# The Role of the High-Density Lipoprotein Receptor SR-BI in the Lipid Metabolism of Endocrine and Other Tissues

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Because cholesterol is a precursor for the synthesis of steroid hormones, steroidogenic tissues have evolved multiple pathways to ensure adequate supplies of cholesterol. These include synthesis, storage as cholesteryl esters, and import from lipoproteins. In addition to endocytosis via members of the low-density lipoprotein receptor superfamily, steroidogenic cells acquire cholesterol from lipoproteins by selective lipid uptake. This pathway, which does not involve lysosomal degradation of the lipoprotein, is mediated by the scavenger receptor class B type I (SR-BI). SR-BI is highly expressed in steroidogenic cells, where its expression is regulated by various trophic hormones, as well as in the liver. Studies of ge-

netically manipulated strains of mice have established that SR-BI plays a key role in regulating lipoprotein metabolism and cholesterol transport to steroidogenic tissues and to the liver for biliary secretion. In addition, analysis of SR-BI-deficient mice has shown that SR-BI expression is important for  $\alpha$ -tocopherol and nitric oxide metabolism, as well as normal red blood cell maturation and female fertility. These mouse models have also revealed that SR-BI can protect against atherosclerosis. If SR-BI plays similar physiological and pathophysiological roles in humans, it may be an attractive target for therapeutic intervention in cardiovascular and reproductive diseases. (Endocrine Reviews 24: 357–387, 2003)

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Abbreviations: ABC, ATP-binding cassette; apo, apolipoprotein; C/EBP, CCAAT/enhancer-binding protein; CETP, cholesteryl ester transfer protein; CLAMP, carboxy-terminal linking and modulating protein; CNS, central nervous system; E, embryonic development; eNOS, endothelial NO synthase; FH, familial hypercholesterolemia; FXR, farnesoid X receptor; HDL, high-density lipoprotein; HMG CoA, hydroxymethylglutaryl coenzyme A; IDL, intermediate-density lipoprotein; KO, knockout; LCAT, lecithin:cholesterol acyltransferase; LDL, low-density lipoprotein; LDLR, LDL receptor; LRH-1, liver receptor homolog 1; LIMPII, lysosomal integral membrane protein II; LPS, lipopolysaccharide(s); LXR, liver X receptor; NO, nitric oxide; PPAR, peroxisome proliferator-activated receptor; RBC, red blood cell; SF-1, steroidogenic factor-1; SR-BI, scavenger receptor class B type I; SR-BIatt, attenuated SR-BI; SRE, sterol regulatory element; SREBP, SRE-binding protein; VLDL, very LDL.

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# I. Introduction

C HOLESTEROL METABOLISM IS intimately associated with the proper functioning of the endocrine system. In addition to the housekeeping functions of cholesterol in all mammalian cells as a key contributor to membrane structure and function, it is the precursor for cytochrome P450 cholesterol side chain cleavage enzyme-initiated synthesis of steroid hormones. (Cholesterol can also be converted to bile acids in the liver and vitamin D in the skin and kidney.) Thus, it is not surprising that endocrine, especially steroidogenic, tissues and other cell types have evolved multiple pathways to ensure the adequate provision of this crucial lipid.

Cells can obtain cholesterol by endogenous synthesis from

mevalonate and isoprenoid precursors (1). An important rate-controlling step in biosynthesis is catalyzed by the enzyme hydroxymethylglutaryl coenzyme A (HMG CoA) reductase. Hydrolysis of cholesteryl esters stored in cytoplasmic lipid droplets can also provide cholesterol. Although most body cells have relatively small cholesteryl ester pools, cytoplasmic cholesteryl ester stores are especially abundant in steroidogenic cells, providing a ready supply of cholesterol for rapidly inducible steroidogenesis. Additionally, cells use surface receptors to extract exogenous cholesterol from the lipoprotein particles that transport this waterinsoluble molecule through the aqueous circulatory system (2). In fact, circulating lipoproteins are a major physiological source of cholesterol for steroidogenic cells. Plasma lipoproteins play a critical role not only in normal cholesterol homeostasis, but also in pathophysiological states such as atherosclerotic cardiovascular disease [increased risk associated directly with the plasma concentrations of low-density lipoprotein (LDL) and inversely with those of high-density lipoprotein (HDL)] (3, 4). Here, we will review the role of the scavenger receptor class B type I (SR-BI), the first HDL receptor to be characterized, in the cellular metabolism of lipoproteins and its relevance for body lipid homeostasis and disease.

#### **II. Lipoprotein Metabolism**

Plasma lipids, i.e., mainly cholesterol, triglycerides, and phospholipids along with low levels of other hydrophobic compounds such as vitamin E, are carried in the blood by water-soluble lipoproteins. Lipoproteins have a polar outer shell of protein and phospholipid and inner core of neutral lipid. The largest lipoprotein particles are chylomicrons, which are synthesized in the intestine. Dietary fat and lipid secreted via bile into the gastrointestinal lumen are absorbed and packaged into chylomicrons containing triglycerides as their major core lipid component and apolipoproteins (apo)B<sub>48</sub> and apoE as key major protein constituents. Chylomicrons are secreted into lymph, and, after their entrance into the bloodstream, their core triglycerides are hydrolyzed by lipoprotein lipase (LPL), an enzyme bound to the luminal surfaces of capillary endothelial cells located in fat and muscle tissue. Hydrolysis of triglycerides reduces the volume of the lipoprotein core. Hydrolysis also results in the release of excess surface shell components, i.e., phospholipids, unesterified cholesterol, and exchangeable apolipoproteins, and their transfer to other circulating lipoproteins, especially to circulating HDL. The residual chylomicron particles remaining in the circulation after lipolysis are called chylomicron remnants, which are rapidly taken up by the liver by receptor-mediated endocytosis (reviewed in Ref. 5).

Very LDL (VLDL) are triglyceride-rich lipoproteins whose major apolipoprotein components include  $apoB_{100}$  (in rodents, also  $apoB_{48}$ ) and apoE. VLDL is synthesized by hepatocytes and secreted into the blood. As is the case for chylomicrons, VLDL triglycerides are hydrolyzed by LPL, giving rise to smaller intermediate-density lipoprotein (IDL) particles and excess surface components that can be transferred to other lipoproteins. IDL is either cleared from the

circulation by hepatic endocytosis or, through the action of hepatic lipase and cholesteryl ester transfer protein (CETP), further converted to LDL (reviewed in Ref. 5). LDLs are the major carriers of cholesterol (as cholesteryl esters) in humans, but normally there is very little LDL in rodents that lack CETP. LDL is removed from the circulation by LDL receptor (LDLR)-mediated endocytosis, in which LDL is internalized and delivered to lysosomes for degradation (see below). Most LDLR activity, and thus clearance of plasma LDL, occurs in the liver.

HDLs are not a single macromolecular entity, but rather a group of lipoprotein particles containing nearly equal amounts of lipid and protein that has been subclassified according to physical properties and apolipoprotein composition (5-8). The major apolipoproteins of HDL are apoA-I and apoA-II (with the minor components apoA-IV, apoC, apoD, and apoE; Refs. 6–8). Both of these apolipoproteins play structural roles and serve as regulators of HDL metabolism (6-8). In some cases, the apolipoproteins are involved in the recognition of HDL by cell surface receptors. There are three major classes of HDL particles: 1) discoidal particles comprising phospholipids and apoA-I, which are present only transiently in the plasma; 2) small, very lipid-poor apoA-I/phospholipid particles, called pre- $\beta$  HDL because of their electrophoretic mobilities, that are present in low concentrations in the plasma; and 3) the most abundant,  $\alpha$ -HDLs, which are large spherical particles with neutral lipid cores and two or more apolipoproteins on their outer shells.  $\alpha$ -HDLs are comprised of two major subpopulations differing in their relative contents of apoA-I and apoA-II; these are lipoprotein A (LpA)-I HDL, which contains apoA-I only, and LpA-I:A-II HDL, which contains both apoA-I and apoA-II.

HDL metabolism is complex, involving several HDLremodeling enzymes, lipid transfer proteins, and cell surface receptors (reviewed in Refs. 6-18). HDL originates as discoidal particles secreted by the liver and intestine or as byproducts of triglyceride-rich lipoprotein metabolism (release of surface components during lipolysis). These nascent HDL particles contain mostly apoA-I and phospholipids. They apparently mature into spherical HDL particles primarily by incorporation of unesterified cholesterol and phospholipids from cells followed by esterification of cholesterol. The transfer of cellular lipids to nascent HDL requires activity of the ATP-binding cassette (ABC) A1 transporter, and its absence results in the HDL deficiency disease called Tangier disease. The unesterified cholesterol incorporated into plasma HDL is converted to cholesteryl esters by the plasma enzyme lecithin:cholesterol acyltransferase (LCAT). Esterification creates an unesterified cholesterol concentration gradient between HDL and cell membranes and is considered critical for efficient cholesterol efflux from cells to HDL. In species that express plasma CETP, a significant fraction of HDL cholesteryl ester is transferred to other plasma lipoproteins (e.g., VLDL, IDL, and LDL) for further transport, primarily to the liver (9, 10). Thus, a substantial fraction of the plasma HDL cholesterol is indirectly delivered to the liver via hepatic endocytic receptors for IDL and LDL. In rodents and rabbits, and probably in humans, there are additional pathways for HDL lipid transport in which HDL directly delivers its cholesteryl esters to cells.

Although cellular endocytic uptake of HDL has been described (reviewed in Ref. 19), both *in vitro* and *in vivo* studies have established that a key mechanism for the direct delivery of HDL cholesterol to cells is fundamentally different from the classic receptor-mediated endocytic pathway initially described for the LDLR (Refs. 20-22; also reviewed in Ref. 23). Instead, receptor-mediated HDL binding to the cell surface results in the transfer of its cholesteryl esters to the cell and the subsequent release of the lipid-depleted HDL back into the extracellular fluid rather than the lysosomal degradation of the particle. This novel cellular mechanism, which can extract cholesteryl esters from LDL as well as HDL, is called selective lipid uptake. This pathway appears to involve temperature-dependent reversible incorporation of HDL cholesteryl ester into the plasma membrane followed by a process in which cholesteryl ester molecules are irreversibly internalized and subsequently hydrolyzed through a nonlysosomal pathway (24-32). The lipid-depleted HDL particles released from cells after selective lipid uptake have the potential for reacquiring cellular cholesterol from peripheral tissues as described above, or they can be catabolized by the kidney (33) as a consequence of glomerulofiltration and subsequent reabsorption and degradation in the proximal tubules by a cubilin-associated endocytic pathway (34, 35). In rats, the liver removes 60-70% of HDL cholesteryl esters from plasma via the selective uptake pathway (Refs. 20 and 33; also reviewed in Ref. 23), a process that appears to be efficiently coupled to biliary lipid secretion (reviewed in Ref. 36). At least in rodents, selective uptake of HDL cholesterol also plays an important role in the transport of cholesterol to steroidogenic tissues (adrenal gland, ovary, and testes; Refs. 20-22 and 37-39), providing cholesterol as substrate for steroid hormone synthesis and for storage in cytoplasmic cholesteryl ester droplets. For example, in the rodent adrenal gland, selective uptake accounts for 90% or more of the cholesterol destined for steroid hormone production (40).

The pathway by which cholesterol is removed from peripheral cells and transported via plasma lipoproteins, such as HDL, into the liver for further metabolism (*e.g.*, VLDL formation, bile acid synthesis, and biliary secretion) is essential for cholesterol homeostasis. This is because peripheral cells (apart from low levels of catabolism in steroidogenic and skin cells) are not able to degrade cholesterol. This pathway, known as reverse cholesterol transport (41), is likely to be responsible for some of the antiatherogenic activity of HDL.

## **III. Lipoprotein Receptors**

To secure an adequate supply of cholesterol to cells, multiple mechanisms for cholesterol uptake from plasma lipoproteins have evolved. Through the work of many investigators, but especially the pioneering studies of Brown and Goldstein (42) and their colleagues, we have a detailed picture of the cellular metabolism of LDL via the LDLR endocytic pathway and the role of LDLRs in body cholesterol transport in health and disease. Other members of the LDLR family of proteins (*e.g.*, LDLR-related protein) participate in the hepatic metabolism of chylomicron and VLDL remnants, and they also appear to have functions independent of lipid metabolism (43–45). All of these receptors process lipoproteins via clathrin-coated pit-mediated endocytosis and lysosomal degradation, which releases cholesterol for subsequent cellular metabolism. The autosomal recessive hypercholesterolemia protein, a cytosolic polypeptide with a phosphotyrosine-binding domain, was recently identified by genetic analysis of patients with defects in LDL metabolism as a regulator of LDLR-mediated endocytosis (46). It presumably influences LDLR activity by binding to the NPYX endocytic motif of the cytoplasmic region of the receptor (46).

A series of metabolic regulatory responses linked to the LDLR pathway helps ensure cellular cholesterol homeostasis. For example, increase of the intracellular cholesterol pool due to the endocytosis of LDL leads to decreased cholesterol synthesis, increased cholesterol esterification for storage, and reduced LDLR levels to prevent excessive intracellular cholesterol accumulation. Substantial progress has been made in understanding the mechanisms by which these processes are regulated via membrane-bound transcription factors known as sterol regulatory element (SRE)-binding proteins (SREBPs; Ref. 47). Furthermore, knowledge of these regulatory mechanisms contributed to the development of statin drugs, which inhibit HMG CoA reductase and consequently lower plasma LDL cholesterol levels by stimulating, via the SREBP pathway, LDLR expression. The statins represent a major breakthrough in the treatment and prevention of atherosclerotic cardiovascular disease.

About 70% of the LDLR activity is concentrated in the liver, where LDLRs remove LDL and, working together with LDLR-related protein, internalize LDL, VLDL, and chylomicron remnants from the circulation. Based on both in vitro and in vivo studies, all steroidogenic tissues from human and nonhuman mammals appear to express the LDLR pathway of lipoprotein cholesterol uptake for steroid hormone synthesis (48). If the LDLR was the sole source of sufficient amounts of cholesterol for steroidogenesis, then subjects with abnormalities in LDLR-mediated endocytosis would be expected to exhibit significantly abnormal steroid hormone production. This does not appear to be the case. Abetalipoproteinemia, which is characterized by the absence of circulating LDL, is not associated with abnormal basal plasma and urinary corticosteroids, but the response of these patients to ACTH stimulation is somewhat impaired (49, 50). Post-ACTH aldosterone and androstenedione secretion is not affected in these patients. Ovarian, testicular, and placental function of abetalipoproteinemic patients has not been exhaustively studied; however, abetalipoproteinemic females, who exhibit decreased plasma progesterone during menstrual luteal phase, have normal pregnancies (51). In addition, various reports of familial hypercholesterolemia (FH), due to LDLR deficiency, have not described major adrenal, ovarian, or testicular steroidogenic dysfunction. Plasma cortisol levels in the basal state are within normal range in heterozygous FH patients; however, plasma cortisol is reduced in homozygous FH subjects relative to controls (52-54) after ACTH administration (however, see Ref. 55). In addition, LDLR-deficient Watanabe rabbits have impaired functional adrenal (56) and ovarian (57) reserves. Although fecundity of the Watanabe rabbit is somewhat impaired (58), no apparent other major endocrine abnormalities have been reported in these rabbits, as is the case for homozygous null LDLR knockout (KO) mice. Furthermore, female homozygous FH patients can get pregnant and give birth to normal offspring. Interestingly, adverse effects on adrenal or gonadal function have not been reported in patients with FH receiving cholesterol synthesis inhibitors (53, 59, 60). Taken together, these data suggest that alternative pathways for lipoprotein cholesterol delivery to cells might be available to supply functionally adequate amounts of lipoproteinderived cholesterol to sustain hormone synthesis in various steroidogenic tissues.

