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Scavenger Receptor class B type I (SR-BI): a versatile receptor with multiple functions and actions

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Abstract

Scavenger receptor class B type I (SR-BI), is a physiologically relevant HDL receptor that mediates selective uptake of lipoprotein (HDL)-derived cholesteryl ester (CE) *in vitro* and *in vivo*. Mammalian SR-BI is a 509-amino acid, ~82 kDa glycoprotein, that contains N- and C-terminal cytoplasmic domains, two-transmembrane domains, as well as a large extracellular domain containing 5-6 cysteine residues and multiple sites for N-linked glycosylation. The size and structural characteristics of SR-BI, however, vary considerably among lower vertebrates and insects. Recently, significant progress has been made in understanding the molecular mechanisms involved in the posttranscriptional/posttranslational regulation of SR-BI in a tissue specific manner. The purpose of this review is to summarize the current body of knowledge about the events and molecules connected with the posttranscriptional/posttranslational regulation of SR-BI and to update the molecular and functional characteristics of the insect SR-BI orthologs.

Keywords

HDL receptor; selective uptake; steroid hormones

Introduction

Scavenger receptor class B type I (SR-BI), is a physiologically relevant HDL receptor that mediates selective uptake of lipoprotein (HDL)-derived cholesteryl ester (CE) *in vitro* and *in vivo* [1-3]. The SR-BI-mediated CE uptake/selective pathway is different from that of the LDL receptor (LDLR)/endocytic pathway in that it binds CE-rich lipoprotein on the cell

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surface and selectively delivers the CE from the hydrophobic core of the lipoprotein to the inside of the cells without internalization of the intact lipoprotein particle [1, 4]. Recent studies have expanded the lipids it facilitates across the plasma membrane to include lipid-soluble vitamins such as vitamin E and carotenoids [5, 6]. SR-BI facilitates the bidirectional flux of free cholesterol (FC) and phospholipids between HDL and cells, thus influencing plasma membrane cholesterol content [7, 8]. It has also been implicated in the entry into cells of the hepatitis C virus (HCV) [9, 10], phagocytosis of apoptotic cells [11], protection against female infertility [12], modulation of platelet reactivity [13, 14], and plays a regulatory role in HDL-induced signaling in the vasculature [15, 16]. Most recently, it has been shown that SR-BI expression in bone marrow-derived cells is protective against diet-induced atherosclerosis and myocardial infarction [17]. SR-BI is evolutionally conserved, but exhibits diverse molecular properties among the various species in which it is expressed. In this review, we aim to summarize the current knowledge about the events and molecules connected to the regulation of SR-BI and to update the molecular and functional characteristics of the insect SR-BI orthologs.

SR-BI/CD36 family: distribution across different species and different tissues

SR-BI is a member of the class B scavenger receptor family, which in mammals includes the cluster determinant 36 (CD36) family, lysosomal integral membrane protein II (LIMPII, a lysosomal protein) and SR-BII (an isoform of SR-BI with an alternate C-terminal cytoplasmic tail). Structurally, all these proteins contain N- and C-terminal cytoplasmic domains, two-transmembrane domains, as well as a large extracellular domain containing 5-6 cysteine residues and multiple sites for N-linked glycosylation [1, 18]. In murine SR-BI, 11 N-linked glycosylation sites have been shown to be glycosylated, of which two glycosylation sites (Asn-108 and Asn-173) are required for proper expression and function of SR-BI [18]. Both SR-BI and CD36 are physiologically regulated by palmitoylation [19-22].

As seen with selective CE uptake [23-26], prominent expression of SR-BI has been observed in the liver and steroidogenic cells of the adrenal and gonads [27-31]. In the liver, SR-BI is mainly expressed in parenchymal cells (hepatocytes), which account for 90% of liver mass. Thus, on an organ basis, the liver expresses the highest amount of SR-BI. Furthermore, hepatocytes express twice as much SR-BI as that of Kupffer cells [32]. Ovarian steroidogenic cells, such as luteinized ovarian granulosa cells [4], luteal cells [29], and theca cells [33], express high levels of SR-BI. High SR-BI expression is also detected in fetal and adult adrenals, adrenocortical tumor cells, adrenal glomerulosa cells and adrenal carcinoma cells [31, 34]. Rat SR-BI expression is induced to high levels in response to treatment of animals with gonadotropin [30]. Exceptionally high levels of SR-BI are also reported in R2C rat testicular Leydig tumor cells [35]. In contrast to rodents, high levels of SR-BI/CLA-1 (the human homolog) are detected in human placental trophoblasts and in trophoblast-like human choriocarcinoma cell lines [36, 37]. Interestingly, SR-BI is also expressed in testicular Sertoli cells, which are not generally classified as steroid producing cells [38]. Testicular germ cells, on the other hand, preferentially express SR-BII, an isoform of SR-BI

[39]. Brain astrocytes, which synthesize neurosteroids, and microglia express SR-BI [40]. Finally, the expression of SR-BI, albeit at varying levels, is also reported in many non-steroidogenic cells, including adipocytes [1, 41], macrophages [42, 43], endothelial cells [44, 45], smooth muscle cells [46], intestinal cells [47, 48], retinal cells [49] and in skin keratinocytes [50].

