Anchoring Proteins as Regulators of Signaling Pathways

Alessia Perino, Alessandra Ghigo, John D. Scott, Emilio Hirsch

Abstract: Spatial and temporal organization of signal transduction is coordinated through the segregation of signaling enzymes in selected cellular compartments. This highly evolved regulatory mechanism ensures the activation of selected enzymes only in the vicinity of their target proteins. In this context, cAMP-responsive triggering of protein kinase A is modulated by a family of scaffold proteins referred to as A-kinase anchoring proteins. A-kinase anchoring proteins form the core of multiprotein complexes and enable simultaneous but segregated cAMP signaling events to occur in defined cellular compartments. In this review we will focus on the description of A-kinase anchoring protein function in the regulation of cardiac physiopathology. (Circ Res. 2012; 111:482-492.)

Key Words: AKAP ■ PKA ■ cAMP ■ cardiac disease

Spatial and temporal control of signal transduction events is frequently achieved by compartmentalization of intracellular effectors through adaptors or anchoring proteins. In particular, elements of the cAMP signaling cascade are localized in the cell via scaffold proteins referred to as A-kinase anchoring proteins (AKAPs). cAMP is a second messenger involved in the regulation of different cellular events that occur in response to extracellular stimuli. Binding of an extracellular stimulus to a selective G-protein coupled receptor (GPCR) triggers the activation of a heterotrimeric Gs protein and its effector, the adenylyl cyclase (AC), which generates the second messenger cAMP. In turn, cAMP exerts its effects through the activation of 3 effectors: protein kinase A (PKA), the exchange protein directly activated by cAMP and the cyclic nucleotide-gated ion channels. The primary effector of cAMP in the heart is PKA, a tetramer formed by 2 catalytic subunits that are inactivated by the binding of the 2 regulatory subunits. Binding of cAMP to the regulatory subunits induces the dissociation and the activation of the catalytic subunits, resulting in the phosphorylation of local substrates.

Several studies have demonstrated that cAMP is not uniformly distributed throughout the cell. Indeed, numerous imaging studies have shown that cAMP levels rise selectively in a specific cellular compartment in a stimulus-specific manner and do not diffuse from one compartment to the other, allowing fidelity of the response. Spatially restricted activation of PKA is guaranteed by the binding of this kinase with AKAPs, a family of functionally related proteins that interact with the regulatory subunits of the PKA holoenzyme. The molecular feature of AKAPs is to possess a structurally conserved PKA anchoring domain, consisting of an amphipatic helix of 14 to 18 residues that selectively binds the dimerization and docking domain at the N-terminus of the PKA regulatory subunit dimer. Although the vast majority of AKAPs bind the type II regulatory subunit of PKA, several AKAPs are referred to as dual-function anchoring proteins because they bind both the type I (RI) and the type II (RII) regulatory subunits of PKA. More recently, type I PKA specific anchoring proteins have been described. Several evidences have demonstrated that PKA-RI and PKA-RII isoforms are indeed anchored to specific subcellular sites via binding to these different AKAPs.

AKAPs do not only position PKA inside the cell but they also ensure that this kinase is coupled to its upstream activators, including membrane receptors and ACs, and to signal termination enzymes, such as phosphodiesterases (PDE) and phosphatases. In this way, AKAPs help to establish intracellular cAMP gradients, generated via activation of a specific GPCR and uniquely modulated by different subsets of PDEs, resulting in stimulus-specific activation and action of PKA. AKAPs also coordinate signaling enzymes such as other kinases, GTPases, and regulatory proteins into multivalent transduction signalosomes. Thus, AKAPs provide the structural integrity for multiprotein complexes that often represent hubs for processing of multiple signals. A further layer of specificity proceeds through protein- or lipid-targeting domains on AKAPs that direct AKAP signaling complexes to intracellular membranes. A concerted research effort over the past 20 years has identified more than 50 genes encoding distinct anchoring proteins. Furthermore, numerous splice variants are transcribed from each gene in a cell type and tissue-specific manner.
To narrow the focus of this article, we will restrict our discussion to the actions of compartmentalized cAMP signaling and AKAP function in the cardiovascular system. In the heart, several AKAPs play a critical role in modulating multiple signaling pathways at the basis of cardiac physiopathology (Table).20 This review will especially focus on the importance of anchored-PKA in the regulation of cardiac cAMP compartmentation.