The LDLR-independent accumulation of cholesterol in macrophages in artery walls is one of the earliest steps in atherosclerosis. It is generally thought that macrophage surface receptors that are not under cholesterol-feedback regulation and that recognize and endocytose modified lipoproteins (e.g., aggregated or oxidized LDL) are essential for massive cholesteryl ester lipid droplet formation in these cells. The multiligand receptors that bind and internalize modified lipoproteins are called scavenger receptors (43, 61-63). There are now many members of a superfamily of scavenger receptors that have diverse structures, expression patterns, and functions (reviewed in Refs. 12 and 61-66). In vivo experiments have implicated scavenger receptor class A types I and II (SR-AI/II) and the class B scavenger receptor CD36 in atherogenesis (12, 66, 67). There is strong support for the proposal that some scavenger receptors also participate in host defense as multiligand pattern recognition receptors for pathogens (65, 66).

Using either direct binding or ligand blotting assays and a variety of preparations from tissues of different species, many laboratories have reported HDL binding activities (6, 7, 19, 68, 69). Serendipitously, SR-BI, originally identified by expression cloning because of its ability to bind modified LDL (70), was the first molecularly well characterized HDL receptor to be discovered (71). Its properties and functions are described below.

#### **IV. Structure and Subcellular Distribution of SR-BI**

The predicted sequences of SR-BI proteins from different mammalian species share 70-80% sequence identity over their 509-amino-acid lengths (Fig. 1). An alternatively spliced mRNA of SR-BI and its corresponding protein have been identified and designated SR-BII (72). SR-BI is a member of a family of structurally related proteins, called the CD36 superfamily (73), which includes the mammalian proteins CD36 (74) and LIMPII (a lysosomal integral membrane protein; Ref. 75); two Drosophila melanogaster proteins, emp (76) and croquemort (a hemocyte/macrophage receptor; Refs. 77 and 78); SnmP-1 (a silk moth olfactory neuron membrane protein; Ref. 79); a putative Caenorhabditis elegans protein (GenBank accession no. Z54270), and others. There are several similarities in the intron/exon organization of the SR-BI (80) and CD36 (81) genes. Human SR-BI was first cloned as a homolog of CD36 and LIMPII of unknown function that

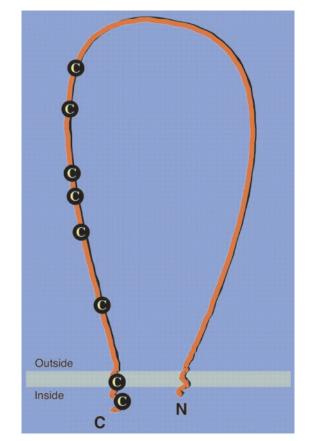


FIG. 1. Model of SR-BI. SR-BI is a 509-amino-acid glycoprotein with a large extracellular domain anchored to the plasma membrane at both the N and C termini by hydrophobic transmembrane regions that have short extensions into the cytoplasm. SR-BI is highly glycosylated on all its potential N-glycosylation sites (84, 85). SR-BI is also palmitoylated on the cysteines located at the C-terminal cytoplasmic and transmembrane domains (84, 87). SR-BI contains a well conserved set of cysteines in its carboxy-terminal half. [Reproduced with permission from M. Krieger: *J Clin Invest* 108:793–797, 2001 (372).]

mapped to chromosome 12 (73, 80) and was called CLA-1 (82). In addition, phylogenetic analysis of the CD36 gene family indicated that LIMPII, SR-BI, emp, and CD36 diverged from a common ancestor gene very early during evolution (73).

With the exception of croquemort and a potential third spliced isoform of SR-BI called SR-BIII (83), each of which has a single hydrophobic domain at the carboxy terminus (77, 83), all of the CD36 family members contain two internal hydrophobic, putative membrane-spanning domains adjacent to short cytoplasmic amino- and carboxy-terminal tails (Fig. 1). The bulk of the proteins lies between the two hydrophobic plasma membrane-anchoring domains on the extracellular side of cells and contains a set of conserved cysteines. SR-BII only differs from SR-BI in that the C-terminal 42 amino acids in the C-terminal cytoplasmic domain of SR-BI are replaced by 40 residues encoded by an alternatively spliced exon (72).

As predicted from the presence of consensus motifs for N-linked glycosylation sites in the cDNA, SR-BI is heavily N-glycosylated (84). This accounts for the difference between its mass predicted from the amino acid sequence ( $\sim$ 57 kDa;

Ref. 81) and that observed using immunochemical methods (~82 kDa; Refs. 71 and 84). In cultured cells, SR-BI is cotranslationally modified on all of its potential N-glycosylation sites (84, 85). Some, but not all, of these N-glycosylated oligosaccharides are transformed into complex carbohydrate chains during transit through the Golgi apparatus (84). Furthermore, metabolic labeling studies have established that SR-BI is fatty acylated (84), a structural feature shared with CD36 (86). Analysis of point mutants has shown that the major sites of palmitoylation of SR-BI are cysteine residues 462 and 470 located in its carboxy-terminal transmembrane and cytoplasmic domains (87).

In cultured cells, SR-BI and SR-BII appear to be concentrated in microdomains that under certain growth conditions correspond to cholesterol and sphingolipid-enriched plasma membrane microdomains (lipid rafts) called caveolae (see below) (84, 88). For some proteins, fatty acylation can serve as a sorting signal for concentration in caveolae. However, inhibition of fatty acylation of SR-BI by simultaneous mutation of cysteines 462 and 470 has no apparent effect on SR-BI surface localization in transfected cultured cells (87). Currently, the motifs in SR-BI that determine its subcellular localization are unknown.

SR-BI is expressed in a variety of polarized epithelial cells, including hepatocytes, colangiocytes, and enterocytes. Adenovirus-mediated in vivo overexpression of SR-BI in murine hepatocytes results in SR-BI expression on both the apical (canalicular) and basolateral (sinusoidal) surfaces of the cells (89). Examination of normal murine liver sections for expression of endogenous SR-BI established that SR-BI is primarily located in the basolateral domain of hepatocytes (90, 91). It is also seen in the basolateral membranes of SR-BItransfected MDCK cells (92, 93). In contrast, SR-BI is predominantly found in the apical domain of enterocytes (94, 95), the epithelial intestinal cell line CaCo2 (94), and colangiocytes (96). The marked differences in the subcellular distribution of SR-BI in polarized cells are likely to be related to important differences in sorting pathways, and possibly in the expression and function of adapter/chaperone proteins. Candidate modulators of the localization, stability, and function of SR-BI have been isolated from rat liver membrane homogenates (97). These proteins interact with the carboxyterminal cytoplasmic domain of SR-BI. Molecular characterization of one of these proteins established that it is a soluble protein composed of multiple PDZ domains (97). This protein, called CLAMP (carboxy-terminal linking and modulating protein), recognizes SR-BI via its N-terminal PDZ domain. Coexpression of CLAMP with SR-BI in transfected cells affects the stability of SR-BI as well as the efficiency of conversion of HDL cholesteryl esters taken up via SR-BI to intracellular unesterified cholesterol (97). Furthermore, CLAMP has been proposed to be involved in determining the basolateral distribution of SR-BI in hepatocytes (97). In fact, a recent study using carboxy-terminal deletions of the SR-BI protein indicates that the CLAMP-interacting domain of SR-BI is essential for its cell surface expression in liver (98). Further studies will be required to identify the polarity and subcellular localization targeting signals in SR-BI, the role of SR-BI associating proteins such as CLAMP, and the functional consequences of the differential plasma membrane localizations of SR-BI.

#### V. Ligand Binding Activities of SR-BI

SR-BI is a multiligand receptor (11, 12, 14). It was initially discovered as a scavenger receptor, because of its modified (acetylated and oxidized) LDL binding activity (70, 99). SR-BI also binds hypochlorite-modified HDL (100). However, SR-BI does not bind the wide array of polyanionic molecules (e.g., fucoidin, polyguanosine, carrageenan) that are all ligands of other classes of scavenger receptors (11, 12, 14, 61, 62, 64–67, 70). In addition to lipoprotein ligands (see below), cell culture ligand binding studies show that SR-BI recognizes a diverse set of ligands. SR-BI binds maleylated BSA (70), advanced glycation end product modified proteins (101), and anionic, but not zwitterionic, phospholipids in the form of liposomes (102, 103). Indeed, SR-BI and CD36 were the first molecularly well defined cell surface receptors for phosphatidylserine to be identified (102). These findings suggested that SR-BI might be able to bind senescent, damaged, and apoptotic cells with high levels of phosphatidylserine on the exofacial surface of the plasma membrane, and thus might play a role in the recognition and clearance of these cells during development, tissue remodeling, and disease (102). In fact, transfected cultured cells expressing exogenous SR-BI can bind apoptotic cells (103–107). Furthermore, SR-BI mediates binding of  $\beta$ -amyloid to transfected Chinese hamster ovary cells (108) and cultured microglia and brain vascular smooth muscle cells (109, 110), suggesting a potential role in Alzheimer's disease. More recently, the hepatitis C virus envelope glycoprotein E2 was reported to be a ligand for human SR-BI, suggesting its role as hepatitis C virus receptor (111). Analysis of the mechanisms by which multiple ligands with very different structures bind SR-BI indicates very complex interactions, suggesting multiple classes of binding sites (11, 12, 112).

Most of the studies of ligand binding to SR-BI have focused on native lipoproteins. The first native lipoprotein shown to bind to SR-BI with high affinity ( $K_d \sim 10$  nM) was LDL (70). Before that finding, the only molecularly defined receptor for LDL was the classic LDLR (1, 2). SR-BI-mediated internalization and degradation of LDL was, however, far less efficient than that by the classic LDLR (70). Similarly, inefficient SR-BI-mediated endocytosis and degradation was observed for modified LDL (Ref. 70; however, see Ref. 99). SR-BI has also been shown to bind to VLDL (113).

Although the potential of SR-BI to function as a new "second" LDLR was intriguing, most investigations of SR-BI have been influenced by the unanticipated discovery that SR-BI was the first molecularly well defined and physiologically relevant HDL receptor to be identified (71). SR-BI binds HDL with high affinity in a calcium- and apoE-independent fashion. The ability of SR-BI to bind to several native lipoproteins suggests that it may be responsible for some of the multilipoprotein binding activities previously reported in a wide variety of cells types and tissues (6, 7, 19, 68, 69, 114). There may, however, be additional cell surface HDL receptors, and they may have diverse structures, tissue expressions, and functional activities.

As is the case for some of the other classes of scavenger receptors (43, 115), SR-BI exhibits nonreciprocal cross competition, wherein one ligand effectively blocks the binding of a second ligand, but the reverse is not the case (112). For example, HDL effectively blocks all LDL binding, whereas LDL inhibition of HDL binding is poor, relative to the K<sub>d</sub> for LDL binding to SR-BI (71). Because of nonreciprocal crosscompetition, LDL is not expected to substantially interfere with the binding of HDL to SR-BI in vivo. Using a method called "retroviral library-based activity dissection," Gu et al. (112) have identified double mutations in murine SR-BI  $(^{402}\text{Glu}\rightarrow\text{Arg} \text{ and } ^{418}\text{Glu}\rightarrow\text{Arg})$  that together block most of the binding of HDL to SR-BI without significantly altering LDL binding. The same method also showed that a single methionine to arginine mutation at position 158 disrupts binding to SR-BI of both HDL and LDL, but not acetylated LDL (116).

SR-BI binds spherical  $\alpha$ -HDL. The lower the density of the  $\alpha$ -HDL particles (larger, higher lipid content), the more tightly they bind to SR-BI (117, 118). Pre- $\beta$ -HDLs are poor substrates of SR-BI (117). Several reports (117, 119) suggest that lipid-free apoA-I is also a poor substrate for SR-BI (however, see Ref. 120), whereas reconstituted discoidal complexes of phospholipid/cholesterol/apolipoprotein (i.e., apoA-I, apoA-II, apoE, or apoC-III) bind more tightly to SR-BI than native spherical  $\alpha$ -HDLs (117, 119, 121). SR-BI appears to be able to bind some lipid-free apoE, which has been reported to facilitate lipoprotein cholesterol uptake (122). The receptor binding domain is located in the aminoterminal 1–165 region of the apoE protein (121). The relative amounts of apoA-I and apoA-II in spherical HDL particles apparently influence their interactions with SR-BI, although the precise nature of the interactions is not yet clear. One report suggests that enriching plasma HDL with additional copies of apoA-II enhances its affinity for SR-BI but inhibits cholesteryl ester uptake (123). Another study reported that reconstituted apoA-I/apoA-II-containing particles exhibit decreased binding relative to particles containing apoA-I only (124). The binding of reconstituted discoidal apoA-I complexes by SR-BI requires either the amino- or carboxyterminal amphipathic helices of apoA-I (117). These (117-119) and other (125) studies strongly suggest that the conformation/organization of apoA-I in HDL particles critically affects the nature of the interaction of the particle with SR-BI. Using phospholipid particles reconstituted with fragments of apoA-I and a model peptide, Williams et al. (120) have provided strong evidence that amphipathic helices play critical roles in the binding of apolipoproteins to SR-BI. This may explain the ability of SR-BI to bind to a wide variety of lipoproteins.

