

Minireview

Genetic Alterations Affecting Cholesterol Metabolism and Human Fertility¹

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ABSTRACT

Single nucleotide polymorphisms (SNPs) represent genetic variations among individuals in a population. In medicine, these small variations in the DNA sequence may significantly impact an individual's response to certain drugs or influence the risk of developing certain diseases. In the field of reproductive medicine, a significant amount of research has been devoted to identifying polymorphisms which may impact steroidogenesis and fertility. This review discusses current understanding of the effects of genetic variations in cholesterol metabolic pathways on human fertility that bridge novel linkages between cholesterol metabolism and reproductive health. For example, the role of the low-density lipoprotein receptor (LDLR) in cellular metabolism and human reproduction has been well studied, whereas there is now an emerging body of research on the role of the high-density lipoprotein (HDL) receptor scavenger receptor class B type I (SR-BI) in human lipid metabolism and female reproduction. Identifying and understanding how polymorphisms in the *SCARB1* gene or other genes related to lipid metabolism impact human physiology is essential and will play a major role in the development of personalized medicine for improved diagnosis and treatment of infertility.

cholesterol metabolism, genetics, infertility, lipoproteins, mutation, polymorphism, reproduction

INTRODUCTION

Infertility represents a serious health problem affecting approximately 15% of reproduction-aged couples in the United States and is defined as the failure to achieve a successful pregnancy after 12 or more months of appropriate, timed, unprotected intercourse or therapeutic donor insemination [1–4]. According to the American Society for Reproductive Medicine, approximately 30% of infertility cases can be attributed to female causes and 30% to male factors, and the

remaining cases involve a combination of male and female factors in addition to unexplained causes [5]. Understanding the various pathologic mechanisms underlying infertility represents an active area of research and serves as an important first step in our ability to treat this health problem.

Genetic mutations leading to functional alterations in proteins involved in the steroidogenic pathway have been shown to adversely impact human fertility. Moreover, research of the molecular biology, biochemistry, and physiology of human steroidogenesis and its disorders as they relate to fertility have been well characterized and thoroughly reviewed [6–11].

An often overlooked, but important, area of research relates to genetic mutations affecting cholesterol metabolism and their impact on human fertility. Cholesterol serves as an essential substrate for steroid hormone production and membrane synthesis. Genetic mutations altering the function of proteins involved in cholesterol uptake, mobilization from stored intracellular pools, and synthesis significantly alter normal cellular function and, in turn, impact fertility. This review summarizes some of these known genetic mutations. In particular, we highlight work focused on the functional impact of genetic mutations involved in cholesterol uptake, mobilization, and de novo cholesterol synthesis and review how these alterations can affect cholesterol metabolism and human fertility.

CHOLESTEROL METABOLISM

Cholesterol is essential for plasma membrane synthesis and fluidity. In steroidogenic cells of the gonads, adrenal glands, and placenta, cholesterol also acts as a necessary precursor for the biosynthesis of steroid hormones, which in turn, regulate vitally important physiologic functions including but not limited to the control of reproductive pathways, development of secondary sexual characteristics, and salt balance [12, 13]. Activated steroidogenic cells demand high levels of cholesterol substrate. Several mechanisms within the cell work in a coordinated manner to ensure adequate replenishment and availability of the cholesterol pool. These major mechanisms include receptor-mediated uptake of lipoprotein-derived cholesterol (i.e., low-density lipoprotein receptor [LDLR] and/or scavenger receptor class B type I [SR-BI]), hydrolysis of stored intracellular cholesteryl esters by hydrolases such as hormone-sensitive lipase, and de novo cholesterol synthesis by a multistep process using acetate as the starting substrate (Fig. 1).

Most species, including humans, depend mostly on cellular uptake of lipoprotein cholesterol as the major precursor for steroidogenesis [14, 15]. There are various mechanisms that