## Cardiac AKAPs

### Cardiac Development

The heart is the first organ to form during embryogenesis and all subsequent events in the life of the organism are dependent on its function. Cardiac organogenesis is characterized by the precise temporal and region-specific regulation of cell proliferation, migration, death, and differentiation.21,22 All these processes are finely tuned by a variety of signal transduction pathways. Among these, anchored cAMP signaling is essential for cardiomyocyte differentiation and heart morphogenesis. AKAP-Lbc (also referred to as AKAP13 or BRX) is a key regulator of these events and the deletion of this AKAP in the mouse results in a thin and enlarged myocardium that leads to an arrest in cardiac development and subsequent embryonic lethality.23 This failure in cardiac development is consistent with decreased activity of the small GTPase Rho, a direct target of AKAP-Lbc.24 Reduced Rho function in turn correlates with a repressed activity of the myocyte enhancer factor-2, a transcription factor important for the proper regulation of cardiac gene expression.25

AKAP-Lbc is thus a platform that links Rho signaling to an essential transcription program that drives cardiomyocyte development.26

### Contractility

In the adult heart, cardiac contractility and relaxation are mediated by rapid changes in cytoplasmic Ca$^{2+}$ concentration.

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<th>Table. AKAPs in the Heart</th>
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<td><strong>Gene Name</strong></td>
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**Non-standard Abbreviations and Acronyms**

- β-AR: β-adrenergic receptor
- AC: adenyl cyclase
- AKAP: A-kinase anchoring protein
- cAMP: cyclic AMP
- GPCR: G protein-coupled receptor
- GRK-2: G protein-coupled receptor kinase 2
- HIF-1α: hypoxia-inducible factor 1α
- LTCC: voltage-gated L-type Ca$^{2+}$ channel
- NFAT: nuclear factor of activated T cells
- PDE: phosphodiesterase
- PKA: protein kinase A
- PLN: phospholamban
- ROS: reactive oxygen species
- RyR: ryanodine receptor
- SERCA: sarcoplasmic reticular Ca$^{2+}$-adenosine triphosphatase
- SR: sarcoplasmic reticulum

