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REVIEW ARTICLE

## Caveolae, caveolin, and cavins: Potential targets for the treatment of cardiac disease

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### Abstract

Caveolae are omega-shaped membrane invaginations present in essentially all cell types of the cardiovascular system, including endothelial cells, smooth muscle cells, macrophages, cardiac myocytes, and fibroblasts. Numerous functions have been ascribed to this omega-shaped structure. Caveolae are enriched with different signaling molecules and ion channel regulatory proteins and function both in protein trafficking and signal transduction in these cell types. Caveolins are the structural proteins that are necessary for the formation of caveola membrane domains. Mechanistically, caveolins interact with a variety of downstream signaling molecules, as, for example, Src-family tyrosine kinase, p42/44 mitogen-activated protein (MAP) kinase, and endothelial nitric oxide synthase (eNOS) and hold the signal transducers in the inactive condition until activated with proper stimulus. Caveolae are gradually acquiring increasing attention as cellular organelles contributing to the pathogenesis of several structural and functional processes including cardiac hypertrophy, atherosclerosis, and heart failure. At present, very little is known about the role of caveolae in cardiac function and dysfunction, although recent studies with caveolin knock-out mouse have shown that caveolae and caveolins play a pivotal role in various human pathobiological conditions. This review will discuss the possible role and mechanism of action of caveolae and caveolins in different cardiac diseases.

**Key words:** *Caveolae, caveolin, cavins, lipid raft, heart*

### Introduction

The cell membrane is a heterogeneous mixture of proteins, cholesterol, and lipids including glycerolipid, phospholipid, and sphingolipids. The sphingolipids and cholesterol are associated with one another within the plasma membrane and form lipid microdomains, commonly known as lipid rafts (1,2). Lipid rafts are sphingolipid- and cholesterol-rich domains of the plasma membrane, which contain a variety of signaling and transport proteins. Different subtypes of lipid rafts can be distinguished according to their protein and lipid composition. Caveolae, a subset of lipid rafts, are flask-like invaginations of plasma membrane that contain proteins of the caveolin family (caveolin-1, caveolin-2, and caveolin-3). The organization and function of caveolae are mediated by coat proteins (caveolins) and support or adapter

proteins (cavins). In addition, lipid rafts have been implicated in the modulation of multiple different types of ion channel proteins. Various types of lipid rafts have been proposed based on different protein markers, morphological features, and their relative cholesterol-to-sphingolipid content (3,4).

### Caveolae and caveolins

Caveolae were first identified in 1953 by Palade using electron microscopy to examine the endothelial cells of rat capillaries (5). Caveolae were named based on their morphological appearance on electron microscopy as 'little caves'. Typically, caveolae exhibit a flask-shaped invaginated structure of 50–100 nm in diameter which is contiguous with the surface plasmalemma (6,7). Different cell types possess different densities of caveolae in their plasma

membrane. For example, approximately 50% of the surface plasmalemma of the adipocyte consists of caveolae (8), while only 5% of fibroblast plasma membrane is made up of caveolae (9). A major component of caveolae is the presence of caveolin proteins (10,11). Cav-1 (also called vesicular integral membrane protein (VIP-) 21) was the first protein to be identified as a prominent resident of caveolae (11,12). Cav-1 and -2 are co-expressed in most cell types, while expression of caveolin-3 is muscle-specific. Thus, endothelial cells and fibroblasts are rich in Cav-1 and -2, while cardiac myocytes and skeletal muscle fibers express cav-1 and caveolin-3. Recent work of Chow et al. provided evidence that cav-1 is found in cardiomyocytes (13,14) and that cav-1 and membrane-bound matrix metalloproteinase-2 (MMP-2) co-localize as another means to keep MMP-2 activity in check, and that caveolin-2 knockout (KO) mice have enhanced cardiac MMP-2 activity (15). The hearts from young cav-1 KO mice do not necessarily show defects in contractile function (16). In contrast, smooth muscle cells express all three caveolins (Cav-1, -2, and -3) (17).

Caveolins are multiple acylated 22–24 kDa proteins embedded in the cytosolic leaflet of cell membranes, with both N and C termini residing in the cytosol (18,19). Caveolins are first inserted into the membrane of the endoplasmic reticulum; they then transit through the secretory pathway, form

homo- and hetero-oligomeric complexes in the Golgi apparatus, and are thought to exit the Golgi for delivery to the plasma membrane as assemblies of around 100–200 caveolin molecules (20,21). Cav-1 expression is necessary for Cav-2 to be exported from the Golgi, and for its stability (22,23). Importantly, no morphological caveolae are found in the Golgi (24).

The recent identification of a family of proteins termed cavins has the potential to lead to significant advances in our understanding of the biology of caveolae. Cavins are localized to caveolae and are important for caveolar biogenesis, caveolin expression, caveola morphology, and have differential tissue distributions.