## VI. Lipid Transfer Activity of SR-BI

## A. Selective cholesterol uptake

SR-BI mediates the transfer of a variety of lipids between cells and lipoproteins. Unlike the interaction of LDL with the LDLR, the binding of HDL to SR-BI does not lead to its lysosomal degradation (71). Instead, SR-BI mediates selective lipid uptake from native lipoproteins (71). As noted above,

selective lipid uptake involves the net transfer of lipids from lipoproteins to cells and the subsequent release of the lipiddepleted lipoprotein into the extracellular medium. SR-BI mediates selective uptake from HDL of cholesteryl esters (71), unesterified cholesterol (126–129), phospholipids (130), triglycerides (131), α-tocopherol (132, 133), DiI (71), BODIPYcholesteryl ester (134), pyrene-labeled phospholipids (130), and cholesteryl ethers (often used as nonhydrolyzable analogs of cholesteryl esters; Ref. 71). The rate constant analyses of lipid transfer from reconstituted HDL to the plasma membrane of SR-BI-expressing cells have shown that the more hydrophobic lipids (e.g., unesterified cholesterol, cholesteryl esters, and triglycerides) can transfer more easily than the more polar phospholipid molecules (135). The physiological relevance of SR-BI-mediated selective lipid uptake in cultured cells was first directly established using steroidogenic cells, which express high levels of SR-BI (see below), HDL binding and selective cholesterol uptake, and use HDL cholesterol for steroidogenesis. An anti-SR-BI antibody simultaneously inhibited HDL binding, selective HDL lipid uptake, and HDL cholesterol-dependent steroidogenesis in murine adrenocortical cells (136). Similar results have been reported for rat ovarian granulosa cells in primary culture (137).

Several investigators have established that selective cholesteryl ester uptake is not dependent on a single class of lipoprotein. HDL (20-31, 37-40, 138-140); reconstituted HDL-like particles prepared with apoA-I, apoC, or native or modified apoE (141); IDL (141, 142); and LDL (38, 140, 143-146) have all been shown to be sources of cholesterol for selective lipid uptake *in vitro* and/or *in vivo*. It seems likely that SR-BI is responsible for many of these activities. For example, SR-BI mediates selective uptake of cholesteryl esters from LDL (128, 146-148) and the uptake of fluorescent lipids from VLDL (113); however, the fractional transfer of surface-bound LDL-cholesteryl esters to cells via SR-BI was significantly lower compared with HDL-cholesteryl esters (149). With regard to HDL subclasses, SR-BI-mediated selective cholesteryl uptake is greater from LpA-I compared with LpA-I:A-II (150). However, it is noteworthy that recent studies provide support for the existence of additional, SR-BI-independent selective lipid uptake mechanisms, such as one facilitated by cell surface proteoglycans (151–155).

SR-BI (71, 104, 113) and its homolog CD36 (87, 148, 156) can both bind HDL with high affinity, but of the two, only SR-BI mediates efficient selective lipid uptake (87, 148). Thus, the cell surface binding of HDL is not sufficient for selective lipid uptake. SR-BI apparently directly facilitates a lipid transfer step that follows binding (two-step mechanism of selective uptake; Ref. 87). Analysis of SR-BI/CD36 chimeras established that sequences in the extracellular domain of SR-BI are sufficient to confer efficient selective lipid uptake activity on the cytoplasmic and transmembrane domains of CD36 (87, 148). However, the carboxy-terminal cytoplasmic domain of the receptor can influence the efficiency of selective lipid uptake, because SR-BII, the isoform of SR-BI with an alternative carboxy-terminal cytoplasmic domain, facilitates selective uptake less well than SR-BI (88). Analysis of the interaction of discoidal HDL particles prepared with wild-type and mutant apoA-Is with wild-type and mutant forms of SR-BI established that, somewhat analogously to enzyme/ substrate interactions, there must be productive binding of an HDL particle to SR-BI to permit subsequent efficient lipid transport (125). Inhibition of SR-BI-mediated selective lipid uptake using small molecules identified in a chemical library screen (blockers of lipid transport) also supports a mechanistic coupling between HDL binding and lipid transport (157). Furthermore, apoA-I-deficient HDL binds with high affinity to SR-BI, but does not mediate efficient lipid uptake, indicating that the HDL features required for binding to SR-BI are distinct from those properties necessary for the selective cholesterol uptake from HDL to cells (158). The molecular details of the interactions between HDL and SR-BI that result in productive binding and lipid transport remain to be defined. Similarly, the precise mechanism of lipid transport has not been elucidated. The discovery of chemical inhibitors of the selective transfer of lipids mediated by SR-BI should provide new mechanistic insights into this lipid uptake pathway (157).

Just as specialized regions in the plasma membrane (clathrin-coated pits) are required for LDLR-mediated endocytosis (1, 25), specialized surface structures may sometimes be involved in SR-BI-dependent selective lipid uptake. Under certain culture conditions, SR-BI has been localized in cell surface caveolae (84, 88). Interestingly, SR-BI stabilizes caveolin-1 protein, independently of its transcriptional control, in cultured cells but not vice versa (159). The apparent clustering of SR-BI in caveolae in cultured cells under some culture conditions raises the possibility that these or similar lipid raft-like plasma membrane domains might be relevant for SR-BI-mediated cholesterol trafficking between lipoproteins and cells (84). Indeed, caveolae appear to be the sites where the initial steps of SR-BI-mediated selective cholesterol uptake into the plasma membrane take place before irreversible internalization of cholesterol into intracellular compartments (87, 160). Furthermore, selective uptake activity in certain cells appears to correlate with levels of caveolin-1 (161), which has cholesterol binding activity (162) and has been implicated in intracellular cholesterol transport (163, 164). One study has suggested that a caveolin-containing multiprotein complex may facilitate movement of SR-BI-derived cholesteryl esters from the cell surface to intracellular compartments (165). However, other studies have shown that: 1) caveolin-1 negatively regulates SR-BI-mediated selective uptake of HDL cholesteryl esters (166); 2) SR-BI-mediated selective uptake of HDL cholesteryl esters is not affected by caveolin-1 expression (167); and 3) localization of SR-BI in caveolae or raft-like domains is not required for selective cholesteryl ester uptake (168). In murine adrenocortical cells, SR-BI was found in numerous circular and oval structures of the cell surface that appear to represent crosssections through previously described microvilli-rich intercellular channels (Fig. 2; and Ref. 169). HDL has been shown to accumulate in these channels (170-172), and they may play an important role in the selective lipid uptake process (134, 169-172). SR-BI has been reported to: 1) be present in microvillar channels in vivo (39, 137); 2) induce microvillar channel formation when overexpressed in insect cells (134); and 3) play a role in the formation of microvillar channels in murine steroidogenic cells in vivo (173). The important question as to whether the selective uptake of lipid from HDL occurs at the cell surface, in some internal compartment followed by retroendocytosis (secretion) of the lipid-depleted lipoprotein particle, or both has not yet been unequivocally resolved (11, 12, 14, 38, 39, 93, 137, 169–171, 174). Recent studies in which purified SR-BI was reconstituted into phosphatidylcholine/cholesterol liposomes have established that SR-BI can mediate HDL binding and selective lipid uptake without the required intervention of other proteins or specialized cellular structures or compartments (175).

The abilities of various tissue-associated lipases and plasma lipid transfer proteins to remodel HDL lipid composition might play a role in modulating the ability of SR-BI to mediate selective HDL-cholesterol uptake. Among these, hepatic lipase has been proposed to participate in HDL metabolism through several mechanisms (16, 176), including selective HDL-cholesterol uptake (11, 12, 14). It has been suggested that hepatic lipase and SR-BI might act coordinately for efficient selective transport of cholesteryl esters from HDL into cells (11, 12, 14, 16, 177-179) based on the following experimental evidence: 1) hepatic lipase activity facilitates selective HDL cholesteryl ester uptake mediated by SR-BI (180, 181); 2) SR-BI (71, 182) and hepatic lipase (183, 184) are highly expressed in tissues that exhibit the highest rates of HDL-cholesterol transport through selective lipid uptake; 3) adrenal SR-BI expression is increased in hepatic lipase KO mice (177) and in rats injected with antihepatic lipase antibodies (185); and 4) the formation of unusual vesicular lipoproteins in apoE/hepatic lipase double KO mice (179). Hepatic lipase-facilitated selective HDL-cholesterol uptake is stimulated by the presence of SR-BI and is dependent on both the lipolytic and nonlipolytic (i.e., hepatic lipase-mediated HDL binding to cell surface proteoglycans) functions of hepatic lipase (180). In addition, CETP remodeling of HDL, particularly in conjunction with hepatic lipase modification, apparently stimulates SR-BI-mediated selective HDL-cholesterol uptake (181, 186). Both in vitro and in vivo SR-BI-mediated selective cholesteryl ester uptake is increased after hydrolysis of HDL phospholipids by secretory group IIa phospholipase A2 (187, 188). Consistent with the importance of enzyme-dependent lipid modification of HDL on the efficiency of cholesterol transfer activity mediated by SR-BI, a higher triglyceride content of HDL decreased the ability of SR-BI to mediate selective HDL cholesteryl ester uptake (144). Furthermore, apoA-I-dependent LCAT-mediated reorganization of HDL is also important for efficient selective HDL-cholesterol uptake by SR-BI (189). Taken together, these findings show that HDL-cholesterol metabolism through the SR-BI-mediated pathway can depend on complex metabolic interactions between different HDL remodeling enzymes and their effects on the lipid composition of HDL.

The precise mechanisms for the intracellular transport of the HDL lipids taken up by SR-BI-mediated selective uptake remain mostly unknown (31). Current evidence indicates that certain lipid transfer proteins, an intact Golgi apparatus, and some cytoskeletal elements are not required for intracellular traffic of cholesterol derived from plasma lipoproteins by selective lipid uptake. However, this process seems

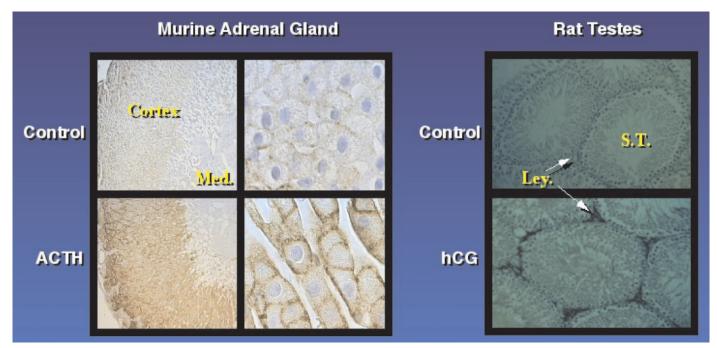


FIG. 2. Regulation of SR-BI expression in rodent steroidogenic tissues. *Left*, In murine adrenal glands, SR-BI immunostaining (*brown*) was found in the adrenal cortex but not in the medulla (Med.) of saline-treated control animals [*top panels* (169, 182)]. SR-BI staining was strongest in the outer zona fasciculata of the adrenal cortex and decreased toward the inner zona reticularis. ACTH treatment markedly increased SR-BI immunostaining in the cortex (*bottom panels*). At higher magnification, SR-BI was most abundantly detected in the plasma membrane of zona fasciculata cells, and the increased intensity of staining in the ACTH-treated mice was seen at both the sinusoidal surface and the intercellular junctions of steroidogenic cells. SR-BI was found in numerous circular and oval structures of the cell surface that appear to represent cross-sections through microvilli-rich intercellular channels (169). *Right*, In rat testes, little immunodetectable SR-BI was found in testicular steroidogenic Leydig cells of control animals [*top* (182)], but not in the seminiferous tubules (S.T.). After human chorionic gonadotropin (hCG) hormone administration, a dramatic increase in SR-BI expression was exclusively localized to Leydig cells [*bottom* (182)]. [Reproduced or derived with permission from A. Rigotti *et al.*: *J Biol Chem* 271:33545–33549, 1996 (169); and K. Landschulz *et al.*: *J Clin Invest* 98:984–995, 1996 (182).]

to be somewhat energy-dependent and mediated by N-ethylmaleimide-sensitive protein(s) that are yet to be identified (31). The role of the hepatic neutral cholesteryl ester hydrolase (reviewed in Ref. 190) as well as cholesterol-rich carrier vesicles or protein complexes (165) in controlling the availability and traffic of unesterified cholesterol derived from the uptake of HDL cholesteryl esters by SR-BI deserves to be explored. Indeed, the generation of unesterified cholesterol after delivery of cholesteryl esters from HDL to cells via SR-BI involves cell type-specific neutral cholesteryl ester hydrolases (32). In addition, CLAMP modulates the efficiency of conversion of HDL cholesteryl esters taken up via SR-BI to intracellular unesterified cholesterol (97). A caveolin and annexin II-containing complex may in some cases be involved in the movement of SR-BI-derived cholesteryl esters from the plasma membrane to intracellular sites (165). Further studies of the detailed molecular mechanism(s) of intracellular cholesterol traffic linked to selective cholesterol uptake will provide new insights to the understanding of this pathway for lipoprotein metabolism.

## B. Cholesterol efflux

The discovery of SR-BI-mediated selective lipid uptake (influx) raised the possibility that SR-BI might be able to mediate another step in the reverse transport process, cholesterol efflux from cells to appropriate acceptors in the extracellular fluid (11, 89). Consistent with this proposal were

the observations that: 1) caveolae, the plasma membrane domains in which SR-BI appears, at least under some conditions, to be concentrated in cultured cells, have been proposed to be major sites of cholesterol efflux from cells (191); and 2) SR-BI expression levels in different cell lines correlate with rates of unesterified (free) cholesterol efflux to HDL in those cells (126). The ability of SR-BI to mediate cholesterol efflux from cells was directly established by studies in which SR-BI-transfected cultured cell lines were shown to exhibit increased radiolabeled unesterified cholesterol efflux to HDL and phosphatidylcholine liposomes, but not lipid-free apoA-I (127). SR-BI has also been reported to influence cholesterol efflux from cells to exogenously added apoE (192). SR-BI-mediated transfer of unesterified cholesterol between cells and HDL is bidirectional (188). Because SR-BI-mediated transport does not appear to be dependent on ATP, net flux of lipids is likely driven by the concentration gradient between cells and extracellular donor/acceptor particles. Although it mediates efflux to lipid-poor HDL from macrophages loaded with nonmetabolizable cholesterol, SR-BI apparently facilitates selective cholesterol uptake from cholesterol-rich particles to the plasma membrane of hepatocytes and steroidogenic cells down a gradient determined by further intracellular cholesterol metabolism.

In all studies performed to date, SR-BI-mediated cholesterol efflux has been correlated with the ability of this receptor to mediate selective uptake (116, 193), suggesting that the mechanisms of influx and efflux may be linked. Analysis of mutant forms of SR-BI that have lost the ability to bind and mediate selective uptake from either HDL alone or HDL and LDL (but not acetylated LDL), combined with the analysis of the effect of antibodies that block lipoprotein binding to SR-BI, strongly suggests that lipoprotein binding is required for SR-BI-dependent cholesterol efflux (116). Furthermore, decreased SR-BI-mediated cholesterol efflux to HDL particles reconstituted with mutant apoA-I forms suggests that the formation of a productive complex between HDL and SR-BI is required for efficient cholesterol transport activity (125). However, an alternative view that cholesterol-acceptor binding to SR-BI is not required for SR-BI-dependent cholesterol efflux has been proposed (194, 195). Interestingly, it has been shown that SR-BI expression in cultured cells alters the accessibility of cellular cholesterol to modification by cholesterol oxidase added to the culture medium (194, 195). The relationship between this change in surface cholesterol accessibility and efflux is not yet certain, but this important observation is likely to lead to new insights into the mechanisms underlying SR-BI-mediated lipid transport.

