Minireview

Caveolins, a Family of Scaffolding Proteins for Organizing “Preassembled Signaling Complexes” at the Plasma Membrane

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Caveolae are vesicular invaginations of the plasma membrane. The chief structural proteins of caveolae are the caveolins. Caveolins form a scaffold onto which many classes of signaling molecules can assemble to generate preassembled signaling complexes. In addition to concentrating these signal transducers within a distinct region of the plasma membrane, caveolin binding may functionally regulate the activation state of caveolae-associated signaling molecules. Because the responsibilities assigned to caveolin continue to increase, this review will focus on: (i) caveolin structure/function and (ii) caveolin-associated signal transduction. Studies that link caveolae to human diseases will also be considered.

The Caveolin Gene Family: Caveolin-1, -2, and -3

Molecular cloning has identified three distinct caveolin genes (1–6), caveolin-1, caveolin-2, and caveolin-3. Two isoforms of caveolin-1 (Cav-1α and Cav-1β) are derived from alternate initiation during translation. Caveolin-1 and -2 are most abundantly expressed in adipocytes, endothelial cells, and fibroblastic cell types, whereas the expression of caveolin-3 is muscle-specific. Caveolin proteins interact with themselves to form homo- and hetero-oligomers (7–9), which directly bind cholesterol (10) and require cholesterol for insertion into model lipid membranes (10, 11). Caveolin oligomers may also interact with glycosphingolipids (12). These protein-protein and protein-lipid interactions are thought to be the driving force for caveolae formation (7). In addition, the caveolin gene family is structurally and functionally conserved from worms (Caenorhabditis elegans) to man (13), supporting the idea that caveolins play an essential role. Caveolin-1 assumes an unusual topology. A central hydrophobic region of the plasma membrane, caveolin binding may functionally regulate the activation state of caveolae-associated signaling molecules. Because the responsibilities assigned to caveolin continue to increase, this review will focus on: (i) caveolin structure/function and (ii) caveolin-associated signal transduction. Studies that link caveolae to human diseases will also be considered.

Caveolin-1 is a multifunctional protein that is thought to function as a scaffold for many signaling molecules. It is expressed in many cell types and is thought to be involved in the regulation of cell growth and differentiation. Caveolin-1 is also involved in the modulation of cell adhesion and motility, and it is implicated in the development and progression of various diseases, including cancer and obesity.

Caveolin-2 is expressed in a variety of cell types, including adipocytes, endothelial cells, and fibroblasts. It is involved in the regulation of lipid metabolism and cell growth. Caveolin-2 is also involved in the modulation of cell adhesion and motility, and it is implicated in the development and progression of various diseases, including cancer and obesity.

Caveolin-3 is expressed in muscle cells, and it is involved in the regulation of muscle contraction and relaxation. Caveolin-3 is also involved in the modulation of cell adhesion and motility, and it is implicated in the development and progression of various diseases, including obesity and diabetes.

The caveolin gene family, caveolin-1, -2, and -3, have been shown to interact with caveolin-1 (20, 23). Using a detergent-free procedure and a polychystidine-tagged form of caveolin-1 for affinity purification of caveolin-rich membranes, G-proteins, Srf family kinases, and Ha-Ras were all found to co-fractionate and co-elute with caveolin-1. Wild-type Ha-Ras also interacted with recombinant caveolin-1 in vitro. Ras binding activity was localized to a 41-amino acid membrane-proximal domain (61–101) of the multifunctional protein GRP78. caveolin-1 dramatically suppresses the tyrosine kinase activity of c-Src. Thus, it appears that caveolin-1 functionally interacts with c-Src and caveolin-1 residues within caveolae microdomains. Srf Family Tyrosine Kinases—Caveolin-1 interacts with wild-type Src (c-Src) but does not form a stable complex with mutationally activated Src (v-Src) (20). Thus, caveolin prefers the inactive conformation of Ga subunits, Ha-Ras, and c-Src. Deletion mutagenesis indicates that the Srf-interacting domain of caveolin is located within residues 61–101. A caveolin peptide derived from this region (residues 82–101) functionally suppressed the autoactivation of purified recombinant c-Src tyrosine kinase and a related Srf family kinase, Fyn. Co-expression of caveolin-1 with c-Src shows that caveolin-1 dramatically suppresses the tyrosine kinase activity of c-Src. Thus, it appears that caveolin-1 functionally interacts with wild-type c-Src via caveolin residues 82–101.