### Caveola regulatory proteins

Cavins act a regulator of caveolar function and organization, and each of them has been assigned different roles based on caveola morphologies and cell type. Cavin proteins function primarily as scaffolding proteins and also regulate availability of caveolins. So far, four different cavin proteins have been identified that include cavin-1 (polymerase transcript release factor (PTRF)), cavin-2 (serum deprivation protein response (SDPR)), cavin-3 (Sdr-related gene product that binds to c-kinase (SRBC)), and cavin-4 (muscle-restricted coiled-coil protein (MURC)) (Figure 1).

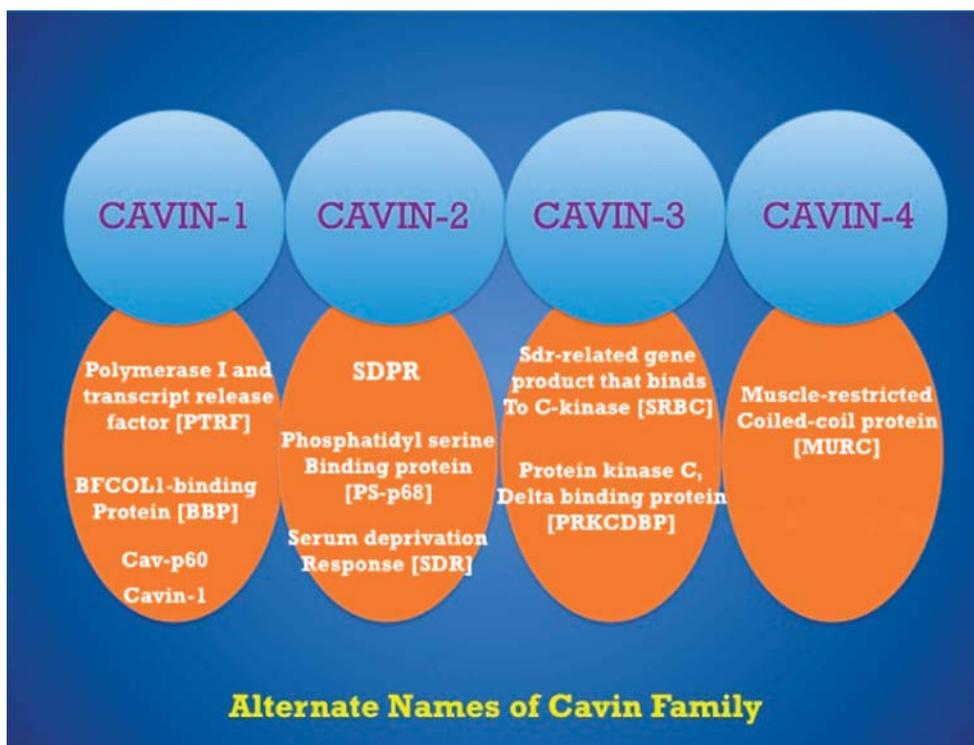


Figure 1. Different names of Cavin family protein.

*Cavin-1 (PTRF)*

Cavin-1 was initially identified in a yeast two-hybrid screen using transcription termination factor (TTF)-I as the bait (25). TTF-I is involved in the polymerase (Pol) I-mediated transcription of ribosomal RNAs (26,27). Cavin-1 was shown to interact both with TTF-I and Pol I and to function as a trans factor for dissociation of TTF-I-paused Pol I transcription complexes (22,28). The original name for cavin-1 was, therefore, polymerase I and transcript release factor (PTRF) (25). Early studies showed that cavin-1 co-localizes with Cav-1 in adipose tissue and co-distributes with Cav-1 in lipid rafts (29). Regulation of Cav-1 bioavailability by cavin-1 was demonstrated *in vitro*, as cavin-1 over-expression causes increased levels of Cav-1, and cavin-1 knock-down reduces Cav-1 levels (29). These data are similar to the well appreciated stabilizing effect of Cav-2 with Cav-1 and vice versa (29). In 2008, Liu et al. (30) showed that genetic deletion of cavin-1 resulted in global loss of caveolae through decreased availability of all caveolin proteins, e.g. dyslipidemia, reduced adipose tissue, and glucose intolerance—similar phenotypes to Cav-1/Cav-3 KO mice. In 2008, Hill et al. (31) showed that cavin-1 associates with caveolae at the plasma membrane, where it is required for the formation of caveolae via sequestration of caveolins into caveolae. These authors also demonstrated that

the loss of cavin-1 enhances the lateral mobility of Cav-1 and its accelerated lysosomal degradation (27). The function of cavin complexes is shown in Figure 2.