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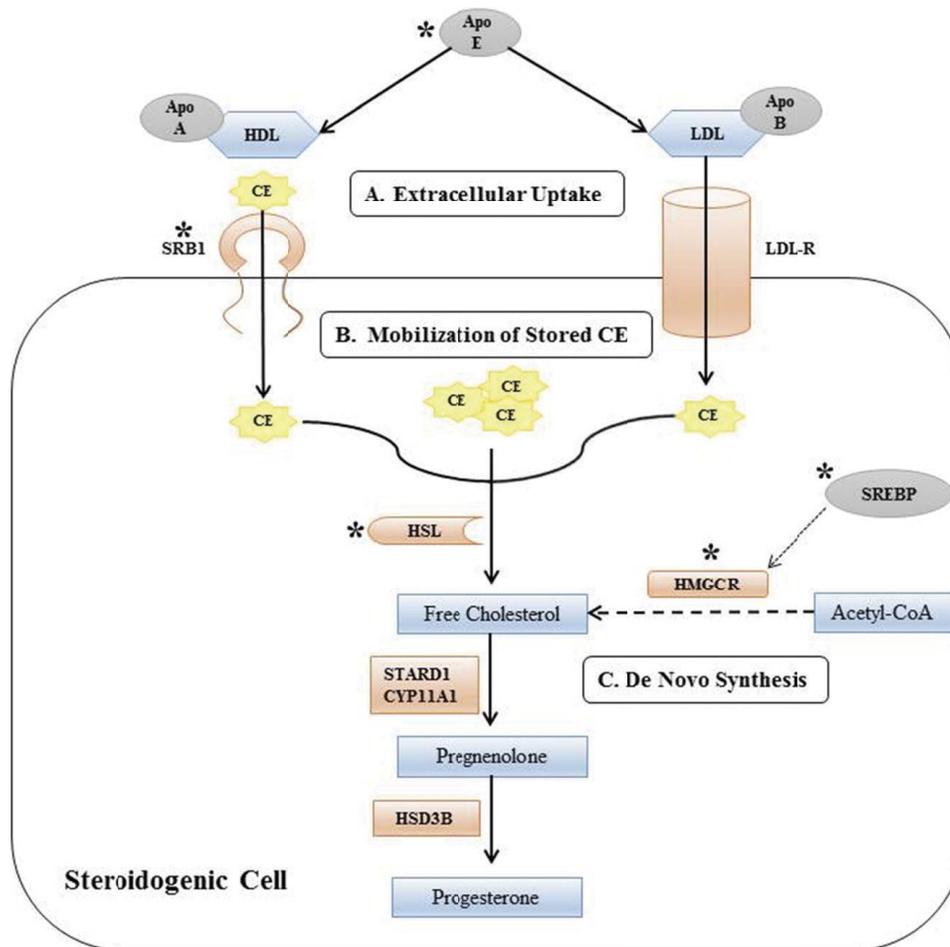


FIG. 1. Sources of cellular cholesterol. The three pathways by which cells maintain an adequate intracellular cholesterol pool are outlined here, including uptake (A), mobilization (B), and de novo synthesis (C). Asterisks denote the location of SNPs discussed in this review. ApoA = apolipoprotein A; CYP11A1 = cytochrome P450, family 11, subfamily A, polypeptide 1; HSD3B = 3 beta-hydroxysteroid dehydrogenase; STARD1 = steroidogenic acute regulatory protein D1.

facilitate cholesterol uptake into a cell. The two dominant mechanisms include uptake via the LDLR [15–17] and selective cholesteryl ester uptake mediated by SR-BI [18]. LDLR-mediated uptake involves the binding of apolipoprotein B (ApoB)- and ApoE-enriched cholesterol particles with subsequent endocytosis of the LDL receptor and uptake of the cholesterol-containing lipoprotein particles into the cell. In contrast, SR-BI mediates high-capacity selective uptake of cholesteryl esters from the core of high-density lipoprotein (HDL), LDL, and very-low-density lipoprotein (VLDL) lipoproteins [19]. Selective uptake refers to the process whereby lipoproteins dock on the extracellular loop of SR-BI (Fig. 2), and the cholesteryl esters within the core of the lipoprotein are transferred into the interior of the cell via a channel formed by dimerization of SR-BI receptors. The lipoprotein, now depleted of cholesteryl esters, dissociates from the receptor and is not internalized. The internalized cholesteryl ester is then hydrolyzed by hydrolases such as hormone-sensitive lipase to generate free or unesterified cholesterol (UC), which is then used for cellular processes such as steroidogenesis or membrane integrity [20].

Following stimulation by tropic hormones, cholesterol may be recruited from the hydrolysis of stored cytoplasmic cholesteryl esters. This process involves the participation of hormone-sensitive lipase (HSL), an enzyme expressed in steroidogenic tissues and which functions to convert stored

cholesteryl esters to UC [21]. This mechanism generates UC for the immediate synthesis of steroid hormones following cellular activation [22].

Intracellular cholesterol may also be derived via de novo synthesis in the endoplasmic reticulum (ER) from acetyl-coenzyme A (CoA), a process regulated by the enzyme 3-hydroxy-3-methylglutaryl CoA reductase (HMG-CoA reductase) [23–25]. The contribution of this pathway in providing cholesterol substrate varies among species, and is heavily influenced by the amount of intracellular cholesterol, and is regulated by the activation of the sterol regulatory element-binding proteins (SREBPs). When cells sense abundant intracellular cholesterol stores, the de novo cholesterol synthetic pathway remains inactive or quiescent. During this time, immature or large SREBPs remains complexed with two other proteins, SREBP cleavage-activating protein (SCAP) and INSIG1, which prevent its translocation to the nucleus. Following a decrease in the intracellular cholesterol pool, as seen in stimulated steroidogenic cells, which in turn would signal a demand for more intracellular cholesterol, there is dissociation of INSIG1 from the complex and subsequent mobilization, cleavage, and translocation of SREBP to the nucleus. In the nucleus, SREBP functions as a transcription factor, resulting in upregulation of the LDL receptor and HMG-CoA reductase, leading to both increased plasma membrane

