in the testes, and small amounts are also secreted from theca cells in the ovaries. Progesterone is a critical progesterone to establish and maintain pregnancy. Progesterone is produced from cholesterol in the corpus luteum of the ovary during early pregnancy and the production is sustained by the placenta in humans and rodents. In addition to their well-recognized effects on reproductive tissues, the sex steroid hormones are also being recognized as having broad physiological effects on non-reproductive tissues, such as nervous, cardiovascular, skeletal,

immune, and hematopoietic systems. It is known that females and males differ in innate and adaptive immune responses, and these sex-biased differences in the immune system contribute to variations in the prevalence of autoimmune diseases and malignancies, susceptibility to infectious diseases, and responses to vaccines (42).

### Androgens and Lympho-Hematopoiesis

Several studies have shown that androgens negatively regulate B lymphopoiesis. Castration of male mice leads to spleen enlargement and expansion of the B-cell population in the bone marrow and spleen (43–45). This effect is reversed by androgen replacement with either testosterone or dihydrotestosterone (DHT) (46). Androgen-resistant “testicular feminization” mutant male mice also show expansion of B-cell populations in the bone marrow and spleen (45, 47). In addition to the regulation of B lymphopoiesis, castrated mice and testicular feminization male mice also show thymic hypertrophy, which can be rescued by DHT administration (43, 45, 48–50). Experiments transplanting wild-type bone marrow cells into testicular feminization male mice suggest that androgen receptors expressed by bone marrow stromal cells or thymic epithelium modulate B-cell development or thymus size, respectively (50, 51). Velardi et al. showed that one mechanism by which androgens influence thymopoiesis is through direct inhibition of the Notch ligand *Dll4* in cortical thymic epithelial cells (52). Immune function progressively declines with age in mice and humans (53). In male mice, castration rejuvenates aged bone marrow and thymus, enhances peripheral T- and B-cell functions, and promotes immune recovery following chemotherapy-induced immunodepletion and HSC transplantation (54–62). These studies indicate that androgens are critical mediators of age-related lymphoid decline. Castration also enhances the recovery of bone marrow-resident HSCs after chemotherapy-induced immunodepletion (62). Khong et al. demonstrated that the number of HSCs marked by CD34<sup>-</sup>Flt3<sup>-</sup>LSK was significantly increased at 7 days after castration of 9-month-old mice as compared to sham-treated mice, and the repopulation potential during serial bone marrow transplantations was enhanced when using these mice as donors (63). Their gene expression analyses suggest that castration induces qualitative changes in both HSCs and their bone marrow environment.

### Estrogens and Lympho-Hematopoiesis

B lymphopoiesis in the bone marrow and T lymphopoiesis in thymus are drastically reduced during pregnancy (64, 65). Ovariectomy stimulates B lymphopoiesis and results in increased numbers of B cells in the bone marrow (66, 67), and it is reversed by administration of E2 (68). Genetically hypogonadal female mice which have a partial deletion of the hypothalamic gonadotropin-releasing hormone gene have a secondary deficiency in gonadal steroidogenesis and show expansion of B cell progenitors. Estrogen replacement with E2 reversed the increased numbers of B cell progenitors in these hypogonadal mice (69). Exogenous E2 treatment suppresses B cell development in both male and female mice (68, 70, 71).

Very early lymphoid precursors marked by Lineage marker<sup>-</sup>IL-7R $\alpha^+$ c-Kit<sup>lo</sup>Terminal deoxynucleotidyl transferase<sup>+</sup> in the bone marrow are selectively depleted by exogenous E2 treatment (72). Both stromal-dependent and independent pathways of estrogen action on developing B cells have been postulated. It is proposed that bone marrow stromal cells expressing estrogen receptors mediate negative regulatory effects of E2 on early pre-B development (47, 73). A study of estrogen receptor  $\alpha$  (ER $\alpha$ ) male knockout mice by Thurmond et al. indicated that ER $\alpha$  is necessary for development of normal numbers of B cells in the bone marrow (74). They investigated the effect of E2 on lymphopoiesis by performing bone marrow transplantation using ER $\alpha$ -deficient mice as donors, recipients, or both, and treated with E2. They demonstrated that exogenous E2-induced alteration of B cell populations was primarily caused by a hematopoietic cell-intrinsic mechanism rather than by their environment.

Estrogens also regulate other hematopoietic lineages. Administration of a high-dose of estrogen induces anemia in rodents and dogs, regardless of their sex (75–77). Schroeder et al. reported that E2 sustained proliferation of erythroid progenitors from chick bone marrow, but E2 also caused erythroid differentiation arrest and blocked erythrocyte gene expression (78). Blobel et al. also showed that E2 added to the culture also reduced the number of erythroid progenitors from human bone marrow (79). They demonstrated that the transcriptional activity of GATA1, an erythroid master transcription factor that is necessary for full maturation of erythrocytes, was strongly repressed by direct binding of ER in an E2-dependent manner in NIH 3T3 and COS cell lines. The same group subsequently reported that inhibition of GATA1 activity by ER induced apoptosis in a murine Friend virus-induced erythroleukemia cell line (80). E2 treatment also stimulates the megakaryocyte colony formation potential of CD34<sup>+</sup> human cord blood cells *in vitro* (81). E2 promotes megakaryocyte polyploidization and maturation via activation of ER $\beta$  accompanied by a significant upregulation of the expression of GATA1, which is also a key regulator of megakaryocyte differentiation (82). Differentiation of dendritic cells with characteristics of Langerhans cells from myeloid progenitors in culture, as induced by granulocyte-macrophage colony-stimulating factor (GM-CSF), is promoted by addition of E2 and inhibited by ER antagonists and ER $\alpha$ -deficiency (83). Interferon regulatory factor 4 (IRF4), a transcription factor induced by GM-CSF and critical for Langerhans cell development, is a target of ER $\alpha$  signaling during this process (84). In contrast, E2 significantly inhibits Flt3-ligand-induced plasmacytoid and conventional dendritic-cell differentiation in culture by decreasing numbers of viable differentiated cells (85). Thus, the effects of E2 are likely to be dependent on the cytokine pathways that might be operative in the steady state or during inflammation and disease.

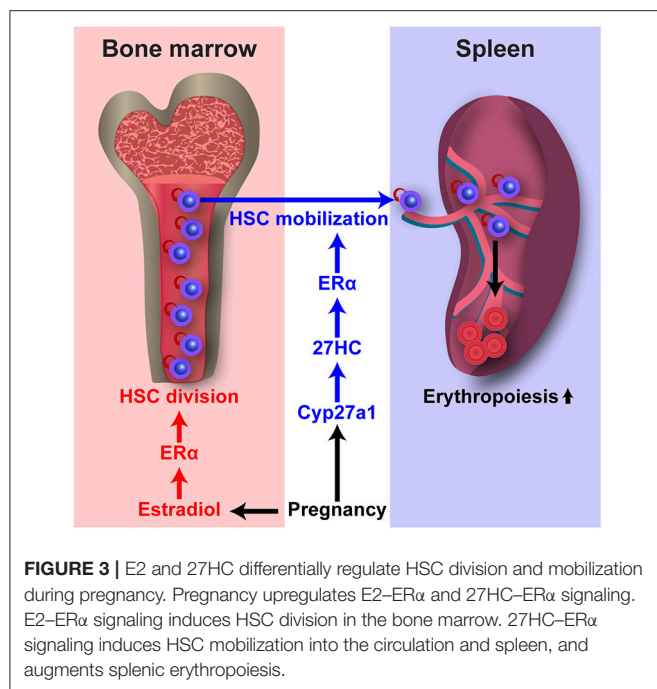
## Estrogens Regulate HSC Division Rate

Estrogens also regulate HSC behavior. In our previous study, we observed that HSCs divide more often in female mice as compared to male mice (14). Ovariectomy in females (which

depletes both estrogens and progesterone) significantly reduced HSC division to male levels, while castration of males has no effect on HSC division. Conversely, administration of exogenous E2, but not progesterone or dihydrotestosterone, significantly increased HSC division in both female and male mice. Because E2 treatment also increased HSC division in ovariectomized female mice and castrated male mice, its action is independent of the gonads. Although HSC division rate was increased in untreated female mice as compared to male mice and in E2-treated mice of either sex as compared to vehicle-treated control mice, we did not observe an increase in absolute HSC numbers in those untreated female mice or E2-treated mice. Instead, we observed an increased generation of megakaryocyte-erythroid progenitors (MEPs) in female mice as compared to male mice, and increased splenic erythropoiesis in E2-treated mice of both sexes as compared to vehicle-treated control mice. Given that increased myeloid progenitors including MEPs may arise directly from the asymmetric division of HSCs (Figure 1) (86), our observations raise the possibility that the increased MEPs in female mice reflects increased asymmetric division of an HSC to produce one HSC and one MEP in response to E2. ER $\alpha$ , but not ER $\beta$ , is highly expressed by HSCs. Conditional deletion of *Esr1*, which encodes ER $\alpha$ , from hematopoietic cells significantly reduced the HSC division rate in female mice, but not in male mice. *Esr1*-deficient HSCs of both sexes were insensitive to exogenous E2 treatment. Moreover, E2 treatment of chimeric recipient mice transplanted with equal numbers of wild-type and *Esr1*-deficient hematopoietic cells revealed that E2 significantly induced division of wild-type HSCs but not *Esr1*-deficient HSCs in the same recipient mice, indicating that E2 acts directly on HSCs, rather than acting indirectly by stimulating secondary signals from other cells. E2 levels increase in females during pregnancy (87), when extramedullary hematopoiesis is induced to increase the production of red blood cells. Notably, pregnant mice exhibit significantly increased HSC division rate relative to non-pregnant female mice, and the deletion of *Esr1* in hematopoietic cells significantly reduced the normal increase in HSC division during pregnancy (Figure 3). Increased spleen size is observed during pregnancy in mice and humans (88, 89). In addition to the increased HSC division rate, we found that pregnant mice exhibited significantly increased cellularity, erythropoiesis, myelopoiesis, and HSC number in the spleen, indicating extramedullary hematopoiesis and HSC mobilization, and these processes also depend upon ER $\alpha$  function in HSCs. Pregnant mice also had increased absolute HSC numbers in the bone marrow, but deletion of *Esr1* in hematopoietic cells did not reverse this phenomenon, suggesting the existence of ER $\alpha$ -independent factor(s) that increase(s) HSC numbers in pregnant mice. Nevertheless, ER $\alpha$  signaling is critical for the induction of HSC division and mobilization to the spleen for the expansion of splenic erythropoiesis.

Illing et al. also reported the effects of E2 on HSC function (90). In this study, they treated mice with E2 at a dose of 0.24 mg/kg/day for 30 days, which is a higher dose and longer treatment than our study at a dose of 0.1 mg/kg/day for 7 days. In this condition, they observed a profound reduction





in bone marrow cellularity by E2 treatment. E2 treatment caused more HSPCs to enter the S phase. They also observed an increased frequency of long-term reconstituting HSCs in E2-treated mice by performing bone marrow transplantation with a limiting dilution assay. However, donor-derived HSPCs of the bone marrow of the recipient mice after tertiary transplantation was decreased in the recipients that received bone marrow cells from E2-treated mice, suggesting exhaustion of reconstituting cells during serial transplantation. Deletion of *Esr1* reversed the reduction of bone marrow cellularity by E2 treatment, however it did not reverse the increased frequency of long-term reconstituting HSCs by E2 treatment. Sanchez-Aguilera et al. reported the effect of tamoxifen, a selective estrogen receptor modulator (SERM), on HSC function (91). Tamoxifen induced HSC division as well as apoptosis in MPPs, and these effects are mediated by ER $\alpha$  but not by ER $\beta$ . Tamoxifen treatment significantly reduced MPP number, but not HSC number, and compromised activation of hematopoiesis after chemotherapy. They observed increased expression of *Myc* in HSCs after tamoxifen treatment, and *Myc*-deficient MPPs did not undergo apoptosis upon tamoxifen treatment. Interestingly, female immunodeficient recipient mice support reconstitution of the blood system by transplanted human HSCs more efficiently than male immunodeficient recipient mice (92, 93). Since female mice have higher E2 levels than male mice and E2 induces HSC division, it is anticipated that higher E2 levels in female recipient mice will promote proliferation and differentiation of transplanted HSCs as compared to male recipient mice with very low E2 levels. The molecular mechanisms by which E2 regulates HSCs are not fully understood. Chapple et al. proposed that HSCs from mice treated with E2 had increased regenerative capacity after

transplantation or irradiation (94). They demonstrated that E2-ER $\alpha$  signaling induced expression of *Ern1*, which encodes Ire1 $\alpha$ , to activate the Ire1 $\alpha$ -Xbp1 pathway of the unfolded protein response, and promoted resistance of HSCs against proteotoxic stress.