Endothelial Nitric Oxide Synthase (eNOS)—Several independent co-immunoprecipitation and domain-mapping studies demonstrate that eNOS interacts directly with caveolin-1 residues 82–101 (30, 34, 36–38). In support of these data, recombinant co-expressors correspond to caveolae membranes as visualized by immunoelectron microscopy (9). Thus, caveolin-2 may function as an “accessory protein” in conjunction with caveolin-1.

Caveolin-interacting Proteins

A number of studies support the hypothesis that caveolin proteins provide a direct means for resident caveolae proteins to be sequestered within caveolae microdomains. These caveolin-interacting proteins include G-protein α subunits, Ha-Ras, Src family tyrosine kinases, endothelial NO synthase, 1 EGF-R and related receptor tyrosine kinases, and protein kinase C isoforms (11, 15, 18, 20–32).

Heterotrimeric G-proteins—G-proteins are dramatically enriched within caveolae membranes, where caveolin-1 directly interacts with the α subunits of G-proteins (18). Mutational or pharmacological activation of Gα prevents its co-fractionation with caveolin-1 and blocks its direct interaction with caveolin-1 in vitro, indicating that the inactive GDP-bound form of Gα preferentially interacts with caveolin-1. G-protein binding activity is located within a 41-amino acid region of the cytoplasmic N-terminal domain of caveolin-1 (residues 61–101). A polypeptide derived from this region of caveolin-1 (residues 82–101) effectively suppresses the basal GTPase activity of purified G-proteins by inhibiting GDP/GTP exchange. In contrast, the analogous region of caveolin-2 possesses GTPase-activating protein activity with regard to heterotrimeric G-proteins (3). However, both of these activities (GDI and GAP) actively hold or place G-proteins in the inactive GDP-ligated conformation (3).

Ha-Ras—Ha-Ras and Srf family tyrosine kinases also directly interact with caveolin-1 (20, 23). Using a detergent-free procedure and a polychystidine-tagged form of caveolin-1 for affinity purification of caveolin-rich membranes, G-proteins, Srf family kinases, and Ha-Ras were all found to co-fractionate and co-elute with caveolin-1. Wild-type Ha-Ras also interacted with recombinant caveolin-1 in vitro. Ras binding activity was localized to a 41-amino acid membrane-proximal domain (61–101) of the cytosolic N-terminal domain of caveolin-1, i.e. the same caveolin-1 region responsible for interacting with G-protein α subunits. Reconstituted caveolin-rich membranes interacted with a soluble recombinant form of wild-type Ha-Ras but failed to interact with mutationally activated soluble Ha-Ras (G12V) (23). Thus, a single amino acid change (G12V) that constitutively activates Ras prevents this interaction. Recombinant overexpression of caveolin in intact cells was sufficient to functionally recruit a non-farnesylated mutant of Ras (C186S) onto membranes (23). This is consistent with the hypothesis that direct interaction with caveolin-1 promotes the sequestration of inactive Ha-Ras within caveolae microdomains. Srf Family Tyrosine Kinases—Caveolin-1 interacts with wild-type Srf (c-Src) but does not form a stable complex with mutationally activated Srf (v-Src) (20). Thus, caveolin prefers the inactive conformation of Ga subunits, Ha-Ras, and c-Src. Deletion mutagenesis indicates that the Srf-interacting domain of caveolin is located within residues 61–101. A caveolin peptide derived from this region (residues 82–101) functionally suppressed the autoactivation of purified recombinant c-Src tyrosine kinase and a related Srf family kinase, Fyn. Co-expression of caveolin-1 with c-Src shows that caveolin-1 dramatically suppresses the tyrosine kinase activity of c-Src. Thus, it appears that caveolin-1 functionally interacts with wild-type c-Src via caveolin residues 82–101.