SR-BI-dependent cholesterol efflux activity is modulated by enzymatic and nonenzymatic changes in HDL lipid composition (188). Both phosphatidylcholine and sphingomyelin enrichment of HDL increase net cholesterol efflux from SR-BI-expressing cultured cells. Cholesterol efflux mediated by SR-BI is significantly correlated with HDL phosphatidylcholine content, suggesting that the relative phospholipid/cholesteryl ester composition of HDL influences the efficiency of cholesterol efflux. This may be due to a dependence on the cholesterol gradient between HDL particles and cell plasma membrane (reviewed in Refs. 68 and 196).

Tangier disease, characterized by impaired cholesterol efflux from cells to lipid-free or lipid-poor apoA-I and dramatically reduced plasma HDL levels, is a consequence of mutations in the gene encoding the ABCA1 transporter (197– 200). This discovery has had a major impact on the study of cellular cholesterol efflux. The potential structural and/or functional interaction between ABCA1 and SR-BI in regulating cellular cholesterol efflux has only just begun to be explored (201). It is also interesting to note that although ABCA1 facilitates efflux of cholesterol, it may be a primary transporter for phospholipid efflux that secondarily drives cholesterol transport out of cells (202-204). It is conceivable that SR-BI and ABCA1 might act coordinately in cellular cholesterol efflux because nascent HDL particles formed from lipid-free apoA-I by ABCA1-mediated phospholipid efflux (202-204) could serve as an acceptor for further cholesterol efflux mediated by SR-BI. In this regard, it is interesting that ABCA1 binds lipid-free apoA-I in preference to spherical HDL particles (203–206), and the opposite is true for SR-BI (117–119). A study involving coexpression of high levels of SR-BI and ABCA1 suggested that SR-BI and ABCA1 may have distinct and, under some circumstances, opposite effects on unesterified cholesterol flux between HDL and cells (201).

The SR-BI-mediated transfer of unesterified cholesterol between cells and the extracellular fluid need not always involve lipoproteins or phospholipid carriers. SR-BI can facilitate the cellular uptake of unesterified cholesterol added directly to culture medium in the absence of lipoproteins (147, 207). This lipoprotein-independent activity of SR-BI may be related to the recent report that SR-BI is indeed a cholesterol binding protein (206).

## VII. Tissue Expression, Regulation, and Function of SR-BI

Immunochemical methods have shown that SR-BI is most highly expressed in adult mammal tissues that are the principal sites of selective lipid uptake in vivo, i.e., the liver and steroidogenic tissues (71, 182). In addition, SR-BI has been observed at lower levels in intestine (94, 95, 182, 207), mammary glands of pregnant rats (71, 182), trophoblast, yolk sac and placenta during intrauterine development (208, 209), and uterine endometrium (210). The presence of SR-BI has also been reported in lung (211), biliary tree (96), macrophages (104, 126, 212-214), endothelial cells (132, 208, 215-217), smooth muscle cells (217), neuroglia (109, 110, 218), retinal pigmental epithelial cells (219), and keratinocytes (220). Substantial amounts of SR-BI mRNA have been detected in 3T3-L1 adipocytes and murine adipose tissue (70); however, the relationship between the mRNA and protein levels of SR-BI in fat is not yet resolved (71, 182). In addition, regulation of SR-BI protein expression is not always correlated with variations in mRNA levels (91, 211, 221-223). Thus, evaluation of the absolute levels and changes in SR-BI mRNA levels may not necessarily reflect the levels of SR-BI protein and SR-BI activity in tissues or cells.

## A. Liver

The liver expresses the highest levels of total tissue SR-BI protein, a finding consistent with the major role of the liver in selective HDL-cholesterol uptake. The liver accounts for 90% of selective HDL cholesteryl ester uptake as well as 50% of total HDL cholesteryl ester clearance in non-CETP-expressing rodents (rats and mice; Refs. 20–23), and it mediates approximately 20% of total HDL cholesteryl ester clearance in CETP-expressing animals (224). SR-BI may account for much of the previously described hepatic lipoprotein binding site activity (225), because both SR-BI (70, 71, 113, 128, 146) and lipoprotein binding site (114, 140, 142, 143, 226) exhibit multilipoprotein binding as well as selective cholesterol uptake activities for different classes of lipoproteins.

Under basal conditions, most hepatic SR-BI expression is in parenchymal cells (90, 91, 212). Although SR-BI can be detected in the canalicular domains of hepatocytes in mice overexpressing hepatic SR-BI (89) and in cultured hepatocyte couplets (93), immunofluorescence analysis indicates that SR-BI is almost exclusively expressed on the sinusoidal surface of hepatocytes in wild-type animals (90, 91). In addition to its expression in liver parenchymal cells, SR-BI protein expression has been reported in Kupffer (212, 227) and liver endothelial cells (227).

Hepatic SR-BI expression can be regulated by a series of dietary, hormonal, and pharmacological manipulations. In the hamster, dietary plant-derived polyunsaturated fatty acids have been shown to stimulate hepatic SR-BI expression and HDL cholesteryl ester uptake (228). In contrast, dietary myristic acid decreased liver SR-BI levels in association with increased plasma HDL levels in hamsters (229). SR-BI expression is inversely regulated by cellular  $\alpha$ -tocopherol concentrations in the HepG2 human hepatocyte cell line and by dietary vitamin E supply in the mouse liver (223). In hamsters, a novel acyl-coenzyme A:cholesterol acyltransferase inhibitor has been reported to increase hepatic SR-BI, but not LDLR, expression (230). In contrast, lipopolysaccharide (LPS), TNF, and IL-1 decreased hepatic SR-BI mRNA and protein levels in the Syrian hamster (231). Streptozotocin administration in genetically hypercholesterolemic RICO rats increased SR-BI protein levels, which correlated with lower plasma HDL (232). On the other hand, insulin-treated diabetic hamsters exhibited lower levels of SR-BI compared with similar hamsters injected with saline only (233). In rats, estrogen administration at pharmacological levels suppresses total hepatic SR-BI expression (182, 212, 234, 235), which also correlates with decreased hepatic selective cholesterol uptake (236). Interestingly, estrogens increase hepatic SR-BII expression (235). The decrease in hepatic SR-BI expression was an indirect effect that was abolished by hypophysectomy and dependent on the estrogen-induced increase in LDLR activity (90). Other studies established that administration of high levels of estrogen increases hepatic Kupffer cell (macrophage) expression while lowering parenchymal cell expression (212). This study also demonstrated similar reciprocal changes in parenchymal and Kupffer cell expression after cholesterol feeding (212). However, studies with hamsters and mice did not find that hepatic SR-BI levels and/or HDL cholesteryl ester transport were regulated by changes in dietary cholesterol (237–239). In addition, a deficiency of plasma HDL in apoA-I KO mice does not increase hepatic SR-BI expression (240). Taken together, these studies indicate that, at least in some species, *in vivo* hepatic levels of SR-BI are not under sensitive feedback control by hepatic cholesterol content and/or plasma HDL-cholesterol concentration.

A recent study has shown that prolonged adrenal stimulation by ACTH in rats and mice decreased hepatic SR-BI protein expression associated with increased plasma HDLcholesterol levels (241). This effect was not reproduced by exogenous corticosteroid administration and was abolished by adrenalectomy (241). These findings suggest that under chronic ACTH stimulation, adrenals release a factor that represses hepatic SR-BI levels as a potential mechanism for preferential channeling of plasma lipoprotein cholesterol to the adrenal tissue during stress.

In addition, the effects of pregnancy and lactation on hepatic SR-BI expression in female rats has been described (242). Hepatic levels of SR-BI increase in late gestation, are maintained at those levels early after birth, return to non-pregnant levels by 3 d postpartum, drop under control levels in late lactation, and revert to basal levels in postlactating females. Interestingly, the regulation of SR-BI and LDLR expression was not the same, suggesting that the roles of these receptors during pregnancy and lactation differ substantially.

The regulation of hepatic SR-BI expression by nuclear receptors (91, 243–245) and the roles of hepatic SR-BI expres-

sion in lipoprotein metabolism and associated diseases are considered below.

## B. Adrenal gland

The highest expression levels of SR-BI per gram of tissue have been found in rodent adrenal glands (71, 182). High levels of SR-BI expression also have been detected in the human adrenal gland (80). Immunofluorescence and immunohistochemical methods have established that SR-BI is expressed primarily on the surfaces of steroidogenic parenchymal cells, such as in the zona fasciculata and zona reticularis cells of the adrenal cortex (Refs. 169 and 182; Fig. 2). High resolution immunohistochemistry established that in murine adrenocortical cells, SR-BI was found in numerous circular and oval structures on the cell surface that appear to represent cross-sections through previously described structures rich in microvillar channels (Ref. 182 and Fig. 2). These channels accumulate HDL, and they seem to play an important role in the selective lipid uptake process (38, 170, 172). The formation of similar cell surface double-membrane channels has been observed in insect cells expressing high levels of recombinant SR-BI (134). In addition, hormonal regulation of adrenal SR-BI expression is closely associated in vivo with changes in microvillar mass and microvillar channel formation in this rat steroidogenic tissue (246). By ultrastructural analysis of adrenal glands obtained from SR-BI-deficient mice, it has been established that SR-BI expression is essential for microvillar channel formation and the localization of HDL particles on the plasma membrane of adrenocortical cells (173). This finding indicates that expression of SR-BI can induce channel formation, probably directly as a consequence of the high-density expression of the receptor on the surfaces of cells.

ACTH treatment of mice, which induces adrenal steroidogenesis in concert with enhanced selective uptake of HDL cholesterol (reviewed in Ref. 247), increases SR-BI protein expression in adrenocortical cells (Ref. 169; Fig. 2). It seems likely that ACTH acts directly on the adrenocortical cells, rather than indirectly, because it also dramatically stimulates SR-BI protein and mRNA levels in cultured murine adrenal cells (169, 177, 248). The effect of ACTH on SR-BI expression is likely mediated by the second messenger cAMP (80, 249, 250). SR-BI expression in cultured human adrenal cells and its regulation by ACTH (249, 250) are similar to those observed in murine cells (169, 177, 248). The ACTH-mediated regulation of human SR-BI in vivo is probably similar to that of the mouse, because levels of SR-BI mRNA in normal adrenal tissue adjacent to Cushing adenoma are low, likely due to the reduced plasma ACTH levels found in these patients (249).

*In vivo* administration of the glucocorticoid dexamethasone, which suppresses ACTH secretion and thus adrenocortical steroidogenesis, dramatically suppresses SR-BI protein expression in the murine adrenal gland, suggesting that the relatively high basal levels of SR-BI in this tissue may be due to endogenous basal ACTH production (169). Taken together, these studies of hormonal regulation of adrenal SR-BI expression strongly support the hypothesis that in this tissue SR-BI mediates physiologically relevant selective uptake of cholesteryl esters to supply substrate for steroid hormone synthesis.

In addition to the activity of the hypothalamic-hypophyseal-adrenal axis, the adrenal cholesterol content can independently regulate adrenal SR-BI levels, although this cholesterol-dependent effect is overridden by ACTH regulation *in vivo* and *in vitro* (80, 248). Increased adrenal SR-BI expression has also been reported in apoA-I-deficient (177), hepatic lipase-deficient (177), and LCAT-deficient (251) mice, suggesting that the expression of these lipoprotein metabolismrelated genes directly or indirectly influences the levels of SR-BI in the adrenal gland. However, another study of apoA-I KO mice detected no changes in SR-BI mRNA or protein in the adrenal gland when compared with apoA-Iexpressing animals (240). Further studies are required to established the basis for these divergent results.

In vivo estrogen treatment of rats: 1) induces adrenocortical expression of SR-BI (182); 2) enhances binding of HDL (apoA-I) to the surface of adrenal cells (182); 3) stimulates uptake of a fluorescent lipophilic dye surrogate for cholesteryl esters, Dil (71), from circulating Dil-labeled HDL (182); and 4) increases adrenocortical selective uptake of HDL cholesteryl ester (252). The relationship in the rat between estrogen's stimulation of adrenocortical expression and suppression of hepatic expression of SR-BI is not established. Hypophysectomy dramatically decreases adrenal SR-BI expression (182), and chronic estrogen therapy affects ACTH secretion (253), strongly suggesting that trophic hormones play a key role in the estrogen-induced regulation of this receptor. In fact, dexamethasone administration, which inhibits endogenous ACTH production, blocked the increase in SR-BI expression in the adrenals of estrogen-treated hypophysectomized rats, demonstrating that ACTH is a critical factor involved in the estrogen-associated increase in adrenal SR-BI expression (90).

The functional significance of adrenocortical SR-BI expression has been established in vitro and in vivo. Anti-SR-BI antibodies that block HDL binding inhibit HDL-dependent steroidogenesis in cultured murine adrenocortical cells (136). Furthermore, SR-BI can provide HDL cholesteryl esters for steroidogenesis in cultured human adrenocortical cells, suggesting a potential role for SR-BI in human adrenals (254). Under normal physiological conditions, however, cultured human adrenocortical cells may derive more cholesterol from the LDLR pathway than the HDL pathway (250), suggesting that in humans LDL may be the primary lipoprotein delivering cholesterol to the adrenals via LDLRs. Nevertheless, in FH patients or patients with abetalipoproteinemia, plasma cortisol responses to ACTH are normal except under prolonged maximal stimulation (see above), indicating the existence of LDLR-independent pathways for adrenal lipoprotein cholesterol uptake. Furthermore, treatment of FH patients with mevinolin, a statin that inhibits cholesterol synthesis, did not result in impairment in adrenal function (53, 59). These results suggest that normal LDL uptake via LDLRs is not required for essentially normal adrenal function and that SR-BI might be able to supply cholesterol for steroidogenesis in human adrenals, at least when the LDLR pathway is impaired.