SR-BI has also been identified in the livers of many non-mammalian species (turtle, goldfish, shark, chicken, frog, and skate), suggesting it emerged early in vertebrate evolutionary history. The expression of SB-RI in turtles is up-regulated during egg development, correlating with peak cholesterol efflux during developmental stages [51].

Multiple orthologs have been identified for the SR-BI/CD36 family in invertebrates. There are six CD36-like proteins identified in *Caenorhabditis elegans*; these proteins have been shown to be involved in pathogen recognition and the clearance of apoptotic cells [52, 53]. A genome-wide analysis identified thirteen SR-BI orthologs in the silk worm (*Bombyx mori*) [54], some of which are responsible for selective uptake of carotenoids into the silk gland [55, 56]. Multiple genes have been identified within the CD36 family in insects as well, eight in hymenopteran and twelve to fourteen in dipterans [57, 58]. Recent studies analyzing the expression pattern of the fourteen genes in *Drosophila melanogaster* during three different developmental larval stages prior to and during the peak of the insect steroid hormone ecdysone show highly regulated expression patterns of these genes, specifically three of the genes are up-regulated in steroidogenic tissues at the onset of pupariation when steroidogenesis is crucial [57]. These studies show the conserved function of SR-BI across species, revealing its role as an important regulator for cholesterol efflux and steroid hormone production.

In order to understand the mechanisms underlying the structure-function relation of the SR-BI/CD36 gene family, we aligned various orthologs of SR-BI/CD36 genes from different species and analyzed the structural features that are important for the function of SR-BI. As shown in the phylogenetic tree of some of the orthologs of SR-BI from the fruit fly to human (Fig. 1), the SR-BI homologs from mammals to other vertebrates are clustered together; similarly, those of nematodes and silk worms are clustered. The orthologs from the fruit fly, however, seem to have diverged into different groups. The 14 fruit fly SR-BI orthologs are clustered into four groups: 1) CG2736 seems to have diverged from most of the other SR-BI orthologs; 2) CG10345 and CG40006 of the fruit fly are more closely related to silkworm SR-BI homologs (SR-B11, SR-B12, SR-B13 and SR-B15); 3) CG3829, CG1887 and emp are more closely related to SR-BI homologs of nematodes (SCAV-4, SCAV-5 and SCAV-6); 4) crq, CG31741, CG7227, ninaD, peste, santa_maria, snmp1 and snmp2 are more closely related to those SR-BI from mammals and other vertebrates.

Some of the structural features of SR-BI have been demonstrated to be important for its function. The N-terminal transmembrane glycine dimerization motif (G15_G18_G25) has been defined to be required for normal receptor oligomerization and lipid transport [59]. Recent studies of the crystal structure of LIMP-2 shed light on the structure of this group of proteins, and showed that the main ectodomain of the protein contains an antiparallel β -barrel core with many short α -helical segments [60]. Two disulfide bridges stabilize the fold.

The disulfide bridge pattern for LIMP-2 (C274-C329 and C312-C318) is similar to that predicted for SR-BI (C321-C323, C274-C329) and that of CD36 (C313-C322, C272-C333), and is consistent with experimental data [61-64]. There are nine N-linked glycosylation sites that have been confirmed with well-defined electron density. When the sites Asn-68 and Asn-325 from LIMP-2 were mutated, the protein failed to be targeted to lysosomes and was retained in the endoplasmic reticulum. With regard to N-linked glycosylation, human SR-BI has 11 putative sites, and a mutational study of each of them shows that the protein failed to locate to the plasma membrane and has a marked reduction in the ability to transfer lipid from HDL to cells when Asn-108 or Asn-173 was mutated [18]. Most of the proteins in this family have lipid transport activity, and the crystal structure of the LIMP-2 showed that 8 amino acids work coordinately to form a tunnel that forms an interconnected cavity through the entire length of the ectodomain to facilitate lipid transfer. These 8 acidic and basic amino acids form a network of hydrogen and ionic bonds and contribute to the lining of the cavity, which is predominately hydrophobic to accommodate lipid moieties.

We have analyzed the above-mentioned structural features in the different SR-BI orthologs, and summarized them in Table 1. The alignment of the sequences highlights some of the structural features (Figure 2). As shown, the orthologs that are more closely related to the SR-BI of nematodes all have extended N-terminal and C-terminal extensions and stretches of internal insertions within their sequences (CG4006_fruitfly, CG3829_fruitfly, emp_fruitfly, CG1887_fruitfly, SRB11_silkworm, SRB13_silkworm, SRB15_silkworm, SCAV-4_c.elegans, SCAV-5_c.elegans, SCAV-6_c.elegans). Most of the proteins have at least one of the two disulfide bridges that stabilize the fold; specifically, the C274-C329 bridge of LIMP-2 is present in all the proteins except the fruit fly protein CG31741. The N-terminal transmembrane glycine dimerization motif is conserved in SR-BI from human to frog, and also in the fruit fly group that is more closely related to mammals and other vertebrates (crq_fruitfly, ninaD_fruitfly, santa maria_fruitfly).