*AKAP indicates A-kinase anchoring protein; PKA RI, type I regulatory subunit of protein kinase A; PKA RII, type II regulatory subunit of protein kinase A; PDE, phosphodiesterases; LTCC, L-type Ca$^{2+}$ channels; β-AR, β-adrenergic receptor; AC, adenyl cyclase; CAV3, caveolin 3; RyR2, ryanodine receptor 2; NFAT, nuclear factor of activated T cells; Epac, exchange protein directly activated by cAMP; HIF-1α, hypoxia-inducible factor-1α; WHL, von Hippel-Lindau; Siah2, Seven in Absentia Homolog 2; PNN, protein kinase N; PTD1, protein tyrosine phosphatase D1; AMY-1, associate of Myc-1; RSK, ribosomal S6 kinase; SAP97, Synapse-associated protein 97; NCX1, sodium-calcium exchanger-1; PLB, phospholamban; KSR1, kinase suppressor of Ras1.*
following the electric stimulation of the myocardium. During the excitation-contraction coupling, brief openings of sarcoplasmic voltage-gated L-type Ca\(^{2+}\) channels (LTCCs) in response to an action potential generate local elevations in intracellular Ca\(^{2+}\). This highly localized Ca\(^{2+}\) rise in turn activates closely apposed ryanodine receptors (RyRs) in the sarcoplasmic reticulum (SR), via a mechanism referred to as Ca\(^{2+}\)-induced Ca\(^{2+}\) release. This results in a substantial release of Ca\(^{2+}\) form the SR, thereby inducing a global rise in Ca\(^{2+}\) concentration that activates cardiac contractile proteins. LTCCs and RyRs are rapidly inactivated by Ca\(^{2+}\)-dependent mechanisms and allow the cardiac sarcoplasmic reticulum Ca\(^{2+}\)-adenosine triphosphatase (SERCA2) pump to recover the released Ca\(^{2+}\) in the SR before the next heart beat. Tight regulation of Ca\(^{2+}\) handling is thus required for proper force and rate of contraction of the heart. The sympathetic nervous system (SNS) is one of the major regulators of heart rate in response to exercise or emotional stress. SNS controls cardiac electric activity through the activation of \(\beta\)-adrenergic receptors (\(\beta\)-ARs) that modulate the function of selected ion channels via phosphorylation by PKA. These Ca\(^{2+}\)-related signaling events are regulated by different combinations of AKAPs that finely modulate the PKA-dependent signaling (Figure 1). Displacement of PKA from AKAPs by PKA anchoring dis-
channel, resulting from a shift in gating mode. Regulation of LTCCs requires PKA targeting to the distal C terminus (DCT) of the channel. Truncation of Cav1.2 DCT abolishes the regulation of LTCCs by the β-AR/PKA pathway, consistently with the finding of PKA phosphorylation sites at the distal C terminus of Cav1.2. Several lines of evidence have emphasized the importance of AKAPs in targeting PKA in the vicinity of LTCCs. In skeletal muscle and in cardiomyocytes, a low molecular weight AKAP, AKAP15/18 (also known as AKAP18α or AKAP7) has been identified as the anchoring protein that targets PKA to Cav1.2. In higher detail, AKAP15/18 targets PKA to the C terminus of Cav1.2 through a modified leucine zipper motif located in its C-terminal region. Disruption of this interaction inhibits PKA-dependent enhancement of LTCC activity, both in skeletal muscle cells and in rat ventricular cardiomyocytes. The C terminus of Cav1.2 undergoes proteolytic processing in vivo, giving rise to two isoforms that differ by truncation of the C terminus. The proteolytically cleaved DCT acts as a regulatory domain of LTCC normal function, by binding to the truncated channel and inhibiting its function. Accordingly, mice expressing only truncated Cav1.2 develop severe cardiac hypertrophy and die perinatally. Deletion of the DCT disrupts the expression and localization of the AKAP15/18-PKA complex, resulting in an impaired regulation of LTCC function.

Ca\(^{2+}\) signaling is regulated not only by AKAP15/18-PKA-Cav1.2 complex at the cell surface but also at the level of the sarcoplasmic reticulum. In this respect, two different AKAPs are involved: mAKAP and AKAP188.

**mAKAP-RyR Complex**

The muscle specific AKAP (mAKAP) is prominently expressed in cardiomyocytes and it is localized both at the sarcoplasmic reticulum, where it regulates Ca\(^{2+}\)-induced Ca\(^{2+}\) release, and at the nuclear envelope, where it assembles a macromolecular complex integrating cAMP and Ca\(^{2+}\) signals. Accordingly, it has been shown that a mAKAP-PKA–RyR complex is strategically located within the cell to modulate both SR-dependent cytoplasmic Ca\(^{2+}\) rise and the perinuclear Ca\(^{2+}\) fluxes. mAKAP functions as a scaffold for a wide range of proteins including type II PKA, AC5, protein phosphatase 2A, the MAP kinases MEK5 and ERK5, the small GTPase Rap1, and the cAMP-activated Rap1 exchange factor Epac1. Within this macromolecular complex, mAKAP-mediated PKA phosphorylation of the RyR is considered to promote opening of this channel and to increase cardiac function. Within this context, cAMP may increase Ca\(^{2+}\) fluxes via PKA-dependent phosphorylation of the RyR, in a manner tightly controlled by the PKA-activated PDE4D3 and protein phosphatase 2A-mediated dephosphorylation. Alternatively, recent studies report that PKA/PDE4D3-mediated control of RyR phosphorylation is irrelevant to normal cardiac function and sympathetic stimulation of the heart.