*Cavin-2 (SDPR)*

Cavin-2 was first purified as a phosphatidylserine (PS)-binding protein from human platelets and was shown *in vitro* to be a substrate for protein kinase C (PKC) isoforms (32,33). Mineo et al. also identified a stretch in the middle part of cavin-2 that binds to the regulatory domain of PKC and showed that cavin-2 localizes to caveolae (33). Cavin-2 was also separately identified as a protein with greater expression upon serum deprivation (hence the alternative name serum deprivation protein response (SDPR)) (34,35). In 2009, Hansen et al. (32) showed that cavin-2 directly binds cavin-1 and recruits it to the plasma membrane and that cavin-2 is required for the stable expression levels of both Cav-1 and cavin-1 proteins. Cavin-1/cavin-2 binding results in the formation of complexes containing Cav-1 contributing to stable caveola structures (36). Interestingly, the over-expression of cavin-2 in cultured cells results in the formation of elongated tubular caveolae, implying that it provides an organizational role to generate membrane curvature (36).

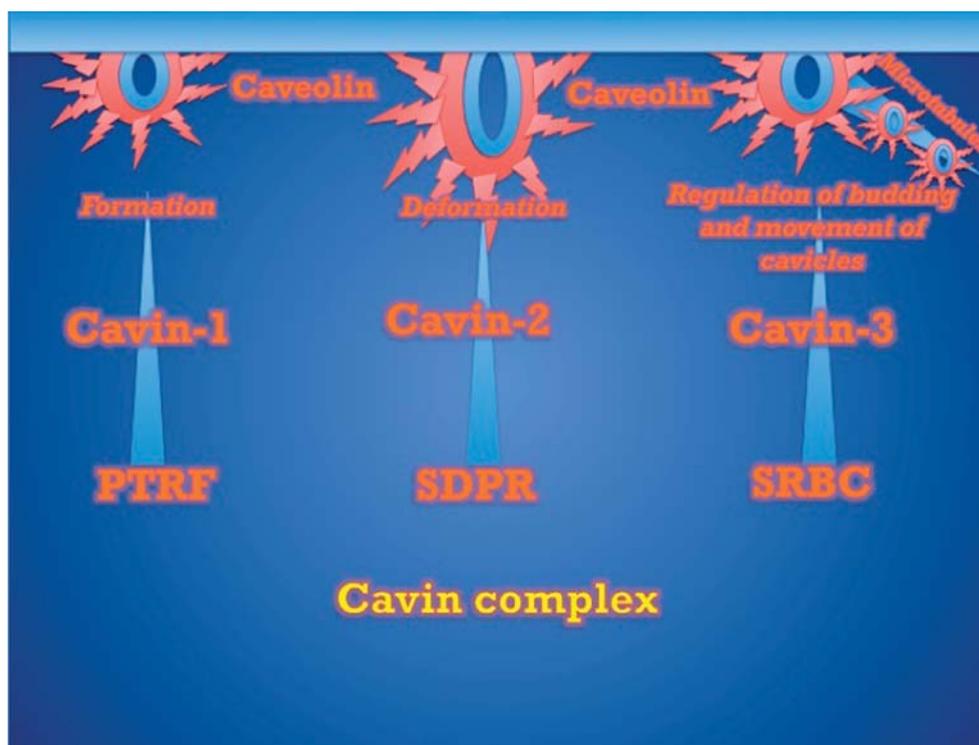


Figure 2. The function of Cavin complexes.

*Cavin-3 (SRBC)*

Cavin-3, or SRBC (Src-related gene product that binds to c-kinase), was initially identified as a PKC $\delta$ -binding protein (37,38). In 2009, it was discovered that cavin-3 is localized to caveolae, hence prompting determination of its role in caveolar function. Cavin-3 co-precipitates with Cav-1 and has a similar distribution to Cav-1; either Cav-1 or Cav-3 must be present for cavin-3 localization to the plasma membrane (39). Furthermore, cavin-3 participates in the formation of caveolar vesicles based on two observations: cavin-3 remains associated with caveolae when budding occurs, and the absence of cavin-3 impairs intracellular vesicular/cavicle trafficking (39).

*Cavin-4 (MURC)*

The most recent addition to the cavin family is cavin-4, MURC (muscle-restricted coiled-coil protein). This cavin was discovered as a cardiac and skeletal muscle-specific cytosolic protein (40–42). In 2009, cavin-4 was characterized as a predominantly muscle-expressed protein component associated with sarcolemmal caveola complexes. On the basis of its expression in muscle and co-localization with Cav-3, it was suggested that cavin-4 plays a predominant role in caveolin-associated muscle disease and disturbs cavin-4 distribution in patients with caveolinopathies (42).

**Caveolin knock-down**

A vast scientific literature confirmed the roles of caveolae and caveolin in the regulation of many cellular processes in cultured cells, and many investigators considered them as an essential platform of signaling molecules and also as the new therapeutic target. However, in the past few years, development of animal models and usage of genetically altered mice have been instrumental in deciphering their physiological functions *in vivo*. The most appropriate approach for the study of caveolin is the use of conditional KO mice, tissue-specific KO mice, or a system biology approach. Caveolin KO mice (Cav-1, -2, -3) and Cav-1/3 double KO mice have already been developed. They are viable as well as fertile but display numerous phenotypes. Transgenic over-expression of Cav-1 or Cav-3 in mice or targeted disruption of each of the caveolin gene loci in mice (Cav-1, Cav-2, and Cav-3 genes) has provided significant insight into the roles of caveolin and caveolae (43). The potential role of caveolin in cardiovascular physiology has become apparent by the discovery of Cav-1 and Cav-3 KO mice and double KO mice which have a cardiomyopathic phenotype. Cav-1 KO mice show complete ablation of the presence of the

