Calcium Signaling in Cardiomyocyte Function

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Rhythmic increases in intracellular Ca^{2+} concentration underlie the contractile function of the heart. These heart muscle-wide changes in intracellular Ca^{2+} are induced and coordinated by electrical depolarization of the cardiomyocyte sarcolemma by the action potential. Originating at the sinoatrial node, conduction of this electrical signal throughout the heart ensures synchronization of individual myocytes into an effective cardiac pump. Ca^{2+} signaling pathways also regulate gene expression and cardiomyocyte growth during development and in pathology. These fundamental roles of Ca^{2+} in the heart are illustrated by the prevalence of altered Ca^{2+} homeostasis in cardiovascular diseases. Indeed, heart failure (an inability of the heart to support hemodynamic needs), rhythmic disturbances, and inappropriate cardiac growth all share an involvement of altered Ca^{2+} handling. The prevalence of these pathologies, contributing to a third of all deaths in the developed world as well as to substantial morbidity makes understanding the mechanisms of Ca^{2+} handling and dysregulation in cardiomyocytes of great importance.

THE PHYSIOLOGY OF CALCIUM SIGNALING IN CARDIOMYOCYTES

The Heart and Circulation

The pump function of the heart is mediated by the synchronous contraction of its constituent muscle cells, the cardiomyocytes. Cardiomyocyte contraction is triggered by an electrical stimulus, the action potential (AP), which induces transient depolarization of the cardiomyocyte plasma membrane (the sarcolemma). The AP is generated by specialized cells known as pacemaker cells located at the sinoatrial node (SAN), which set the frequency of contraction of the heart. This electrical signal propagates through specialized conduction pathways and via myocyte-to-myocyte transfer through gap junctions, across the atria until it reaches the atrioventricular node (Rohr 2004). After a short delay to allow atrial systole, the impulse propagates through the ventricles via the bundle of His and Purkinje fibers to induce ventricular systole (Stephenson et al. 2012). Opening and closing of valves further defines the filling and ejection of blood from the chambers. Eventually, blood is propelled from the left ventricle into the aorta to the systemic circulation and from the right ventricle into the pulmonary artery to the lungs. The AP is a transient phenomenon and repolarization of the cardiomyocytes is associated with relaxation, again in a sequential manner for each chamber of the heart. This relaxation phase (diastole) is important for the filling of the chambers, and is an essential part

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of the cardiac cycle (Fukuta and Little 2008). This highly coordinated contraction and relaxation of the four chambers of the heart is necessary for optimal support of the circulation and ensures a supply of nutrients and signals throughout the body.