## 27-Hydroxycholesterol Regulates HSC Mobilization

Oxysterols are oxygenated derivatives of cholesterol and key substrates for bile acid synthesis (Figure 2) (16). In the classic pathway of bile acid synthesis, cholesterol is converted into 7 $\alpha$ -hydroxycholesterol (7 $\alpha$ HC) by cholesterol 7 $\alpha$ -hydroxylase CYP7A1, a rate limiting step that occurs in the liver. In alternative pathways that occur primarily in extrahepatic tissues, cholesterol is converted into 24-hydroxycholesterol (24HC), 25-hydroxycholesterol (25HC), and 27-hydroxycholesterol (27HC) by cholesterol 24-hydroxylase CYP46A1, cholesterol 25-hydroxylase CH25H, and sterol 27-hydroxylase CYP27A1, respectively. Oxysterols are considered to be bioactive lipids and recent studies have started to reveal their important roles in both the hematopoietic and immune systems. 27HC is the most abundant circulating oxysterol and acts as an endogenous SERM which can bind to ERs and regulate their function (95). Plasma 27HC levels strongly correlate with total cholesterol levels (96), as 27HC is generated directly from cholesterol by the sterol 27-hydroxylase CYP27A1. Plasma 27HC levels are greatly reduced in *Cyp27a1*-deficient mice (97). CYP27A1 is abundant in the liver, but it is also expressed in extrahepatic tissues (16). Dietary or genetic changes that elevate 27HC levels modulate ER activity, thereby inhibiting vascular repair in cardiovascular disease (95), promoting ER-positive breast cancer growth (98, 99), and increasing the severity of atherosclerosis (100).

We have demonstrated that the increases in HSC division, HSC mobilization, and extramedullary hematopoiesis during pregnancy require ER $\alpha$  in HSCs, and E2 treatment induces HSC division as described above (14). Interestingly, our recent study revealed that treatment of mice with E2 did not increase HSC number in the spleen, indicating that E2 treatment does not induce HSC mobilization (101). In contrast, treatment with 27HC, another endogenous ER ligand, increased HSC number in the spleen but not HSC division in the bone marrow, indicating a role in inducing HSC mobilization. We demonstrated that the effect of 27HC on HSC mobilization is nullified by deletion of *Esr1* in hematopoietic cells, indicating that 27HC-induced HSC mobilization is dependent on ER $\alpha$ . Plasma cholesterol levels increase in humans during pregnancy (102). During pregnancy in mice, we observed significant increases in 27HC levels in HSPCs. *Cyp27a1*-deficient mice had significantly reduced HSC mobilization and extramedullary hematopoiesis during pregnancy, while the increased rate of HSC division in the bone marrow during pregnancy was not affected. These findings indicate that 27HC acts in concert with E2 to promote hematopoiesis during pregnancy by regulating ER $\alpha$  signaling in HSCs (Figure 3). As described above, increased cholesterol



levels promote HSC mobilization in mice and humans, and increased HSC mobilization in *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> mice is associated with elevated serum G-CSF levels (33). In our study, we observed that 27HC treatment significantly induced HSC mobilization in mice deficient for *Csf3*, which encodes G-CSF (101). Together, 27HC and G-CSF additively increased the numbers of colony-forming HSPCs in the peripheral blood. Therefore, 27HC and G-CSF likely act through distinct mechanisms to induce HSC mobilization. These findings suggest an alternative model that the ability of elevated cholesterol levels to promote HSC mobilization is mediated by increases in 27HC production, because treating mice with 27HC induces HSC mobilization and 27HC levels increase as cholesterol levels increase.

## E2, 27HC, and ER $\alpha$

ER $\alpha$  is a nuclear receptor transcription factor and E2 is the most potent endogenous estrogen. Different ER ligands are known to have distinct effects on ER $\alpha$ -mediated regulation of gene expression, and ER ligands differ in their structures and their effects on ER conformation (103–106). For example, Wardell et al. used breast cancer cell lines to test E2 and five different synthetic ER ligands and observed different gene expression patterns regulated by different ER–ligand complexes (106). 27HC induces a unique conformational change in the ER that is different from that mediated by E2 and other ER ligands (107). Different ER–ligand complexes also engage functionally distinct coregulators by selective recruitment of coactivators and corepressors to activate and repress expression of target genes, respectively (108). Thus, as different ER ligands can act through the ER $\alpha$  to differentially regulate gene expression, this may explain why E2 and 27HC have distinct effects on HSCs even though both act through ER $\alpha$  (Figure 3). It will be interesting to explore the nature of the ER $\alpha$  target genes as well as the mechanism by which ER $\alpha$  function is differentially regulated by E2 and 27HC, two major endogenous ER ligands.

## Bile Acids

Bile acids are synthesized from cholesterol in the liver (Figure 2), secreted into the bile, and delivered to the lumen of the small intestine where they act as emulsifiers of dietary lipids, cholesterol, and fat-soluble vitamins (16). However, bile acids have additional roles (109). Tauroursodeoxycholic acid (TUDCA) serves as a chemical chaperone and reduces endoplasmic reticulum stress (110). HSCs are predisposed to apoptosis through misfolded protein accumulation in the endoplasmic reticulum caused by cellular stress that subsequently activates the unfolded protein response (111). Addition of TUDCA to cultured mouse HSCs alleviates endoplasmic reticulum stress and increases their capacity to reconstitute the hematopoietic system in recipient mice upon transplantation (112). In contrast to the quiescent state of adult HSCs in the bone marrow, HSCs undergo a rapid expansion in the fetal liver during development (113). Adult HSCs in the bone marrow have a lower rate of protein synthesis as compared to most other hematopoietic cells (114). Sigurdsson et al.

reported that although fetal-liver HSCs had a higher rate of protein synthesis as compared to adult HSCs in the bone marrow, fetal-liver HSCs had lower expression of endoplasmic reticulum stress response genes (115). In addition to the role of CYP27A1 for side chain oxidation of cholesterol for the generation of 27HC to initiate the alternative acidic bile acid biosynthetic pathway, CYP27A1 also catalyzes another side chain oxidation after the ring modification step of both classic and alternative acidic bile acid synthesis pathways (Figure 2) (16). *Cyp27a1*-deficient mice have significantly decreased bile acids (97). Sigurdsson et al. also reported that fetuses in *Cyp27a1*-deficient mothers displayed significantly reduced levels of total bile acids as well as secondary bile acids in the fetal liver, suggesting that maternal bile acids are transferred to the fetus during pregnancy (115). Interestingly, the livers of *Cyp27a1*-deficient fetuses in *Cyp27a1*-deficient mothers contained a significantly lower number of long-term reconstituting HSCs, as assessed by limiting dilution transplantation assay, and these fetal HSCs showed significantly higher levels of protein aggregation. These findings imply that bile acids enable fetal-liver HSCs to have a higher level of protein synthesis without activating a stress response, allowing expansion of the HSC pool during fetal development.

## 25-Hydroxycholesterol

25HC is generated directly from cholesterol by CH25H, and 25HC is further converted into 7 $\alpha$ ,25-dihydroxycholesterol (7 $\alpha$ ,25HC) by the oxysterol 7 $\alpha$ -hydroxylase CYP7B1-mediated hydroxylation (Figure 2) (116). Expression of *Ch25h* is upregulated in macrophages and dendritic cells when they are exposed to various inflammatory mediators (117–120). 25HC augments the production of inflammatory cytokines in macrophages, and mediates feedback inhibition of *IL1b* expression and inflammasome activation in activated macrophages in the DNA sensor protein absent in melanoma 2 (AIM2)-dependent manner (121–124). 25HC is strongly induced following viral infection and by interferon, and it inhibits the replication of a wide range of enveloped viruses (125, 126). 25HC also promotes macrophage foam cell formation (127). Epstein-Barr virus-induced gene 2 (EBI2), a G protein-coupled receptor also known as GPR183, controls follicular B-cell migration and T-cell-dependent antibody production (128, 129). 7 $\alpha$ ,25HC acts as a ligand for EBI2 and directs migration of B cells in the spleen during the adaptive immune response (130, 131). EBI2 and 7 $\alpha$ ,25HC also regulate splenic CD4<sup>+</sup> dendritic cells for positioning in marginal zone bridging channels to maintain their homeostasis and mount a response against certain antigens, and positioning of activated CD4 T cells at the interface of the follicle and T zone to interact with activated dendritic cells (132–134). Thus, 25HC broadly regulates innate and adaptive immune cell behavior. The 7 $\alpha$ ,25HC/EBI2 axis also regulates bone mass homeostasis (135). EBI2 is expressed in monocyte/osteoclast precursors, and 7 $\alpha$ ,25HC is secreted by osteoblasts. EBI2 guides osteoclast precursors toward bone surfaces by promoting their movement and positioning, which facilitates fusion of osteoclasts and enhances the development of large osteoclasts to maintain bone mass homeostasis.

## CHOLESTEROL SYNTHESIS/METABOLISM AND HEMATOLOGIC MALIGNANCIES

Cholesterol metabolism is dysregulated in hematologic malignancies. The rate of cholesterol synthesis is higher in cells from acute myeloid leukemia (AML) patients as compared to healthy subjects (136). Hypocholesterolemia is frequently observed due to elevated LDL uptake by leukemia cells (137–139), but elevated cholesterol levels in leukemia cells have also been reported (140–143). Yvan-Charvet et al. reported that HFHC diet administered *Ldlr*<sup>+/-</sup> mice transplanted with cellular cholesterol efflux pathway-deficient *Abca1*<sup>-/-</sup>*Abcg1*<sup>-/-</sup> bone marrow cells displayed a myeloproliferative neoplasm (MPN)-like phenotype, and expression of an *APOA1* transgene that elevates HDL levels suppressed this phenotype (32). Thus, changes in intracellular cholesterol levels are associated with the development and maintenance of hematologic malignancies. Statins have cytotoxic effects in various types of malignant hematopoietic cells including AML (144–158), chronic myeloid leukemia (CML) (153, 159–161), MPNs (162), acute lymphocytic leukemia (ALL) (163, 164), chronic lymphocytic leukemia (CLL) (165–167), adult T-cell leukemia (ATL) (168), lymphoma (169, 170), and multiple myeloma (171–176). To identify compounds that can inhibit the stem cell activity of leukemia-initiating cells (LICs), Hartwell et al. performed a high-throughput screen in a bone marrow-mimicking culture system in which LICs expressing the *MLL-AF9* fusion oncogene were co-cultured with a bone marrow stromal cell line (177). Among the compounds that selectively inhibited LICs but not normal HSPCs, lovastatin also inhibited LIC stem cell activity in an *in vivo* bone marrow transplantation model. Although these reports demonstrate the effectiveness of statins, the mechanisms of their anticancer effects are not fully understood. Griner et al. reported that MPN-associated *JAK2*<sup>V617F</sup> localized to lipid rafts, subdomains of the plasma membrane that contain protein receptors and a high concentration of cholesterol, and simvastatin inhibited this localization and *JAK2*<sup>V617F</sup>-dependent cell growth in MPN model cell lines (162). Simvastatin also inhibited erythroid colony formation of primary cells from MPN patients, but had no effect on cells from healthy individuals. Other than the cholesterol-lowering effect, inhibition of the mevalonate pathway by statins also reduces the levels of farnesyl pyrophosphate and geranylgeranyl pyrophosphate and thereby inhibits protein farnesylation and geranylgeranylation, modifications that are important for a variety of cellular processes including cell proliferation, survival, and migration (Figure 2). Thus, the anticancer effects of statins could also be rendered through changes in these other cellular processes (157, 158, 170, 176).