Regulation of the expression of CD36/SR-BI gene family

As noted above, human and rodent SR-BI is expressed most abundantly in the liver parenchymal cells and steroidogenic cells of the adrenal gland and gonads, where the selective pathway exhibits its highest activity [27-31]. In steroidogenic cells, SR-BI is primarily localized on the cell surface, and its expression is regulated by trophic hormones (adrenocorticotrophic hormone [ACTH] or gonadotropins luteinizing hormone [LH] or follicle-stimulating hormone [FSH]) in concert with the regulation of steroid hormone production [28, 65]. SR-BI expression in both lower vertebrates (i.e., turtle) and fruit fly correlates with their developmental stage when peak cholesterol flux is required. On the other hand, many dietary, hormonal and pharmacological agents can regulate hepatic SR-BI expression [66]. Dietary polyunsaturated fatty acids up-regulate, whereas myristic acid decreases, liver SR-BI expression [67, 68]. Fibrates down-regulate SR-BI levels in the liver, while they upregulate SR-BI levels in macrophages and have no effect on SR-BI levels in the adrenal gland [69]. Therefore, SR-BI is regulated in a cell type specific fashion and may have different modes of selective uptake depending on the cell type.

Recently, in the search for the cellular and molecular mechanisms involved in the regulation of SR-BI expression and function, particularly posttranscriptional/posttranslational regulation, we have shown that two microRNAs, miRNA-125a and miRNA-455, can bind to specific sites in the 3' UTR of SR-BI mRNA and regulate the expression of SR-BI [70]. The expression of miRNA-125a and miRNA-455 is detected in adrenal, ovarian granulosa, and model Leydig cell lines, and their expression is down-regulated by trophic hormones or the second messenger, cAMP. When either miRNA-125a or miRNA-455 is overexpressed or inhibited, SR-BI-mediated selective HDL uptake and SR-BI-supported steroid hormone synthesis is inhibited or stimulated, respectively. Therefore, our findings suggest that miRNA-125a and miRNA-455 act as SR-BI attenuators to negatively regulate SR-BI-mediated selective delivery of lipoprotein cholesterol in steroidogenic cells and, consequently, inhibition of SR-BI-supported steroidogenesis. Furthermore, in a recent report, Wang et al provided evidence that the 3'-UTR of human SR-BI contains binding sites for miR-185, miR-96 and miR-223, and these three miRNAs were shown to inhibit selective HDL-CE transport into HepG2 cells via inhibition of SR-BI protein expression [71].

Mechanism of Actions

SR-BI facilitates selective HDL cholesteryl ester uptake in two separate independent steps: lipid-rich lipoprotein binding to the extracellular domain of SR-BI and the selective transfer of lipid to the plasma membrane [72, 73]. Studies with CD36/SR-BI chimeras and SR-BI mutants show that high affinity lipid rich-lipoprotein binding to SR-BI is important yet not sufficient for efficient lipid transfer [74]. Meanwhile, efficient lipid uptake via SR-BI or SR-BI/CD36 chimeric receptors is dependent on the extracellular domain of SR-BI [75]. In addition, compounds that can increase CE-rich lipoprotein binding to SR-BI can actually block lipid transfer [76]. Furthermore, protein-protein interaction involving SR-BI with many of its CE donors could be the predominant feature that drives productive SR-BI-lipoprotein complex formation. It has been shown that many of the CE donors (HDL, apoA-I/phospholipid bilayer disks, and lipid-free apoA-I) for SR-BI all share class A amphipathic helices that could be the structural feature to which SR-BI is binding [77, 78]. In addition, SR-BI exists as a multimeric complex with itself or other membrane proteins on the cell surface to facilitate lipid transfer, and the extracellular domain of SR-BI is essential for efficient CE transfer.

Many studies have also observed the formation of specialized cell surface structures, termed 'microvillar channels', whose expression is induced by SR-BI, that facilitate selective lipid transfer to the cell interior [79-82]. Immunolocalization studies at the electron microscopic level in rat ovarian luteal, testicular Leydig, and adrenocortical cells have demonstrated that SR-BI is preferentially localized on the microvillar membrane domains that form channels in which various lipoproteins, including HDL, get trapped [80, 81]. In addition, SR-BI was also shown to affect the flux of free cholesterol and the properties of the plasma membrane, and to facilitate the formation of specific lipid rafts that are necessary for the formation of the microvillar channels [82]. It is in these microvillar channels that HDL particles are trapped, apparently to boost the efficiency of the selective HDL-CE transport process.

Recently, we have also shown that the physical state of the SR-BI protein (i.e., monomeric versus dimeric and high-order oligomeric forms) and SR-BI-dependent architectural changes on the cell surface also play significant roles in SR-BI-mediated selective HDL-CE uptake [83]. Using a sulfhydryl-reactive reagent, such as cell-impermeant dithiothreitol (DTT), we showed that disulfide bond(s) exist in SR-BI and contribute to the oligomerization of SR-BI as well as to selective HDL-CE uptake. In addition, the reduction of higher complexes by DTT suggested that ectodomain (or ECD) dimer/oligomer formation may be mediated, at least in part, by disulfide bond formation via the six conserved cysteine residues (C251, C280, C321, C323, C334, and C384) found on the ECD of SR-BI.