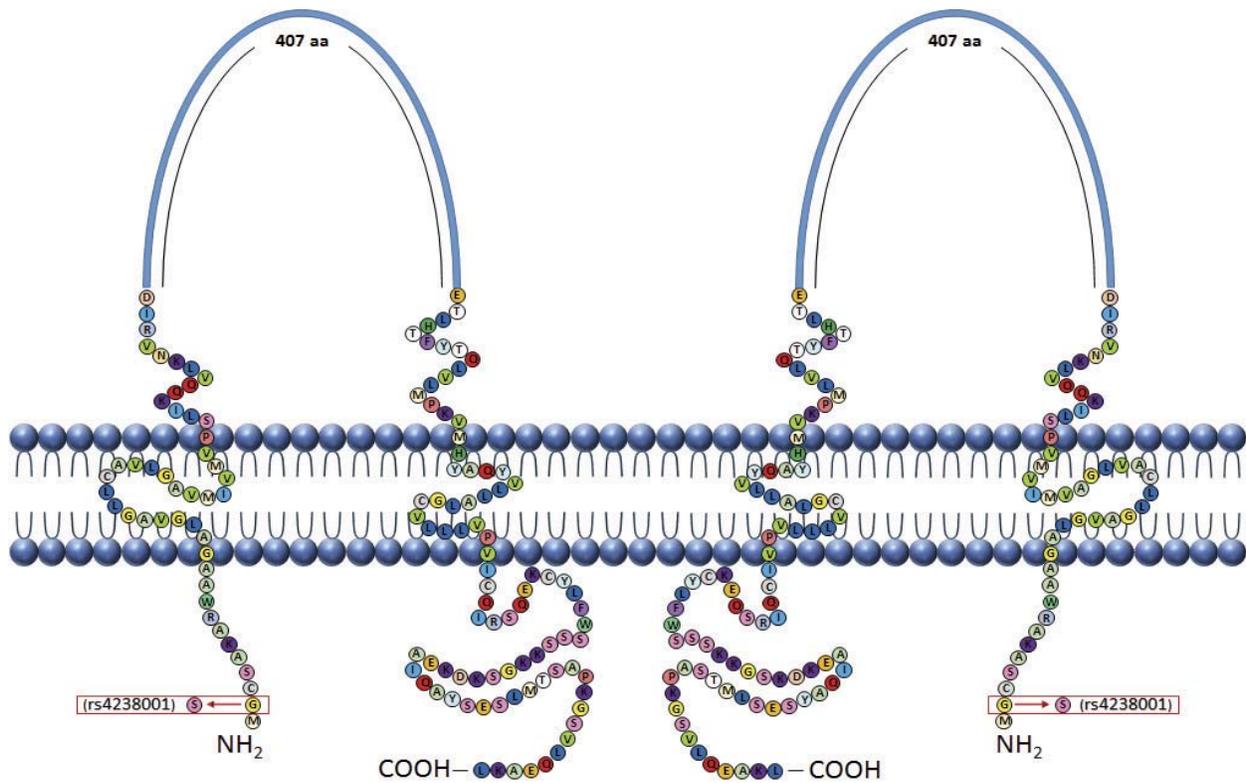


FIG. 2. Structure of the scavenger receptor class B type 1 (SR-BI). SR-BI is a receptor that mediates high-capacity selective uptake of cholesteryl esters from the core of HDL, LDL and VLDL via lipoprotein docking on the extracellular loop. A deficiency in SR-BI is associated with infertility, and the location of the rs4238001 SNP discussed in this review is highlighted here.

receptor-derived cholesterol uptake and de novo cholesterol production [26, 27].

GENETIC ALTERATIONS AFFECTING CHOLESTEROL UPTAKE AND THEIR INFLUENCE ON HUMAN FERTILITY

Lipoprotein particles serve as vehicles for cholesterol transport throughout the body and function to regulate intracellular cholesterol levels within a tight physiologic range, as an excess or insufficiency is typically deleterious to normal cellular function [28, 29].

Lipoprotein-mediated cholesterol uptake is an important mechanism by which cells obtain cholesterol for steroidogenesis. In fact, extracellular uptake has been shown to provide approximately 80% or more of cholesterol substrate for steroidogenic cells of the adrenal glands, corpus luteum, and placenta, with the other 20% supplied by de novo cholesterol synthesis from acetate and other precursors and cholesteryl ester hydrolysis [30–32]. In humans, LDLs, which are composed of the major apoproteins ApoB100 and ApoE as ligands to the LDLR, bind to the LDLR, and this is followed by endocytosis, which leads to internalization of the lipoprotein and the LDLR. In contrast, cholesterol-mediated uptake by SR-BI occurs by selective cholesteryl ester uptake and not by endocytosis. Several known polymorphisms in *APOE* have been discovered and found to significantly impact cholesterol metabolism and human fertility.

Apolipoprotein E

ApoE is a constituent apoprotein of VLDL, intermediate density lipoproteins (IDL), HDL, and chylomicron particles. It

is produced in the liver and in macrophages and serves an important role in lipid transport by mediating the binding of lipoprotein particles to their receptors [33]. ApoE-mediated delivery of cholesterol represents an important mechanism by which steroidogenic cells obtain cholesterol for steroid hormone production.