Among the metabolites of cholesterol, oxysterols such as 7βHC, 25HC, 7β,25HC, 7-ketocholestanol, and 7-ketocholestanol have cytotoxic effects on leukemia and lymphoma cells (178–183). Tsujioka et al. reported that DNA methyltransferase inhibitors induced *CH25H* expression with enhanced 25HC production and promoted apoptosis in leukemia and myelodysplastic syndrome (MDS) cell lines, while

exogenous 25HC treatment suppressed cell growth of leukemia and MDS cell lines (184). Other than oxysterol, Sanchez-Aguilera et al. reported that tamoxifen treatment blocked development of *JAK2*<sup>V617F</sup>-induced MPN in mice and induced apoptosis of human MPN cells from patients with *JAK2*<sup>V617F</sup> mutation in a xenograft model (91). They also demonstrated that tamoxifen treatment reduced leukemic burden in a mouse model of AML using mice transplanted with bone marrow cells expressing the *MLL-AF9* oncogene. Their findings have uncovered the potential role of estrogen signaling in leukemia and suggest the potential use of SERMs as a treatment for leukemia. The roles of cholesterol metabolites in hematologic malignancies are not yet fully explored, and further studies of cholesterol metabolites are expected to elucidate their roles in hematologic malignancies and their potential in preventing and treating hematologic malignancies.

## CONCLUSION AND FUTURE DIRECTIONS

Cholesterol and its metabolites are now being recognized to have important roles in broad biological processes by regulating a wide variety of molecular machinery. Advances in understanding these molecular mechanisms will benefit human health. One potential clinical application of molecules that regulate or are regulated by cholesterol metabolism is to enhance mobilization of HSCs for transplantation. To enable efficient collection of mobilized HSCs from the peripheral blood for HSC transplantation, donors are treated with HSC-mobilizing agents such as G-CSF (185). However, a significant proportion of donors fail to reach the minimum HSC collection threshold required for transplantation using traditional strategies (186). The failure of mobilization can increase patient morbidity because patients cannot proceed to transplantation. Thus, advances in mobilization strategies that could increase the success of HSC collection without introducing additional side effects are needed to improve patient outcomes. For example, administration of 27HC enhances the mobilization of HSPCs by G-CSF (101). Identification of the genes downstream of 27HC-ERα signaling that mediate HSC mobilization may contribute to the development of new methods that improve the yield of mobilized HSCs for transplantation, while also offering an explanation for the long-standing observation that increased cholesterol levels are associated with increased HSC mobilization in mice and humans.

High blood cholesterol levels are associated with the development of atherosclerosis. Atherosclerosis is a progressive disease in which the inside of the artery become thick and stiff due to the buildup of the atheromatous plaque which consists of cholesterol, fat and other substances, and restricts blood flow and causes complications including myocardial infarction, peripheral artery disease, and stroke. In addition to lipids, various types of leukocytes also accumulate in the atheromatous plaque. Hypercholesterolemia causes monocytosis, and these monocytes give rise to macrophages which eventually turn into foam cells by ingesting LDL in the plaque, and promotes plaque growth and inflammation. Other than monocytes, diverse immune-cell subsets, such as neutrophils, mast cells,

B and T lymphocytes, are associated with atherosclerosis [reviewed in (187, 188)]. Oxysterols are formed and accumulate in the plaque as a result of LDL oxidation due to the inflammatory response. Although atherosclerotic properties of oxysterols have been tested, it is still unclear whether oxysterols have pro- or anti-atherosclerotic properties [reviewed in (189)]. Estrogens also affect atherogenesis. Despite of reports that support the atheroprotective effects of estrogens, it is also controversial whether they have pro- or anti-atherosclerotic properties [reviewed in (190)]. After myocardial infarction, monocyte recruitment is increased, and sustained and accelerated atherosclerosis is observed in a mouse model. Interestingly, myocardial infarction causes HSPC mobilization into the spleen and sustains augmented monocyteopoiesis, providing a possibility of novel therapy to mitigate progression of atherosclerosis (191, 192). Thus, cholesterol and its metabolites link hematopoiesis with cardiovascular health, and deciphering this link is critical for developing new targeted therapies.

The molecular mechanisms underlying the regulation of normal and malignant hematopoiesis by cholesterol and its metabolites are not yet fully understood. There are many drugs that target cholesterol synthetic and metabolic

pathways, and further studies are expected to generate novel strategies for enhancing hematopoiesis, augmenting hematopoietic recovery after hematopoietic injuries, improving collection of mobilized HSCs for transplantation, and treating hematologic malignancies.

## AUTHOR CONTRIBUTIONS

The author confirms being the sole contributor of this work and has approved it for publication.

## FUNDING

The study was supported by The Jackson Laboratory and the National Blood Foundation Scientific Research Grants Program.

## ACKNOWLEDGMENTS

The author gives appreciation to colleagues and collaborators, and apologizes to researchers whose work could not be cited and this review owing to space limitations. The author thanks Carmen Robinett for thoughtful editing of the manuscript.

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**Conflict of Interest Statement:** The author declares that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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# Oxysterols and Gastrointestinal Cancers Around the Clock

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## OPEN ACCESS

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equally to this work

### Specialty section:

This article was submitted to  
Cancer Endocrinology,  
a section of the journal  
Frontiers in Endocrinology

**Received:** 08 January 2019

**Accepted:** 03 July 2019

**Published:** 17 July 2019

### Citation:

Kovač U, Skubic C, Bohinc L,  
Rozman D and Režen T (2019)  
Oxysterols and Gastrointestinal  
Cancers Around the Clock.  
Front. Endocrinol. 10:483.  
doi: 10.3389/fendo.2019.00483

This review focuses on the role of oxidized sterols in three major gastrointestinal cancers (hepatocellular carcinoma, pancreatic, and colon cancer) and how the circadian clock affects the carcinogenesis by regulating the lipid metabolism and beyond. While each field of research (cancer, oxysterols, and circadian clock) is well-studied within their specialty, little is known about the intertwining mechanisms and how these influence the disease etiology in each cancer type. Oxysterols are involved in pathology of these cancers, but final conclusions about their protective or damaging effects are elusive, since the effect depends on the type of oxysterol, concentration, and the cell type. Oxysterol concentrations, the expression of key regulators liver X receptors (LXR), farnesoid X receptor (FXR), and oxysterol-binding proteins (OSBP) family are modulated in tumors and plasma of cancer patients, exposing these proteins and selected oxysterols as new potential biomarkers and drug targets. Evidence about how cholesterol/oxysterol pathways are intertwined with circadian clock is building. Identified key contact points are different forms of retinoic acid receptor related orphan receptors (ROR) and LXRs. RORs and LXRs are both regulated by sterols/oxysterols and the circadian clock and in return also regulate the same pathways, representing a complex interplay between sterol metabolism and the clock. With this in mind, in addition to classical therapies to modulate cholesterol in gastrointestinal cancers, such as the statin therapy, the time is ripe also for therapies where time and duration of the drug application is taken as an important factor for successful therapies. The final goal is the personalized approach with chronotherapy for disease management and treatment in order to increase the positive drug effects.

**Keywords:** oxysterols, circadian rhythm, hepatocellular carcinoma, pancreatic cancer, colorectal cancer, ROR, LXR, FXR

## INTRODUCTION

### Cholesterol and Oxysterols

Cholesterol is an essential molecule that participates in many cellular processes. It enables proper functioning of cellular membrane, is a precursor for synthesis of steroid hormones, oxysterols and bile acid, and functions as a signaling molecule regulating cell cycle, modifying proteins, and affecting its own synthesis (1–3). Most of the cholesterol in cells resides in the cellular membranes, where it plays a crucial role in stabilization of membranes, affects its fluidity and has an important role in lipid rafts (3). Oxysterols also have multiple functions, such as affecting membrane fluidity,

regulating SREBP (sterol regulatory element binding transcription protein) signaling pathway through regulation of INSIGs (insulin induced genes) and by this sterol synthesis, interacting with NPC1 (NPC intracellular cholesterol transporter 1) and OSBP/OSBPL [oxysterol-binding proteins (like)] and, most importantly, are ligands and activators of several nuclear receptors, such as RORs (NR1F1-3, retinoic acid receptor related orphan receptors A, B, C), FXR (NR1H4, farnesoid X receptor alpha), PXR (NR1I2, pregnane X receptor), ESR1/2 (NR3A1/2, estrogen receptor alpha/beta), and LXR (NR1H3, liver X receptor alpha) (4, 5). The term oxysterol usually means oxidized sterols that are produced from cholesterol enzymatically or by auto oxidation (**Figure 1**). However, also other sterols, including intermediates of cholesterol synthesis can be oxidized at least enzymatically by cytochrome P450 (CYP) enzymes (6). Auto oxidation of cholesterol usually happens in the presence of reactive oxygen species and oxidation occurs on the B ring of sterol nucleus, mainly at positions C7 or C6. With this process  $7\alpha/\beta$ -hydroxycholesterol, 7-ketocholesterol and 6-hydroxycholesterol are formed (7, 8). Enzymatic synthesis includes the side chain oxidation by CYP or non-CYP. For example, 24-hydroxycholesterol is synthesized by CYP46A1, 25-hydroxycholesterol by 25-hydroxylase (non-heme iron-containing protein) and 27-hydroxycholesterol by CYP27A1 (7, 9). Other oxysterols are formed by oxidation of the sterol nucleus, like  $4\beta$ -hydroxycholesterol synthesized by CYP3A4 or  $7\alpha$ -hydroxycholesterol by CYP7A1 (10). The concentration of oxysterols in normal healthy tissue and blood is  $10^4$ - to  $10^6$ -fold lower compared to cholesterol (11). In addition to endogenous synthesis, oxysterols can also derive from the diet. The cholesterol-rich food contains 10 to  $100\ \mu\text{M}$  concentration of oxysterols. Most common are  $7\alpha$ - and  $7\beta$ -hydroxycholesterol, 7-ketocholesterol, cholestane- $3\beta,5\alpha,6\beta$ -triol,  $5\alpha,6\alpha$ -epoxycholesterol, and  $5\beta,6\beta$ -epoxycholesterol (12). When oxysterols were fed to humans, they were found in chylomicrons and lipoproteins (13).