Tissue Specific Mechanism of Actions

As summarized above, the regulation of steroidogenic SR-BI expression primarily occurs at the gene transcription level by trophic hormones. In contrast, the functional expression of hepatic SR-BI is primarily regulated at the post-transcriptional level. Many recent studies have shown that SR-BI interacts with other proteins, which, in turn influence the SR-BI-mediated HDL-CE transport into cells [84-89]. In the liver, the four PDZ (PSD-95/Disc-large/ZO-1) containing adaptor protein, PDZK1 (also called NHERF3), interacts with the C-terminal end of SR-BI (mouse sequence: EAKL), and is responsible for the post-transcriptional control of the expression, stability, localization, and function of SR-BI [89-94]. PDZK1 does not bind to the C-terminus of SR-BII, a minor splice variant of SR-BI (mouse sequence: SAMA) [87, 95]. Inactivation of the *PDZK1* gene in mice (*PDZK1*^{-/-}) leads to almost complete (~95%) suppression of SR-BI protein expression in hepatocytes, ~50% reduction of SR-BI protein expression in the small intestine, but no significant reduction in SR-BI protein levels in macrophages, steroidogenic tissues, adrenal, ovary and testis and endothelial cells [91, 96, 97]. In addition, overexpression of small PDZK1-associated protein (SPAP) downregulated PDZK1 in a liver-specific fashion, causing the subsequent down-regulation of hepatic SR-BI, but again having no effect on the levels of SR-BI in the adrenal gland or peritoneal macrophages [98]. The significance of these functional interactions has been shown in *PDZK1*^{-/-} mice, *SPAP* transgenic mice and mice treated with fibrates [69, 91, 98], where plasma HDL levels are markedly increased due to a deficiency of hepatic SR-BI. *PDZK1*^{-/-} mice differed from *SR-BI*^{-/-} mice in that the ratio of unesterified to total plasma cholesterol was normal, females were fertile and CE stores in steroidogenic organs were unaffected in *PDZK1*^{-/-} mice in contrast to the abnormalities observed in *SR-BI*^{-/-} mice [91, 99]. These differences are presumably due to normal expression of SR-BI in extrahepatic tissues.

In other recent studies to search for factors involved in regulating SR-BI expression and function in steroidogenic tissue, we examined the expression pattern of PDZ domain containing proteins related to PDZK1 [100]. In fact, PDZK1, also known as Na⁺/H⁺ exchanger regulator factor-3 (NHERF3), belongs to a family of scaffolding proteins that also includes NHERF1 (EBP50), NHERF2 (E3KARP), and NHERF4 (IKEPP) [84, 101, 102]. All of these family members possess tandem PDZ domains; NHERF1 and NHERF2 have two and PDZK1/NHERF3 and NHERF4 have four tandem PDZ domains [84, 102]. In addition to PDZ domains, NHERF1 and NHERF2 possess C-terminal MERM (merlin-ezrin-radixin-moesin) binding domains, which indirectly tether these proteins to the actin

cytoskeleton [103]. We have shown that NHERF1 and NHERF2 mRNA and protein are expressed at varying levels in model steroidogenic cell lines and the adrenal, with only low expression of PDZK1 (NHERF3) and NHERF4. Dibutyryl cyclic AMP decreased NHERF1 and NHERF2 and increased SR-BI mRNA expression in primary rat granulosa cells and MLTC-1 cells, whereas ACTH had no effect on NHERF1 and NHERF2 mRNA levels but decreased their protein levels in rat adrenals [100]. Co-immunoprecipitation, colocalization, bimolecular fluorescence complementation, and mutational analysis indicated that SR-BI associates with NHERF1 and NHERF2. NHERF1 and NHERF2 down-regulated SR-BI protein expression by inhibiting its de novo protein synthesis. NHERF1 and NHERF2 also inhibited SR-BI-mediated selective CE transport and steroidogenesis, which were markedly attenuated by partial deletions of the PDZ1 or PDZ2 domain of NHERF1, the PDZ2 domain of NHERF2, or the MERM domains of NHERF1/2 or by gene silencing of NHERF1/2. Moreover, an intact COOH-terminal PDZ recognition motif (EAKL) in SR-BI is needed. Transient transfection of hepatic cell lines with NHERF1 or NHERF2 caused a significant reduction in endogenous protein levels of SR-BI. Additional studies demonstrated that another member of the NHERF family, NHERF4, had no effect on either SR-BI protein levels or its selective transport function when CHO cells were transiently co-transfected with SR-BI plus NHERF4 as compared with SR-BI alone. In contrast, co-transfection of CHO cells with SR-BI plus PDZK1/NHERF3 up-regulated the expression of SR-BI protein as compared with SR-BI protein levels seen in cells transfected with the SR-BI construct alone. These results are in agreement with the earlier reports showing that PDZK1/NHERF3 is essential for normal expression of SR-BI in mouse hepatocytes. Our results further demonstrate that the presence of PDZK1/NHERF3 can stimulate SR-BI protein expression even in non-hepatic cells expressing SR-BI [100]. Collectively, these data establish NHERF1 and NHERF2 as SR-BI protein binding partners that play a negative role in the regulation of SR-BI expression, selective CE transport, and steroidogenesis.