caveolae, cellular organelles, in the endothelium and fat. Similarly, Cav-1 and Cav-3 KO mice lack caveolae in cells that normally express this protein such as skeletal muscle, heart, and diaphragm. Heart tissue is made up of different types of cells. In heart, differentiated cardiomyocytes are surrounded by a network of cardiac fibroblasts and endothelial cells and less abundant vascular smooth muscle cells. There is also a controversy regarding expression of caveolin isoforms in the heart muscle. It is well known that cardiac myocytes express Cav-3, and other cell types in the heart express Cav-1 and Cav-2. But recent studies provided the evidence of the existence of Cav-1 in cardiomyocytes (44). Cav-1 KO mice develop progressive cardiac hypertrophy as demonstrated by transthoracic echocardiography (TTE) and magnetic resonance imaging (MRI) (45). In contrast, Cav-3 KO mice develop cardiomyopathy characterized by hypertrophy, vasodilatation, and reduced contractility as well (46). Cav-1 and Cav-3 double KO mice completely lacking caveolae are deficient in all three caveolin proteins because Cav-2 is degraded in the absence of Cav-1. The double KO mice developed a severe cardiomyopathic phenotype with cardiac hypertrophy and decreased contractility (47). Additionally, Cav-1 KO mice exhibited myocardial hypertrophy, pulmonary hypertension, and alveolar cell hyperproliferation caused by constitutive activation of p42/44 mitogen-activated protein kinase and Akt (48). Interestingly, in Cav-1-reconstituted mice, cardiac hypertrophy and pulmonary hypertension were completely rescued (48). Again, genetic ablation of Cav-1 leads to a striking biventricular hypertrophy and to a sustained eNOS hyperactivation yielding increased systemic NO levels (49). Furthermore, a diminished ATP content and reduced level of cyclic AMP in hearts of KO mice was also reported (49). Taken together, these results indicate that genetic disruption of Cav-1 is sufficient to induce severe biventricular hypertrophy with signs of systolic and diastolic heart failure (49).

Interestingly, Cav-3 KO mice show a number of myopathic changes, consistent with a mild to moderate muscular dystrophy phenotype. However, it remains unknown whether a loss of Cav-3 affects the phenotypic behavior of cardiac myocytes *in vivo*. Cav-3 KO hearts display significant hypertrophy, dilation, and reduced fractional shortening as revealed by gated cardiac MRI and transthoracic echocardiography. Histological analysis reveals marked cardiac myocyte hypertrophy, with accompanying cellular infiltrates and progressive interstitial/perivascular fibrosis. It has also demonstrated that p42/44 MAPK (ERK1/2) is hyperactivated in heart derived from Cav-3 KO mice, which can lead to cardiac hypertrophy (46) (Figure 3).

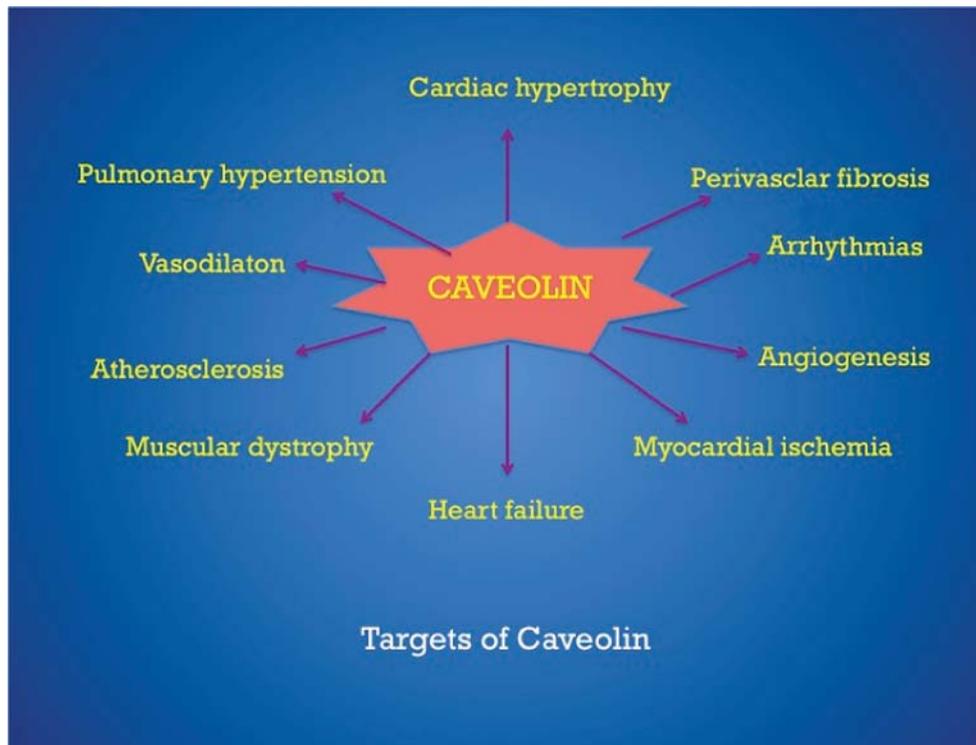


Figure 3. Caveolin and cardiovascular disease.