**AKAP188-SERCA2 Complex**

SERCA2 controls Ca\(^{2+}\) reuptake into the sarcoplasmic reticulum, a rate-limiting step for cardiac relaxation. SERCA2 activity is regulated by numerous factors, including the cytoplasmic/SR Ca\(^{2+}\) gradient, the protein concentration of SERCA2, and the SR inhibitory protein phospholamban (PLN). Diphosphorylated PLN binds to SERCA2 and suppresses its activity, whereas phosphorylation of PLN on Ser16 by PKA dissociates PLN from SERCA2, increasing the Ca\(^{2+}\) reuptake into the SR. This PKA-mediated phosphorylation of PLN is strictly dependent on the function of AKAP188, a long splice variant of the AKAP18 gene. Both the displacement of AKAP188 from PLN or the silencing of AKAP188 significantly reduce the PKA-dependent PLN phosphorylation after β-adrenergic stimulation, resulting in a decrease in Ca\(^{2+}\) reuptake into the sarcoplasmic reticulum. Alterations in the function of PLN-SERCA2 complex are linked to cardiac dysfunction. Because AKAP188 mediates PLN phosphorylation and subsequent increase in SERCA2 activity, modulation of AKAP188 could represent a novel pharmacological target in the treatment of heart failure.

**Sarcomeric AKAPs**

Several actin-associated (ezrin, gravin, WAVE-1, and AKAP79/150) and microtubule-associated (MAP2, AKAP350/450, hAKAP220, pericentrin, flagellar radial spoke protein 3) AKAPs have been described in different tissues. In the heart, multiple evidences have demonstrated the crucial role of AKAPs in targeting PKA at the sarcomere. In particular, 3 different AKAPs are involved in mediating PKA-dependent phosphorylation of sarcomeric proteins, crucial regulators of myocardial contractile function.

Synein is the first intermediate filament protein shown to bind PKA RI and to localize a pool of PKA, allowing local substrate phosphorylation within the myocyte cytoskeleton. Intermediate filament-targeted PKA could phosphorylate substrates found at the Z-line or regulate intermediate filament structure. Synein is overexpressed in failing hearts: this correlates with an increase in PKA targeting to sites undergoing molecular remodeling.

Cardiac troponin T has been recently characterized as a novel dual-specificity AKAP able to dock PKA at the thin filaments in proximity of its main sarcomeric substrates. Within the myocardial contraction machinery, PKA phosphorylates cardiac myosin binding protein C and this event results in enhanced cardiac contractility due to the rearrangement of the myosin crossbridges and thick filament structure. This configuration ensures that PKA is tethered near its substrate thanks to the recently characterized dual AKAP myomagelin (MMGL). Myomagelin is a PDE4D-interacting protein involved in assembling a cAMP/PKA/PDE signaling module at the sarcomere. The translocation of myomagelin to the sarcomere is therefore compatible with a mechanism that would lead to increased β-adrenergic-stimulated phosphorylation of cardiac myosin binding protein C and cTnI, thus enhancing cardiac contraction as well as cardioprotection.

**Cardiac Rhythm and Arrhythmias**

Cardiac contractility and rhythm respond rapidly to physical activity and emotional stress to meet the changes in the metabolic needs of the organism. The sympathetic nervous system is the main player of this response and acts by enhancing the current amplitude of the slowly activating delayed rectifier \(I_{Ks}\), potassium channel (also referred to as...
HERG).\(^8\) \(I_{\text{Ks}}\) channel is composed by the pore-forming α-subunit KCNQ1 that conducts the ionic current and the auxiliary β-subunit KCNE1 that controls the biophysical properties of the channel.\(^9,10\) \(I_{\text{Ks}}\) channels are regulated by the sympathetic nervous system via the β-AR/cAMP/PKA pathway. High cAMP levels cause an increase in the \(I_{\text{Ks}}\) amplitude and a slowdown in the current decay during deactivation.\(^8\) This cAMP-mediated regulation of the channel is controlled by the scaffold protein Yotiao (also referred to as AKAP9), which recruits PKA and the protein phosphatase 1 to the C-terminal domain of the KCNQ1 subunit.\(^1,12\) PKA-dependent functional regulation of \(I_{\text{Ks}}\) channels is lost when the binding site for Yotiao on the KCNQ1 subunit is mutated (KCNQ1-G589D).\(^1,13\) Mutations in both subunits of the \(I_{\text{Ks}}\) channel are associated with at least 2 heritable arrhythmic syndromes, referred to as catecholaminergic polymorphic ventricular tachycardia\(^14\) and long-QT syndrome.\(^15\)