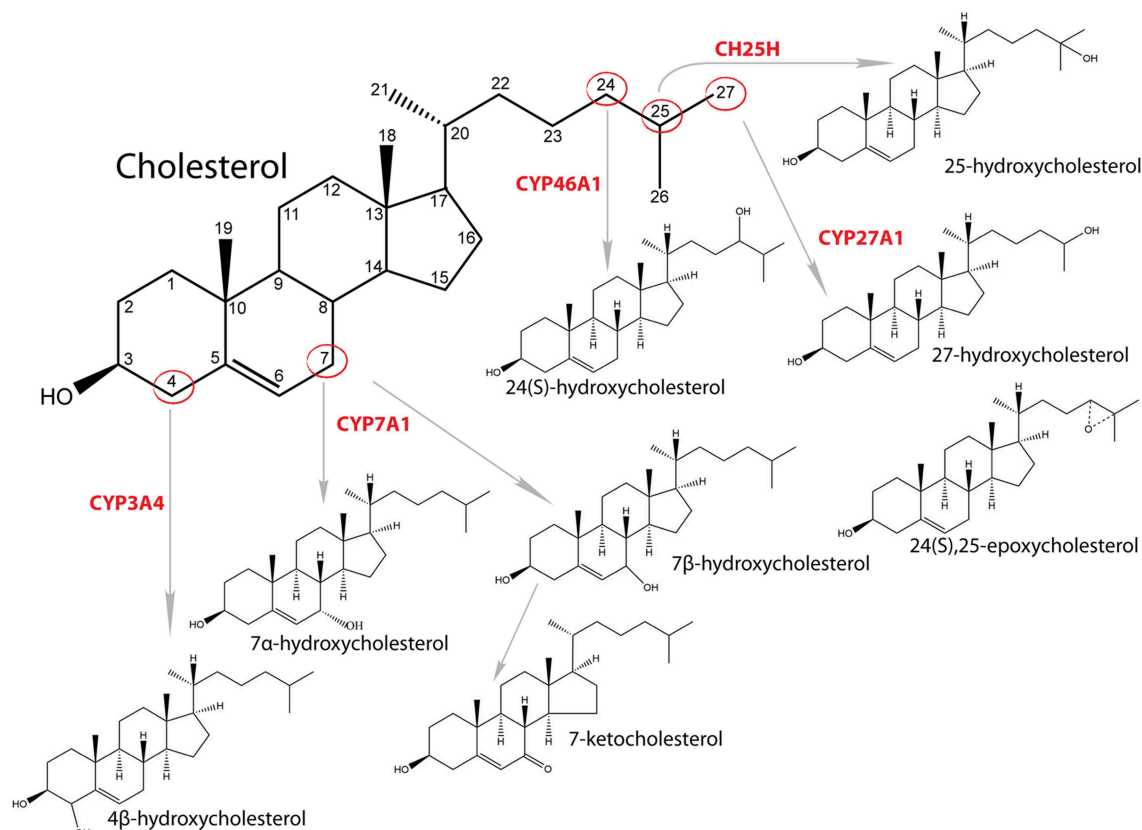
SREBPs are transcription factors that activate transcription of genes necessary for cholesterol synthesis and uptake. Mammalian cells express three SREBP isoforms, SREBP-1a, SREBP-1c, and SREBP-2, which are responsible for expression of different lipid associated genes. SREBPs are located in endoplasmic reticulum (ER) together with SCAP (SREBP cleavage-activating protein) the escort protein, and INSIGs, the inhibitors of translocation. When cholesterol level declines, SREBPs are translocated to Golgi apparatus together with SCAP where they are proteolytic cleaved. A smaller SREBP is translocated to nucleus where it induces transcription of target genes (14). The major regulator of cholesterol homeostasis is SREBP-2 (15) as shown by the early mouse knockout experiments as well as in follow-up studies (16, 17). When SCAP is bound to INSIG, the vesicular transport of SREBP from ER is disabled. The cholesterol and oxysterols level regulate the INSIG inhibition of SCAP/SREBP transport (18, 19). Interestingly, cholesterol and oxysterols both induce the SCAP-INSIG interaction but by different mechanisms. Cholesterol acts by binding to SCAP and causing its conformational change that promotes binding to INSIG. Oxysterols, on the other hand, act directly on INSIG. For INSIG-2 it was shown that hydroxyl

group on the side chain of sterols (22, 24, 25, or 27 position) is necessary for successful binding. A study confirmed these results, when 27-hydroxycholesterol levels were upregulated by CYP27A1 overexpression in mice or when primary hepatocytes were treated with 27-hydroxycholesterol, *Insig-2* expression was induced and SREBP-1 translocation was prevented (20). In this way, oxysterols regulate cholesterol synthesis and uptake through regulation of SREBP signaling pathway (18).

All these pathways are regulated by cholesterol and cholesterol synthesis intermediates but also by oxysterols themselves. Oxysterol synthesis itself is regulated in a similar manner as cholesterol and bile acid synthesis since many enzymes, transporters, and transcription factors are common. The excess of oxysterols is toxic for cells; therefore, oxysterols are transported to the liver, where they are metabolized to bile acid products and excreted from the body (21). FXR is a nuclear receptor of bile acids and is also the major regulator of bile acid synthesis. Hence, FXR regulates directly or indirectly expression and activity of oxysterol producing enzymes (CYP7A1, CYP27A1, CYP3A) (22). Also 22(R)-hydroxycholesterol has been shown to regulate expression of ABCB11 (ATP binding cassette subfamily B member 11, alternatively also BSEP- bile salt export protein) through FXR in hepatocytes (23). Since bile acids can act through different signaling pathways not connected to oxysterols, we will focus only on FXR direct involvement in selected cancers.

## Circadian Rhythm

Circadian clock as the inner rhythm in mammals is recognized as a cell-autonomous and self-sustaining mechanism, which controls almost every aspect of our life. The period of these rhythms is  $\sim 24$  h long, thus circadian (from latin *circa*—approximately; *diem*—day) (24). The circadian rhythmicity is known to be a crucial endogenous process of organisms, described in almost every live species from cyanobacteria to human, and is capable to adapt to the environmental rhythm of the day. Circadian homeostasis in mammals is maintained by the central clock located in the suprachiasmatic nucleus (SCN) of the hypothalamus which orchestrates numerous clocks in peripheral tissues. The peripheral clocks have been observed in cells and tissues all over the mammalian body. Light, however, is not the only signal for entrainment of internal clocks. Systemic cues including hormones, body temperature, feeding/fasting cycles also influence the circadian rhythm in tissues throughout the body (25). The molecular basis of clock is constituted of periodical expression of clock genes driven by the autoregulatory transcription-translation feedback loops involving *cis*-regulatory elements such as E-boxes, D-boxes, and ROREs (ROR-elements) (26). The positive transcriptional loop is formed by transcriptional activators ARNTL/BMAL1 (Aryl Hydrocarbon Receptor Nuclear Translocator Like) and CLOCK (Clock Circadian Regulator, NPAS2 in neuronal tissue, Neuronal PAS Domain Protein). The CLOCK:BMAL1 heterodimer binds to conserved E-box sequences in target gene promoters of *PER1,2,3* (Period Circadian Regulator 1, 2, 3), *CRY1,2* (Cryptochrome 1, 2), and *DEC1,2* (Deleted In Esophageal Cancer 1, 2) genes contributing to the activation of their expression (27). PER and CRY proteins dimerize in the

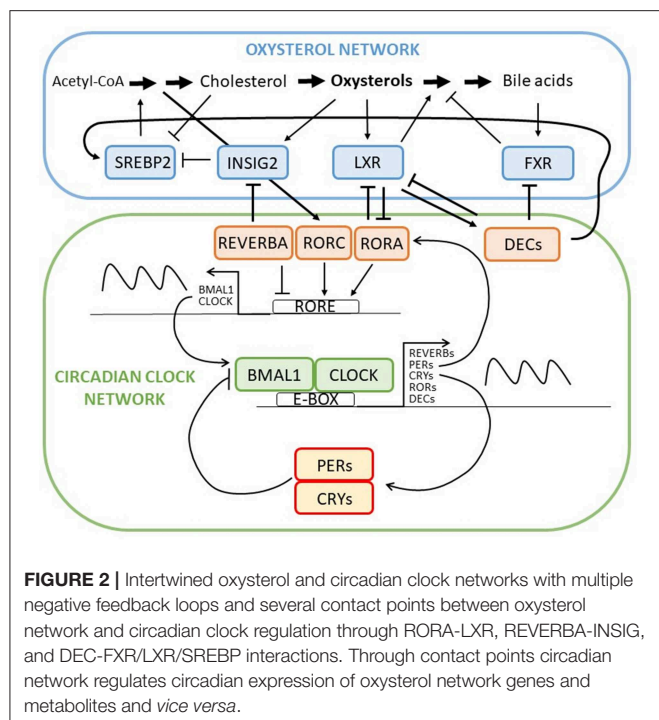


**FIGURE 1 |** Synthesis of oxysterols and catalyzing enzymes.

cytoplasm and after translocation to the nucleus inhibit further *CLOCK:BMAL1* transcription, forming the negative feedback loop. Also DEC1 and DEC2 can interact with the component of the SCN core clock genes. DEC1 and DEC2 proteins form dimers and translocate to the nucleus where they inhibit the activity of *CLOCK:BMAL1* heterodimer (28). The degradation of PER, CRY and DEC proteins is essential for the restart of a new cycle of the transcription with ~24 h periodicity. An additional regulatory loop of BMAL1 and CLOCK dimer activity is through interaction with RORs and REVERBA (Nuclear Receptor Subfamily 1 Group D Member 1, NR1D1). RORs and REVERBA compete for ROR response element in the promoter region of *BMAL1*, where REVERBA acts as inhibitor and RORs as activators of *BMAL1* transcription. In turn, *CLOCK:BMAL1* heterodimers activate *REVERBA* transcription. Besides E-boxes and ROREs, D-boxes play an important role as well. Transcription regulation through D-boxes goes via different transcription factors, such as DBP (albumin gene D-site binding protein) expressed in the SCN with a clear rhythm in the light-dark or constant dark conditions. The role of TIMELESS (timeless circadian regulator gene), which is mammalian ortholog of *Drosophila* TIM, remains ambiguous (29). In *Drosophila* TIM protein plays an important role and entrains the internal clock through light. After heterodimerization with PER, translocation to the

nucleus occurs and transcription of core clock cycle genes is inhibited.

Regulation of circadian rhythm, however does not stop with transcription-translation regulatory loops. Post-translational changes such as phosphorylation, ubiquitination and acetylation as well as epigenetic changes have been proven to play an important role in regulation of circadian rhythms (30–32). PER1–3 proteins are subjects to temporal changes in phosphorylation by CKIε (casein kinase Iε) and CKIδ, reaching a peak right before its destruction. Their reversible phosphorylation is a dynamic process with kinases and phosphatases as counterparts, their net effect leading to altered PER2 protein stability and cellular location, ultimately affecting the length of circadian period (33). Additionally, *CLOCK* has been found to have HAT (histone acetyltransferase) activity (34). While HAT activity results in transcription chromatin states, its counterpart, histone deacetylase, would condense chromatin and silence gene expression. Indeed, SIRT1 (sirtuin 1), a NAD<sup>+</sup> (nicotinamide adenine dinucleotide) dependent protein deacetylase, is a representative of HDAC (histone deacetylase) family, whose deacetylation is under circadian control. In the liver, SIRT1 deacetylates BMAL1 and PER2 as well as histone H3 in promoters of clock controlled genes (31, 35). With its reaction depending on NAD<sup>+</sup>, SIRT1 scopes far beyond its circadian



regulation. Primarily known physiological effects of SIRT1 deacetylation were regulation of metabolism and response to oxidative stress. It therefore represents a functional link between cellular metabolic activity and stress response, cell proliferation and genome stability, standing at crossroads of the processes we are tackling (31, 36–38).

## Cholesterol and Oxysterols Around the Clock

Disorders of lipid metabolism are responsible for many adverse pathologies, including tumor development. It is already well-established that circadian clock controls every aspect of our life, also the lipid metabolism (Figure 2). The core circadian machinery is placed in the hypothalamus and orchestrates other peripheral clocks in tissues like liver, colon, and pancreas. Peripheral clocks can be synchronized through different channels. They can be directly synchronized by SCN (neural and hormones signals), through food entrainment or body temperature (39). Lipid metabolism focusing on cholesterol metabolism is under a daytime specific regulation. Recently it was shown that adropin, identified as a protein that has a role in maintaining the energy homeostasis, could represent a link between circadian clock and cholesterol metabolism. Expression of adropin is diminished by cholesterol and 7-oxygenated sterols that can modulate the RORA/C signaling. The RORA/C and REVERB receptors might thus link adropin and its synthesis to circadian rhythm of lipid metabolism which is a novel and important connection (40).