ECC and Ca²⁺: Generation of the Ca²⁺ Transient and Induction of Contraction

The mechanism by which the AP is transduced into the contractile response is termed "excitation-contraction coupling" (ECC) (Fozzard 1977; Bers 2002; Fearnley et al. 2011; Eisner 2014). Changes in intracellular Ca²⁺ concentration are central to this mechanism and couple (within a few msec) membrane depolarization with the engagement of the actomyosin cytoskeleton (via the energy of ATP hydrolysis) and thus sarcomere contraction (Fig. 1). During diastole (when the heart is relaxed), the cells are in their most extended state; their membrane potential (i.e., difference between inside and out) lies between -70 mV and -90 mV for atrial and ventricular cardiomyocytes and -60 mV for nodal cells. This negative resting membrane potential is close to the equilibrium potential for K⁺ channels, which are the dominant conductance (through Kir2.x channels) at rest (Miake et al. 2003; Zobel et al. 2003; Cordeiro et al. 2015). The negative equilibrium potential results from the large K⁺ gradient across the sarcolemma. This ionic gradient is generated and maintained by the Na⁺K⁺ATPase pumping three Na⁺ ions out of the cell in exchange for two K⁺ ions (Glitsch 1979; Gadsby 1984; Shattock et al. 2015). This pump also maintains the Na⁺ gradient across the cell membrane, compensating for the Na⁺ influx during the upstroke of the AP. Arrival of the AP results in an increase in membrane potential (depolarization) to the activation threshold of sodium channels (Na_V; pore-forming subunit Na_V1.5), -40 mV, and induces a rapid influx of Na^+ (Fig. 1(1)). This increase in intracellular Na⁺ further depolarizes the cell, to an extent that the threshold for activation of voltage-gated L-type Ca2+ channels (LTCCs) is crossed (comprising its poreforming subunit, $Ca_V 1.2$). The activation of these channels and ensuing Ca²⁺ influx underlies the plateau phase of the AP (Fig. 1(2)). Although the magnitude of this Ca^{2+} influx is not by itself sufficient to induce effective contraction, it represents a key triggering step in ECC. Specifically, Ca²⁺ entering the cell is amplified by Ca²⁺ release from the sarcoplasmic reticulum (SR) Ca²⁺ store through a mechanism called Ca²⁺-induced Ca²⁺ release (CICR) (Fabiato and Fabiato 1977; Fabiato 1983; Roderick et al. 2003). Through this mechanism, the Ca^{2+} entry signal arising via LTCC stimulates the opening of ryanodine receptor Ca²⁺ channels (RyR; type 2 isoform) located on the SR (Cannell et al. 1987; Beuckelmann and Wier 1988; Stern 1992; Wang et al. 2001). The RyR channel is a multimeric protein complex that is comprised of an RyR tetramer as well as a number of accessory proteins that contribute to modulating its activity under basal conditions as well as in response to physiological agonists and altering cell conditions. One of the first such proteins to be described is the archetypal Ca²⁺ sensor CaM, which acts to inhibit the channel activity (Xu and Meissner 2004). An interaction with the immunophilin FKBP12.6 is also well established. Although this interaction was at one time considered dynamic (Wehrens et al. 2003), evidence now supports a model in which the interaction is highly stable and serves to maintain the closed state of RyRs (Guo et al. 2010). Other interacting proteins include protein phosphatases and kinases that may act to couple kinase signaling cascades with RyR function (Zalk et al. 2007). In the SR, Ca²⁺ is primarily stored bound to the lowaffinity Ca²⁺-binding protein calsequestrin (Cala et al. 1990). Notably, calsequestrin associates with the RyR through the proteins junctin and triadin (Györke et al. 2004). This efficient coupling between plasmalemma Ca2+ influx and Ca²⁺ release from the SR is ensured through a close apposition (10-15 nm) of the associated channels (LTCC and RyR2) and their host membranes in a confined space called the dyadic cleft (Fig. 1(3); Hayashi et al. 2009; Scriven et al. 2010; Pinali et al. 2013). This architecture ensures that RyRs are exposed to high levels of Ca^{2+} entering the cardiomyocyte during the AP, which are necessary for their opening and subsequent Ca^{2+} release.



Figure 1. Excitation–contraction coupling (ECC). (1) An action potential depolarizes the cardiomyocyte and induces Na⁺ influx through voltage-gated Na⁺ channels (Na_v). (2) This further depolarizes the cell membrane and induces Ca²⁺ influx through voltage-gated L-type Ca²⁺ channels (LTCCs). (3) This Ca²⁺ entry stimulates Ca²⁺ release via dyadic RyR2 on the SR (4), which in turn triggers cell contraction through activating myofilament crossbridges. (5) LTCC inactivate and RyR close. (6) Cytosolic Ca²⁺ is then moved out of the cell by the Na⁺/Ca²⁺ exchanger (NCX) and pumped back into the SR by SERCA2a, thereby decreasing cytosolic Ca²⁺ concentration and bringing about relaxation. (7) A family of K⁺ channels participate in cell repolarization with K⁺ efflux as a last step for returning membrane potential to its resting value before a new cycle starts. (8) Tuning ECC to meet cardiovascular demands involves β-adrenergic pathways that induce the activation of CaMKII and of cAMP/ PKA, which phosphorylates voltage-gated LTCCs and RyRs to enhance their activity and phospholamban (PLB) to remove its inhibition of SERCA activity.