Variants of long-QT syndrome have been shown to be caused by mutations in both the \(I_{\text{Ks}}\) channel α (KCNQ1, LQT1) and β (KCN1, LQT5) subunits.\(^16,17\) Recently, a cohort of patients with genotype-negative long-QT syndrome have been described to carry a missense mutation in Yotiao (S1570L). The S1570L mutation is in the binding domain of Yotiao for KCNQ1. Disruption of the Yotiao/KCNQ1 interaction reduces the PKA-mediated phosphorylation on KCNQ1 amino terminus (Ser27) and eliminates the functional response of \(I_{\text{Ks}}\) channel to cAMP.\(^18\) The interaction between Yotiao and KCNQ1 is thus essentially required for the maintenance of a normal heart rhythm.

Recent evidences suggest that AKAP79/150 is also involved in heart rhythm regulation. In physiological conditions, AKAP79/150 coordinates the binding of PKA and PKCα to Cα,1.2 and facilitates the coordinated opening and closing of the channel.\(^9,10\) A gain of function mutation (G406R) in a cytoplasmic loop of Cα,1.2 correlates with an abnormal coupling with AKAP79/150, eventually leading to LQT8, a disease also known as Timothy syndrome.\(^10\) This occurs through a mechanism whereby AKAP79/150 functions like a subunit of Cα,1.2 that stabilizes the open conformation of the channel. Ablation of this anchoring protein restores normal gating of Cα,1.2 and protects the heart from arrhythmias.\(^10\)

Besides Yotiao and AKAP79/150, heart rhythm modulation involves D-AKAP2 (also referred to as AKAP10). D-AKAP2 controls the sensitivity of pacemaker cells to cholinergic stimulation, both in mouse embryonic stem cell-derived cardiomyocytes and in vivo, in mouse hearts. Accordingly, D-AKAP2–deficient mice display heart rhythm abnormalities, eventually leading to premature death from arrhythmia.\(^10\) Interestingly, a human polymorphism (I646V) affecting the affinity of D-AKAP2 for the regulatory subunit RI of PKA has been described. This variant correlates with increased basal heart rate and decreased heart rate variability, 2 events that are indicative of high risk of sudden cardiac death.\(^10\) Thus, heart rhythm regulation relies on the coordinated action of Yotiao, AKAP79/150, and D-AKAP2. Furthermore, a growing body of evidence indicates that arrhythmogenesis can also be linked to mitochondrial function.\(^10\)

### Oxidative Stress (Mitochondria, Hypoxia)

Mitochondria constitute a major generator of cellular energy and their activity is controlled by normal cellular homeostasis. A key aspect of mitochondrial function is the dynamic balance of fusion and fission, events that alter mitochondrial morphology and activity.\(^10,12\) Control of mitochondrial dynamics is evolutionary conserved and its deregulation is implicated in pathological conditions, including cardiovascular disorders such as dilated cardiomyopathy, myocardial infarction, and heart failure.\(^10,12,13\) The cAMP/PKA pathway has been recently found to regulate mitochondrial respiration, dynamics, and cellular apoptosis.\(^10\) Localization of PKA in proximity to mitochondrial substrates ensures efficient propagation of cAMP signals from the plasma membrane to this target organelle. cAMP signals are carried to mitochondria by a set of mitochondrial AKAPs that regulate mitochondrial function through the organization of signalosomes in this cellular compartment.\(^10\)

#### mAKAP

Reduced oxygen levels, referred to as hypoxia, affect mitochondrial function by increasing glycolysis and lactate production. At the molecular level, hypoxia stabilizes hypoxia-inducible factor 1α (HIF-1α), which controls transcription of a wide range of genes, including factors implicated in the regulation of mitochondrial energy metabolism.\(^10,11\) Under normoxic conditions, the levels of HIF-1α are kept low through its ubiquitin-mediated proteasomal degradation.\(^10\) This multiprotein signaling complex is compartmentalized inside the cell by mAKAP. mAKAP sequesters HIF-1α at the perinuclear membrane, thereby minimizing the translocation distance to its site of action in the nucleus. Furthermore, mAKAP assemblies and compartmentalizes components of the protein ubiquitin machinery that determine the bidirectional control of HIF-1α stability.\(^10\) During normoxia, mAKAP clusters HIF-1α with negative regulatory factors, like prolyl hydroxylase domains and Von Hippel Lindau, that enhance the efficiency of its degradation. Under hypoxic conditions, positive regulatory factors, including the ubiquitin E3 ligase seven in absentia, bind to mAKAP and favor the stabilization of HIF-1α. The expression of HIF-1α target genes protects the heart from oxygen-deprivation injury that occurs under pathological stresses, and, in this condition, mAKAP favors the enhancement of the hypoxic response. Displacement of mAKAP from perinuclear membranes of cardiomyocytes alters the stability of HIF-1α and the transcription of genes associated with hypoxia.