SR-BI and Clinical Relevance

In addition to mediating selective cholesteryl ester transport from HDL to cells [1, 2, 34], bi-directional flux of unesterified cholesterol between HDL and cells [104, 105], phospholipid uptake by cells [106], and hepatic reverse cholesterol transport [107], it is becoming increasingly clear that SR-BI performs many other functions including its involvement in atherosclerosis [108, 109], apoptosis [110-113], platelet function [109, 114], immune responses [115], hepatitis C virus (HCV) [116-118] and dengue virus [119] entry, malaria parasite infection [120], and human HDL homeostasis [121, 122]. Evidence for the atheroprotective role of SR-BI is shown in genetically modified mouse models [108]. Both SR-BI transgenic [123, 124] and adenovirus-mediated [125] hepatic overexpression of SR-BI has been shown to markedly suppress atherosclerosis in LDL-receptor deficient mice that were chronically fed a high-fat diet. Conversely, complete deficiency of the SR-BI gene in chow-fed apoE-deficient (SR-BI/apoE DKO) mice [126] or high-fat diet-fed LDL receptor-deficient (SR-BI/LDLR DKO) mice [127] accelerated the development of atherosclerosis. Interestingly, SR-BI/apoE DKO mice exhibited severe dyslipidemia, developed early occlusive atherosclerotic coronary artery disease, spontaneous myocardial infarctions, severe cardiac dysfunction and died prematurely around 6 to 8 weeks of age [128, 129]. Other

studies demonstrated that attenuated expression of SR-BI in LDL-receptor KO mice [130] or feeding a high-fat/high cholesterol diet to SR-BI-deficient mice [131, 132] also led to development of atherosclerosis. In addition, evidence is accumulating that SR-BI influences the functions of a number of vascular cells relevant to atherosclerosis, including macrophages, lymphocytes, endothelial cells and endothelial progenitor cells [109].

SR-BI is also implicated in modulating platelet function and mediating platelet-HDL interactions [109, 114]. Imachi et al [133] first provided evidence that human (h) SR-BI/CLA-1 is expressed in platelets and megakaryocytes, the platelet precursors within the bone marrow. Furthermore, it was reported that hSR-BI/CLA-1 abundance was significantly reduced on the surface of platelets from patients with atherosclerotic disease and that such attenuated levels showed an inverse correlation with increased cholesteryl ester content and platelet aggregation. Subsequent work of Dole et al [134] demonstrated that a high plasma UC:TC ratio in SR-BI deficient mice was associated with platelet abnormalities, including cholesterol content, abnormal morphology, high clearance rates, and thrombocytopenia. It was further demonstrated that abnormal circulating lipoproteins containing a high UC:TC ratio in SR-BI KO mice, rather than the SR-BI deficiency itself, variably impacted platelet structure, function and clearance. A similar functional phenotype has been observed in human carriers of an SR-BI genetic variant in which a proline was substituted for a serine at amino acid position 297 (P297S) [121]. Recently, it was reported that increased platelet activation in response to SR-BI deficiency in mice is caused by dyslipidemia and platelet cholesterol overload [13, 135].

While various metabolic functions of SR-BI have been well studied in rodents, the understanding of the role of hSR-BI/CLA-I in human lipid metabolism, particularly HDL metabolism and atherosclerotic disease, is still in its infancy stage. Human genetic studies of hSR-BI/CLA-I function have primarily focused on polymorphisms in hSR-BI/CLA-I for potential association with HDL-cholesterol and other metabolites [107]. As summarized by Kent and Stylianou, most of the early studies focused primarily on three SNPs located in exon-1, intron-5, and exon-8 [107]. However, these studies reported only a weak association between hSR-BI/CLA-I and HDL-cholesterol levels. A recent, large, genome-wide association study (GWAS) involving over 10000 individuals reported that genetic polymorphism in *SCARBI* was associated with a small, but significant elevation in plasma HDL-cholesterol [136]. More recently, Vergeer et al [121] identified a single loss-of-function mutation (P297S) in SR-BI that was associated with increased HDL cholesterol levels, reduced cholesterol efflux from macrophages, and reduced adrenal steroid secretion, but had no effect on atherosclerosis. Another study identified two novel missense mutations, S112F (nucleotide C588T) and T175A (nucleotide A776T), in the hSR-BI/CLA-I gene that were also associated with elevated HDL-cholesterol in heterozygous carriers [122]. Currently, however, there is no evidence that any of these mutations in anyway impact atherosclerosis in humans.