Liver X receptors whose natural ligands are oxysterols have been found to regulate *Dec1*, a transcription factor involved in hepatic clock system and metabolism (41). *In vivo* observation showed reciprocal suppression between RORA and

LXR (42). Research on *Reverba* mutant mice showed a circadian controlled expression of *Cyp7a1*. Furthermore, Martelot et al. also demonstrated that REVERBA cooperates in modulation of cholesterol and bile acid synthesis through control of SREBP. Thus, REVERBA control the rhythmic abundance of *Insig2* and is further responsible for diurnal translocation of SREBP to the nucleus. The circadian activation of SREBP drives the circadian transcription of cholesterol biosynthesis genes and hence the oxysterols, which activate LXR. The cyclically activated LXR is responsible for cyclic expression of *CYP7A1* (43). Both, *Cyp7a1* and *Cyp27a1* showed circadian expression where sex differences in circadian variation were observed, indicating the importance of sex when planning the therapy (44). In the *Clock* mutant mice on a diet containing cholesterol and cholic acid showed reduced and disrupted *Cyp7a1* expression and high liver cholesterol accumulation (45). Timed high fat diet in mice, on the other hand, resulted in changed *Cyp7a1* expression via PPARα (peroxisome proliferator activated receptor alpha) as well as increased hepatic cholesterol (46). *Cyp7a1* anomalies were found in *Reverba* deficient mice as well as *Per1*<sup>-/-</sup> and *Per2*<sup>-/-</sup> mice, where bile acid homeostasis was disrupted (47, 48). Other CYP enzymes involved in cholesterol biosynthesis have been reported in association with circadian clock metabolism. CYP3A has a circadian pattern, but researched did not find it to be important for drug therapy due to small changes observed (49). mRNA levels and metabolic activity of CYP3A4 in serum-shocked HepG2 cells showed a 24 h rhythmicity. DBP was responsible for CYP3A4 activation (50). CYP8B1, an important player in bile acid and liver metabolism, is also under the RORA regulation resulting in its diurnal rhythm and fasting induction (51). Furthermore, DEC2 was shown as an important regulator that convey the circadian signal to the liver that has role in *CYP7A*, *CYP8B*, and *CYP51A1* expression (52).

## HEPATOCELLULAR CARCINOMA (HCC)

Hepatocellular carcinoma (HCC) is one of the most common causes of death worldwide and represents the most common primary malignancy in the liver. It is commonly associated with chronic hepatitis B virus (HBV) or hepatitis C virus (HCV) infection, aflatoxins and alcoholic cirrhosis (53). It is a global health problem and over 80% of HCC cases are seen in developing countries with the highest incidence in areas endemic for HCV and HBV (54). Most patients with HCC have liver cirrhosis but there is also a number of cases where patients with non-alcoholic fatty liver disease (NAFLD) and without cirrhosis develop HCC, demonstrating the role of NAFLD in its pathogenesis (55, 56). The incidence is increasing rapidly and is higher in men compared to women (57). Other types of liver cancers like intrahepatic cholangiocarcinoma, hepatoblastoma, and angiosarcoma are not so common in comparison to HCC. The molecular pathogenesis of HCC is extremely complex where circadian clock and lipid metabolism play an important role (58). Genetic and epigenetic alterations have been shown to also drive hepatocarcinogenesis. Knowing the crucial signaling pathways in HCC will enable us to provide better therapies to treat this cancer



**TABLE 1** | Oxysterol-circadian factors influencing HCC development.

Factor	Notes	Proposed function	References
Oxysterols	Increased in serum of NAFLD, HCV infected patients	Potential biomarkers	(60, 61)
	Treatment of HepG2	Cytotoxicity	(62)
25-hydroxycholesterol	Treatment of rat hepatoma cells	Pro-apoptotic	(62, 63)
25-hydroxycholesterol and OSBPL8	Treatment and overexpression in HepG2	Pro-apoptotic	
OSBPL8	Downregulation in Huh7 and HepG2	Pro-proliferative	(62)
	Overexpression in HCC cell line	Pro-apoptotic	(64)
LXR	Lower expression in HCC tumors	Lower post-operative survival rate	(65)
	Activity	Anti-proliferative via SOCS3	(66)
FXR	Lower expression and activity in HCC tumors	Association with multiple malignant characteristics	(67–72)
	Overexpression in HCC cell lines	Anti-proliferative, suppressed tumor growth in nude mice	(69)
	Downregulation in HCC cell lines	Pro-proliferative, increased migration and invasion, accelerated tumor growth in nude mice	(70)
SREBP1	Increased expression in HCC cell line	Required for tumor proliferation	(73)
CLOCK (NPAS2)	Increased expression in HCC tumors		(74)
	SNPs	Associated with increased risk for HCC, survival of TACE treated patients	(75)
PER3	SNP	Association with survival	(76)
PER2	Knockout mice	Higher diethylnitrosamine induced carcinogenesis	(77)
Chronic circadian disruption	Spontaneous hepatocarcinogenesis in mice	Metabolic disruption, CAR activation	(77–79)
TIMELESS	HepG2	Oncogenic	(80)

(59). The overview of factors associated with HCC are presented in **Table 1**.

In patients infected with HCV, the cholesterol transport in the liver is modified and serum concentration of cholesterol was lower compared to healthy individuals. Interestingly, the serum levels of oxysterols 4 $\beta$ -hydroxycholesterol, 25-hydroxycholesterol, and 7 $\alpha$ -hydroxycholesterol were elevated despite lower cholesterol concentration. When patients with HCV were treated with anti-viral therapy the oxysterols were reduced back to normal values. Further analyses indicated that these oxysterols were probably not elevated because of the activity of liver enzymes CYP3A4 and CYP7A1. CYP7A1 expression was unchanged in patients with HCV (61) and CYP3A4 activity was even downregulated (81). Direct effect of higher oxysterol concentrations on the development of HCC remains unknown, but oxysterols may be potential biomarkers and even potential novel targets for inhibiting disease progression (61). One of the major primary risk factors for HCC is NAFLD. With increasing control over hepatitis infections, it is predicted that NAFLD will soon become the major risk factor for HCC development. NAFLD is a complex multi systemic disease, caused by many factors such as genetics, dietary, environmental, and others (82, 83). In NAFLD patients, serum cholesterol is elevated and consequently some oxysterols (4 $\beta$ -, 25-, and 27-hydroxycholesterol) are also elevated. These oxysterols can affect the resorption of cholesterol in some tissues, through LXR activation, which regulates ATP-binding cassette transporters. In this way oxysterols affect the cholesterol concentration in NAFLD, which can evolve in HCC (60). In rat model with induced hepatoma tumor in the

liver, the measurements showed elevated levels of following oxysterols: 24S-, 25- and 27-hydroxycholesterol, and 24S,25-epoxycholesterol, which are all known to bind to LXR. In these tumors, the ABCA1 (ATP binding cassette subfamily A member 1) and ABCG1 (ATP binding cassette subfamily G member 1) cholesterol transporters were elevated on mRNA and protein levels, most likely through LXR activation. There is some data indicating that 25-hydroxycholesterol has a pro-apoptotic function in rat hepatoma cells and is able to induce sub-G1 apoptosis (63). Authors suggested that local addition of 25-hydroxycholesterol in combination with other drugs could be potentially used in treatment of hepatoma patients. HCC cells have changed metabolism to sustain the fast proliferation. Because of this, many cellular functions are altered, including cholesterol metabolism and transport. It was shown that oxysterols are cytotoxic, can induce cell death in HepG2 cells, and can suppress the growth of HCC cells by inhibiting ACAT2 (Acyl-coenzyme A:cholesterol acyltransferase) enzyme, which results in intracellular unesterified oxysterol accumulation (62). When OSBPL8 (also known as ORP8) is downregulated, cell proliferation is promoted. When ORP8 was overexpressed in HepG2 cells and 25-hydroxycholesterol was added, the ER stress and apoptosis were promoted (62). ORP8 overexpression was already enough to trigger apoptosis in primary HCC cells isolated from human liver and cell lines (64). Lower LXR expression was associated with lower post-operative survival rate (65). LXR regulated HCC response to TGF $\beta$ 1 (transforming growth factor beta 1), which acts as cytostatic and pro-apoptotic (84). LXR suppressed HCC proliferation through activation of SOCS3 (suppressor of cytokine signaling 3) (66).

FXR's role in HCC development was indicated when whole body *Fxr* knockout mice developed spontaneous HCC by the age of 14 months (85, 86). These mice had abnormal level of bile acids in the serum and administration of cholestyramine decreased HCC incidence (85). Many studies confirmed a significant decrease in FXR expression and activity in human HCC tumors and this was associated with multiple malignant characteristics (67–72). However, intestine-specific *Fxr* reactivation in *Fxr* knockout mice restored bile acid enterohepatic circulation, limiting hepatic inflammation and proliferation while preventing spontaneous hepatocarcinogenesis (87). Also only 20 and 5% incidence of hepatic tumors was observed in hepatocyte specific and enterocyte specific *Fxr* knockout mice, respectively. No serum or hepatic increase in bile acid level was observed in either of cell specific knockout models and no change in expression of cell-cycle regulators (88). These results lead to a hypothesis that high bile acid levels and FXR deregulation are needed for HCC development. There is, however, a mounting data pointing to a direct involvement of FXR in tumor suppression.

Overexpression of FXR decreased proliferation of HCC cell line and suppressed tumor growth in nude mice (69). Inhibition of FXR expression resulted in enhanced cell proliferation, migration and invasion in HCC cell lines and accelerated tumor growth in nude mice. FXR was shown to directly interact with  $\beta$ -catenin and repress its transcriptional activity (70). FXR also directly upregulates NDRG2 (N-myc downregulated gene family member 2) (72). NDRG2 is a known tumor suppressor, whose expression is reduced in HCC samples and correlates with aggressive tumor characteristics (72, 89). FXR also directly inhibited gankyrin expression via C/EBP $\beta$ -HDAC1 (CCAAT enhancer binding protein beta/ histone deacetylase 1) complex (90). Gankyrin is a known oncogene and is increased in HCC (91). In this study, they also showed that long-lived Little mice, which have high FXR liver expression, do not develop liver cancer after diethylnitrosoamine injection in comparison to wild type mice (90). FXR upregulated miR-122 which suppressed proliferation of HCC cells and the growth of HCC xenografts *in vivo* (71). In HCC human tumors miR-122 was significantly downregulated and this correlated with FXR expression (71). FXR and its agonist waltonitone repressed HCC cell proliferation by activating miR-22 repression of CCNA2 (Cyclin A2) (92). In HCC tumors FXR and miR-22 were downregulated while CCNA2 expression was opposite (92, 93). FXR also repressed inflammation via SOCS3 and via inhibiting NF $\kappa$ B (nuclear factor Kappa B) signaling (94, 95). FXR is a direct regulator of SOCS3, which enabled FXR-mediated cell growth repression, and their expression is correlated in HCC human samples (96). In summary, a direct role of FXR in protection against hepatocarcinogenesis could also be *via* defense against bile acid-induced injury, prevention of liver injury and apoptosis, prevention of ROS generation, promoting liver repair and generation after injury, suppressing cancer cell proliferation, etc. (97). There are some potential explanations available for the mechanisms behind FXR downregulation in HCC. In HCC cell lines miR-421 downregulated FXR and by this promoted cell proliferation, migration and invasion (98). Increased expression of miR-421 and its correlation with patient's survival was

confirmed in HCC patients (99). Another factor decreasing the expression and activity of FXR is inflammation and inflammatory cytokines were shown to inhibit HNF1A (HNF1 homeobox A) binding to FXR promotor (68). SIRT1 overexpression leads to deacetylation of FXR in the mouse liver, and inverse expression of SIRT1 and FXR was confirmed in human HCC samples (100). In spite of many tumor suppressor actions discovered, there is also some caution needed. FXR also upregulates FGF19 (fibroblast growth factor 19) which is anti-cholestatic and anti-fibrotic factor in the liver and was proposed for the treatment of NASH. However, FGF19, but not its rodent counterpart FGF15, is potentially pro-tumorigenic as shown by ectopic expression in mice (101). FGF19 expression is upregulated in HCC samples and correlates with poor prognosis (102). This is an important factor to consider when translating results from studies in rodent models to humans. However, new engineered FGF19 variants have been developed excluding pro-tumorigenic activity and are currently in evaluation for the treatment of NASH (103).