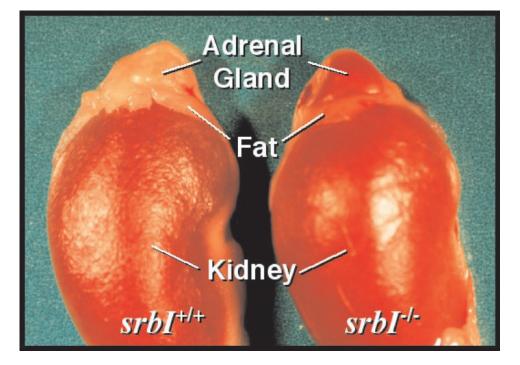
Analysis of mice with targeted null mutations in the SR-BI

gene has established that SR-BI plays a role in murine adrenocortical cholesterol metabolism. Biochemical and histochemical studies established that these mice exhibit depleted adrenal cholesterol stores (cytoplasmic cholesteryl ester storage droplets) in a gene-dose-dependent manner with reductions of 42% in heterozygotes and 72% in homozygote null SR-BI mutants (SR-BI KO mice; Ref. 255; Fig. 3). Similar lipid depletion is also observed in the ovaries (see below). Comparable adrenal cholesterol depletion has been observed in other murine mutants with disturbances in HDL metabolism, including apoA-I-deficient (172) and LCAT-deficient (251) mice, both of which exhibit abnormally high adrenal SR-BI mRNA levels (177, 251) that presumably represent regulatory responses made to compensate for reduced uptake of HDL-derived cholesterol. Furthermore, apoA-I KO mice also had blunted adrenal steroidogenic response to ACTH stimulation (172). Although SR-BI KO mice show no gross phenotypic indications of adrenal insufficiency, additional studies will be required to determine whether there are more subtle alterations in adrenal steroidogenesis in these mice. It is important to note that, except under conditions of very high demand, endogenous cholesterol synthesis via the HMG CoA reductase pathway would be expected to provide adequate amounts of substrate cholesterol for steroidogenesis in the adrenal glands, ovaries, and testes, even when LDLR- or SR-BI-mediated cholesterol import was not available.

It has long been known that plasma lipoproteins, in particular HDL, are able to neutralize bacterial LPS (endotoxin) and thus are protective against endotoxemia and bacterial sepsis (256–258). This is believed to be due, in part, to the binding of LPS by HDL (259), thus preventing LPS from stimulating the production of cytokines (TNF $\alpha$ , IL-1, and IL-6) by monocyte/macrophages (257). In rats, HDL-bound LPS accumulates in the adrenal gland, ovary, and liver (260, 261), precisely those tissues that express high levels of SR-BI. Furthermore, the accumulation of HDL-bound LPS in the adrenal gland is increased by ACTH and decreased by dexamethasone (260, 261) in a manner similar to HDL binding and SR-BI expression (169). In the case of the adrenal gland, the SR-BI-dependent removal of LPS from HDL may contribute to the occurrence of acute adrenocortical insufficiency or hemorrhage observed in severe gram-negative sepsis, particularly fulminant meningococcemia (reviewed in Ref. 262). Therefore, SR-BI may influence the tissue distribution of LPS, and thus the body responses to septic shock.

## C. Ovary

The distribution and regulation of SR-BI in ovaries has been investigated both *in vitro* and *in vivo* (106, 137, 182, 263–269). In the preovulatory rodent and bovine ovary, SR-BI mRNA and protein are found in the theca interna cells, which actively synthesize androgens from cholesterol, but not in the granulosa cells, which convert androgens into estrogens. SR-BI expression appears in granulosa cells during formation of the corpus luteum in rodents and cows (106, 137, 182, 263–268) and correlates with increased serum progesterone levels *in vivo* (137, 267). Analysis of *in vitro* and *in vivo* luteinized rat ovarian cells reveals SR-BI expression on the cell FIG. 3. Adrenal lipid depletion in SR-BI-deficient mice. In normal animals (srbI+/+, left), the adrenal gland is *light yellow* due to the massive accumulation of cholesterol in lipid droplets in the cytosol of steroidogenic cells. In SR-BI KO animals  $(srbI^{-/-}, right)$ , the adrenals are *brownish-red* because of a substantial reduction in the cellular cholesterol pool (255). [Photograph by Bernardo Trigatti, Massachusetts Institute of Technology and McMaster University.]



surface in microvilli and microvillar channels, which bind HDL and show selective HDL fluorescent cholesteryl ester uptake (137, 267). Consistent with the coordinate regulation of SR-BI expression with selective HDL-cholesterol uptake and progesterone production during luteinization, prostaglandin F2 $\alpha$ -induced luteolysis in the rat is associated with a decrease in both SR-BI expression and serum progesterone concentration (266).

Estrogen administration concomitantly induces SR-BI expression, steroidogenesis, and selective uptake in the rat ovary (182). In rat ovaries, high-dose estrogen treatment decreases SR-BI expression in theca cells and increases it in luteal cells (182). The overall estrogen-induced increase in SR-BI in the luteinized ovary correlates with higher uptake of DiI from DiI-labeled HDL (182).

Gonadotropin treatment of immature female rats induces a rapid increase in SR-BI mRNA expression in the theca interna cells during folliculogenesis followed by the appearance of SR-BI protein expression in luteal cells during luteinization (264). These gonadotropin-induced changes in rat ovarian SR-BI expression correlate with concomitant changes in selective HDL-cholesterol uptake (137, 267). Similar findings have been reported in SR-BI expression during endogenous ovarian cycling in cows (265).

The role of cholesterol in the modulation of physiological SR-BI expression in the ovary is unclear. Cholesterol loading apparently does not affect SR-BI levels in luteinized granulosa cells of the rat (267), whereas cholesterol depletion only modestly stimulates SR-BI expression (137). However, ovary desensitization by multiple gonadotropin administrations in rats, which decreases ovarian cholesterol content and progestin synthesis, induces selective HDL cholesteryl ester uptake and SR-BI expression compared with that in the luteinized ovary (137). These data suggest that under some conditions SR-BI might be regulated by the cholesterol con-

tent of the luteal cell independently of gonadotropic stimulation. There is a striking defect in ovarian function in SR-BI KO mice that will be discussed below.

## D. Testis

In the testis, SR-BI is most abundantly expressed in steroidogenic Leydig cells (182), with lesser amounts in Sertoli cells (105). SR-BI expression in Sertoli cells has been suggested to have a role in phagocytosis of apoptotic spermatogenic cells (105); however, additional studies will be required to test this proposal. In the testis of the normal mature rat, SR-BI is barely detectable by Western blot analyses or immunohistochemical techniques (Fig. 2), which correlates with very low selective HDL-cholesterol uptake and steroidogenesis from HDL-derived cholesterol (39), suggesting that Leydig cells are not dependent on exogenous lipoprotein-cholesterol during normal steroid hormone production. In contrast, SR-BI expression in Leydig cells is dramatically stimulated after gonadotropin treatment (182) that also induces HDL binding, cholesteryl ester uptake, and testosterone synthesis (137, 182). SR-BI expression is also stimulated by testicular desensitization in vivo (39). These data suggest that SR-BI may be important for cholesterol metabolism in Leydig cells in vivo (182). Under gonadotropin-mediated desensitization, some Leydig cells show SR-BI localized to surface microvilli, as is the case in steroidogenic cells of the adrenal and ovary, but most receptors are found in a complex membrane channel system deep within the cytoplasm of these cells (39). Although it is possible that there may be subtle functional defects in the testes in SR-BI KO mice, there are no overt defects in male fertility in these SR-BI-deficient animals (255). Thus, SR-BI expression is not required for adequate testosterone synthesis and any other function necessary for functional sperm production.

## E. Gut

Although the liver and steroidogenic tissues are the sites of greatest SR-BI expression, SR-BI is expressed in other sites throughout the body. SR-BI is expressed in the intestines (71, 182, 208, 270), primarily on the apical surfaces of epithelial cells (94, 95, 207). There is a gradient of expression along the gastrocolic axis of the small intestine with the highest expression levels of SR-BI found in the proximal (duodenal) region (94, 95, 270). SR-BI is also expressed in the CaCo-2 human colonic adenocarcinoma cell line (94, 207). Intestinal SR-BI expression is regulated by treatments that alter biliary lipid composition. In rodents, expression is suppressed coordinately with decreased intestinal cholesterol absorption when biliary lipid delivery into the intestinal lumen is impaired as a consequence of bile duct ligation, bile diversion, or null mutations in the genes encoding either the multidrug resistance-2 glycoprotein or cholesterol  $7\alpha$ -hydroxylase (95). These *in vitro* and *in vivo* data supported the suggestion that SR-BI might play a critical role in intestinal cholesterol absorption (207). This suggestion was especially attractive in light of the observation of SR-BI-mediated cell uptake of unesterified cholesterol in the absence of lipoproteins (147) and that the cholesterol absorption inhibitors ezetimibe and its derivatives bind to and block the activity of SR-BI (271). However, SR-BI is not essential for absorption of cholesterol by the intestine (see Section X.D). At least some of the longsought cholesterol transporters for controlling net absorption of cholesterol from the intestine appear to include members of the ABC transporter family (see below).

As would be expected from its common embryological origin with the intestine, the gallbladder also expresses SR-BI. Both murine and human gallbladders have SR-BI in the apical domains of their epithelial cells (96, 272). Furthermore, diet-induced biliary lipid hypersecretion in mice is associated with decreased gallbladder SR-BI expression (96, 272). These findings suggest that SR-BI might be involved in lipid transport across the gallbladder epithelium and, as appears to be the case for the small intestine, its expression is regulated by biliary lipid content.

## F. Lung

Within the lung, type II pneumocytes are involved in significant lipid uptake from lipoproteins for alveolar surfactant production. In particular, vitamin E supply from plasma HDL is important for protecting surfactant from oxidative damage in the alveolar space. Interestingly, SR-BI, which can mediate selective vitamin E ( $\alpha$ -tocopherol) uptake (132, 133, 273), is expressed in the embryonic lung from 1 d before birth, increasing thereafter in type II pneumocytes (211, 273). Its expression in these cells is inversely regulated with dietary vitamin E supply, apparently by posttranscriptional mechanisms (273). These findings strongly suggest that the expression of SR-BI on alveolar type II cells may help determine the cellular supply of vitamin E. The relevance of SR-BI for pneumocyte metabolism of nonvitamin E lipids remains to be established.

#### G. Nervous system

Apolipoproteins, lipoprotein-remodeling enzymes, and lipoprotein receptors are present in peripheral nerves and brain, including the cerebrospinal fluid (274). Furthermore, it is interesting to note that very large plasma lipoproteins cannot cross the blood-brain barrier by simple diffusion, indicating the presence of a distinct receptor-mediated lipid transport system between plasma and the central nervous system (CNS). SR-BI is found in endothelial cells derived from the blood-brain barrier, suggesting an important function in supplying lipids and vitamins from plasma lipoproteins to the CNS (132). In addition, SR-BI expression has been reported in glial, but not neuronal, cells of the CNS (109, 110, 218). SR-BI has been detected in cultured human fetal and murine newborn, but not adult, microglia (109, 110, 218). In contrast, it is found in astrocytes and vascular smooth muscle cells in normal adult mouse and human brains (109, 110, 218). SR-BI expression in cultured human glia appears to be regulated by lipoprotein availability (218). SR-BI mRNA has been localized by RT-PCR in the parietal cortex as well as in the cerebellum of the human brain (275). Interestingly, SR-BI has been found in brains from Alzheimer's disease patients (110, 275), which together with its  $\beta$ -amyloid binding activity (108, 109), suggests a potential role for this receptor in the pathogenesis of Alzheimer's disease. On the other hand, rat peripheral sympathetic neurons, which internalize lipids from both LDL and HDL, do not express SR-BI (276).

## H. Mammary gland

SR-BI is expressed in pregnant rat mammary gland (182) and a human breast carcinoma cell line (277). In the latter, cholesterol acquisition from HDL is dependent on SR-BI-mediated selective cholesterol uptake (277). The transfer by a LDLR-independent pathway of a lipid-depleted lipoprotein particle from plasma across the mammary epithelium into the milk of lactating mice has been reported (278). The relevance of SR-BI expression in this latter process, as well as mammary gland physiology in general, remains to be established. The absence of SR-BI in gene-targeted mice does not appear to significantly impede the ability of mothers to nurse their young (279).

## I. Endothelium

Endothelial SR-BI expression was initially reported in the decidual tissue surrounding the embryo during early mouse development (208). SR-BI has also been found in caveolar fractions of human microvascular endothelial cells in culture (215). In this latter system, SR-BI appears to mediate the protective effect of HDL on oxidized LDL-induced cholesterol depletion of caveolar cholesterol and subcellular redistribution of endothelial nitric oxide (NO) synthase (eNOS; Ref. 215). More recently, SR-BI was detected in ovine fetal pulmonary arterial endothelial cells (280) and endothelial cells derived from the blood-brain barrier (132), suggesting a role in lipid transfer from plasma lipoprotein into the CNS (216). Functional studies also indicate that SR-BI is expressed in murine aortic endothelial cells and participates in the regulation of NO synthase (Ref. 280; also see below).

#### J. Macrophages

SR-BI mRNA and protein levels are low in human monocytes, but increase upon differentiation into macrophages (Refs. 126 and 213; however, see Ref. 104). Agonists of the nuclear receptors peroxisome proliferator-activated receptor (PPAR)- $\alpha$  and PPAR- $\gamma$  (214), 15-deoxy- $\delta$ -12,4-prostaglandin J2 (281), testosterone (282), and advanced glycation end products (283) increase macrophage SR-BI expression; whereas it is decreased by LPS (221), interferon- $\gamma$  (Ref. 221; however, see Ref. 281), TNF- $\alpha$  (221), and TGF- $\beta$  (284). The suppression of SR-BI by LPS in macrophages is dependent on the modulation of SR-BI gene promoter activity by p21- activated protein kinase-1 (285). The LPS-activated p21activated protein kinase-1 pathway decreases the binding of a novel transcription factor to a myeloid zinc finger protein-1-like element present in the human SR-BI promoter (285). Reduced mRNA SR-BI levels in LPS-treated macrophages also appear to involve nuclear factor-*k*B activation (286). Oxidized LDL also seems to reduce macrophage SR-BI mRNA and protein levels (Ref. 287; however, see Ref. 213). The ability of oxidized LDL to decrease SR-BI expression is dependent on the degree of LDL oxidation and can be mimicked by 7-ketocholesterol, but not unoxidized cholesterol (287). Interestingly, SR-BI has been found in macrophagederived lipid-loaded cells of apoE KO mice (126), human atherosclerotic lesions (213, 214), and cholesterolotic gallbladders (96), raising the possibility that it may play a role in lipid deposition in these disease conditions.

## K. Skin

SR-BI has been found in cultured human and murine epidermis (220). Calcium-induced keratinocyte differentiation is associated with decreases in both SR-BI expression and uptake of HDL cholesterol (220). Although keratinocyte SR-BI mRNA levels were higher after inhibiting cholesterol synthesis, they were decreased by 25-hydroxycholesterol (220). In both human and murine epidermis, SR-BI mRNA content was higher after skin barrier disruption (220), suggesting that SR-BI may facilitate cholesterol uptake required for barrier restoration, which includes the deposition of lipids to form a water impermeant seal.