Concluding Remarks

SR-BI is a member of the class B family of receptors, is evolutionarily conserved but exhibits variable molecular properties among the various species in which it is found. It

serves as an HDL receptor that preferentially mediates the selective uptake of HDL-CE in the liver for biliary cholesterol secretion and bile acid formation and also mediates a bulk delivery of cholesterol to the adrenal, ovary and testis for steroidogenesis. In addition to the central role of SR-BI in facilitating selective CE uptake, it is becoming increasingly clear that this receptor protein performs many other important functions; e.g., SR-BI appears to regulate processes involved in cellular cholesterol homeostasis, bi-directional cholesterol flow, membrane lipid expression, female fertility (oocyte maturation), apoptosis, platelet function and, in addition, SR-BI may act as an athero-protective agent. SR-BI, along with CD81, has been implicated in the entry of the hepatitis C virus into liver cells. Recent findings of mammalian SR-BI provide new insights into the posttranscriptional/posttranslational regulation of this receptor, but also raise many questions. Understanding the molecular mechanisms and relative importance of various miRNAs and how they regulate and contribute to the function of SR-BI in a tissue specific manner will be very informative. Furthermore, investigations into NHERF1 and NHERF2 mediated negative regulation of SR-BI in steroidogenic cells, the liver and in other SR-BI expressing cells should clearly establish their critical role in SR-BI-dependent selective HDL-CE transport and potentially other SR-BI linked functions. This information will be especially useful for liver, where, until now, another member of the NHERF family, PDZK1/NHERF3, is considered to be a major regulator of the post-transcriptional/posttranslational control of the expression, stability, localization, and function of SR-BI. Finally, very little information is currently available about the expression, structural organization and function of SR-BI from lower vertebrates as well as insects. Further exploration of their properties may lead to identification of a 'super SR-BI' that can be exploited to increase the efficacy of selective HDL-CE function, especially in the liver for the removal (excretion) of excessive cholesterol.

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Abbreviations

CD36	cluster determinant
CE	cholesteryl ester
CHO	Chinese hamster ovary cells
CLA-I	the human <u>CD36</u> and <u>LIMPII A</u> -analogous-1
FSH	follicle stimulating hormone
HCV	Hepatitis C virus
HDL	high-density lipoprotein
LH	luteinizing hormone
LIMPII	lysosomal integral membrane protein II
NHERF1	Na ⁺ /H ⁺ exchange regulatory factor 1

NHERF2	Na ⁺ /H ⁺ exchange regulatory factor 2
NHERF3	Na ⁺ /H ⁺ exchange regulatory factor 3
PDZ	<u>P</u> SD-95/ <u>D</u> iscs-large/ <u>Z</u> O-1
SR-BI	scavenger receptor class B type I

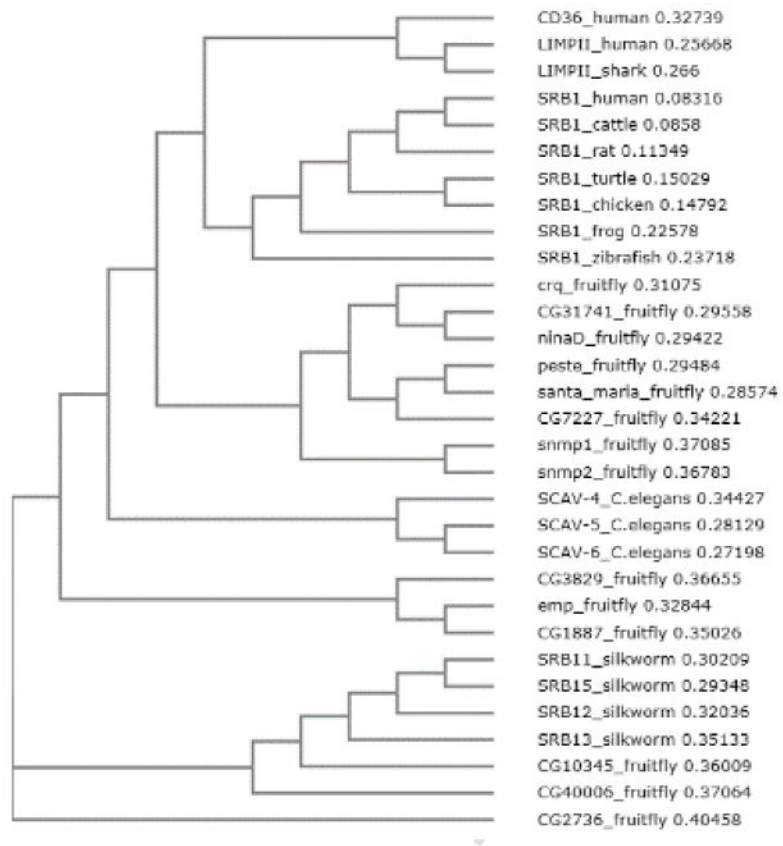


Figure 1. Phylogenetic tree of representative orthologs of SR-BI from different species. Amino acid sequences from the various SR-BI orthologs were analyzed using the multiple sequence alignment program Clustal Omega from EMBL-EBI (<http://www.ebi.ac.uk/Tools/msa/clustalo>).