However, these couplons do not provide a sufficient Ca^{2+} influx to overcome the highbuffering capacity of the cardiomyocyte cytosol to induce RyR-mediated Ca^{2+} release throughout the volume of large ventricular cardiomyocytes (150 µm long × 20 µm deep on average) and induce contraction (Hüser et al. 1996; Smyrnias et al. 2010). To overcome this problem, and convey the AP to the entire cell volume, ventricular cardiomyocytes are endowed with a highly elaborate network of membrane tubules extending from invaginations of the sarcolemma (Smyrnias et al. 2010; Scardigli et al. 2018a). This network comprises transverse tubules (T-tubules [TTs]), which are distributed along the Z-lines of the sarcomere and axial

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tubules that are arranged along the long axis of the cardiomyocyte (together, the transverse and axial tubule system [TATS]). Further, TATS brings the sarcolemma and SR and its associated LTCCs and RyRs, respectively, into close proximity, forming couplons to generate a homogenous cell-wide Ca²⁺ transient (Scriven et al. 2010; Pinali et al. 2013). At this location, RyRs are organized in clusters, thereby optimizing release at each site (Walker et al. 2014; Shen et al. 2019). Although clusters of more than 100 RyRs have been reported, recent superresolution imaging experiments describe average cluster sizes ranging between 9 and 23 RyRs (Jayasinghe et al. 2018b; Shen et al. 2019). The localization of dyads to the Z-line of the sarcomere ensures exposure of contractile machinery to maximal Ca²⁺ elevation and flux (Fig. 1(4)). In atrial cardiomyocytes or ventricular cardiomyocytes from fetal and neonatal animals (Mackenzie et al. 2004; Zima and Blatter 2004; Bootman et al. 2006), TATS are however either absent or at a very low density (Brandenburg et al. 2016). In these cells, Ca²⁺ entry across the sarcolemma and its coupling with subsarcolemmal RyRs is sufficient to support their relatively lower contraction. Through the action of a number of players, such as kinases (e.g., calmodulin kinase II [CaM-KII] and protein kinase A [PKA]), phosphatases, and reactive/nitric oxygen species, Ca²⁺ release in the dyad is regulated by many signal transduction cascades (for review, see Zalk et al. 2007).

Cardiomyocyte Relaxation and Ca²⁺ Clearance

Depending on species, size of animal, and level of activity, the heart beats between 1 and 12 times per second. Thus, subsequent to systole and to allow the next round of contraction to occur, efficient mechanisms are required to bring about relaxation (diastole), and allow refilling of the chambers with blood. An initial step in this relaxation phase is the termination of mechanisms responsible for raising cytosolic Ca^{2+} . RyR2 release channels behave stochastically and their opening terminates rapidly through a combination of attrition, store depletion, regulation of their gating by luminal Ca^{2+} , and inactivation at the cytosolic side (Cannell and Kong 2017). LTCC also rapidly inactivates by a Ca²⁺- and voltage-dependent mechanism (Cens et al. 2006; Tadross et al. 2008). Repolarization of the cell membrane potential is the result of an outward current of K⁺ via different voltage-activated K⁺ channels (I_{Kr}, I_{Ks}) and, finally, opening of K⁺ channels that maintain the resting membrane potential (IK1-Kir2.1, 2.2, and 2.3) (Fig. 1(6); Cordeiro et al. 2015). Overall, these channel activities determine the time course and phases of the AP (Carmeliet 1999; Chiamvimonvat et al. 2017). It is also important to note that it is not possible to trigger a new AP during the plateau phase of the ventricular cardiomyocyte AP. This refractory period protects the heart from prematurely unwanted contractions (Burton and Cobbe 2001).