More and more results show the importance of SREBPs, especially SREBP-1, as a link between oncogenic signaling and tumor metabolism. It was shown that cancerous cells have higher *de novo* lipogenesis, which is required for rapid tumor proliferation. In the cancer cells, SREBP-1 is highly activated and it was shown, that pharmacological targeting of SREBP-1 greatly inhibits tumor growth. This rises hope for SREBP-1 to be potential anti-cancerous target (73). Higher expression of SREBP-1 was shown in different cancer cell lines (104) and higher expression of SREBP-1 is associated with many metabolic diseases; including NAFLD and NASH. One of the factors activating SREBP-1 in HCC is hepatoma-derived growth factor (HDGF). Co-expression of HDGF and SREBP-1 is an indicator of poor HCC prognosis. HDGR knockdown or its mutation in HepG2 cells resulted in decreased expression of SREBP-1 targeted genes (105). A study on a mouse model of HCC showed that lipid biosynthesis (fatty acids and cholesterol) is crucial for HCC development and that targeting SREBP pathway can be used as an anti-tumor strategy (106). Study on hepatic stellate cells, which have an important role in liver fibrosis, showed that in these cell line INSIG-1 and INSIG-2 expression is downregulated. By downregulation of INSIGs, SREBP signaling is promoted, which is the characteristic of HCC and crucial for cancer proliferation (107). Bioinformatics analysis showed that two miRNA (has-miR-221 and has-miR-29c) are potential HCC diagnostic markers and that they have one common target, which is *INSIG1* (108). All these data show the importance of SREBP signaling and its potential as drug target.

Data on human and mice reported a connection between circadian rhythms and liver disease where alterations in rhythmicity had a profound effect on metabolic pathways resulting also in adverse outcomes, like HCC. NPAS2 or CLOCK was shown to have a critical role in HCC and expression of the protein was significantly upregulated in HCC patients (74). In other study, single nucleotide polymorphisms (SNPs) in NPAS2 were associated with the increased risk for HCC or with overall survival in HCC patients treated with transcatheter arterial chemoembolization (TACE) (75). The rs2640908 polymorphism within *PER3* was also associated

with overall survival in HCC patients treated with TACE (76). SNPs from circadian negative feedback loop genes were further studied and were suggested to have an independent role as prognostic biomarkers for prediction of HCC clinical outcome (109). Study on mice showed that circadian disruption due to *Per2* mutation or jet lag has a profound role in liver carcinogenesis induced by diethylnitrosamine (77). Other research addressed the importance of the circadian clock metabolism in hepatocarcinogenesis where the changes in expression of several core clock genes were downregulated (*BMAL1*, *CLOCK*, *PER1*, *PER2*, *CRY1*, *CRY2*), while upregulation of clock related genes (*NR1D1* and *DBP*) was observed (110). Circadian metabolism and carcinogenesis are highly interconnected and the connection is complicated. Kettner et al. demonstrated that chronic circadian disruption induces NAFLD and spontaneous hepatocarcinogenesis, promotes genome-wide deregulation and metabolic disruption, and activates CAR (NR1H3, constitutive androstane receptor) which drives NAFLD to NASH, fibrosis and HCC progression (78). Chronic circadian disruption in mice had a profound effect on metabolism, what was also observed in humans and circadian disruption with or without steroid receptor Coactivator-2 (SRC-2) ablation showed association with human HCC gene signature (79). The TIMELESS protein has oncogenic function in human HCC as well (80). Studies on HepG2 cell line demonstrated the importance of *RORA* in different steps in liver carcinogenesis (111).

## PANCREATIC CANCER (PC)

Pancreatic cancer is one of the most malignant cancers, estimated to cause 432 242 deaths in 2018 and ranking seventh among estimated cancer deaths in the world (112). Estimated 5-year survival rate is extremely low and only 4% of patients will live 5 years after diagnosis. An important risk factor is smoking, since around 20% of tumors are attributable to smoking. Other risk factors include family history of chronic pancreatitis or pancreatic cancer, male sex, advancing age, diabetes mellitus, obesity and occupational exposure (113, 114). Novel epidemiological studies propose that dietary factors also impact pancreatic cancer risk. In a large population saturated fatty acid intake was linked to higher pancreatic cancer risk, while omega-3 fatty acids, increased vitamin C and vitamin E intake lowered cancer risk (115). Pancreatic cancer patients have unspecific signs, making the diagnosis difficult, often discovering already advanced stages of the disease. The overview of factors associated with PC are presented in **Table 2**.

Very little is known about the oxysterol role in the development of pancreatic cancer. Serum cholesterol, 5 $\alpha$ ,6 $\alpha$ -epoxide, and lanosterol were identified as highly discriminating between pancreatic cancer patients and healthy subjects (116). Two meta-analyses showed that dietary cholesterol may be associated with pancreatic cancer in worldwide populations (128, 129). OSBPL have been shown to be involved in pathology of PC. Increased expression of OSBPL5 was associated with higher

invasion and poor prognosis of pancreatic cancer patients (117, 118). In pancreatic ductal adenocarcinoma (PDAC) patients, OSBPL3 was found as differentially expressed in four studies and was correlated with poor prognosis of these patients (119). The role of nuclear receptors also remains unknown. Activation of LXR by synthetic ligands had anti-proliferative effects on PDAC cells (120). Very few studies measured the expression FXR and its role in pancreatic cancer. Moreover, there are conflicting results available. The increase in FXR mRNA and protein expression was confirmed in pancreatic tumors in comparison to adjacent tissue, and high FXR expression was correlated with the poor prognosis. FXR inhibition reduced cell proliferation, migration and invasion in pancreatic cancer cell lines (121, 122). It was proposed that FXR induced phosphorylation of SP1 (Sp1 transcription factor) and by this promoted cancer progression (122). While another study found correlation between high FXR expression with less aggressive phenotype, smaller tumors, absence of metastases and better prognosis (123). The difference in FXR expression and correlation between studies can simply be attributed to a low sample number, different groups of patients, different length of time in survival analyses, correlation with other factors etc. However, bile acids were increased in plasma and pancreatic juice in PC patients, and the mouse model confirmed the correlation between the increase in serum bile acids level with the severity of the disease (124). FXR was significantly increased in pancreatic cancer cell lines in comparison to normal pancreatic cells and FXR was found as the regulator of FAK (PTK2, protein tyrosine kinase 2)/c-Jun (JUN, Jun proto-oncogene, AP-1 transcription factor subunit) / MUC4 (mucin 4) signaling pathway (124). Similar to HCC, SREBP1 pathway and *de novo* lipogenesis is upregulated in PC. Study on 60 PC patients showed high correlation between elevated SREBP1 expression and poor disease prognosis. Inhibition of SREBP1 in a mouse model lead to decreased *in vivo* weight of tumor, indication the importance of SREBP1 upregulation for cancer cell growth (130). Study on PC cell model showed that inhibitors of SREBP1 decrease PC cell viability and proliferation. This indicate that targeting SREBP1 pathway is potential target for PC disease management and should be further explored (131). One of the potential molecules for targeting SREBP1 is resveratrol. Recent study on mouse model of PC and human cell lines treated with gemcitabine (chemotherapy medication) showed that resveratrol suppressed stemness induced by gemcitabine. Resveratrol should be considered as an additive for chemotherapeutic drugs (132).

Circadian activity in pancreas is also controlled by SCN (133, 134). The clock genes expression (*BMAL1*, *PER1*, *PER2*, *PER3*, *CRY2*, *TIMELESS*, and *CK1 $\epsilon$* ) is altered in PDAC which is the most common type of pancreatic malignant tumors (135, 136). In humans, lower *BMAL1* expression was associated with poorer survival rate, and correlated with higher tumor stage, poorer histological differentiation, and increased vascular invasion in PDAC (125, 126). Since knockdown of *Bmal1* resulted in an anti-apoptotic and pro-proliferative profile, while its overexpression had the opposite effect, *Bmal1* can act as an anti-oncogene by binding directly to *p53* promoter region (126). Since circadian rhythms and metabolic pathways go both ways, and pancreatic

**TABLE 2 |** Oxysterol-circadian factors influencing PC development.

Factor	Notes	Proposed function	References
Cholesterol, 5 $\alpha$ ,6 $\alpha$ -epoxide, and lanosterol	Increased in serum of PC patients	Potential biomarkers	(116)
OSBPL5	Increased expression in PC tumors	Higher invasion and poor prognosis	(117, 118)
OSBPL3	Increased expression in PDAC tumors	Poor prognosis	(119)
LXR	Activation by ligands in PDAC cell lines	Anti-proliferative	(120)
FXR	Increased expression in PC tumors	Poor prognosis	(121, 122)
	Increased expression in PC tumors	Better prognosis	(123)
	Inhibition in PC cell lines	Anti-proliferative, lower migration and invasion	(121, 122)
BMAL1	Increased expression in PC cell lines	Regulator of FAK/JUN/MUC4 pathway	(124)
	Lower expression in PC tumors	Poor prognosis	(125, 126)
	Knockdown in PC cell lines	Anti-apoptotic, pro-proliferative	(126)
SIRT1	Significant down regulation in PC tumors	Lower mortality rate	(127)

cancer risk is increased in people with metabolic syndrome (137), the role of metabolism and its disruption plays an important role in pancreatic cancerogenesis. A recent study evaluating dietary influence on cancer risk in women confirmed the role of obesity (138). *Bmal1* and its downstream regulation seems to play a crucial role in pancreatic regulation of metabolic processes, as *Bmal1* knock out in mouse  $\beta$ -cells led to glucose intolerance and development of diabetes (139). Since glucose metabolism is also under the circadian control, it is not surprising that alterations in clock genes (*Clock*, *Bmal1*) lead to impaired glucose tolerance (140), with a profound role in pathogenesis of pancreatic cancer (141). Deregulation of SIRT1, which regulates the central and peripheral clock, has an important role in PDAC as well (127).

## COLORECTAL CANCER (CRC)

Colorectal cancer is the third most commonly diagnosed cancer, the second most common cause of oncological death in the world estimated in 2018 (112) and as such represents a major public health issue worldwide. About 6% of CRCs are predetermined by a defined hereditary syndrome, while around 25% of CRCs are familial, the latter being tightly intertwined with many of the modifiable risk factors as well as genetic factors. Non-modifiable risk factors for CRCs include increasing age, male gender, African American race and residence in high-income countries (142), while modifiable factors include obesity, moderate to heavy alcohol consumption, smoking, high consumption of red or processed meat and a diet with low fiber, fruit, and vegetables intake (112, 142). Also, genetics plays an important role in its pathogenesis (142). In CRC one of the most commonly dysregulated pathway is the Wnt/ $\beta$ -catenin signaling, leading to  $\beta$ -catenin accumulation, ultimately resulting in activation of several gene targets, including oncogenes that contribute to the development of cancerous phenotype (143). Its component APC (APC regulator of WNT signaling pathway) mutations are present in majority of sporadic CRCs (144). Since onset and progression of CRC are tightly intertwined

with its mutational pathways, detailed knowledge of their regulation is crucial for obtaining new markers in order to better understand risk factors as well as treatment and prognosis. The overview of factors associated with CRC are presented in **Table 3**.