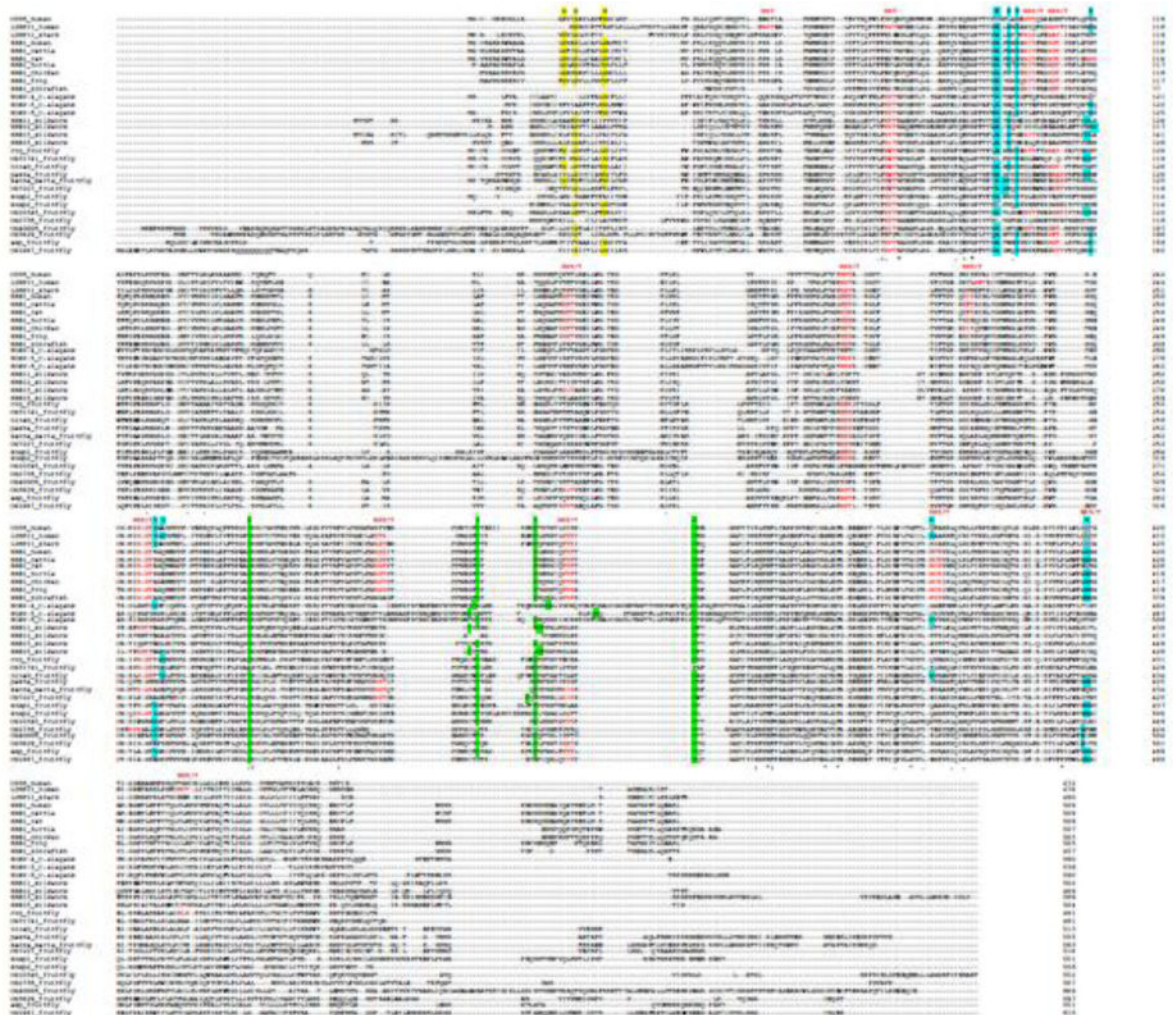


Figure 2. Sequence alignment of SR-BI orthologs from different species. Amino acid sequences from the various SR-BI orthologs were analyzed using the multiple sequence alignment program Clustal Omega from EMBL-EBI (<http://www.ebi.ac.uk/Tools/msa/clustalo>). Colored amino acids represent the structural features discussed in the text. G_G_G is the glycine dimerization motif, NXS(T) is the N-glycosylation site, C-C is the S-S bond, ERKKDDKE is the tunnel cavity.

Table 1

Structural features of SR-BI orthologs from different species. % similarity was calculated using the T-coffee program from EMBL-EBI (<http://tcoffee.org.cat/apps/tcoffee>).