Active mechanisms substantially contribute to return intracellular cytosolic Ca²⁺ concentration to its resting levels and to bring about relaxation. These mechanisms also serve to replenish intracellular Ca²⁺ stores to prepare the cell for its next contraction. The primary contributor to cytosolic Ca²⁺ clearance as well as SR refilling is the sarco/endoplasmic reticulum Ca²⁺ ATPases (SERCA) pump. The SERCA 2a isoform is primarily expressed in the heart where it is localized to the SR membrane proximal to RyR2 and the contractile machinery (Dally et al. 2010). Subsequent to its Ca^{2+} -dependent activation (K_{1/2} 0.4 µм) (Lytton et al. 1992), via ATP hydrolysis, SERCA actively pumps Ca²⁺ from the cytosol into the SR (Fig. 1(5)). Ca2+ is also extruded out of the cell by a Na⁺/Ca²⁺ exchanger (NCX) in its forward mode to exchange one Ca²⁺ out of the cell and three Na⁺ into the cell (Fig. 1(5); Shattock et al. 2015). Although expressed in cardiomyocytes, the plasma membrane Ca²⁺ ATPase does not make a major contribution to Ca²⁺ extrusion during ECC (Hammes et al. 1998; Bers 2002). Although SERCA dominates in cytosolic Ca²⁺ clearance, its contribution varies according to species ranging between 70% and 90% of all Ca²⁺ removed from the cytosol (Bassani et al. 1994; Piacentino et al. 2003). The remainder is predominantly via NCX. In steady state, extrusion via NCX equals influx via LTCC and Ca²⁺ release and reuptake into the SR are in equilibrium at a set level of Ca^{2+} in the store (Eisner 2014). Dysregulation of any of these transport mechanisms will lead to a new equilibrium, with a new filling level of the store (e.g., an increase in intracellular Na⁺ will raise the Ca²⁺ store filling by reducing NCX-mediated Ca²⁺ extrusion) (Eisner 2014).

Tuning ECC to Modulate Cardiac Function

Heart function is dynamically regulated to meet the changing needs of the organism during alterations in the body activity, by the autonomic nervous system (Lymperopoulos et al. 2013; Eisner 2014; Wang et al. 2018). For example, during the fight-or-flight response, cardiomyocytes show inotropic (increased force of contraction) and lusitropic (increased relaxation) responses (Lymperopoulos et al. 2013). An increase in heart rate is also observed, although this is mediated by an effect on the spontaneous generation of AP at the SAN. This fight-or-flight response is primarily mediated by the adrenergic system and its hormone mediators noradrenaline and adrenaline. In altering cardiomyocyte function, the latter acts through β -adrenergic receptors (primarily β 1) expressed on the cardiomyocyte plasma membrane. B-Adrenergic receptors are 7-transmembrane G-protein-coupled receptors (GPCRs) that couple via the stimulatory G-protein (Gs) to activate adenylate cyclases and increase levels of the intracellular messenger cyclic AMP (cAMP) (Wang et al. 2018). Increased cAMP activates protein kinase A (PKA), which then phosphorylates multiple targets involved in ECC to augment cardiomyocyte contraction, and in turn cardiac function. Indeed, PKA phosphorylation targets each of the key functional components of ECC. Specifically, PKA phosphorylation of LTCC results in increased Ca²⁺ current, and phosphorylation of RyR leads to greater sensitivity to Ca²⁺ (Valdivia et al. 1995; van der Heyden et al. 2005). PKA also phosphorylates myofilament proteins (troponin C, myosin-binding protein C [MyBPC] and troponin I), most notably troponin I, decreasing the affinity of the myofilaments for Ca²⁺ and thereby enhancing crossbridge cycling (Fig. 1 (8); Metzger and Westfall 2004). In bringing

about the effects of PKA, and modulation of Ca²⁺ handling, phospholamban (PLB) is an important target. PLB is a small 5 kDa protein that interacts with SERCA, inhibiting its activity. On phosphorylation by PKA, PLB dissociates from SERCA resulting in its disinhibition (Fig. 1; for review, see MacLennan and Kranias 2003). As well as bringing about the cardiomyocyte lusitropic response via more rapid clearance of cytosolic Ca^{2+} , enhancing of SERCA activity results in an elevated SR Ca^{2+} load. The latter in turn increases Ca²⁺ availability in the SR for release, also sensitizing the open probability of RyRs. Many of the proteins targeted by PKA, most notably RyR and PLB, are also phosphorylated during β -adrenergic stimulation by CaMKII with similar consequences for cardiomyocyte function (Ullrich et al. 2012; Grimm et al. 2015; Uchinoumi et al. 2016; Potenza et al. 2018). Recently, a number of new micropeptide regulators of SERCA such as DWORF have been described (Nelson et al. 2016). Although these proteins are not modulated by PKA, their interaction with SERCA appears to act in competition with PLB. A direct regulation of SERCA by a long noncoding RNA has also been reported (Vervliet et al. 2018; Zhang et al. 2018). β-Adrenergic stimulation also shortens the AP duration by enhancing K⁺ channel activity (Hegyi et al. 2018). Together, these combined actions of β-adrenergic stimulation facilitates the increased heart rate and cardiac output required under times of stress.