High total cholesterol level is associated with a higher risk for colon cancer in men (145). Another study taking into account also genetic factors again confirmed a link between hypercholesterolemia and colorectal cancer risk (146). A *CYP7A1* haplotype and SNPs were significantly associated with colorectal cancer and it was proposed to be the effect of fecal bile acids (147–150). Whole grain food significantly reduces colon cancer risk and phytochemicals that are involved in this protection are especially interesting (182).

Studies in colon cancer cell lines indicate that different oxysterols are cytotoxic and induce apoptosis. A study of wheat bran showed that it contains several different oxyphytosterols with anti-proliferative effect on colon cancer cell lines, some could also induce apoptosis (151). Dietary-representative oxysterol mixture induced apoptosis in differentiated colonic CaCo-2 cells (152). A study in major cell line models for CRC, Caco2 and SW620 cells, showed that 27-hydroxycholesterol decreased proliferation of these cells (153). This effect was not due to cellular cytotoxicity or induction of apoptosis and it was independent of nuclear receptors LXR and ESRs. 7 $\alpha$ - and 7 $\beta$ -hydroxycholesterol, 5 $\alpha$ ,6 $\alpha$ -epoxycholesterol and 7 $\beta$ -hydroxysitosterol were all able to induce apoptosis in human colon cancer cell line Caco-2 (154, 155). 7 $\beta$ -hydroxycholesterol was cytotoxic to colon cancer cell lines in concentrations from 3 to 10  $\mu$ M (156). 7-ketocholesterol and 25-hydroxycholesterol reduced barrier functions, apoptosis and induced viability of Caco-2 cells (158). 7-ketocholesterol besides decreasing epithelial barrier also induced inappropriate development of inflammatory response to food (159). 7-ketocholesterol induced ER stress in HT-29 colon cancer cell line (160) and affected mitochondrial functionality in Caco-2 cells, while co-treatment with 7-ketostigmaterol reduced the toxic effect (161). Only 25-hydroxycholesterol, but not the



**TABLE 3 |** Oxysterol-circadian factors influencing CRC development.

Factor	Notes	Proposed function	References
Total serum cholesterol	Increased in humans	Higher risk for CRC	(145, 146)
CYP7A1	SNP and haplotype	Associated with CRC	(147–150)
Oxyphytosterols	Treatment of CRC cell lines	Anti-proliferative, pro-apoptotic	(151)
Dietary oxysterols	Treatment of Caco-2	Pro-apoptotic	(152)
27-hydroxy cholesterol	Treatment of CRC cell lines	Anti-proliferative	(153)
7 $\alpha$ - and 7 $\beta$ -hydroxycholesterol, 5 $\alpha$ ,6 $\alpha$ -epoxycholesterol, and 7 $\beta$ -hydroxysitosterol	Treatment of Caco-2	Pro-apoptotic	(154–156)
7 $\beta$ -hydroxycholesterol	Treatment of Caco-2	Induced expression of inflammatory and chemotactic cytokines	(157)
7-ketocholesterol	Treatment of Caco-2	Reduced barrier functions, anti-apoptotic, induced viability, lower inflammatory response	(158, 159)
25-hydroxycholesterol	Treatment of HT-29	Induction of ER stress	(160)
	Treatment of Caco-2	Mitochondrial functionality	(161)
	Treatment of Caco-2	Reduced barrier functions, anti-apoptotic, and induced viability	(158)
	Treatment of DLD-1	Induction of cell death, anoikis	(162)
	Treatment of Caco-2	Enhanced IL1B induction of IL8	(163)
LXR	Induction by agonist in CRC cell lines	Anti-proliferative	(164)
CYP8B1, CYP46A1, CYP2R1	Higher expression in CRC	Poor prognosis	(165)
CYP7B1	Higher expression in CRC	Good prognosis	(165)
OSBPL9	Downregulation in CRC tumors	Poor prognosis	(166)
LXR	Increased expression	Good prognosis	(167)
FXR	Activation in HT-92	Anti-proliferative	(168, 169)
	Decreased expression in CRC tumors	Poor prognosis	(170–175)
	Knockout in mice	Increased susceptibility to chemically-induced	(171, 176)
PER1, PER3	Overexpression in CRC cell lines	Reduced tumor growth, anti-proliferative, pro-apoptotic	(92, 171, 175–177)
	Decreased expression in CRC tumors	Poor prognosis	(178)
PER1, BMAL1	Decreased PER1 and increased BMAL1 in CRC tumors	Poor prognosis	(179)
PER2	Increased in CRC tumors	Good prognosis	(178)
RORA	SNPs	Risk of development of CRC	(180)
SIRT1	Lower expression in CRC tumors	Good prognosis	(180)
	Transgenic mice and human tumor specimens	Suppression of <i>in vivo</i> tumor formation	(181)

22-(R)-hydroxycholesterol and other oxysterols (7 beta-hydroxycholesterol and 5-cholesten-3beta-ol-7-one) induced anoikis, a type of programmed cell death, in DLD-1 cells (162). Some of these effects could be through activation of LXRs, since LXR induction by GW3965 had anti-proliferative effects on colon cancer cells (164).

On the other hand, oxysterols also affect expression of inflammatory molecules in colon cancer cells. Inflammatory bowel disease is an important risk factor for development of CRC and chronic inflammation and oxidative stress are part of pathogenesis (183). 7 $\beta$ -hydroxycholesterol induced expression of key inflammatory and chemotactic cytokines in CaCo-2 cell line (157). 25-hydroxycholesterol pre-treatment enhanced IL1B (interleukin 1 beta) induced IL8 (interleukin 8) production in Caco-2 cells (184). Representative mixture of oxysterols increased oxidative stress in differentiated Caco-2 cells and

was followed by the production of cytokines IL6 (interleukin 6) and IL8 (163). In CRC patients, serum level of IL8 was increasing with the progression of cancer (185). Expression of enzymes and oxysterol receptors is modulated in CRC. Human tissue microarray analyses revealed significantly higher protein expression of CYP2R1, CYP7B1, CYP8B1, CYP46A1, CYP51A1, while CYP27A1 and CYP39A1 had no significant change, in primary colorectal tumor compared to normal colonic mucosa (165). In this study, they also showed a significant association between patient prognosis and survival with CYP expression. For example, higher expression of CYP8B1, CYP2R1, CYP27A1, and CYP46A1 in tumor was associated with poor prognosis, while high CYP7B1 expression correlated with good prognosis. OSBPL1A short transcript variant was down-regulated in colon cancer tumors, but the long variant was unchanged in comparison to normal samples (186). OSBPL9 was

included in a gene expression signature as a predictor of survival in colon cancer and was downregulated in poor prognosis patients (166).

LXR expression was proposed to be a prognostic indicator for CRC and its expression was associated with favorable clinical outcome. Positive LXR expression was associated with better survival rate and there was a significant negative association between LXR expression and vascular invasion, but no association was found between LXR expression and the patient's age, sex, tumor size, grade or TNM (tumor/node/metastasis) stage (167). A genome wide analyses revealed regulatory programs of LXR activation which lead to inhibition of HT29, a colorectal cancer cell line, proliferation (168). LXR was shown to directly bind to  $\beta$ -catenin and suppress its activity and cellular proliferation (169). A recent review has already summarized FXR and bile acids role in the development of colon cancer (187). Several studies showed that FXR expression is reduced in intestinal tumors in humans and that it is inversely correlated with the degree of malignancy and clinical outcome (170–175). The FXR knockout mice have increased susceptibility to chemically-induced colorectal carcinogenesis, while FXR overexpression in gut cells reduced tumor development and growth (171, 176). The activation of FXR was shown to suppress proliferation and induce apoptosis in colon cancer cell lines (171, 177). The observed downregulation of FXR expression is due to increased methylation of FXR promotor by the loss of APC function, which was confirmed in CRC cell lines, animal models and colonic tumors from patients (174, 188, 189). However, FXR is also downregulated by intestinal inflammation, western diet, and microRNA (187, 190). The current hypothesis is that the decreased FXR regulation in combination with Western diet and hence higher levels of secondary bile acids results in pro-tumorigenic colon environment leading to the development of colon cancer. Moreover, recent studies showed that FXR exhibits anti-cancerogenesis effects beyond regulation of bile acid level, by also affecting other cellular signaling pathways in colon cells. A study in mouse and organoid models, showed that FXR regulated proliferation of intestinal cancer stem cells (191). FXR repressed proliferation of colon cells by inhibiting the MMP7 (matrix metalloproteinase 7), a known intestinal tumor promotor expression; by activating mir-22 repression of CCNA2 (Cyclin A2); and by activating the EGFR/SRC (epidermal growth factor receptor/SRC proto-oncogene) pathway in colon cells (92, 175, 177). Upregulation of SREBP1 pathway is also present in CRC (192). Inhibition of SREBP1 in CRC shows promising result for cancer management. It was shown that ordonin (diterpenoid isolated from *Rabdosia rubescens*) reduced expression of SREBP1 and induce apoptosis in CRC cells cultures (193).

Epidemiological studies have shed light on connection between circadian disruption and elevated risk of cancer, including colorectal cancer (128, 194, 195). Meta-analysis showed increased incidence of colorectal cancer in people with long-term exposure to night light (shift work). The proposed mechanism for circadian disruption on oncogenesis is melatonin suppression and loss of its protective effect against cancer via apoptosis, anti-angiogenesis, anti-oxidation and regulation

of the immune system. One of the proposed additional factors is low level of 25-hydroxyvitamin D due to lower sun exposure (128). In mouse models, physical destruction of the SCN as well as functional disturbance of circadian rhythms (chronic jet lag) resulted in accelerated tumor growth in transplantable tumor models (Glasgow osteosarcoma and Pancreatic adenocarcinoma), indicating a role of circadian system in controlling malignant growth (196). In human CRC, there are multiple studies reporting abnormal expression of circadian genes including altered expressions of *CLOCK*, *BMAL1*, *PER1*, *PER2*, *PER3*, and *CK1 $\epsilon$*  (179, 197–200). Whether the disruption originates in core clock genes and drives tumorous transformation or measured disruption is a consequence of cancer, remains unclear. However, studies suggest that clock genes have an important role in tumor suppression (201). Although clinical correlations between specific mechanisms of clock gene disruption and colorectal cancer phenotype and prognosis have not been conclusive, some pathways show typical clinical and pathological features. Decreased expression of *PER1* and *PER3* in tumor tissue as such indicate poorer survival rate (178), decreased *PER1* and high *BMAL1* expression correlate with poorer outcome and liver metastasis (179), and high *PER2* expression correlate with significantly better disease outcome (178). In recent systematic evaluation of genetic variants in the circadian pathways connected with CRC, examining 119 SNPs in *RORA* was proposed as potentially important marker for CRC risk and prognosis. While people carrying SNP in *RORA* were much more inclined to developing CRC, lower *RORA* correlated with better differentiated tumors and better disease outcome (180). On the other hand, changes in cellular metabolism may cause circadian disruption, further influencing colorectal cancer phenotype (202). It has been shown that SIRT1 suppresses colorectal tumor formation *in vivo* by  $\beta$ -catenin deacetylation (181). A recent study showed that both metabolic and circadian dysregulation progressed during cancer progression. Their findings suggested that clock-related glycolysis genes alterations might add to a clock-driven rewiring of metabolism, connected to cancer progression and altering response to cancer therapy (203).

## NEW THERAPEUTIC STRATEGIES

### Targeting Oxysterol-Cholesterol Network

Statins are widely used lipid-lowering drugs which inhibit HMGCR, a rate limiting enzyme from cholesterol synthesis. Statins have been proposed in several studies as potential drugs used for reducing the risk of development and mortality in gastrointestinal cancers. Statin use was associated with a decreased risk of mortality in several cancers also colorectal cancer (204). However, another study showed no association with colorectal cancer incidence in United States cohort (205). Longer statin use was connected to a reduction in all-cause mortality in patients after colorectal diagnosis (206). However, overall conclusion of meta-analyses of 42 studies was that statin use was associated with a modest reduction in risk of CRC (207). This association was confirmed for lipophilic

statins but not for hydrophilic statins. In addition, long-term statin use (>5 years) did not significantly affect the CRC risk.