In the endoplasmic reticulum, Cav-3 initiates the biogenesis of caveola organelles by forming homo-oligomers and hetero-oligomers with Cav-1 (50). At the plasmalemma, Cav-3 interacts with dystrophin and its associated glycoproteins (51,52). Cav-3 and dystrophin competitively bind to the same site of  $\beta$ -dystroglycan, suggesting that Cav-3 may regulate the membrane recruitment of dystrophin and the assembly of the dystrophin glycoprotein complex (DGC) (53). At the cell surface, Cav-3 co-localizes also with signaling molecules such as Gi2 $\alpha$ , G $\beta$  $\gamma$ , c-Src, other Src kinases, as well as nitric oxide synthases (neuronal and inducible NOS), indicating that muscle caveolae might be involved in the modulation of these signaling processes (54,55). In addition, Cav-3 localized a glycolytic enzyme in striated muscle and plays a role in the regulation of energy metabolism of muscle cells as it is required for the cell membrane targeting of phosphofructokinase, an enzyme that catalyzes a rate-limiting reaction in glycolysis (56). It is Cav-1 that targets various glycolytic enzymes including phosphofructokinase in smooth muscle, lymphocyte, and astrocyte (56).

*In-vitro* studies have shown that Cav-3 plays a critical role in myoblast cell differentiation and survival and in myotube formation (57). The relevance of Cav-3 in muscle physiology was further confirmed by the findings that mutations in the *CAV3* gene result in distinct neuromuscular and cardiac disorders, such as limb girdle muscular dystrophy

(LGMD) 1-C, idiopathic persistent elevation of serum creatine kinase (hyperCKemia), inherited rippling muscle disease (RMD), distal myopathy, and familial hypertrophic cardiomyopathy (HCM) (58–60).

The *CAV3* gene (OMIM no. 601253) spans 12 kb of genomic DNA on chromosome 3p25 and contains two exons. At present, 20 different point mutations, 2 base-pair deletions, and 1 novel splice site mutation have been reported (57). More recently, four novel *CAV3* mutations have been identified in patients affected by congenital long-QT syndrome (LQTS) in the absence of signs of primary cardiomyopathy, suggesting a possible role for Cav-3 in the regulation of cardiac ion channels (61,62).

### Caveolae and cardiac arrhythmia

Modulation of ion channel activity plays a critical role in regulating cardiovascular function. Recently, it has become apparent that the regulation of channel function is not the only means of controlling excitability; the trafficking and localization of ion channels with signaling molecules also play a significant role. The cardiac action potential is generated by the highly orchestrated activity of different ion channel proteins as well as membrane transporters and exchangers. These transmembrane proteins govern the flux of ions across the sarcolemma of cardiomyocytes generating the ionic currents

responsible for excitation. Abnormalities in the function or regulation of the ion channel proteins underlie many different forms of arrhythmias.

Most cells in the cardiovascular system express multiple channel types (e.g. voltage-gated  $\text{Na}^+$ ,  $\text{K}^+$ , and  $\text{Ca}^{2+}$  channels) and even multiple isoforms of a particular channel, with each channel uniquely contributing to excitability (63,64). Voltage-gated  $\text{Na}^+$  channels are responsible for the initial depolarization of the cardiac sarcolemma, to permit the opening of voltage-gated L-type  $\text{Ca}^{2+}$  channels, resulting in  $\text{Ca}^{2+}$  influx and contraction. Membrane repolarization is controlled by  $\text{K}^+$  channels. Therefore, altering the number of channels and/or their function can have significant impact on both resting membrane potential and the cardiac action potential wave form. Defects in either of these processes can have life-threatening implications (63,64).

Along with the essential scaffolding protein Cav-3, a number of different ion channels and transporters have been localized to caveolae in the heart, including L-type  $\text{Ca}^{2+}$  channels (Cav1.2),  $\text{Na}^+$  channels ( $\text{Na}_v1.5$ ), pacemaker channels (HCN4),  $\text{Na}^+/\text{Ca}^{2+}$  exchanger (NCX1), and others. Closely associated with these channels are specific macromolecular signaling complexes that provide highly localized regulation of the channels. Mutations in the Cav-3 gene (*CAV3*) have been linked with the congenital long QT syndrome (LQTS), and mutations in caveolar localized ion channels may contribute to other inherited arrhythmias. Changes in the caveolar microdomain in acquired heart disease may also lead to dysregulation and dysfunction of ion channels, altering the risk of arrhythmias in conditions such as heart failure (65).