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The abbreviations used are: NOS, nitric oxide synthase; EGF-R, epidermal growth factor receptor; eNOS, endothelial NOS; PKC, protein kinase C; MAP, mitogen-activated protein; PDGF, platelet-derived growth factor; PtdIns, phosphatidylinositol; PKF-M, phosphohexokinase-M; GPI, glycosylphosphatidylinositol; Gα1, II7′NouAcG5OsCer.
The Caveolin Scaffolding Domain

What is the mechanism by which the caveolin scaffolding domain recognizes this diverse group of signal transducers? Perhaps the caveolin scaffolding domain recognizes a common sequence motif within caveolin-binding signaling molecules. To investigate this possibility, we have used the caveolin scaffolding domain as a receptor to select caveolin-binding peptide ligands from random peptide sequences displayed at the surface of bacteriophage. Two related caveolin-binding motifs (φXφXXXφ and φXXXφXXXφ, where φ is aromatic amino acid Trp, Phe, or Tyr) were elucidated, and these motifs exist within most caveolae-associated proteins (31). Thus, caveolin-binding motifs mediate the interaction of caveolin-binding proteins with the scaffolding domain of caveolin. These caveolin-binding motifs are present within most G-protein α-subunits and the kinase domains of many distinct families of tyrosine and serine/threonine protein kinases (Src family kinases; PKCα; MAP kinase; EGF-R; insulin receptor; and PDGF receptor).

As many known caveolae or caveolin-associated proteins contain caveolin-binding motifs (see Table II in Ref. 31), this may be a general mechanism for caveolin-mediated sequestration and inactivation of a diverse group of signaling molecules within caveolae membranes for regulated activation by receptor ligands. Thus, the caveolin scaffolding domain may function like other modular protein domains. Expression of constitutively active Ha-Ras (Gly-12 → Val) does not affect the activity of Ha-Ras; and (iv) it is membrane-proximal, suggesting that this caveolin domain may be involved in other potential protein-protein interactions. As a consequence, this caveolin-derived protein domain has been termed the caveolin scaffolding domain (Fig. 1).

Caveolin-1 is Down-regulated in Transformed Cells

Direct interaction of caveolin with signaling molecules leads to their inactivation (18). Since many signaling molecules can cause cellular transformation when constitutively activated, it is reasonable to speculate that caveolin may possess transformation suppressor activity. Consistent with this hypothesis, both caveolae and caveolin are most abundantly expressed in terminally differentiated cells: adipocytes, endothelial cells, and muscle cells. In addition, caveolin-1 mRNA and protein expression are lost or reduced during cell transformation by activated oncogenes such as v-abl and Ha-ras (G12V); caveolae are absent from these cell lines (42).

The potential "transformation suppressor" activity of caveolin-1 has recently been evaluated by using inducible expression in onco-genically transformed cells. Induction of caveolin-1 expression in v-abl- and Ha-ras (G12V)-transformed NIH 3T3 cells abrogated the anchorage-independent growth of these cells in soft agar and resulted in the de novo formation of caveolae (43). Thus, down-regulation of caveolin-1 expression and caveolae organelles may be critical to maintaining the transformed phenotype. These findings may also have relevance to human cancers. Sager and co-workers (44) identified caveolin-1 as one of 26 gene products whose mRNAs were down-regulated in human mammary carcinoma cell lines.