HCC occurs mainly in cirrhotic liver and statins may affect the risk of HCC by their anti-fibrotic effect. Three meta-analyses confirmed that statin use is associated with lower risk of HCC in different populations (58, 208, 209). Fluvastatin was pointed out in one of these studies. A registry-based study also confirmed an association between statin use and the risk of HCC and additionally showed a dose response relationship (210). Statin use also significantly decreased the risk of HCC in patients with HBV (211, 212). Studies suggest that statins lower the risk of cancer in general in chronic hepatitis patients (213). Overview of studies on statin effect on mean survival rate revealed a link to extended survival, but the length of survival was variable among studies (214). Perioperative statins have been associated with improved recurrence-free survival in HCC patients (215, 216). Meta-analysis confirmed an association between statin use and decreased risk in mortality in pancreatic patients, but other studies found no association (217, 218). A review of studies revealed that observational studies found the association but randomized controlled trials did not. Statins have anti-neoplastic properties through anti-proliferative, pro-apoptotic, anti-angiogenic and immunomodulatory effects and can affect multiple signaling pathways in cells (219). Most important is the inhibition of HMGCR and by this synthesis of mevalonic acid. *HMGCR* genetic variant significantly modified the protective association between statins and CRC risk (220). Mevalonate pathway is upregulated in several cancers, also pancreatic and hepatic, and is responsible for activation of small G proteins (221). All these data make statins compelling therapy for decreasing the risk of cancer and lowering mortality of patients, but due to conflicting results, it is difficult to form final recommendations. An important issue in prescribing statins are the side effects of statins such as hepatotoxicity and drug-induced myopathy.

Since SREBPs target genes are upregulated in many cancers, SREBPs could have therapeutic potential (106). Several studies showed a successful targeting of SREBP pathway and suppression of lipid metabolism with substances like TAK1, Emodin and using different miRNA (222–225). Since oxysterols bind to INSIG and affect SREBP signaling pathway, oxysterols also have a potential to be used in cancer proliferation inhibition, but more studies on oxysterol-INSIG interaction are needed.

Oxysterols activate several nuclear receptors most importantly LXR, which is hypothesized to exert their anti-cancerogenic effects. Targeting LXR for prevention and therapy of cancers is already evaluated in clinical studies. LXR is an interesting target, because it is activated by phytosterols, which can reduce the incidence of colon cancer (226). LXR is connected to TGF $\beta$ 1 actions and was also proposed as a potential target for treatment of HCC (84). Bergapten, a LXR agonist, was already evaluated for HCC treatment (227). LXR agonists were proposed also for treatment of CRC since LXR activation reduced intestinal tumor formation in a mouse (APC<sup>min/+</sup>) CRC model and also blocked proliferation of human colorectal cells

(228). LXR is a promising target, but majority of evidence was gathered through studying the effects of LXR activation in cell lines (4).

FXR is also a promising target for cancer treatment. Activation of FXR would prevent toxic bile acids build up, but also repress other tumorigenic proteins. In preclinical and clinical trials FXR agonists show a potential for treatment of different liver disease among them also HCC (175, 229, 230). In the mouse (APC<sup>min/+</sup>) CRC model on high fat diet, treatment with FexD, a deuterated analog of fexaramine with the gut-restricted activity, resulted in slower tumor progression, improved bile acid homeostasis and improved survival (191). However, FXR's role in pancreatic cancer is conflicting and the fact that in humans it activates a potentially pro-tumorigenic FGF19 emphasizes the needed for more studies that will confirm the positive role of FXR agonists.

## Chronotherapy as a New Therapeutic Strategy

Cancer represents the second leading cause of death worldwide (231). The available treatment is not always the most efficient thus new therapeutic strategies are needed to be developed. In addition to standard therapy (chemotherapy, radiation, and surgery), additional factors need to be taken into consideration, such as lifestyle and biology, when providing integrative treatment for different cancer types (232). Since the circadian clock metabolism has a profound role in pathogenesis of cancers, chronotherapy might be a better therapeutic strategy. We need to adjust the pattern of drug delivery to improve the treatment efficiency, by reducing the drug at the time point where tissue is most susceptible to toxicity, and increasing the dose at times with most susceptibility to the positive drug effect (233).

Therapeutic strategy for HCC is well-established. Since the incidence is rising drastically, early diagnosis and definitive treatment is currently the only way to increase the survival rate of HCC patients. Great research breakthroughs in chronobiology led to the development of this field. Recently it was demonstrated that isoform of the HNF4A (nuclear factor 4 alpha) plays a crucial role in HCC progression. Forced expression of *BMAL1* in HCC that is positive for HNF4A stops the growth of tumors *in vivo* (234). Furthermore, SULT1A1 (sulfotransferase 1a1) that has a circadian pattern at the mRNA and protein level and is responsible for detoxifications of various drugs in the liver is regulated through *BMAL1*. Knockdown of *Bmal1* resulted in changed rhythmicity in Hepa-1c1c7 cells (235). The role of IFNA (interferon alpha) was assessed in circadian manner in HepG2 cells as well. It was proposed that IFNA could have pharmacological role, since its continuous administration resulted in significantly decreased levels of *CLOCK* and *BMAL1* protein (236).

Pancreatic cancer is one of the most aggressive tumors, responding poorly to therapy; therefore, new therapeutic strategies are in high demand. Circadian gene *Per2* overexpression increases the sensitivity to cisplatin, possibly by inducing a reduction in of the BCL (B-cell lymphoma) proteins

(237). In search of cancer cell growth inhibitors downstream circadian controlled pathways, ligands of PPARG (peroxisome proliferator activated receptor gamma) showed to be reducing tumor aggressiveness and enhancing cytotoxic action of anti-cancer agents (238, 239). Another mechanism showing promise in pancreatic cancer treatment might be TIMELESS, involved in DNA damage response, whose expression was found to be altered in pancreatic cancer (135).

Chronotherapy has also proven to be effective in CRC. In metastatic CRC patients chemotherapy induced circadian disruption correlated with poorer disease outcome, suggesting its prevention could improve treatment results (240). Furthermore, a meta-analysis of five randomized controlled trials showed a significant improvement in overall survival in metastatic CRC patients treated with chronobiologically timed chemotherapy compared to conventional chemotherapy (241). Chronomodulated hepatic arterial infusion also showed promise as a possible drug administration strategy in heavily pretreated patients with CRC liver metastases (242). Recent study examining the role of PER3 in CRC found that its overexpression enhanced fluorouracil sensitivity in CRC cells, proposing it as a potential target in CRC treatment (243). Moreover, another study showed sex-specific expression and sex-specific prognostic value of clock and clock-controlled genes, shedding light on colorectal cancer and patient characteristics that have to be taken into consideration in order to provide optimal treatment (244).

## CIRCADIAN-OXYSTEROL NETWORK IN CANCEROGENESIS

Members of the oxysterol and circadian clock networks were exposed as the new promising prognostic biomarkers, genetic risk factors and potential therapeutics in gastrointestinal cancers. The roles of oxysterols in various cancers have been reviewed previously and mechanisms by which oxysterol can affect cancer pathogenesis and disease development were pointed out (8). Oxysterols activate different signaling pathways in cells which can either promote or inhibit cancer development. For example, 22(R)-, 24-, 25-, and 27-hydroxycholesterol are *in vivo* ligands of LXR and act as tumor suppressor in selected cancers. Increased LXR activity was shown to be beneficial in all three presented cancers exposing LXR as a promising drug target in oncology. However, one oxysterol can have a different role depending on the tissue. Current hypothesis is that the dual role of oxysterols is due to activation of different signaling pathways resulting in tumor suppressor LXR-dependent or oncogenic LXR-independent actions (245). Oxysterols also interact with OSBP/L proteins and these have been connected to many human diseases, such as dyslipidemia and cancers (246). Studies indicate that OSBP family members could also have a dual role. In HCC and CRC their expression is downregulated and this is correlated with a poor prognosis. While in PC their expression is increased and correlates with a poor prognosis. The opposite roles could be explained by the fact that members of OSBP family have tissue specific expression, which is disturbed in tumors, and also have different roles in cell physiology. Enzymes involved in

oxysterol synthesis are also potential new prognostic biomarkers and drug targets in gastrointestinal cancers. The expression and the SNPs in cytochromes P450 enzymes are associated with the risk for development and prognosis of selected cancers. The level of serum cholesterol itself is a prognostic biomarker associated with a higher risk for development of numerous cancers. The association is consolidated by the fact that statins are emerging novel therapies in gastrointestinal cancers. Cholesterol is the key player not only due to being the oxysterol progenitor molecule but also one of the key cellular ingredients needed in growing cancerous cells. The oxysterol metabolites, the bile acids, and their receptor FXR are emerging new biomarkers and therapeutic targets in gastrointestinal cancers. The role of FXR in these cancers is two faced. FXR downregulation is observed with progression of cancerogenesis and FXR role in suppression of proliferation, migration and invasion in colon cells and hepatocytes was confirmed. However, FXR role in pancreatic cancer seems to be the opposite. These data indicate that FXR activity is essential in tissues with high FXR expression such as liver and colon, while FXR activity in tissues where FXR and bile acids are not common is potentially tumorigenic.

Disruptions of circadian rhythm are clearly tumorigenic in gastrointestinal cancers as indicated by rodent models. The circadian molecular clock genes are also new emerging prognostic biomarkers and therapeutic targets. Several genes involved in regulation of cellular circadian expression have direct oncogenic or tumor suppressor roles. Not only their expression correlates with prognosis in patients, knockouts in rodent models lead to spontaneous cancerogenesis and SNPs are associated with the risk of cancer development and prognosis. They are interesting therapeutic targets, moreover, the time of the therapy must also be considered and chronotherapy has already been shown to be effective in gastrointestinal cancers.

## SUMMARY

Summary of reviewed data revealed that circadian regulatory network, cytochromes P450, nuclear receptors, cholesterol biosynthesis and oxysterols have overlapping roles in gastrointestinal cancers. Several factors from sterol homeostasis and circadian rhythm have been identified as potential novel prognostic biomarkers, genetic risk factors and drug targets. However, there are still several issues that remain open. The role of oxysterols in carcinogenesis is far from being conclusive. The cells are dealing with a variety of oxysterol molecules that promote their actions through modulation of transcription factors, such as LXR, RORs and others. Depending on the type of cancer, an oxysterol modulated pathway can have beneficial or damaging effect on carcinogenesis. This is one of the obstacles in developing new therapeutic strategies, besides statins, where it is clear that a more personalized approach is essential to increase the positive drug effects. The link between cholesterol, oxysterol synthesis and circadian rhythm was until recently



mostly unidirectional: the clock controlled the expression of lipogenic genes. It now becomes evident that both pathways are interconnected by energy metabolism where RORA/C and LXR are at the crossroad. The ROR receptors are circadian regulators, being co-responsible for the rhythmic expression of output metabolic genes. However, their own transcriptional activity depends on sterols and oxysterols whose endogenous synthesis is regulated by the clock. This is again a new field of translational research termed chronotherapy which was proven to be successful particularly in treatments of colorectal cancer.

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## AUTHOR CONTRIBUTIONS

All authors listed have made a substantial, direct and intellectual contribution to the work, and approved it for publication.

## FUNDING

This work was supported by Slovenian Research Agency program grant P1-0390 and research project J1-9176. UK was supported by young researcher scholarship. LB is a masters' student of medicine at the Faculty of Medicine University of Ljubljana.

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**Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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