In several cell types, including smooth muscle and endothelial cells, mediators of calcium signaling, such as  $\text{Ca}^{2+}$ -ATPase, inositol-triphosphate receptor (IP3R),  $\text{Ca}^{2+}$  pumps and L-type  $\text{Ca}^{2+}$  channels, large conductance  $\text{Ca}^{2+}$ -activated  $\text{K}^+$  channel, calmodulin and transient receptor potential (TRP) channels, localize in cholesterol-rich membrane domains. Such localization suggest that membrane rafts and/or caveolae have a role in calcium handling and  $\text{Ca}^{2+}$  entry that control excitation-contraction of heart muscle (66,67). TRP channels, in particular TRPC1, -3, and -4, are enriched in caveolae and Cav-1 and regulate the plasma membrane localization and function of TRP channels (68). Current evidence indicates that caveolae regulate calcium entry, and depletion of cholesterol by methyl- $\beta$ -cyclodextrin reduces co-localization of Cav-1 and TRPC1, and redistribution of TRPC1, thus preventing  $\text{Ca}^{2+}$  influx (69). Moreover, the  $\text{Na}^+$  pump,  $\text{Na}/\text{K}$ -ATPase, contains two caveolin-binding motifs and resides in caveolae in a number of cells, including smooth muscle cells and cardiomyocytes, thereby

helping to maintain the  $\text{Na}^+$  gradient (70). Voltage-gated  $\text{K}^+$  channels are also localized in caveolae and play an important role in maintaining cellular excitability. In fibroblast, the Kv 1.5 subunit co-localizes with Cav-1, Kv 2.5 localizes with membrane raft, and depletion of cholesterol with M $\beta$ CD redistributes and alters the function of  $\text{K}^+$  channels (71). These findings imply that alteration of caveolae and/or caveolin by any disease or drug treatments can shift the localization of the channels, thereby altering cellular excitability and functional activity.

### Caveolae and atherosclerosis

Experimental evidence indicates that caveolae and caveolins have the possibility to influence atherogenesis in many ways. Cav-1 is a cholesterol-binding protein that can transport cholesterol from the endoplasmic reticulum (ER) to the plasma membrane. The major receptors for high-density lipoprotein, SR-B1, and a scavenger receptor for modified forms of LDL, CD36, can also reside in and signal in caveolatype microdomains (72). In addition, oxidized LDL can extract caveola cholesterol, unlocalize eNOS, and impair NO release (73). Conversely, blockade of HMG CoA reductase with statin-based drugs reduces caveolin levels and promotes eNOS activation (74). This concept has been validated in apolipoprotein E-deficient (ApoE<sup>-/-</sup>) mice where statin treatment decreases Cav-1 expression and promotes NOS function *in vivo*. However, to date, there are no data showing changes in Cav-1 levels in atherosclerotic lesions from humans (43).

Several lines of evidence now suggest that Cav-1 might play a pro-atherogenic role. In endothelial cells, Cav-1 is up-regulated on LDL exposure (75). Moreover, down-regulation of Cav-1 is associated with reduced uptake of oxidized LDL by endothelial cells (76). This finding is especially important because caveolae are proposed to play a major role in the transcytosis of native and modified LDL.

Cav-1 translocation to the plasma membrane is also enhanced on incubation of endothelial cells with LDL. This movement is accompanied by increased association of Ras with caveolae and results in the activation of Ras, an important upstream activator of the p42/44 MAP kinase pathway (75). Blair et al. (75) have also shown that oxidized LDL can modify the distribution of both Cav-1 and eNOS. This redistribution is accompanied by a reduction in eNOS activation by acetylcholine. This observation might be the result of disruption of the signal transduction complex containing eNOS, Cav-1, and other molecules required for eNOS activation. Recent work by Kincer et al. has shown that CD36, a class B scavenger receptor associated with caveolae, was probably

responsible for this effect (77). This observation is important in view of the fact that in hypercholesterolemic patients or animal models impairment of endothelium-derived relaxation is observed (78,79). It is also known that in smooth muscle cells Cav-1 and CD36 interacts and Cav-1 plays a role in the increase in apoptosis and lipotoxicity (80). In agreement with this finding, Feron et al. have shown that exposure of endothelial cells to serum from hypercholesterolemic patients promotes an increase in the Cav-1–eNOS interaction (81).

To verify if Cav-1 influenced lesion progression in mice, Lisanti and his co-workers cross-bred Cav-1<sup>-/-</sup> mice with ApoE<sup>-/-</sup> mice that developed atherosclerosis. Interestingly, the loss of Cav-1 in the ApoE<sup>-/-</sup> mice resulted in a pro-atherogenic lipid profile, similar to that seen in CD36<sup>-/-</sup> mice bred to an ApoE background (82,83). Surprisingly, despite a pro-atherogenic lipid profile, the loss of Cav-1 reduced the lesion burden by 80%, suggesting Cav-1 regulated LDL-mediated vascular dysfunction, inflammation, and lesion progression. The authors suggested this may be caused by a decrease in stability of the scavenger receptor for oxidized or modified LDL, CD36 in macrophages, and an increase in endothelium-derived NO production, which would reduce vascular inflammation. These remarkable findings unequivocally support the importance of Cav-1/caveolae in the pathogenesis of atherosclerosis (43).