G-protein-coupled Receptors in Caveolae

Several G-protein-coupled receptors, i.e. endothelin, bradykinin, muscarinic acetylcholine, and β-adrenergic receptors...have been localized to caveolae using a combination of morphological and biochemical techniques (45–49). Caveolar localization may be ligand-dependent or -independent depending on the receptor (Fig. 2). Binding of bradykinin to B2 bradykinin receptors on smooth muscle cells promotes the sequestration of the occupied receptors within caveolae (47). Receptor antagonists did not affect the distribution of these molecules, suggesting that only the activated receptor undergoes translocation to caveolae. Similarly, in cardiac myocytes, the muscarinic cholinergic agonist carbachol promotes the translocation of the muscarinic acetylcholine receptor into caveolin-rich membrane domains that contain caveolin-3 (46). Translocation of this receptor subtype was responsible for the dioligand binding detected in the caveolin-rich fractions. Atrpine, a muscarinic cholinergic antagonist, did not induce translocation of the m2 muscarinic acetylcholine receptor to caveolae. Thus, agonist-induced translocation of G-protein-coupled receptors to caveolae membranes may be an essential step in the initiation of signaling cascades, as many downstream transducers of G-protein-coupled receptors have been localized to caveolae membranes.

Receptor Tyrosine Kinases in Caveolae

EGF initiates activation of the Ras-MAP kinase cascade. Using Rat-1 cells Mineo et al. (27) observed that EGF-R and Ras are greatly enriched within caveolae membranes. Thirty seconds after adding EGF, Raf-1 appears in caveolae but not in other membrane domains. Expression of constitutively active Ha-Ras (Gly-12 → Val, 5420 Minireview: Caveolins, Signaling, and Cell Transformation
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Caveolar Components Undergo Lipid Modification

Caveolin co-purifies with lipid-modified signaling molecules, including Gα subunits, Ha-Ras, eNOS, and Src family tyrosine kinases (23). As many acylated and prenylated proteins are known to be targeted to caveolae, it has been suggested that lipid modification is required or greatly facilitates this targeting event. In support of this notion, myristoylation (GZα) and palmitoylation (CSα) mutants of Gαi2 were poorly targeted to caveolin-enriched membrane fractions (51). Similarly, a myristoylation minus mutant of c-Src was quantitatively excluded from caveolae. The caveolar targeting of Gαi2 was dramatically augmented approximately 4-fold by palmitoylation. Therefore, it is likely that both myristoylation and palmitoylation are important for their correct caveolar localization. The caveolar targeting of Hck and Fyn tyrosine kinases as well as eNOS also supports this hypothesis (21, 25, 30, 35, 36, 38, 52). The C-terminal domain of caveolin-1 also undergoes palmitoylation on three residues, 133, 143, and 156 (53).

Lipid Mediators of Apoptosis within Caveolae

Cholesterol and sphingolipids are two major lipid components of caveolae membranes, and both of these lipid classes have been found to interact directly with caveolin-1 (10–12, 54). Sphingolipids serve as substrates to generate ceramide, a newly characterized intracellular second messenger (55). Caveolin-1 has been shown to interact directly with caveolae or are only associated with caveolae upon cross-linking with antibody probes. In the case of the tissue factor receptor system, this GPI-anchored protein is only associated with caveolae upon binding its natural ligand (66). Thus, antibody probes may mimic natural endogenous ligands and target clustered GPI-anchored proteins to caveolae. Similarly, clustering of a glycosphingolipid (GαM1) with a ligand (the GαM1 binding B-subunit of cholera toxin) increases its association with caveolin-1 by 5-fold (12). Several G-protein-coupled receptors are targeted to caveolae in response to different agonists and antagonists (46, 47, 67). Taken together, these results suggest that clustering or receptor activation by ligand binding is sufficient to promote regulated translocation into caveolae membranes.