#### L. Embryonic and extraembryonic tissues

Placenta and yolk sac are considered to function as active interfaces between maternal circulation and the embryo and, thus, play major roles in the maternal-fetal lipoprotein transport system (reviewed in Ref. 288). The exact mechanisms of this transplacental cholesterol transport are not clear (208, 289–292). In humans, the placenta expresses several lipoprotein receptors, including LDLR (293) and VLDL receptor (294), LDLR-related protein (295), and SR-BI (80). The placental syncytiotrophoblast cell is proposed to play a key role in the exchange of nutrients between the mother and the developing fetus. Interestingly, the presence of SR-BI protein and HDL binding has been observed in the syncytiotrophoblast on the brush border membrane (*i.e.*, the side facing the mother; Refs. 296 and 297) as well as in basal plasma membrane (*i.e.*, the side facing the developing fetus; Ref. 297). Although the physiological significance of this is unknown, it is possible that maternal HDL may have a role in providing cholesterol and other lipids, conceivably via SR-BI, for the needs of the growing fetus.

The expression pattern of SR-BI during embryogenesis was first described for the mouse (208). On d 7.5 of murine embryonic development (E7.5), there are newly formed maternal blood vessels within the endometrium-derived decidua providing nutrients to the developing embryo. At this time, SR-BI is significantly expressed in endothelial cells of the decidua, but little expression is seen in intraembryonic and extraembryonic tissues. On d E8.5, when embryonic vascular structures develop, there is a significant increase in SR-BI expression in the trophoblast cells that surround the developing embryo. On d E10, when the placenta becomes a main site for transport of nutrients, SR-BI is expressed in both the placenta and yolk sac. High expression of SR-BI is also found during hamster embryonic development (209) in the yolk sac apical surface (d E10.5 and E14.5). Analysis of HDL clearance, however, showed that the yolk sac appeared to remove substantial amounts of the entire HDL particles from the maternal circulation, suggesting that selective uptake may not be the only mechanism involved in yolk sac clearance of maternal HDL in the hamster (209).

Within the murine embryo itself, *in situ* hybridization signal of SR-BI mRNA was detected on d E11.5 in the urogenital ridge of both male and female embryos, but on d E12.5, high levels of SR-BI mRNA were detected only in testes, which are active in steroidogenesis at this stage, but not in the ovaries, in which steroidogenesis takes place later in gestation (298). *In situ* hybridization also revealed SR-BI expression in the liver at d E12.5 and E14.5, with declining expression by d E16.5 (298), but immunofluorescence methods did not detect SR-BI expression in the murine embryonic liver up to d E17.5 (208). SR-BI expression is detectable in fetal adrenal gland by d E14.5 (208, 298) and in the hindgut (d E17) outlining the folds of the gut epithelium (208). High levels of SR-BI expression have also been detected in the human fetal adrenal (80, 182).

## VIII. Mechanisms Underlying the Regulation of SR-BI Expression

The mechanisms involved in the control of SR-BI expression have only just begun to be deciphered. The promoter of the human SR-BI gene contains consensus-DNA sequences that bind several transcription factors including steroidogenic factor-1 (SF-1), CCAAT/enhancer-binding protein (C/ EBP), SREBP-1 (80, 299), liver X receptor (LXR; Ref. 243), and liver receptor homolog 1 (LRH-1; Ref. 244). The regulation of SR-BI expression by trophic hormones, cholesterol, and polyunsaturated fatty acids *in vivo* (106, 137, 169, 177, 212, 225, 228, 248, 263–269, 298) is likely to be controlled by transcriptional regulation through these and other as yet unidentified factors.

SR-BI regulation by trophic hormones in steroidogenic cells may depend on cAMP/protein kinase A signal transduction that stimulates the transcriptional function of SF-1 (300) and C/EBPs (301). The SF-1-sensitive site is required for the basal and cAMP-stimulated transcriptional activity of the SR-BI promoter in adrenocortical cells *in vitro* (80, 299), and SF-1 is also critical for the expression of SR-BI during the development of murine steroidogenic tissues *in vivo* (298). Because C/EBPs are intracellular mediators of various trophic factors (301), they may also be involved in the regulation of SR-BI by cAMP-dependent trophic hormones in non-SF-1-expressing tissues. On the other hand, vitamin E-dependent regulation of SR-BI in hepatic cells might be mediated by protein kinase C activity (223). Taken together, these data indicate that activation of multiple signaling pathways may participate in modulating SR-BI expression.

The expression of SR-BI in some steroidogenic cells in culture and in vivo can be regulated by cholesterol (177, 248, 298). Furthermore, SREs reside within the 2.2-kb promoter region upstream of the transcriptional start site of the SR-BI gene (299). The ability of SREBP-1a to stimulate the expression of a reporter gene linked to the SR-BI promoter depends on the presence of these elements (299). SREPB-1a expression is induced by gonadotropin treatment and precedes the increased expression of SR-BI in the ovarian tissue (302). Estrogens appear to stimulate ovarian SR-BI expression through dual activation of estrogen receptors and SREPB-1a, both of which may interact with response elements on the SR-BI gene promoter in vitro (303). Furthermore, SERBP-1adependent regulation of SR-BI expression appears to be synergistic with the increased expression mediated by SF-1 (299). Additional studies have shown that SR-BI expression in macrophages is regulated by activators of PPARs (214) and that estrogen and dietary cholesterol induce activation of SR-BI expression in hepatic macrophages while suppressing parenchymal cell expression (212). Therefore, it is likely that the regulation of SR-BI expression involves complex and interrelated activation of various transcription factors in different tissues.

Hepatic SR-BI expression is regulated and, thus can influence the last step of reverse cholesterol transport and whole body cholesterol homeostasis. Studies with hypophysectomized rats have suggested that the dramatic reduction of hepatic SR-BI expression after high-dose estrogen treatment is a consequence of changes in circulating levels of hypophyseal trophic hormones (90, 182). As noted above, under chronic ACTH stimulation, adrenal glands release a factor that represses hepatic SR-BI levels (241).

Recent *in vivo* and *in vitro* data have emphasized the importance in regulating hepatic SR-BI expression of the nuclear receptors farnesoid X receptor (FXR), LXR, LHR-1, and PPAR- $\alpha$  (91, 243–245). The administration to mice of cholic acid, an activator of the FXR, significantly increases hepatic SR-BI mRNA and protein levels (245). The FXR-dependent regulation of SR-BI in the murine liver was further demonstrated by low SR-BI expression in FXR KO mice as well as the lack of cholic acid-induced up-regulation of SR-BI in FXR-deficient animals (245). It is not known whether FXR regulates SR-BI expression by direct interaction with the SR-BI gene promoter or whether regulation is indirect. LXR $\alpha$ , LXR $\beta$ , and LHR-1 induce SR-BI transcription in human and murine hepatoma cells by binding to the corresponding nuclear receptor response element located in the promoter region of the SR-BI gene (243, 244); however, the in vivo relevance of these activities remains to be established. It is noteworthy that SR-BI mRNA levels are reduced in LRH-1-deficient mice (244), but not in LXR- $\alpha$  KO mice (304).

Stimulation of PPAR- $\alpha$  by fibrates increases SR-BI mRNA levels and protein in macrophages (214). Mardones *et al.* (91) have shown that fibrates do not significantly alter SR-BI mRNA levels in the murine liver, yet they substantially lower hepatic SR-BI protein expression (and correspondingly increase HDL particle size), apparently via a posttranscriptional regulatory mechanism. Posttranscriptional control of SR-BI expression was originally suggested by the initial characterization of its expression pattern in different tissues (70, 71) and subsequently was reported in a variety of experimental models (95, 222, 223). PPAR- $\alpha$  mediates the effects of fibrates on hepatic SR-BI expression, because these effects are abolished in PPAR- $\alpha$  deficient mice (91). The identification of endogenous or exogenous factors and pathways that modulate the expression and/or activity of SR-BI in the liver may provide new insights in developing novel approaches to manipulate HDL metabolism, reverse cholesterol transport, and atherosclerosis in humans (255, 305–307).

## IX. SR-BI and Lipoprotein Metabolism

## A. HDL metabolism

The expression pattern of SR-BI (*i.e.*, most abundantly expressed in the liver and steroidogenic tissues, the principal sites involved in selective HDL-cholesterol uptake), as well as the regulation of SR-BI expression in these tissues (see above) strongly indicated that SR-BI is a physiologically relevant HDL receptor (reviewed in Ref. 12). Direct evidence for the role of SR-BI in HDL metabolism *in vivo* (Fig. 4) has come from studies in which the levels of SR-BI in mice have been manipulated either by overexpressing the SR-BI gene in the liver using adenovirus-mediated gene transfer or transgenic approaches (89, 129, 308, 309) or by introducing targeted mutations into the SR-BI gene (255, 310).

In the first in vivo experiments, recombinant adenovirusmediated gene transfer was used to induce hepatic SR-BI overexpression in mice (89). The resulting transient increase in SR-BI on both sinusoidal and canalicular surfaces of hepatocytes was accompanied by a dramatic transient reduction in the levels of plasma HDL cholesterol and apoA-I and a concurrent increase in the cholesterol concentration in hepatic bile (89). The increased SR-BI-mediated hepatic HDL selective uptake was also associated with increased catabolism of apoA-I (89). In fact, SR-BI overexpression in apoA-I-deficient mice leads to accumulation of small dense HDL remnants and increased HDL apolipoprotein uptake in liver and kidney (311), which are the main sites apoA-I degradation in vivo. The reciprocal relationship between plasma HDL-cholesterol and biliary cholesterol levels in SR-BI-overexpressing mice suggested that increased biliary cholesterol secretion originated from plasma HDL cholesterol taken up by the liver. Consistent with this hypothesis, there was a dramatic increase in the excretion of DiI into the bile of hepatic SR-BI overexpressing mice after iv administration of DiI-HDL (89). These conclusions were subsequently confirmed in studies using transgenic mice overexpressing SR-BI

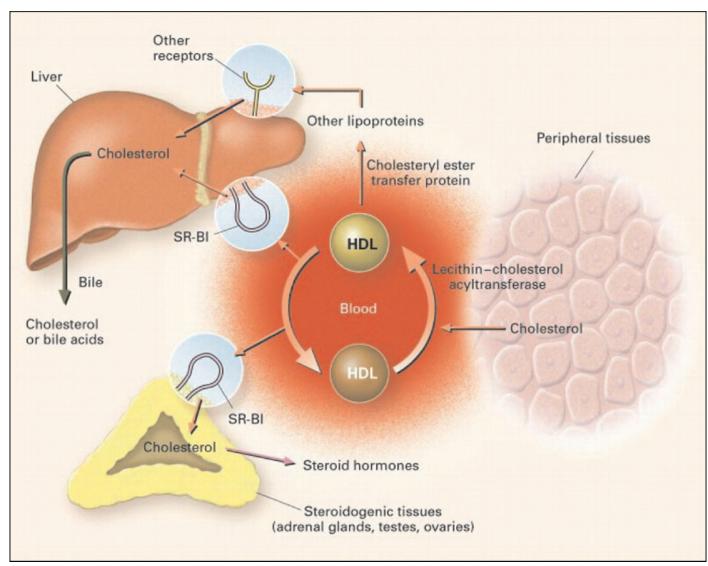


FIG. 4. Role of SR-BI in HDL metabolism *in vivo*. HDL can efficiently remove cellular cholesterol from peripheral tissues by an ATP-dependent mechanism involving the ABC transporter ABCA1 (not shown). Although SR-BI can also mediate cholesterol efflux from cultured cells to HDL, the relevance of this activity *in vivo* remains to be determined. After HDL cholesterol is esterified to cholesteryl esters by the enzyme LCAT (not shown), it is transported to the liver by either direct or indirect pathways. In the indirect pathway, CETP transfers cholesteryl esters from HDL to non-HDL lipoproteins, which then deliver this cholesteryl ester to the liver by receptor-mediated endocytosis. The direct pathway involves SR-BI-mediated selective cholesterol uptake. HDL cholesterol taken up by the liver can be ultimately destined for bile secretion, either as cholesterol or as bile acids, products of hepatic cholesterol metabolism. The delivery of cholesterol uptake by steroidogenic tissues via plasma HDL to the liver and bile is called reverse cholesterol transport. SR-BI also mediates HDL-cholesterol uptake by steroidogenic tissues for steroid hormone synthesis or cholesterol storage. [Reproduced with permission from A. Rigotti and M. Krieger: *N Engl J Med* 341:2011–2013, 1999 (373). © Massachusetts Medical Society.]

specifically in the liver (129, 308, 309, 312, 313). Furthermore, metabolic kinetic analyses of radiolabeled HDL cholesterol have suggested that SR-BI expression in the liver is correlated with hepatic HDL cholesterol (both esterified and free cholesterol) uptake and secretion into bile (129). However, it has not been formally established that SR-BI overexpression in the liver increases overall reverse cholesterol transport (net movement of cholesterol from nonhepatic tissues to the liver and then secretion into the bile, *e.g.*, see Ref. 313).

Analysis of SR-BI KO mice definitively established a role for SR-BI in HDL metabolism in this species (255). SR-BI KO mice have, relative to wild-type control animals, a 2- to 2.5-fold increase in total plasma cholesterol levels, mostly due to increased cholesterol in HDL particles (255). These HDL particles are larger and more heterogeneous in size than those in wild-type animals, and they are enriched with apoE. Despite increased plasma HDL-cholesterol levels, no difference is observed in the plasma apoA-I levels between SR-BI null and wild-type mice, suggesting that the increase in HDL cholesterol was due to impaired selective uptake of cholesterol from HDL (255). An independently derived mutant mouse strain with attenuated SR-BI expression due to a serendipitous promoter mutation (SR-BIatt mice) (310) has a 50% reduction in hepatic SR-BI expression (similar to that of heterozygous SR-BI KO mice; Ref. 255) and more moderate increases in plasma total cholesterol levels as well as in HDL size and cholesterol content, similar to the heterozygous null SR-BI mouse. The reduced hepatic levels of SR-BI in SR-BIatt mice are associated with reductions in hepatic selective HDLcholesterol uptake and plasma clearance of HDL-cholesteryl esters in vivo (310). Together, these studies demonstrate that SR-BI is important for the maintenance of normal plasma HDL-cholesterol levels and HDL structure, and they support the proposal that the increased cholesterol content and size of HDL in SR-BI KO mice are due to impaired selective HDL-cholesterol uptake in the liver (255). Consistent with this, SR-BI KO mice also exhibit reduced biliary cholesterol secretion and gallbladder bile cholesterol content (238, 305) without concomitant changes in either biliary bile acid or phospholipid secretion, bile acid pool size, or fecal bile excretion. Thus, SR-BI deficiency appears to specifically affect biliary cholesterol secretion. Taken together, these studies indicate that SR-BI is important for normal hepatic selective HDL-cholesterol uptake and biliary cholesterol secretion in mice, thus supporting the idea that SR-BI plays a key role in the late stages of reverse cholesterol transport (Fig. 4).