To balance the sympathetic system in the heart, the parasympathetic system with its principal mediator acetylcholine (ACh) lower the heart rate. ACh acts on the M2 muscarinic GPCRs within the heart. On activation of M2 ACh receptors $G_{\beta\gamma}$ subunits are liberated, and through activation of GIRK channels (also known as IK_{ACh}) result in a more negative resting membrane potential and slower heart rate (for review, see Saw et al. 2018).

Multiple circulating hormones act on cardiomyocyte activity to modify contractility, and in so doing, couple other organ systems and cell types with cardiomyocyte function (Drawnel et al. 2013; Mayourian et al. 2018; Smyrnias et al. 2018). Those modulations act through Cold Spring Harbor Perspectives in Biology Merspectives or Biology www.cshperspectives.org altered Ca²⁺ signals as well as through changes in myofilament response to Ca²⁺ (Kobayashi and Solaro 2005). Notable cardioactive hormones include angiotensin II, which is produced in the kidney, endothelin-1, which is released locally and systemically by the endothelium, and by ATP. These hormones/mediators are also produced by cardiomyocytes themselves, thus eliciting an autocrine action (Dostal and Baker 1999; Drawnel et al. 2013). Of these hormones, many engage GPCRs, but in contrast to the β -adrenergic receptors, act via $G_{\alpha q}$ to promote phospholipase C-dependent hydrolysis of phosphatidylinositol 4,5-bisphosphate into inositol 1,4,5-trisphosphate (InsP₃) and diacyglycerol (DAG). DAG acts through protein kinase C (PKC) and InsP₃ acts on InsP₃ receptors (InsP₃R) to modify ECC (Kockskämper et al. 2008b; Drawnel et al. 2013; Smyrnias et al. 2018). In particular, PKC phosphorylates myofilament proteins to alter contractility, and on the Na⁺/H⁺ exchanger to modify intracellular pH and Na⁺ (Russell and Molenaar 2000). In so doing, myofilament sensitivity to Ca²⁺ is altered and Ca²⁺ balance further modulated through NCX consequent to changes in Na⁺ (Despa and Bers 2013; Garciarena et al. 2013). The role of InsP₃ in regulation of ECC is discussed below.

Membrane Tubules and Microdomain Signaling in Cardiomyocytes

Cell-wide increases in Ca²⁺ and efficient contraction rely on TATS in adult ventricular cardiomyocytes (Heinzel et al. 2002, 2011; Smyrnias et al. 2010; Crocini et al. 2014, 2016). Owing to its essential role in ECC, the complexity of TATS has gained great interest over recent years, with detailed knowledge arising from the advances in superresolution and electron microscopical imaging technologies that are able to visualize TATS in all their detail (Ferrantini et al. 2013; Soeller and Baddeley 2013; Crocini et al. 2014; Crossman et al. 2017). The density of TATS varies substantially through development, across the chambers of the heart, between species and during pathology (Song et al. 2006; Jayasinghe et al. 2012; Frisk et al. 2016; Manfra et al. 2017; Jones et al. 2018). During early postnatal development, the organization of TATS in rat cardiomyocytes is completed by 10-12 days postbirth (Ziman et al. 2010), although at this stage, very few LTCCs lie in close proximity to RyRs (Franzini-Armstrong et al. 2005). With development, the colocalization of LTCC with RyR increases (Sedarat et al. 2000), constructing the mature couplon in the dyad to enable efficient CICR. The structure and organization of TATS shows species-dependent differences, with mice having narrower tubules ($\sim 0.17 \mu m$) (Kong et al. 2017) compared with humans, pigs, and rats (~0.25 µm) (Soeller and Cannell 1999) or rabbits (~0.45 µm) (Savio-Galimberti et al. 2008; Kong et al. 2017; Rog-Zielinska et al. 2018). TATS are also more densely distributed in small rodents compared with large mammals including human, with TT flanking each sarcomere (Fig. 2; Manfra et al. 2017). The density of TATS in ventricular cardiomyocytes seems to associate with a high heart rate and the need for a very fast contraction and relaxation (e.g., in mice with a heart rate of 600 bpm). In atrial cardiomyocytes, TATS have been generally considered to be absent or rudimentary in nature. Recent data, however, shows that the nature of TATS in atrial cardiomyocytes is more diverse, with observed differences in right versus left atria, and between species. This diversity is possibly associated with different atrial workloads and cardiomyocyte width (Frisk et al. 2014; Brandenburg et al. 2016, 2018; Gadeberg et al. 2016; Denham et al. 2018). High-resolution microscopy studies in small and large mammals showed distinct populations of atrial cardiomyocytes that possess different configurations of TATS (i.e., organized, disorganized, and empty cells) (Frisk et al. 2014; Glukhov et al. 2015; Yue et al. 2017).