Caveolae Purification and Caveolae-related Domains

Caveolae Purification—Several independent methods have been developed for purifying caveolae (15, 16, 22–24, 29). Initially, these methods took advantage of the natural detergent insolubility of caveolae membranes. More recently, detergent-free methods have become available that are dependent on the intrinsic light buoyant density (22, 23). Purification by all of these methods reveals the dramatic enrichment of caveolins and signaling molecules relative to plasma membrane. Caveolar localization of these signaling molecules has been confirmed in many cases by Schnitzer and colleagues (24, 50, 63). Also, these molecules appear to form a tight complex with caveolin-1, as shown using a polyhistidine-tagged form of caveolin-1 to affinity purify caveolae membranes from cultured cells (23).

Caveolae have also been shown to be detergent-resistant structures in vivo. For example, when intact cells were fixed with paraformaldehyde, extracted with cold Triton X-100, and then examined by electron microscopy, the insoluble membranes that remained were found to be caveolae (64). In support of these morphological findings, caveolin proteins are Triton-insoluble in caveolae (15, 16) but Triton-soluble in the Golgi (65). This compartment-specific Triton insolubility is most likely due to the association of caveolin with cholesterol and sphingolipids, which form a Triton-insoluble microenvironment, termed a liquid-ordered phase.

It has been debated whether GPI-anchored proteins are constitutively associated with caveolae or are only associated with caveolae upon cross-linking with antibody probes. In the case of the tissue factor receptor system, this GPI-anchored protein is only associated with caveolae upon binding its natural ligand (66). Thus, antibody probes may mimic natural endogenous ligands and target clustered GPI-anchored proteins to caveolae. Similarly, clustering of a glycosphingolipid (GαM1) with a ligand (the GαM1 binding B-subunit of cholera toxin) increases its association with caveolin-1 by 5-fold (12). Several G-protein-coupled receptors are targeted to caveolae in response to different agonists and antagonists (46, 47, 67). Taken together, these results suggest that clustering or receptor activation by ligand binding is sufficient to promote regulated translocation into caveolae membranes.

Caveolae-related Domains or Precaveolae or Both?—A number of investigators have purified “caveolae” from cells and tissues that lack apparent expression of caveolin (69–72). These domains have been termed Triton-insoluble complexes, detergent-resistant membranes, and low density membranes. We now suggest the term caveolae-related domains be used to describe these structures. Like caveolae, these microdomains are dramatically enriched in cholesterol.
terol, sphingolipids, and lipid-modified signaling molecules (69, 70). The existence of “caveole-related domains” that fail to contain caveolin has caused considerable confusion (69). However, this was at a time when only one caveolin gene was known to exist, i.e. caveolin (now termed caveolin-1). In addition, it has been shown that caveolin-1 and caveole are down-regulated in response to cell transformation, whereas caveolin-2 levels remain constant (9). As a consequence, many commonly used cell lines lack caveolin-1 protein expression and visible caveolae, as they are immunortalized or transformed. Also, other detergent-insoluble membrane proteins have recently been cloned, and one or more of them may represent functional homologues of the caveolins (63, 68, 69).

Caveolae-related domains can also be produced in vitro simply by mixing cholesterol, sphingolipids, and phospholipids in the appropriate ratio (70). Their Triton insolubility is a physical property of their molecular organization that produces a liquid-ordered membrane domain (rather than fluid or liquid crystalline). As caveolin-1 is found associated with glycosphingolipids in vivo (12), binds cholesterol directly (10), and requires a high local concentration of cholesterol (>30%) to insert into model lipid membranes (10, 11), these findings suggest that a true functional relationship exists between caveole-related domains and mature caveole. For example, during the biogenesis of mature caveole, caveole-related domains would need to exist as precursors for proper insertion of caveolins into membranes. Thus, in cells that express caveolins, these caveole-related domains may represent “precaveole” that simply lack caveolins. In support of this reductionist model, recombinant expression of caveolin-1 in cells that lack morphological detectable caveole is sufficient to drive the formation of mature invaginated caveole (19, 33, 43). This indicates that cells normally make the ingredients that are necessary for the formation of mature caveole, and insertion of caveolin proteins may be only a late phase in this process. Insertion of caveolins into these caveole-related domains may provide a necessary “brake” in signal transduction (43).

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