#### AKAP121

Under hypoxic conditions, HIF-1α availability is controlled by the ubiquitin E3 ligase seven in absentia homolog 2.\(^10,114\) Seven in absentia homolog 2 is normally bound to mitochondrial AKAP121 and the expression levels of this ubiquitin E3 ligase are induced during hypoxia, thereby causing a degradation of AKAP121 and an attenuation of the cAMP/PKA signaling at the mitochondria.\(^11,15\) In normal physiology, AKAP121 regulates mitochondrial morphology by serving as a docking site for PKA at the mitochondrial membrane. Within this compartment, PKA phosphorylates and inhibits the mechanoenzyme dynamin-related protein 1, resulting in an inhibition of mitochondrial fission. Deregulation of
AKAP121, that occurs on increased seven in absentia homolog 2 expression in ischemia-induced cardiomyocyte cell death, alleviates dynamin-related protein 1 inhibition, resulting in mitochondria fission.116

AKAP-dependent activation of the cAMP-PKA signaling at the mitochondria also controls oxidative stress, mainly caused by reactive oxygen species (ROS) production. These cAMP-mediated effects are mainly associated with PKA-dependent phosphorylation of complex I subunits117 that results in an enhanced functional capacity of the mitochondrial respiratory chain and in a reduced ROS production.118 In cardiac physiology, AKAP121 tethers PKA at the mitochondria and is thus involved in the control of ROS production, thereby protecting the cardiomyocyte from oxidative stress. Deregulated ROS production within the cardiomyocyte may contribute to the development of cardiac dysfunction. Indeed, displacement of AKAP121 from mitochondria by competitive peptides increases ROS levels and promotes cardiomyocyte death. Furthermore, in response to pressure-overload, AKAP121 protein expression is downregulated, thus resulting in mitochondrial stress, increased ROS production and cell death.119 All these evidences suggest that deregulated mitochondrial cAMP signaling could contribute to the development of cardiac dysfunction.

Hypertrophy
Cardiac hypertrophy is an adaptive remodeling process of the myocardium that occurs in response to various cardiac stresses. It is associated with an increase in cardiomyocyte size, a qualitative and quantitative change in the expression levels of contractile proteins and an activation of fetal cardiac genes.120,121 Because hypertrophy can ultimately progress to ventricular dilation, contractile dysfunction, and heart failure, significant efforts have been made to investigate the molecular players at the basis of this pathological process. Cardiomyocyte hypertrophy is controlled by membrane receptors that trigger multiple networks of intracellular mediators, which in turn transmit the hypertrophic signal to the nucleus.122 An emerging concept in the field of signal transduction is the existence of hubs where multiple signaling pathways converge and share common molecules, thereby facilitating crosstalk between pathways. In this respect, mAKAP, AKAP-Lbc, and AKAP79/150 are attractive candidates that could coordinate hypertrophic signals elicited from multiple stress stimuli (Figure 2).