In rodents, deletion of the *ApoE* gene results in the development of severe hypercholesterolemia and decreased expression of the steroidogenic enzymes cytochrome P450 aromatase (Cyp19a1) and 3 β -hydroxysteroid dehydrogenase (3 β HSD), essential enzymes involved in the biosynthetic pathway of progesterone and estrogen, leading to a decrease in the level of both hormones [34]. In that study, Zhang et al. [34] showed significant alterations in the ER ultrastructure of *ApoE* null mice, which are described as swollen and tubby, and we speculate that these ER changes contributed to the reduced expression and function of Cyp19a1 and 3 β HSD. Interestingly, no differences between the fertility rates of *ApoE* null and those of wild-type control mice were observed. However, *ApoE* null mice did possess greater numbers of ovarian follicles as well as an increased ratio of ovarian follicle atresia and apoptosis than their wild-type counterparts [34].

Three important polymorphisms have been discovered in the human *APOE* gene [35, 36]. These codominant alleles, designated ϵ 2, ϵ 3, and ϵ 4, give rise to 3 functionally distinct proteins: ApoE2, ApoE3, and ApoE4 [33], which vary in amino acid residues at positions 112 and 158. ApoE2 is characterized by 2 cysteine residues, ApoE3 by a cysteine and arginine residue, and ApoE4 by 2 arginine residues at these sites [37]. Although these genetic polymorphisms represent small changes in the DNA sequence, studies have found that they exert a significant impact on the functional properties of their corresponding proteins and result in the alteration of

plasma cholesterol and apolipoprotein levels [33] and marked differences in reproductive efficiency [38–41].

In one study, Corbo et al. [40] screened 160 European women to investigate the possible impact of *APOE* polymorphisms on reproductive efficiency. Investigators discovered that women harboring the $\epsilon 3/\epsilon 3$ genotype exhibited higher reproductive efficiency, whereas carriers of the $\epsilon 2$ allele had lower numbers of children and pregnancies [40]. *APOE* polymorphisms have also been found to impact male fertility. Setarehbadi et al. [42] found significant differences between the distribution of *APOE* allelic combinations in fertile men and that in infertile men, with a higher percentage of fertile males possessing the $\epsilon 3/\epsilon 3$ genotype. This study mirrors the results of Gerdes et al. [41], who reported higher birth rates for children from fathers possessing the $\epsilon 3/\epsilon 3$ genotype than from fathers possessing other allelic variations.

Overall, these studies suggested that lower reproductive efficiency is associated with the $\epsilon 2$ allele and higher reproductive efficiency with the $\epsilon 3$ allele.

LDL Receptor

The LDL receptor is an important protein that functions to mediate the uptake of LDL cholesterol, the preferred substrate for steroid hormone production [43–47]. Given the important role the LDL receptor plays in providing adequate substrate for steroidogenesis, one might assume that alterations in its function would lead to significant impairment of fertility. However, LDL receptor-deficient mice are fertile and produce normal sized litters despite exhibiting an altered lipid profile [48]. In contrast, a deficiency of SR-BI is associated with infertility [49, 50]. The ability of SR-BI to bind LDL cholesterol may partially explain the normal fertility exhibited by LDL receptor null mice. To date, no significant polymorphisms have been discovered in the LDL receptor which adversely impact human fertility. A recent publication by Rinninger et al. [51] showed that levels of hepatic and adrenal SR-BI protein expression were not different between wild-type and LDLR knockout mice.

Scavenger Receptor Class B Type I

SR-BI has been identified as the primary lipoprotein receptor for HDL, but it also has the capability to bind LDL, VLDL, and other ligands with high affinity [52–56]. SR-BI is highly expressed in liver, adrenal glands, and ovarian tissues [50], where it plays an important role in mediating selective cholesteryl ester (CE) uptake [20]. This process serves as another lipoprotein receptor-mediated mechanism for providing cholesterol substrate to steroidogenic cells [12, 57–63]. In addition, SR-BI has been shown to mediate the bidirectional movement of UC down a concentration gradient between lipoproteins and cells [64–66].

Much of our knowledge of SR-BI function comes from animal studies. In rat ovaries, SR-BI mRNA is present in interstitial cells, thecal cells, corpora lutea, and luteinized granulosa cells [67]. SR-BI protein expression is upregulated after stimulation with tropic hormones [68, 69] and is associated with an increase in CE uptake [70]. SR-BI expression in ovarian tissue plays a particularly important role in female fertility, as substantial amounts of HDL, but not LDL, are present in follicular fluid surrounding oocytes in ovarian follicles [46, 71–75]. LDL is absent from the follicular fluid of pre-ovulatory follicles because particles range in size from 18 to 23 nm, with a molecular mass of 2.3 million daltons (Da), precluding movement across the basement membrane

(size limit, approximately 400 000 Da). [74–77]. In contrast, HDL particles range in size from 8.2 to 13 nm with molecular mass of 200 000 to 400 000 [76, 77]. Due to the absence of other lipoprotein particles in the follicular fluid, SR-BI delivery of HDL may serve as an important mechanism by which cholesterol is delivered to the oocyte and its surrounding steroidogenic support cells. It is not surprising then that genetic alterations in SR-BI have been shown to adversely impact cholesterol metabolism, including that of the ovaries, resulting in alterations in fertility.