	Accession #	Overall similarity	Sequence Extensions	N-terminal length	TM length	ECM similarity	TM length	ECM similarity	TM length	C-terminal length	Glycine dimerization motif	N-Glycosylation	S-S bonds	Tunnel cavity (E93, R95, K97, K115, D252, D254, K381, E413)
CD-36-human	NP_000063.2	76%		9	21	409	80%	20	12	G_G_G	4	2	2/8(000)D(0)E	
LJMP-II_human	NP_005497.1	76%		7	22	395	82%	18	26	0_G_0	10	2	8/8 ERKKDDKE	
LIMPII shark	AFK11285.1	81%		10	22	397	76%	21	25	G_G_0	7	2	4/8 ER(0)D(0)E	
SR-BI Human	NP_005496.4	78%		11	21	395	100%	21	48	G_G_G	9	2	4/8 ERK(0)00E	
SR-BI cattle	NP_777022.1	81%		11	21	395	80%	21	48	G_G_G	9	2	4/8 ERK(0)00E	
SR-BI rat	NP_113729.1	78%		11	21	386	82%	21	48	G_G_G	10	2	3/8 ERK(0)00	
SR-BI turtle	XP_005299633.1	78%		10	21	387	80%	21	47	G_G_G	8	2	4/8 ERK(0)00E	
SR-BI Chicken	XP_415106.2	69%		9	21	406	82%	21	44	G_G_G	9	2	3/8 E0K(0)00E	
SRBI frog	XP_002293533.1	74%		5	21	406	80%	21	39	G_G_G	8	2	3/8 E0K(0)00E	
SR-BI Zebra-fish	NP_944603.1	78%		8	0	358	82%	21	57	0_0_0	6	2	3/8 E0K(0)00E	
SCAV-4_C.elegans	NP_510157.2	74%	internal	7	21	495	80%	21	15	0_0_G	2	*1(no 321-323)	4/8 E0KKD(0)0	
SCAV-5_C.elegans	NP_509651.2	74%	internal	4	21	488	80%	21	16	0_0_G	2	*1(no 321-323)	4/8 E0KK(0)0K	
SCAV-6_C.elegans	NP_492081.1	74%	internal	7	21	492	80%	21	41	0_0_G	2	2	3/8 E0KK(0)00	
SRB11_silk worm	NP_001266430.1	73%	N-terminal	20	21	409	71%	21	31	0_G_0	2	*1(no 321-323)	3/8 ER(0)K(0)00	
SRB12_silk worm	NP_001266422.1	73%		9	21	401	74%	21	33	0_G_0	1	1(no 321-323)	3/8 ER(0)K(0)00	
SRB13_silk worm	XP_004925280.1	73%	N,C-terminal	33	21	371	74%	21	77	0_G_0	3	2	3/8 ER(0)K(0)00	
SRB15_silk worm	BAM67017.1	71%	N-terminal	18	21	404	75%	22	36	0_G_0	2	*1(no 321-323)	2/8 ER(0)0(0)00	
crq_fruitfly	NP_787957.1	77%		12	21	417	73%	21	20	G_G_G	6	2	3/8 E0K(0)D(0)0	
CG31741_fruitfly	NP_724088.2	76%		12	21	415	77%	21	22	0_G_G	3	*1(no 274-329)	2/8(0)KK(0)00	
miniaD_fruitfly	AAO11676.1	76%		12	21	428	77%	21	31	G_G_G	4	2	5/8 ERK(0DK)	
peste-maria_fruitfly	NP_001137808.1	75%	C-terminal	10	21	372	78%	24	73	0_G_G	4	2	4/8 E0KK(0)00E	
santa-maria_fruitfly	NP_723277.3	73%	C-terminal	16	21	368	76%	21	83	G_G_G	6	2	3/8 ERK(0)0000	
CG7227_fruitfly	NP_609169.1	75%	C-terminal	7	21	408	76%	18	47	0_G_0	5	2	3/8 ERK(0)0000	
snmp1_fruitfly	NP_650953.1	74%	C-terminal	7	19	413	77%	21	73	0_0_0	2	2	4/8 E0K(0)D(0)E	
snmp2_fruitfly	ABW70129.1	74%		6	21	492	75%	21	16	0_G_G	3	2	3/8(0)0K(0)D(0)E	

	Accession #	Overall similarity	Sequence Extensions	N-terminal length	TM length	ECM length	ECM similarity	TM length	ECM length	ECM similarity	TM length	C-terminal length	Glycine dimerization motif	N-Glycosylation	S-S bonds	Tunnel cavity (E93, R95, K97, K115, D252, D254, K381, E413)
CG10345_fr uitfly	NP_65056 3.2	75%	C-terminal	7	21	443	76%	21	443	76%	21	19	0_G__G	4	2	2/8 000K0D000
CG2736_frui tfly	NP_61199 1.1	74%		7	21	411	68%	21	411	68%	21	41	0__0__0	2	1 (no 321-323)	2/8 0000D000E
CG40006_fr uitfly	NP_00103 6401.1	65%	N, C-terminal	91	21	337	76%	21	337	76%	22	143	0_G__0	3	2	3/8 E000D000E
CG3829_frui tfly	NP_61199 2.3	76%	N, C-terminal	30	76	405	74%	76	405	74%	21	52	0_G__0	4	2	4/8 E0KK000E
emp_fruitfly	NP_72650 4.2	75%	N,C-terminal	20	20	410	78%	20	410	78%	21	63	0__0__G	4	2	5/8 E0KKD000E
CG1887_frui tfly	NP_00109 7477.1	67%	N,C-terminal	72	22	381	78%	22	381	78%	21	83	0_G__G	5	1 (no 321-323)	4/8 E0KK000E