mAKAP
In addition to its role in regulating cardiac contractility and oxidative stress, mAKAP is also implicated in cardiac hypertrophy. Within this scenario, mAKAP assembles a perinuclear macromolecular complex that regulates gene transcription in response to multiple hypertrophic stimuli. This mAKAP complex includes at least 3 enzymes that are involved in the hypertrophic responses: the mitogen activated kinase ERK5,70 the Ca\(^{2+}\)/calmodulin-dependent protein phosphatase calcineurin A\(\beta\)223 and the epsilon isoform of PLC.124 cAMP-dependent-triggering of the MAP kinase signaling activates the prohypertrophic transcription factor myocyte enhancer factor-2c and its regulated genes.70 On the other hand, Ca\(^{2+}\)-induced activation of the mAKAP-associated calcineurin A\(\beta\) results in a dephosphorylation and in a nuclear translocation of the transcription factor nuclear factor of activated T cells (NFATc) that promotes the transcription of hypertrophic genes.125,126 The control of hypertrophic gene expression by the epsilon isoform of PLC implicates both the myocyte enhancer factor- and NFAT-dependent transcription.124 Whereas ERK-mediated hypertrophy is triggered by cytokine receptors70 and calcineurin A\(\beta\) is activated through the \(\beta\)-AR/cAMP/PKA/RyR2 mediated Ca\(^{2+}\) release,123 the epsilon isoform of PLC integrates multiple upstream signaling pathways that regulate hypertrophy, including endothelin-, norepinephrine-, insulin-like growth factor-1- and isoproterenol-activated signaling.124 The crucial role of mAKAP in the hypertrophic process has been further demonstrated by the reduction of cardiac hypertrophy on the peptide-mediated displacement of mAKAP from the nuclear envelope.70,124

AKAP-Lbc
Several lines of evidence indicate that \(\alpha\)-adrenergic transmission, through the activation of heterotrimeric \(G\) proteins \(Gq\) and \(G12/13\), triggers the GTPase RhoA and its signaling cascade that controls the transcription of genes involved in cardiomyocyte hypertrophy.127 At the cellular level, the activation of small GTPases is controlled by guanine nucleotide exchange factors that facilitate GDP-GTP exchange and the activation of the enzyme. Recent works have identified AKAP-Lbc not only as an AKAP that scaffolds PKA, PKC, and PKD,128 but also as a guanine nucleotide exchange factor for the small GTPase RhoA.24 AKAP-Lbc is activated in response to agonists that stimulate the \(\alpha_1\)-AR-G12/13 signaling pathway129 and is inactivated via anchored PKA-mediated phosphorylation and subsequent recruitment of the regulatory protein 14-3-3, which prevents AKAP-Lbc from being able to activate Rho.130 Thus, suppression of the Rho-specific exchange factor AKAP-Lbc correlates with a negative modulation of the hypertrophic signaling in response to GPCR-Gq/G12/13 stimulation. Furthermore, prolonged \(\alpha\)-adrenergic
stimulation results in an upregulation of AKAP-Lbc protein levels, thereby directing the hypertrophic signal to the transcriptional machinery. In more detail, AKAP-Lbc facilitates the activation of PKD that inactivates the histone deacetylase HDAC5, thereby favoring myocyte enhancer factor-2–dependent transcription and the onset of cardiac hypertrophy. Therefore, AKAP-Lbc may provide a platform for crosstalk between PKD and Rho signaling pathways, in the context of cardiac hypertrophy.

**AKAP79/150**

Cardiac hypertrophy is also controlled by the calcium dependent Ser/Thr phosphatase calcineurin (CaN or PP2B) and the downstream transcriptional effectors, including NFAT. Indeed, hyperactivation of the CaN/NFAT pathway in cardiomyocytes of transgenic mice results in profound hypertrophy that rapidly progresses to heart failure. Several studies have demonstrated the positive effect of the inhibition of the CaN/NFAT signaling pathway in the treatment of cardiac hypertrophy. AKAP79/150 has a CaN-binding domain and is one of the endogenous inhibitors of CaN in the brain. Cardiac-restricted transgenic mice overexpressing the CaN inhibitory domain of AKAP79/150 display inhibited CaN activity that is associated with attenuated cardiac hypertrophy in response to catecholamine stimulation and pressure overload. These findings suggest a primary role for AKAP-mediated control of CaN in the hypertrophic response, even if the precise role of AKAP79/150 in this context still remains to be fully understood.