### Caveolae and angiogenesis

Angiogenesis, a process of new blood vessel formation, occurs in three clearly distinct phases: initiation, proliferation of vascular cells, and morphogenesis. It has been demonstrated that VEGF stimulates endothelial cell proliferation, induces the expression of proteases and receptors important in cellular invasion and tissue remodeling, modifies endothelial cell permeability by stimulating NO and PGI<sub>2</sub> production, and finally prevents endothelial cell apoptosis (84,85). The interaction of VEGF with VEGF receptor-2 (Flk-1/KDR) is required to induce the full spectrum of biological responses involved in angiogenesis (86). It has been recently observed that VEGFR-2 and endothelial NO synthase, activated by VEGF, co-localize with Cav-1 in plasma membrane caveolae of HUVE cells, suggesting the caveolar localization of VEGF signaling machinery in endothelium (87).

It is interesting to note that several important proteins involved in angiogenesis have been localized to caveolae. Some of these macromolecules include the VEGF receptor (VEGFR), the urokinase receptor (uPAR), and eNOS. Recent studies by Labrecque et al. (88) have shown that Cav-1 tonically inhibits VEGFR-2 signaling, but interaction of VEGFR-2

with Cav-1 appears to be required for the proper ligand-induced activation of the receptor within caveolae membranes. Brouet et al. (89) found that eNOS-dependent atorvastatin stabilization of microvascular endothelial cell tube formation was associated with decreased Cav-1 expression, as well as other modifications that enhance eNOS activity. On stimulation of cells with bradykinin, the G protein-coupled bradykinin B2 receptor (B2R) and downstream effectors (Tyk2 and STAT3) are translocated outside the caveolae (90). This finding also has repercussions for eNOS regulation, because B2R can also interact with eNOS and inhibit its activity in a ligand- and calcium-dependent manner (91).

Morphogenesis implicates cell matrix adhesion events dependent on integrins (92) and cell-to-cell adhesion events dependent on interactions between cell surface ligands and receptors, belonging to the family of Eph tyrosine kinase receptors (93).  $\beta_1$ -Integrin was found to be associated with Cav-1, and caveolin appears to be a general regulator of  $\beta_1$ -integrin function involving Fyn kinase activation (94,95). Moreover, caveolae could function as assembling sites on the cell surface to allow the interaction between ephrin–Eph receptor system and integrins—an event preceding capillary morphogenesis. Data showing that knock-down of Cav-1 disrupts caveolae in endothelial cells and inhibits angiogenesis *in vitro* and *in vivo* support a central role of caveolae in angiogenic events (96).

Finally, in support of a role for Cav-1 in the regulation of angiogenesis *in vivo*, scientists have recently shown, using Matrigel plugs supplemented with basic fibroblast growth factor, that angiogenesis in Cav-1-null (-/-) mice is markedly reduced (97). Similar observations were made regarding tumor angiogenesis that was induced by injecting the B16 melanoma cell line into Cav-1-deficient (-/-) and wild-type animals. In addition, ultrastructural analysis of newly formed capillaries within the exogenous tumors revealed disorganized and incomplete capillary formation in Cav-1-null mice.

### Caveolae and hypertrophy

Cardiac hypertrophy is the consequence of an increase in cardiac myocyte size and/or mass. Since cardiac myocytes have no capacity for cellular proliferation, their only means of growth is by cellular enlargement. Given that cardiac failure is the most common result of insufficiency of myocardium, it is not surprising that cardiomyocyte hypertrophy is the dominant cellular response to virtually all forms of hemodynamic overload (98). However, long-term adaptive/compensatory hypertrophy is associated with progressive ventricular dilation. As a consequence

of cardiac enlargement and wall thinning, stress on the wall also increases, despite constant intracavitary pressure. This mathematical increase in wall stress generates its own hemodynamic stress on the heart, further stimulating the overloaded hypertrophy signaling pathway and thereby altering the balance from cell growth response to cell death. Once these processes have progressed to this stage (decompensation, loss of cardiac myocytes), irreversible functional deterioration develops, which leads to heart failure and, ultimately, death (99,100).