Genetically engineered mice lacking SR-BI demonstrate the importance of this protein in reproduction. Female homozygous SR-BI knockout mice are infertile [18, 49, 50], most likely secondary to impaired embryonic development of the offspring, as embryos from SR-BI null females have been shown to develop an abnormal morphology and to arrest in culture. Similar abnormalities were found in unfertilized oocytes, but estrus cycles, progesterone levels, and ovulatory patterns in SR-BI null mice were found to be normal [50]. However, a more recent study by Jimenez et al. [78] found that SR-BI null mice have 50% lower plasma progesterone levels than wild-type controls, as well as ovaries with small corpora lutea, large follicles with hypertrophied theca cells, and follicular cysts with blood-filled cavities. These later data are more consistent with the phenotypic data observed in humans carrying a single nucleotide polymorphism (SNP) in the *SCARB1* gene, which encodes the SR-BI protein. As a result of altered SR-BI function, null mice have elevated and abnormally large ApoE-enriched circulating HDL particles as well as an elevated UC:total cholesterol ratio (known as the UC:TC ratio), a phenotype which is most likely secondary to defective removal of the core CE from these lipoprotein particles [79].

Interestingly, fertility in SR-BI null mice can be rescued by methods that act to restore normal cholesterol metabolism. Miettinen et al. [49] treated SR-BI null mice with the HDL cholesterol-lowering drug probucol [80, 81]. They found that this treatment reduced and remodeled the abnormally large HDL particles and restored fertility. In addition, these investigators also performed bilateral ovarian transplantation in which ovaries were removed from SR-BI null mice and subsequently transplanted into ovariectomized SR-BI-positive hosts. The transplanted SR-BI-negative ovaries began functioning normally in the SR-BI-positive environment and developed the capacity to produce functional oocytes, resulting in restoration of fertility. In support of these findings, Yesilaltay et al. [79] confirmed the presence of abnormally large HDL particles and an elevated UC:TC ratio in SR-BI null mice. Investigators demonstrated that hepatic restoration of SR-BI expression alone via adenoviral transduction or stable transgenesis in SR-BI null mice substantially reduced levels of abnormally large HDL, normalized the UC:TC ratio, and restored fertility [79]. Taken together, these data led the investigators to hypothesize that infertility in SR-BI null mice is not due to irreversible defects in oocyte or embryonic development but rather secondary to abnormal lipoprotein metabolism and/or the abnormal transfer of cholesterol to or from the oocyte or supporting cells.

As in rodents, alterations in human SR-BI function have been shown to adversely impact cholesterol metabolism and fertility. In vitro experiments in the HGL-5 immortalized human granulosa cell line, in which SR-BI had been knocked down using interfering RNA, resulted in significantly reduced progesterone secretion after stimulation with forskolin (an activator of cyclic AMP) compared to that in treated controls [82]. This is in line with recent rodent data by Jimenez et al.

[78], which reported a 50% reduction in circulating plasma levels of progesterone in SR-BI null mice.

Several SNPs in the *SCARB1* gene have been identified and found to impact cholesterol metabolism and human fertility [83] (Fig. 1). In a prospective study of adults with hyperalphalipoproteinemia (defined as subjects with fasting HDL-C levels of >60 mg/dl), West et al. [84] found that certain polymorphisms in *SCARB1* were associated with increased SR-BI protein degradation that resulted in lower receptor protein expression. In addition, these expression levels were inversely proportional to HDL lipoprotein size and positively associated with CE uptake from HDL [84]. In another study, Yates et al. [85] evaluated the association of *SCARB1* polymorphisms and fertility outcomes in women undergoing in vitro fertilization. In that study, investigators found the missense rs4238001 (REFSEQ accession number: NP_001076428.1) SNP (encoding an amino acid change from glycine to serine at amino acid 2) was significantly associated with lower follicular fluid progesterone levels and poor fetal viability [85]. Finally, a study by Velasco et al. [86] found that a cohort of women undergoing in vitro fertilization treatment exhibited low SR-BI-RNA expression, a finding which was associated with lower baseline and peak estradiol levels and lower number of retrieved and fertilized oocytes than in women expressing higher levels of SR-BI [86]. Taken together, research in both animal models and human studies has demonstrated the importance of SR-BI and its role in cholesterol metabolism and fertility.

GENETIC ALTERATIONS AFFECTING CHOLESTEROL MOBILIZATION AND THEIR INFLUENCE ON HUMAN FERTILITY

The ability of the cell to store and mobilize intracellular cholesterol is the result of intricate mechanisms which work to regulate the size and availability of the cholesterol pool. Following uptake, UC can be esterified by acyl CoA:cholesterol acyl transferase (ACAT) and stored as CE in intracellular lipid droplets for later use [87]. Following stimulation with tropic hormones, stored CE can be hydrolyzed by HSL, mobilized to the mitochondria, and subsequently used as a substrate for immediate synthesis of steroid hormones [22, 88]. SNPs in HSL have been discovered and found to impact cholesterol metabolism and fertility.

Hormone-Sensitive Lipase

HSL is an important protein with multiple physiological functions. It plays an essential role in lipid metabolism and is responsible for mediating hydrolysis of diacylglycerol and triacylglycerol [21]. In addition, it mediates the hydrolysis of cholesteryl esters in steroidogenic tissues of the adrenal glands, ovaries, and testis, providing substrate for the immediate synthesis of steroid hormones [89, 90].