## B. Metabolism of other lipoproteins

In addition to binding HDL and selectively taking up HDL cholesterol, SR-BI can also bind non-HDL lipoproteins such as LDL and VLDL (70, 113) and mediate selective cholesterol uptake from LDL (128, 146), suggesting that SR-BI may also participate in the metabolism of non-HDL lipoproteins. This has been supported by several *in vivo* studies. Under standard chow (low-fat) diet conditions, hepatic SR-BI overexpression slightly, but consistently, decreases plasma LDL/IDL cholesterol levels (89, 308, 309), and SR-BI deficiency subtly increases the amounts of LDL/IDL-sized lipoproteins (255). Furthermore, hepatic overexpression of SR-BI increases the clearance of labeled LDL from the plasma (309).

Mice, but not humans, normally transport the majority of their plasma cholesterol in HDL particles and have only very small amounts of non-HDL particles (*i.e.*, apoB-containing particles) in their circulatory systems. Plasma levels of non-HDL lipoproteins (*e.g.*, apoB-containing lipoproteins) can be stimulated in mice by dietary (high-fat/cholesterol; Ref. 314) or genetic (*e.g.*, LDLR deficiency, Ref. 315; and apoE deficiency, Refs. 316 and 317) manipulations.

Overexpression of SR-BI in mice fed high-fat/high cholesterol diets or in heterozygous and homozygous LDLRdeficient mice results in reduced plasma levels of VLDL and IDL/LDL cholesterol compared with non-SR-BI transgenic controls (308, 309, 318). Conversely, SR-BI deficiency in apoE KO mice (SR-BI/apoE double KO mice) increases the levels of cholesterol in VLDL-size lipoproteins when compared with SR-BI-expressing apoE KO mice, suggesting that SR-BI may directly or indirectly contribute to the clearance of the cholesterol in VLDL-sized particles in single apoE KO mice (305). Reduced expression of SR-BI in LDLR KO mice (*i.e.*, SR-BIatt/LDLR KO mice) results in significantly increased levels of plasma LDL cholesterol when these mice are fed a Western type high-fat/cholesterol diet, but not when they are fed a low-fat chow diet (319). In metabolic kinetic anal-

ysis, no differences were observed in hepatic clearance and uptake of LDL protein or cholesterol in SR-BIatt/LDLR double KO mice compared with single LDLR KO control mice. The authors concluded that SR-BI does not appear to have a direct role in LDL cholesterol catabolism in vivo (319), but rather acts indirectly on LDL metabolism (e.g., by inducing LDL production). Similar kinetic studies in SR-BI-overexpressing apoB transgenic mice showed a slight increase in LDL cholesteryl ester clearance, but no change in LDL apolipoprotein turnover (149). Taken together, most, but not all (319), studies suggest that in addition to HDL, SR-BI may, at least in rodents, also function as a receptor for apoBcontaining lipoproteins in vivo. The influence of SR-BI on murine LDL metabolism appears to be substantially less than that of LDLRs, and its influence on HDL metabolism appears to be much greater than its effects on non-HDL lipoprotein metabolism.

#### X. Role of SR-BI in Physiology and Pathophysiology

## A. Reproductive biology: female fertility

Studies showing coordinate regulation of SR-BI expression, steroid hormone production, and HDL-cholesterol uptake in the ovaries in both mice and humans (see above) have all indicated that SR-BI may play an important role in normal ovarian function. Further support for this suggestion has come from the observation that female SR-BI KO mice are infertile (305). Despite the dramatic reduction in ovarian lipid stores in the corpora lutea (see above), SR-BI KO mice are able to produce normal amounts of plasma progesterone during pseudopregnancy (305), suggesting that normal ovarian lipid stores are not required for production of adequate amounts of progesterone, a phenomena also seen in apoAIdeficient and LCAT-deficient (251, 320) mice. Furthermore, several ovarian functions requiring adequate steroid hormone production and proper interaction within the hypothalamic-hypophyseal-ovarian axes apparently seem to be normal in SR-BI KO females. For example, they exhibit no obvious defects in their gross ovarian morphology, estrus cycles, or numbers of ovulated oocytes (305). These findings suggest that SR-BI-independent sources of cholesterol (endogenous cholesterol synthesis, endogenous cholesterol stores, SR-BI-independent pathways of cholesterol uptake) are sufficient to meet most of the steroid biosynthetic precursor requirements of steroidogenic cells.

The ovulated oocytes in SR-BI KO mice, however, are dysfunctional, and preimplantation embryos isolated from SR-BI KO females the morning after mating either are dead or die soon afterward (Ref. 305; Fig. 5). This suggests that SR-BI may either directly (*e.g.*, disturbed cholesterol influx or efflux in the absence of SR-BI) or indirectly (*e.g.*, abnormal plasma lipoproteins due to the lack of SR-BI expression) influence oocyte maturation and development (305). The exact mechanism leading to the defect in oocyte development is currently under study. Genetic, surgical, and pharmacological studies suggest that abnormal lipoprotein metabolism plays a key role in female SR-BI KO infertility (279). Indeed, reduction in the plasma HDL-cholesterol levels by treatment with the cholesterol-lowering drug

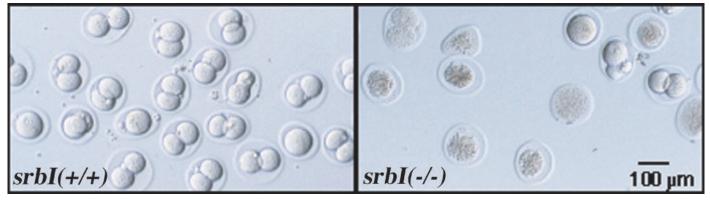


FIG. 5. Infertile SR-BI KO female mice produce abnormal preimplantation embryos. When preimplantation embryos from wild-type females (srbI+/+) are maintained in culture for 1 d, they divide and exhibit normal morphologies (*left*). In contrast, the majority of embryos from  $srbI^{-/-}$  females do not divide and exhibit abnormal nonrefractile morphologies (*right*). [Reproduced with permission from B. Trigatti *et al.*: *Proc Natl Acad Sci USA* 96:9322–9327, 1999 (305). © National Academy of Sciences, U.S.A.]

probucol fully restores fertility to SR-BI KO female mice (279).

It is of interest that in many species, including humans, HDL is the only lipoprotein detected in substantial amounts in the follicular fluid surrounding the developing oocyte in the ovary (321-324). The exact function of follicular fluid HDL is unknown, but it may deliver lipid nutrients to the oocytes and/or the surrounding cumulus cells (e.g., for local steroid hormone production or membrane synthesis required for normal oocyte maturation). HDL may also be involved in cholesterol efflux (reviewed in Refs. 12, 196, and 325) from the oocyte/cumulus cells, thus contributing to maintenance of normal cellular cholesterol balance. In this regard, it is interesting that homozygous ABCA1 transporter KO females have impaired female fertility, presumably due to placental malformation (326). These mice lack spherical plasma HDL particles due to impaired cholesterol efflux from cells to nascent discoidal HDL particles (327, 328). Furthermore, an inactivating mutation in the gene coding for oocyte vitellogenesis receptor, a VLDL receptor-like protein that binds VLDL and vitellogenin (reviewed in Refs. 329 and 330) causes hyperlipidemia in the restricted ovulator strain of chickens. Interestingly, these chickens also exhibit oocyte growth defects and female sterility (331). Although the relationship between the infertility of SR-BI KO and ABCA1 KO mice, as well as restricted ovulatory chickens, remains to be determined, it is conceivable that changes in HDL (structure/composition/abundance) and/or SR-BI structure and function may disturb normal human oocyte development and thus contribute to some forms of human female infertility. The potential influence of dyslipidemia in female infertility of unknown etiology may warrant further exploration (279).

#### B. Atherosclerosis

Epidemiological studies have shown that low serum HDLcholesterol (*i.e.*, the "good" cholesterol) concentration is an independent risk factor for coronary artery disease (reviewed in Ref. 332). Indeed, low HDL cholesterol is the most common dyslipidemia found among patients with premature coronary artery disease, although it is usually combined

with other lipid disorders (333). Although the association between low HDL cholesterol and increased risk of coronary artery disease was first described several decades ago, the underlying mechanism(s) by which HDL protects against coronary artery disease are still uncertain. The most popular proposed mechanism is reverse cholesterol transport (41) in which HDL removes excess cholesterol from peripheral cells, including those in arterial wall, and transports it to the liver where cholesterol can be excreted into bile (reviewed in Ref. 334). In addition, HDL has been suggested to exhibit additional properties that could potentially contribute to its antiatherogenic capacity, including its capacity to inhibit LDL oxidation and protect endothelial cells from the cytotoxic effects of oxidized LDL (reviewed in Ref. 335) as well as having a variety of beneficial effects on coagulation/fibrinolysis, inflammation, and blood cell and endothelial cell biology (280, 336, 337). It has also been suggested that low HDL cholesterol itself may not be atherogenic, but rather a secondary marker of some related atherogenic primary event, such as abnormal metabolism of the triglyceride-rich lipoproteins (338, 339).

SR-BI could influence atherosclerosis and coronary artery disease because of its involvement in the initial step of reverse cholesterol transport (i.e., cholesterol efflux from peripheral cells to HDL), as well as the later steps (*i.e.*, hepatic cholesterol uptake from HDL and subsequent excretion into bile). The role of SR-BI in the development/prevention of atherosclerosis (reviewed in Ref. 306) has been addressed by manipulating the levels of SR-BI in different mice models particularly vulnerable to atherosclerosis [i.e., the LDLR KO mouse (315, 340), the apoB transgenic mouse (341) fed a high-fat/high-cholesterol diet (342), and the apoE KO mouse (316, 317)]. These mice have increased plasma total cholesterol levels, primarily due to increased levels of atherogenic, apoB-containing lipoproteins (LDL-like in LDLR KO and apoB transgenic mice, and VLDL- and IDL/LDL-like in the apoE KO mice). LDLR KO and apoB transgenic mice develop atherosclerotic lesions in the aorta when fed a high-fat/highcholesterol diet (340-342), whereas 3- to 5-month-old mice deficient in apoE spontaneously develop atherosclerosis in their aortic sinus when fed a normal chow diet (316, 317).

When SR-BI/apoE double KO mice are maintained on a

normal chow diet, they exhibit, compared with the apoE single KO mice, increased plasma cholesterol levels, mainly in VLDL-sized particles (305). Also, they have no normalsized HDL, but rather very large HDL-like lipoproteins indicative of impaired selective uptake of HDL cholesterol by the liver (305). Consistent with this, biliary cholesterol levels are decreased, suggesting a substantial reduction in reverse cholesterol transport (305). Atherosclerosis is dramatically accelerated in SR-BI/apoE double KO mice. They exhibit massive atherosclerosis in the aortic sinus and coronary arteries (305) at a surprisingly young age, 4–7 wk. The mechanism(s) by which SR-BI deficiency lead to accelerated atherosclerosis are currently under study and may include changes in plasma lipoprotein levels and/or structures, disturbed cholesterol flux into or out of the arterial wall (e.g., macrophages; Refs. 213 and 214) and impaired reverse cholesterol transport due to loss of selective uptake by the liver (305). The influence of SR-BI on vitamin E transport (Ref. 132; also see below) and on endothelial cell NO metabolism (Ref. 280; also see below) may also contribute to the accelerated atherosclerosis. Remarkably, all of the double KO mice die by approximately 8 wk of age (305, 343). Further examination of these mice has shown extensive coronary artery occlusions and spontaneously developed multiple myocardial infarctions and cardiac dysfunction. Their coronary arterial lesions are strikingly similar to human complex atherosclerotic plaques with the presence of cholesterol clefts and extensive fibrin deposition, indicating hemorrhage and clotting. Thus, SR-BI/apoE double KO mice provide a novel murine model for coronary heart disease and may provide novel insights on the role of lipoprotein metabolism and atherosclerosis in the pathogenesis of myocardial infarction and cardiac dysfunction (343).

SR-Blatt/LDLR KO mice fed a Western-type high-fat/ cholesterol diet also exhibit increased plasma total cholesterol levels (primarily due to increases in LDL cholesterol; Ref. 319) and significantly more aortic root atherosclerosis than the SR-BI-positive LDLR KO controls (319).

Unlike SR-BI deficiency, hepatic overexpression of SR-BI can suppress murine atherosclerosis. For example, a single administration of SR-BI recombinant adenovirus results in transient hepatic overexpression of SR-BI in LDLR-deficient mice fed a Western-type high-fat/high-cholesterol diet and significantly reduced HDL cholesterol, but not non-HDL cholesterol, levels (344). When analyzed 4 wk after virus administration, at a time at which the plasma lipoproteins had returned to pretreatment levels, the SR-BI-overexpressing mice had significantly reduced areas of atherosclerotic lesions relative to controls. The sizes of the lesions in individual mice correlated with their mean HDL-cholesterol levels and in some, but not all, experiments atherosclerotic lesion size also correlated with the mean non-HDL-cholesterol level. These data suggest that the antiatherosclerotic effect of SR-BI overexpression in this model is mediated, at least partly, by changes in HDL-cholesterol flux, and in some cases potentially also by reductions in non-HDL-cholesterol levels. In heterozygous null LDLR KO mice, stable transgenic hepatic expression of SR-BI, significantly reduced atherosclerosis if the animals were fed an atherosclerosis-inducing high-fat/high-cholesterol/cholic acid diet (318). There was no antiatherosclerotic effect of the SR-BI transgene when mice were fed a more modest, Western-type diet lacking cholic acid. In contrast to the conclusions drawn from the adenovirus experiments, the authors of this latter study concluded that the transgene-mediated decrease in atherosclerosis was primarily due to the decrease in non-HDL cholesterol rather than the HDL cholesterol. These SR-BI overexpression studies clearly demonstrate that hepatic overexpression of SR-BI can be antiatherogenic. This may be due to changes in structures and quantities of circulating lipoproteins or increases in HDL-cholesterol flux to the liver, *i.e.*, increased reverse cholesterol transport.