Over-expression of Cav-3 in neonatal cardiac myocytes decreases the ability of the adrenergic agonist phenylephrine or endothelin-1 to increase cell size (101). A similar kind of effect is seen in cardiac myoblasts (H9C2) in which Cav-3 reduces angiotensin II-promoted hypertrophy (102). Other studies indicate that cardiac hypertrophy results in decreased expression of Cav-3 (103,104) and that right heart (103) and left heart (104) hypertrophy is enhanced in Cav-1 KO and Cav-1/3 double KO mice. Down-regulation of growth signals is the most likely cause of expressed caveolin-induced inhibition of cardiomyocyte growth. Cav-1 and -3 KO mice show hyperactivation of p42/44 MAPK (50) and up-regulation of eNOS activity and nitrosative stress (44,104,50). In contrast, increased caveolin expression down-regulates activity of those entities (102,105). Chronic myocardial hypoxia increases eNOS expression while decreasing the expression of Cav-3, consistent with the idea that the expression and activity of eNOS is dependent on caveolin (106). Alterations in caveolin expression almost certainly change the ability of the hypertrophied heart to respond to a variety of physiologic and pharmacologic agonists/stimuli (44).

### Caveolae and ischemic cardiomyopathy

As coronary artery disease is the leading cause of mortality, cardiologists have been attempting for years to identify techniques to minimize the deleterious effects of myocardial ischemia and to diminish the extent of myocardial infarction after coronary occlusion. When the heart is subjected to a transient non-lethal period of ischemia, it quickly adapts itself to become resistant to infarction from a subsequent ischemic insult. This adaptation is called preconditioning (PC). Thus ischemic PC is a protective and adaptive mechanism produced by short periods of ischemic stress, rendering the heart more protective against another similar or greater stress. Although initially it was believed that 'ischemic PC' could be induced by short cyclic episodes of ischemia and reperfusion, it soon became apparent that a similar phenotype could be elicited by a splendid array of stimuli. For example, a number of pharmacological

agents, agonist of adenosine, bradykinin, adrenergic, muscarinic receptor, nitric oxide (NO) donors, phosphodiesterase inhibitors, and various noxious stimuli (endotoxin, cytokine, reactive oxygen species (ROS), etc.) have all been found to generate a PC-like phenotype (107,108), also known as pharmacological preconditioning.

After the discovery of 'ischemic PC' in 1986, the next discovery came in 1993, when it was found that PC has a biphasic pattern: an early phase, which develops very quickly (within few minutes from the exposure to the stimuli) and lasts only 1–2 h, and a late phase, which develops more slowly (needs 6–12 h) but lasts 3–4 days. The early phase develops by rapid post-translational modification of pre-existing proteins through a series of signaling cascades. Protein kinase C (PKC) plays a central role in this signaling cascade, although mitogen-activated protein (MAP) kinase (extracellular kinase, p38 MAP kinase, and c-Jun NH(2)-terminal kinase) is equally involved in PC. The late PC is mediated by cardioprotective gene expression and by the synthesis of new cardioprotective proteins. This mechanism involves redox-sensitive activation of transcription factors through PKC and tyrosine kinase signaling pathways that are in common with the early phase of PC.

Ischemia/reperfusion injury activates p42/44 and p38 MAPK, redistributes Cav-3, and down-regulates expression of Cav-1 (109). Disruption of caveolae using M $\beta$ CD eliminates the ability of ischemia and pharmacological preconditioning to protect the cardiac myocyte from injury (110). This is supported by the decreased ability of Cav-1 KO mice to undergo pharmacological preconditioning (111). Recent investigations also showed that pro-survival signaling components (e.g. ERK1/2, HO-1, eNOS and p38 MAPK $\beta$ ) translocate and/or interact with caveolin in the ischemia/reperfusion heart, rendering the heart less susceptible to a pro-survival signal, and induces myocardial injury. Similarly, death signaling components (e.g. p38 MAPK $\alpha$ , JNK, and Src) translocate and/or interact with caveolin in the preconditioned heart, rendering the heart less exposed to death signaling components and more susceptible to pro-survival signaling components (112). Although the detailed mechanism of action of caveolin is not very clear, evidence indicates that proteasomes play a very important role in the interaction between caveolin and signaling components. However, overall observation indicates that caveolin plays a pivotal role in cardioprotection against ischemic injury.

### Summary and conclusion

Caveolae and caveolins undoubtedly regulate various aspects of the cardiovascular system. The potential

role of caveolin in cardiovascular physiology has become apparent by the discovery of Cav-1 and Cav-3 KO mice and double KO mice which have a cardiomyopathic phenotype. Clearly, loss of Cav-1 has a profound effect on the eNOS pathway, indicating the importance of this interaction, whereas the loss of Cav-3 impacts NOS as well as MAPK activation. Although the detailed mechanisms of actions are not very clear, experimental evidence demonstrates the predominant role of caveolin in cardiac hypertrophy, atherosclerosis, ischemic injury, and different myocardial functions. The most recently discovered proteins, cavins 1–4, are involved in regulation of caveolae and modulate the function of caveolins by promoting membrane remodeling and trafficking. The pathogenic role of caveolins is an emerging area; however, the role of cavins in cardiac disease is just beginning to be explored. Recent investigations are disentangling the complex processes of caveolin and cavin-regulated signaling systems in the myocardium and developing novel approaches, aimed at counteracting heart failure and/or cardiovascular diseases.

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