Disruption of HSL in mice results in an altered metabolic phenotype. HSL null mice exhibit increased hepatic insulin sensitivity and are resistant to diet-induced obesity [91, 92]. With regard to cholesterol metabolism and fertility, the testes of HSL null mice were found to completely lack neutral cholesteryl ester hydrolase activity, resulting in increased accumulation of intracellular CE. This finding was associated with oligospermia with reduced motility and a consequential reduction in fertility [93, 94]. Vallet-Erdtmann et al. [95] found that reintroduction of HSL into the testis of HSL null mice reversed CE accumulation and fully restored fertility.

In humans, several polymorphisms in the *HSL* gene have been identified [96–100]. The C-60 G polymorphism is an *HSL* promoter variant that is associated with a 40% reduction in promoter activity in vitro [99]. A study by Vatannejad et al. [101] observed significant differences between the *HSL* genotype distribution in fertile male mice and that in infertile males (n = 164, n = 169, respectively). Interestingly, the CC genotype conferred a 2.4-fold greater risk for male infertility than for male carriers of the GC or GG genotype [101].

Taken together, these data suggest that HSL mobilization of CE plays an essential role in the process of spermatogenesis and that disruption of HSL function adversely impacts fertility.

GENETIC ALTERATIONS AFFECTING DE NOVO CHOLESTEROL SYNTHESIS AND THEIR INFLUENCE ON HUMAN FERTILITY AND EMBRYONIC VIABILITY

De novo synthesis represents another major source of cellular cholesterol, which is required for structural integrity, steroidogenesis, and oocyte maturation. We refer readers to a recent comprehensive review of malformations caused by enzymatic defects in cholesterol synthesis [102], and we would like to highlight some of these major enzymatic defects that result in embryonic lethality and/or developmental abnormalities.

As shown in Figure 3, there are many enzymatic steps in the conversion of acetate to cholesterol, and multiple enzymatic defects have been reported, particularly involving steps downstream of squalene production [102].

HMGCoA Reductase

3-Hydroxy-3-methylglutaryl-CoA reductase (HMGR) is the rate-limiting enzyme in the early steps of cholesterol synthesis and acts to catalyze the formation of mevalonate from 3-hydroxy-3-methylglutaryl coenzyme A. In 2003, Ohashi et al. [103] showed that mouse embryos genetically engineered to have complete deficiency of *Hmgcr* did not develop past the blastocyst stage; thus, no viable *Hmgcr* null mice were produced from heterozygotic crossings. Investigators determined that pre-implantation embryos (embryonic day 3.5 [E3.5]) appeared to be normal and that the defect in viability likely occurred at the level of implantation. An attempt to infuse replacement mevalonate via a subcutaneous osmotic pump did not overcome the defect in *Hmgcr* null embryos, as the embryos were able to implant but did not progress to viable offspring. Mice heterozygous for this mutation appeared to be normal in development, gross anatomy, fertility, and capacity for cholesterol synthesis despite decreased HMGR activity. Overall cholesterol biosynthesis remained unchanged in the liver of these mice, and lipoprotein profiles were similar to those of wild-type mice profiles, suggesting that one copy of the *Hmgcr* gene produces sufficient HMGR for hepatic cholesterol synthesis.

HMGR is regulated both transcriptionally and post-transcriptionally. It is well established that when cells sense a reduction in intracellular cholesterol mass, activation of the ER-residing SREBPs (1a, 1c, and 2) occurs, which leads to its transformation from a larger ER protein to a smaller nuclear transcription factor [104]. Cholesterol genes known to be activated by SREBP2 include *HMGR*, *LDLR*, and *INSIG*, among others [105]. Complete knockout of SREBP2 in mice is 100% embryonically lethal [104].

Surprisingly, little is known regarding the functional effect of variants in the SREBP2 gene in relation to reproduction or other medical diseases. Liu et al. [106] reported a significant