**Heart Failure**

Heart failure is a complex and multifactorial disease, characterized by the inability of the heart to pump sufficient blood to meet the metabolic needs of the body and represents a leading cause of mortality worldwide. Heart failure can result from aberrant signaling events that normally regulate myocardial function. In addition, altered gene expression is a peculiar feature of the failing heart. Gene expression profiles have pointed out a large scale of rearrangement in the AKAP-PKA signaling modules during end-stage heart failure. For instance, the expression of AKAP-Lbc, AKAP18δ, AKAP2, and SPHKAP was found upregulated, whereas AKAP121 levels were diminished in the failing human heart. An example of altered cAMP compartmentation in the failing human myocardium is given by increased protein levels of AKAP18δ. The enhanced association of PKA RIα with AKAP18δ may result in abnormal calcium reabsorption in the sarcoplasmic reticulum, ultimately leading to altered myocardial contractility.

Another distinctive feature of failing hearts is a chronic activation of the β-AR signaling pathway that initially compensates for contractile dysfunction but then progresses to deterioration of cardiac structure and function. At the molecular level, β-ARs are downregulated and desensitized through the action of a complex signaling module that includes PKA, G protein-coupled receptor kinase 2 (GRK2), and β-arrestin. Tight control of cellular cAMP levels is thus required for normal myocardial contractility. The catalytic subunit of phosphoinositide-3 kinase gamma (p110γ) is an AKAP that controls cAMP levels. p110γ tethers PKA in the vicinity of its negative modulator PDE3B, thereby constituting a feedback module that negatively controls cardiac contractility. Moreover, in physiological conditions, the β-AR pathway activates PKA, which in turn phosphorylates and inhibits the lipid kinase activity of the PKA-bound p110γ. In pressure overload-induced heart failure, p110γ is upregulated and escapes PKA-mediated inhibition. Activated p110γ reduces cell surface expression of β-ARs, thereby contributing to the development of heart failure. Genetic and pharmacological inhibition of p110γ activity renormalizes β-AR density and improves contractility in failing hearts, thus establishing p110γ as a potential target for the treatment of heart failure. Importantly, the spatial localization of β-ARs also plays a critical role in cardiac physiology and in the development of heart failure. Indeed, redistribution of β2-AR signaling from the T-tubules to the cell crest in failing cardiomyocytes results in uncoupling of the β2-AR from the localized pools of PKA that are responsible for the compartmentation of the β2-AR–cAMP signaling. This results in a cell-wide cAMP propagation on β2-AR activation in failing cells that is similar to the patterns observed for β1-ARs, thus contributing to the heart failure phenotype. These findings, together with a still required more complete analysis of the AKAP function in failing cardiomyocytes, will provide a deeper understanding of this cardiac disease and will facilitate the development of new therapeutic strategies.
Conclusion

Evidence accumulated in decades of studies on AKAP and their partners clearly indicate that alteration of such complexes represents a key contributing factor for cardiac diseases (Figure 3). Manipulation of protein–protein interaction at AKAPs is thus emerging as a promising therapeutic strategy. Proof of concept studies show that small molecules can in principle act to pharmacologically modulate AKAP-based signaling complexes. However, the limited number of such attempts has only scratched the surface of a vast potential of pharmacological intervention. Complexes at cardiac anchoring proteins can encompass 10, 20, or more components where each interaction is in principle amenable to pharmacological modulation. Our knowledge of the biological and chemical properties of these protein–protein complexes is only at its infancy. To better define targets of biological and chemical properties of these protein–protein complexes is only at its infancy. To better define targets of biochemical assays that simplify the search for disrupting biochemical activities that are pharmacologically modulate AKAP complexes in knock-in mice will likely provide conclusive proofs for AKAP regulatory subunits. Genetic modeling of the disruption of selected AKAP complexes will thus offer new tools for tackling this issue. Second, the role of such interactions in relevant disease conditions needs a detailed validation. Genetic modeling of the disruption of selected AKAP complexes in knock-in mice will likely provide conclusive proofs for the therapeutic value of such interventions. Third, new biochemical assays that simplify the search for disrupting moieties are required to select small molecules of pharmacological interest. Finally, it is tempting to speculate that the identification of small molecules that act on spatial and temporal restricted signaling will eventually prove to be more effective treatments for different aspects of heart failure, especially because our current therapeutic arsenal of drugs is still inadequate to combat this global health problem.

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Disclosures

None.

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