The complexity of the role of SR-BI on atherosclerosis is highlighted by a study of the effects of hepatic SR-BI overexpression on atherosclerosis in a different murine model, mice expressing the human apoB transgene (345). The effects on lipoprotein metabolism and atherosclerosis of varying levels of stable hepatic SR-BI expression were examined. Surprisingly, only mice with moderately elevated hepatic SR-BI expression were found to be protected against dietinduced atherosclerosis. The reason why high levels of hepatic SR-BI overexpression failed to protect against atherosclerosis is not clear, but may be due to structural/ compositional changes introduced to HDL or non-HDL particles in these animals or changes in reverse cholesterol transport. Thus, the consequences of SR-BI overexpression in the liver on atherosclerosis and lipoprotein metabolism are complex and may depend on levels of SR-BI expression as well as the mouse model of atherosclerosis. However, this study suggests that very high unphysiological levels of SR-BI expression may not always be beneficial.

In most circumstances in the mouse, expression of SR-BI appears to be cardioprotective and conversely, absence of SR-BI is atherogenic. Whether SR-BI has similar functions in humans, remains yet to be seen. If so, the selective modulation of SR-BI-mediated lipoprotein metabolism by dietary, pharmacological, and gene therapy approaches to reduce the risk of atherosclerotic cardiovascular disease would be an appealing subject for basic and clinical research. It is noteworthy that in the murine studies performed to date, low HDL-cholesterol levels may actually reflect accelerated reverse cholesterol transport rather than increased risk for coronary artery disease, and conversely, very high plasma HDL-cholesterol levels may be a sign of impaired reverse cholesterol transport. These observations raise the question of whether, in addition to assessing coronary artery disease risk in humans solely by concentration of plasma HDL cholesterol, more emphasis should be directed to the evaluation of functionality of HDL particles and flux of cholesterol through the plasma HDL pool.

## C. Cholesterol gallstone disease

Because SR-BI controls biliary cholesterol secretion and gallbladder bile cholesterol content (89, 129, 238, 305, 312), it is a candidate gene to be involved in pathogenesis of cholesterol gallstone disease. There has been one report of increased expression of hepatic SR-BI associated with biliary cholesterol hypersecretion and gallstone formation in a gallstone-susceptible mouse strain (346). However, a similar, independent study did not reproduce this finding (347). SR-Blatt mice with a partial deficiency of hepatic SR-BI expression do not exhibit a significant decrease in gallstone susceptibility when fed with a lithogenic diet (348). This latter finding indicates that SR-BI is much less relevant for controlling biliary cholesterol hypersecretion derived from intestinal chylomicrons during murine cholesterol gallstone formation. SR-BI is still likely to be a prolithogenic gene when the underlying pathogenic event is an increased HDLmediated reverse cholesterol transport. If so, SR-BI may provide another target for pharmacological prevention and treatment of this common disease.

#### D. Intestinal cholesterol absorption

The expression of SR-BI in the intestines on the apical surface of epithelial cells (94, 95, 207), the regulation of intestinal SR-BI expression (95), and in vitro cholesterol transport assays in brush border membranes and cultured epithelial cells all suggested that SR-BI might have a role in cholesterol absorption (207). For instance, SR-BI ligands and anti-SR-BI antibodies were reported to inhibit unesterified and esterified cholesterol uptake from bile salt mixed micelles and phospholipid vesicles into intestinal brush border membrane preparations and CaCo-2 cells (207). Furthermore, in cultured cells, the intestinal cholesterol absorption inhibitor ezetimibe binds with high affinity to SR-BI, blocking cholesterol uptake by SR-BI (271). However, intestinal dietary cholesterol absorption in vivo is either slightly higher or not changed in SR-BI-deficient mice (238, 271), clearly demonstrating that SR-BI expression is not essential for murine intestinal cholesterol absorption. Moreover, ezetimibe inhibits cholesterol absorption in SR-BI-deficient mice fed chow and cholesterol-rich diets (271). Thus, if SR-BI normally participates in intestinal cholesterol absorption, SR-BI KO mice must have compensatory, SR-BI-independent mechanisms for cholesterol absorption.

A recent discovery revealed that human sitosterolemia, a condition characterized by extensive accumulation of plant sterols and cholesterol in plasma and tissues and accelerated development of atherosclerosis, is caused by mutations in the two adjacent genes encoding the ABC transporter family members ABCG5 and ABCG8 (349–352). These proteins were suggested to normally have an important role in limiting intestinal cholesterol absorption by promoting cholesterol excretion (349–352). We do not yet know whether SR-BI, which also mediates cholesterol efflux in cultured cells (see above), has a similar role in the intestine, potentially interacting with ABC proteins.

#### E. Embryogenesis and fetal development

SR-BI apparently contributes to the later stages of embryonic development and pregnancy. Developing embryos require substantial amounts of cholesterol for membrane synthesis and for steroid hormone production (reviewed in Ref. 288). This cholesterol is acquired by endogenous synthesis and from exogenous sources, *i.e.*, maternal lipoproteins. SR-BI has been shown to be expressed during murine embryonic development in a variety of extraembryonic and maternal tissues (*see above*), including decidual cells adjacent to the embryo, trophoblast cells, yolk sac, and placenta (208).

Interestingly, SR-BI expression in the trophoblast coincides with increased expression of the trophoblast cell P450 cholesterol side chain cleavage enzyme, which converts cholesterol to pregnenolone, indicative of active local progesterone production (353). The exact function of this progesterone production is unclear but it has been suggested to be involved in preventing rejection of the implanted fetus (354, 355). These studies suggested that SR-BI might provide cholesterol for embryonic membrane production and/or steroid hormone synthesis and that lack of SR-BI in either extraembryonic or maternal tissues may impair these processes. The expression of SR-BI in extraembryonic tissues is correlated with uptake of the lipophilic fluorescent dye DiI from DiIlabeled HDL injected into pregnant mice (208). This pattern of SR-BI expression during embryogenesis, as well as its localization on the apical sides of cells facing the maternal circulation, is consistent with a potential role in cholesterol uptake from maternal lipoproteins into extraembryonic tissues and/or within the developing embryo itself for growth and/or steroidogenesis. In addition, the expression pattern of SR-BI in the murine embryo (see above) resembles that of steroidogenic acute regulatory protein and cholesterol side chain cleavage enzyme, both key proteins in the steroidogenic pathway (356). These studies suggest that SR-BI may deliver cholesterol for steroid hormone synthesis within the embryo itself. Because SR-BI can also mediate the delivery of LDL cholesterol to cells, it is possible that, at least under some conditions (e.g., FH due to LDLR deficiency), SR-BI might deliver cholesterol from LDL as well as HDL to embryonic and extraembryonic tissues (302). Whatever its normal role in embryogenesis, in an appropriate genetic or pharmacological background (279), SR-BI is not absolutely essential for fertilization, pregnancy, or delivery of healthy pups.

The lower than expected yield (50% reduction) of homozygous SR-BI KO mice born to heterozygous parents suggests that SR-BI-deficiency in the tissues of embryonic origin may result in partial embryonic lethality (255). The influence of the absence of SR-BI in maternal tissues on embryogenesis may in part be indirect, *e.g.*, through the changes introduced in maternal lipoproteins, the structure/abundance of which may potentially influence fetal development (357). It is not known whether SR-BI KO fetuses suffer from impaired cholesterol delivery.

#### F. Red blood cell (RBC) maturation

RBCs are derived from multipotential hematopoietic progenitor cells in the bone marrow. A key step in RBC maturation is the formation of reticulocytes by the expulsion of nuclei from erythroblasts in the bone marrow. Early reticulocytes have irregular shapes and contain cytoplasmic RNA and organelles (*e.g.*, polyribosomes, mitochondria; Ref. 358). As reticulocytes mature, they destroy or expel their RNA, surface transferrin receptors, cytoplasmic organelles, and ribosomes. They also remodel their cytoskeletons as they transform into flexible, biconcave, oxygen-carrying erythrocytes. Analysis of SR-BI KO mice (359) has established that specific alterations in plasma lipoprotein metabolism can profoundly influence erythroid differentiation. SR-BI KO mice are mildly anemic, and their RBCs exhibit mild developmental abnormalities that are exacerbated by either feeding the animals a high-cholesterol diet or by inactivating the apoE gene (SR-BI/apoE double KO mice). In the most extreme case-the double KO mice-the cells resemble proposed intermediates in reticulocyte differentiation. They are anucleate, hemoglobin- and RNA-rich; they express surface transferrin receptors, are macrocytic, irregularly shaped, and contain large, membrane-enclosed, intracellular autophagolysosomes. These unusual RBCs contain abnormally high levels of cholesterol, and the severity of their developmental defects is correlated with their cholesterol content. The apparent block in maturation is reversible, because transfusion of RBCs from SR-BI/apoE double KO mice into wild-type recipients results in their apparently normal maturation into erythrocytes. At least some of the maturation process (extrusion of autophagolysosomes, loss of RNA) can be recapitulated in vitro, where extraction of excess cholesterol by addition of the cholesterol sequestering agent methyl cyclodextrin accelerates autophagolysosome expulsion. Thus, autophagocytosis and SR-BI- and cholesterol-sensitive phagolysosome expulsion are probably key steps in normal erythropoiesis. Further analysis of SR-BI KO mice should provide additional insights into the cellular mechanisms of RBC maturation. The severe reticulocytosis in SR-BI/apoE double KO mice may contribute to the accelerated atherosclerosis, cardiac dysfunction, myocardial infarction, and early death of these animals (343).

## G. NO metabolism

Endothelium-derived NO plays a key role in vascular physiology and pathophysiology, including atherosclerosis (360). NO is generated by eNOS, and its decreased availability facilitates atherosclerotic plaque formation induced by hypercholesterolemia. Interestingly, eNOS activity, which is localized in caveolae, and NO production are stimulated by HDL, and this HDL-dependent effect is impaired by anti-SR-BI blocking antibodies in cultured endothelial cells (215). This finding suggested that endothelial SR-BI expression might be the molecular link between the protective effect of HDL with respect to eNOS function and NO synthesis. Using SR-BI and eNOS transfected Chinese hamster ovary cells, Yuhanna et al. (280) have shown that SR-BI mediates the activation of eNOS by HDL. The SR-BI-mediated stimulation of eNOS is dependent on the presence of native HDL particles, but not lipid-free HDL apolipoproteins (280). The mechanism by which HDL binding to SR-BI stimulates eNOS activation appears to be mediated by an increase in intracellular ceramide levels (361). Both eNOS activation and vascular relaxation induced by HDL in murine aortic ring preparations are significantly reduced in samples isolated from SR-BI KO compared with SR-BI-positive control mice (280). These studies indicate that SR-BI-associated atheroprotection may be related not only to its role in reverse cholesterol transport but also to its influence on the modulation of intracellular signal transduction that controls NO production.

#### H. Vitamin E transport

Recent studies have shown that selective lipid uptake, rather than endocytosis, is important for  $\alpha$ -tocopherol delivery to cells (362, 363). Consistent with this, SR-BI can mediate the cellular uptake of  $\alpha$ -tocopherol from HDL (132, 133). Overexpression of SR-BI in cultured cells by either DNA-mediated transfection or recombinant adenovirusmediated transduction increases net selective uptake of  $\alpha$ tocopherol from the HDL (133, 363). Thus, in addition to the previously suggested pathways involving LPL, phospholipid transfer protein, and the LDLR (364, 365), SR-BI-mediated selective uptake can supply physiologically relevant levels of  $\alpha$ -tocopherol to cells. In fact, relative to wild-type control animals, SR-BI-deficient mutant mice exhibit a substantial increase in plasma  $\alpha$ -tocopherol levels due primarily to the elevated  $\alpha$ -tocopherol content of their abnormally large plasma HDL-like particles (133). This increase in plasma  $\alpha$ -tocopherol in SR-BI KO mice is correlated with a decrease in the  $\alpha$ -tocopherol content of both the bile and several tissues, including ovaries, testes, lung, and brain. SR-BI deficiency did not significantly alter the  $\alpha$ -tocopherol contents of the liver, spleen, kidney, or white fat. These data show that SR-BI plays an important role in transferring  $\alpha$ tocopherol from plasma lipoproteins to specific tissues. Also, SR-BI-mediated uptake of  $\alpha$ -tocopherol in the liver is primarily coupled to biliary excretion rather than to accumulation in hepatic tissue. Similar findings have been reported for SR-BI-dependent hepatic cholesterol transport (238). As a consequence of its role in regulating cellular  $\alpha$ -tocopherol content, SR-BI expression may confer protection against oxidative stress in cells. Thus, defective tissue uptake of  $\alpha$ tocopherol carried in lipoproteins in SR-BI-deficient mice might be one of the pathogenic mechanisms underlying the reproductive and cardiovascular disorders exhibited by these animals. Interestingly, a Drosophila class B scavenger receptor mediates cellular vitamin A uptake, and its loss of function is associated with a carotenoid-deficient phenotype characterized by abnormal visual chromophore and blindness in the fruit fly (366).

#### **XI. SR-BI** in Humans

Although the role of SR-BI in rodent lipoprotein metabolism as a physiologically relevant HDL receptor is well established, its role in human lipoprotein metabolism is not well defined experimentally. Both the selective HDL-cholesterol uptake activity of human SR-BI and the similar patterns of SR-BI gene expression [*i.e.*, most abundant expression in liver and steroidogenic tissues, in human and rodent tissues (71, 80, 182) and regulation in human steroidogenic cells (104, 234, 249, 250, 254)] suggest that SR-BI is likely to be involved in human HDL metabolism.

There have not yet been any reports of naturally occurring functionally significant mutations in the human SR-BI gene, although polymorphisms, some weakly associated with plasma LDL cholesterol levels and body mass index, have been described (367). In addition, a small-scale intervention study in human subjects has shown that plant stanol ester consumption changed plasma lipoprotein cholesterol irrespective of the SR-BI gene polymorphisms (368). A Japanese large-scale study also found no association between SR-BI gene variants and increased risk for myocardial infarction (369). However, another study has reported an association between an *SR-BI* gene *Hae*III polymorphism with coronary artery disease and lower body mass index in Korean subjects (370). A recent association study also reported a relationship between a SR-BI gene polymorphism and morbid obesity (371). Additional studies of the relationships of SR-BI polymorphisms and human phenotypes will be required to assess the importance of SR-BI in humans.

#### **XII.** Concluding Remarks

The discovery and analysis of the HDL receptor SR-BI has contributed to our understanding of cellular lipoprotein cholesterol metabolism, especially that which occurs through selective lipid uptake. This receptor is not only relevant for general body cholesterol homeostasis, but also for physiological cholesterol uptake and metabolism in steroidogenic tissues. Furthermore, experimental evidence from various animal models has established that alterations in the levels of SR-BI expression can significantly cause or influence pathology in a number of key physiological systems, *e.g.*, atherosclerosis/cardiovascular disease, female fertility, and RBC maturation. Thus, SR-BI represents a novel target which, after additional basic and clinical research, may prove valuable for the development of new pharmacological or genetic therapies to prevent or treat a variety of human diseases.

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