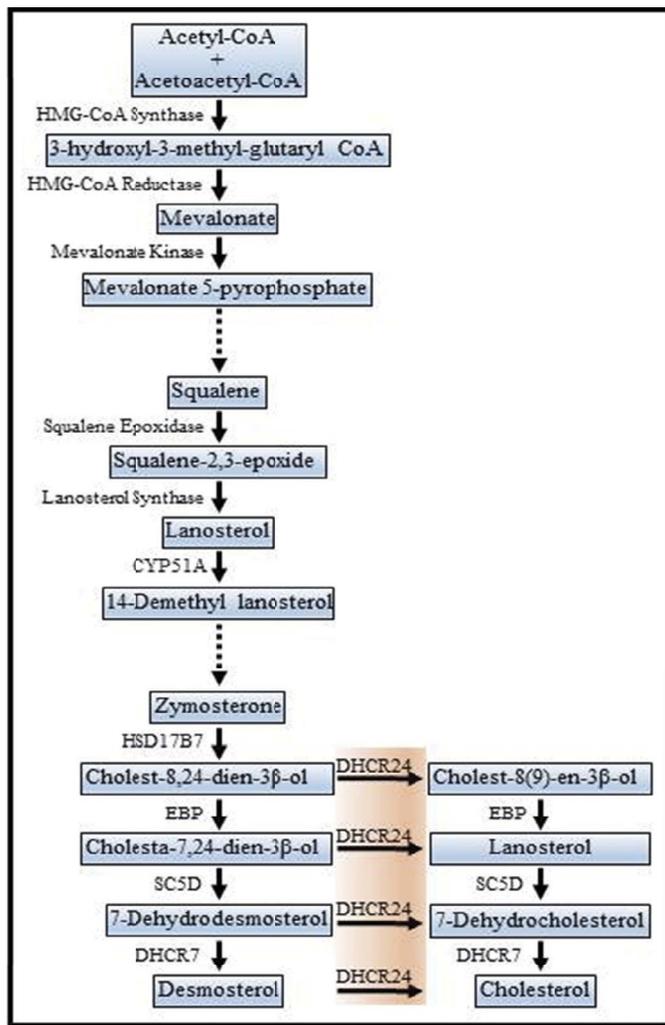


FIG. 3. De Novo cholesterol synthesis. The enzymatic steps in the conversion of acetate to cholesterol are outlined here. Mutations in these enzymes have been shown to result in impaired embryonic viability.

increase in LDL-cholesterol levels in Chinese Han female carriers of the CC genotype for the rs4822063 SREBP2 variant. Incrementally more is known regarding the functional effects of variations in the *HMGCR* gene in human reproduction. In 2007, Steffen et al. [107] examined genetic causes in the mother and infant associated with preterm delivery (PTD). These investigators were particularly interested in examining the effects of genetic variations in cholesterol genes in the mother and infant on the risk of PTD. Cholesterol genes were genotyped in infants born before 37 wk of gestation ($n = 414$) and in at least 1 parent (253 mothers, 351 fathers). Selection of candidate genes was based on a previous publication from Knoblauch et al. [108] which identified haplotypes responsible for most of the genetic variance in LDL, HDL, and LDL/HDL in a German population. Results in the infant dataset showed a significant association of variations in the *APOAI* gene (ApoA-I is the major apolipoprotein in HDL fractions) and *HMGCR* (rs2303152). In the maternal dataset, the *HMGCR* variant rs2303152 was not analyzed due to low allele frequency; however, the results showed a significant association of PTD with *ABCA1*, *LCAT*, *LIPC*, and *APOE*, all genes associated with HDL metabolism. The authors concluded that there might be a benefit in assessing the effect of nutritional risk on PTD by genetic testing for common variations in cholesterol genes.

Lanosterol

Lanosterol represents the first step in sterol formation and can be converted by lanosterol 14 α -demethylase (CYP51, a member of the cytochrome P450 family), to follicular fluid meiosis-activating factor (FF-MAF), a sterol intermediate that has been studied extensively and was shown to activate meiosis in gametes [109]. Recently, Lewinska et al. [110] examined polymorphisms within the *CYP51A1* gene and found significant associations with birth weight and maternal lipid levels. Genotyping for CYP51A1 variants was performed in samples isolated from four different populations of mothers experiencing preterm birth or from neonates affected by growth retardation or preterm birth. In a cohort of women and neonates from Western European descent, the investigators identified 22 sequence variants and reported 10 as novel and rare. Of the polymorphisms identified, the minor allele frequencies (MAF) for the common variants rs6465348 and rs12673910 were significantly higher in neonates and mothers affected by preterm birth than in the general population. Based on its high MAF and its location in the CYP51A1 3' untranslated region (UTR), the investigators chose rs6465348 for further study and found a significant association between low body weight for gestational age and lower LDL cholesterol and total cholesterol in women. These genomic approaches underscore the effort to identify genetic causes for infertility problems related to alterations in lipid metabolism.

In addition to lanosterol's well-known role in generating meiosis-activating factor, other studies have suggested an intriguing role for lanosterol and dihydrolanosterol (a reduction product of lanosterol) in the post-translational regulation of HMGCoA reductase [105, 111]. As mentioned previously, Insig is an ER-resident protein that forms a complex with SREBP. Song et al. [105] showed that lanosterol enhanced Insig-mediated ubiquitination and degradation of HMGCoA reductase. Lange et al. [111] subsequently showed that 24,25dihydrolanosterol could potentially inhibit HMGCoA reductase activity in fibroblasts. Together, these studies strongly suggest that lanosterol exerts a negative feedback inhibition on the rate-limiting enzyme of cholesterol synthesis.

Desmosterol

In the Bloch pathway, the enzyme 3 β -hydroxysteroid- Δ 24 reductase (DHCR24) catalyzes the conversion of desmosterol in the final steps of cholesterol formation [112]. A recent review by Zerenturk et al. [112] highlights the renewed interest in studying the biological effects of desmosterol. DHCR24 was first identified due to high homology with the *DIMINUTO/DWARF1* gene in *Arabidopsis thaliana*; it was also separately identified later as selective Alzheimer's disease indicator 1 (Seladin-1) due to its association with Alzheimer's disease. The *DCHR24* gene is highly expressed in brain, liver, and steroidogenic tissues; missense mutations in this gene lead to desmosterolosis, a rare autosomal recessive disorder characterized by congenital anomalies and elevated desmosterol levels [113].

The first report of a child with congenital malformations and confirmed elevated levels of desmosterol were reported in 1998 by FitzPatrick et al. [113]. The child was born at 34 weeks gestation with extensive developmental abnormalities (including macrocephaly, cleft palate, and short limbs) and died within 1 hour of birth due to respiratory distress. Desmosterol levels were measured using gas chromatography-mass spectrometry (GC-MS) from extracts isolated from liver, kidney, and brain tissues. The highest concentrations of desmosterol were found in the brain tissue of the deceased child, whereas plasma levels

were considered normal in the mother but markedly elevated in the father. The authors also noted that exposure to triparanol, a highly teratogenic inhibitor of DHCR24, results in similar malformations, underlining the importance of this enzyme in human development [113].

More recently, Schaaf et al. [114] reported a third case of desmosterolosis and also examined the functional effects of polymorphisms in the *DCHR24* gene in this case report. These investigators determined that the affected infant was a compound heterozygote for 2 novel missense mutations, c.281G > A (p.R94H, which was inherited from the mother) and c.1438G > A (p.E480K, which was inherited from the father). In yeast expression assays, the two mutations significantly lowered DHCR24 enzymatic activity, as measured by the conversion of desmosterol to cholesterol, compared to that in wild-type DHCR24. Mutations in this infant were not fatal, and a trial of therapy with riboflavin, nicotinamide, and thiamine was initiated, but the investigators reported concerns regarding noncompliance with use of the prescribed treatment. A subsequent analysis of sterol levels at 14 months showed no significant changes in desmosterol or cholesterol levels [109].

Admittedly, the clinical condition of desmosterolosis is rare; however, there have been a number of in vitro studies examining other aspects of desmosterol effects on inflammation and cell proliferation. For instance, McGrath et al. [115] reported an interesting relationship between SR-BI and DHCR24. Using human coronary artery endothelial cells (HCAEC), these investigators incubated the cells with recombinant or native HDLs and found that preincubation of the cells with the HDL particles suppressed NF-κB-mediated DNA transcription. One of the genes transcriptionally regulated by preincubation with HDL was *DHCR24*, which had been shown previously to be a hydrogen peroxide scavenger [116] and have antioxidant properties [117]. Furthermore, after SR-BI expression was silenced in the HCAEC, basal and stimulated mRNA levels of DHCR24 were significantly reduced. These results showed that the effect of DHCR24 in modulating inflammatory responses in endothelial cells was dependent on SR-BI. It is unknown if there is a direct interaction between SR-BI and DHCR24, and this should be explored further.

7-Dehydrocholesterol

Of the enzymatic defects identified in the de novo cholesterol synthesis pathway, the mutation resulting in Smith-Lemli-Opitz syndrome (SLOS) is the best characterized. SLOS is an autosomal recessive disease caused by a defect in the 3β-hydroxysterol Δ7 cholesterol reductase (*DHCR7*) gene leading to reduced cholesterol end-product and accumulation of 7-dehydrocholesterol and 27-hydroxy-7-dehydrocholesterol [118]. This deficiency results in morphological abnormalities, mental retardation, and reduced lifespan (including embryonic lethality) [118]. Knowledge of cholesterol metabolism has proven crucial to both the early diagnosis and treatment of SLOS.

A number of diagnostic approaches have been used to identify affected fetuses, including analysis of synthetic cholesterol intermediates. In 2005, Chevy et al. [119] argued against the utility of molecular diagnostic testing and instead advocated for routine GC-MS profiling of amniotic fluid (AF) in the diagnoses of developmental abnormalities attributed to defects in sterol intermediate synthesis. Clinical indications for AF sampling included fetal growth retardation, external male genitalia defect, and limb defects. Using GC-MS, these

investigators were able to detect significant differences in AF levels of cholesterol, 7-dehydrocholesterol, and 8-dehydrocholesterol between normal and SLOS-affected infants. Of these sterol intermediates, these investigators concluded that 8-dehydrocholesterol level, given its long-term stability, was the best marker for SLOS. Results from this larger clinical population confirmed previous results by Abuelo et al. [120] and Tint et al. [121]. In addition, a urinalysis can also be performed as early as 12 weeks to diagnose SLOS [122].

Because the defect in DHCR7 leads to low plasma cholesterol levels and elevated 7- and 8-dehydrocholesterol levels, current treatment standards include dietary cholesterol supplementation with statin therapy [123]. There are also currently studies examining the benefits of antioxidants in the treatment of SLOS (E. Elias, personal communication).

CONCLUSIONS

Based on current evidence, it is clear that certain genetic polymorphisms leading to functional alterations of proteins involved in cholesterol uptake, mobilization, and de novo cholesterol synthesis can significantly impact human fertility. With the advent of personalized medicine, the identification and functional importance of polymorphisms and other genomic alterations related to reproductive function in men and women remains an important area of research. It is expected and anticipated that in the coming years, cholesterol-related diagnostic studies and therapeutic interventions will be refined based on the principles of personalized medicine.

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