Structural differences in TATS have an impact on cardiomyocyte physiology and function. With a high TATS density, the majority of RyRs reside within couplons (Fig. 2A; Louch et al. 2006; Scriven et al. 2010; Wong et al. 2013). In this situation, for example in small rodents including mice and rats, AP-depolarization and RyR-mediated Ca²⁺ release show high-temporal fidelity. However, a low TATS density (e.g., humans and pigs) results in a significant number of



Figure 2. Difference in the TATS in isolated cardiomyocytes from mouse (*A*), pig (*B*), and human (*C*). The TATS is stained in green (Caveolin-3 [Cav3] or NCX) and RyRs are stained in red. Scale bar, 10 μ m. Images were acquired with a Nikon A1R confocal microscope using a 60× oil immersion objective. A4× zoom of the white square is shown (unpubl.).

RyR that lie outside of couplons/dyad cleft (i.e., noncoupled) and are therefore likely not exposed to the same Ca²⁺ concentration directly following the AP (Fig. 2B,C; Heinzel et al. 2002; Louch et al. 2004; Dries et al. 2013). As a consequence, this fraction of RyRs is activated with a delay, resulting in inhomogeneous Ca²⁺ release during a cell transient/contraction (Heinzel et al. 2002). This role of TATS in Ca²⁺ transient generation is further illustrated in cells in which they are normally absent or sparse, such as atrial cells (Bootman et al. 2011; Brandenburg et al. 2016). On electrical stimulation, these cells show an increase in intracellular Ca²⁺ concentration $([Ca^{2+}]_i)$ that initially occurs at the cell periphery and, which then propagates to the center of the cell via a combination of CICR and Ca²⁺ diffusion (Mackenzie et al. 2004; Sheehan et al. 2006). Conversely, disruption of TATS in ventricular cells by osmotic shock or through maintenance in culture for 6 days leads to inhomogeneous Ca²⁺ release during transients (Lipp et al. 1996; Brette et al. 2005; Smyrnias et al. 2010). The efficiency of CICR is similarly low in ventricular cardiomyocytes isolated from neonatal hearts, which show little evidence of TATS (Haddock et al. 1999). The mechanisms underlying the expression and maintenance of TATS is not yet fully resolved. Titin cap protein (telethonin), junctophilin 2, and the Bin/Amphiphysin/Rvs domain protein amphiphysin II (AmpII or BIN-1) have all been shown, however, to modulate the biogenesis and maintenance of TATS (Chen et al. 2013; Ibrahim et al. 2013; Reynolds et al. 2013; Hong et al. 2014; Fu and Hong 2016).

NON-CANONICAL Ca²⁺ SIGNAL GENERATION IN THE HEART

In addition to the Ca^{2+} signaling mechanisms underlying ECC (described above), other Ca^{2+} transport pathways are expressed in the heart contributing to a more complex picture of the role of Ca^{2+} in cardiomyocyte function. These additional Ca^{2+} signaling pathways interact with the canonical ECC signaling Ca^{2+} mechanism to selectively and simultaneously control ECC as well as other cellular processes (Fig. 3).

InsP₃ and InsP₃ Receptors

Inositol 1,4,5-trisphosphate receptor (InsP₃R) intracellular Ca²⁺ release channels are expressed in cardiomyocytes (Lipp et al. 2000; Kockskämper et al. 2008b; Garcia et al. 2017). Although all

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Figure 3. Noncanonical Ca²⁺ channels. (1) G-protein-coupled receptors activated by endothelin-1 (ET-1) or angiotensin-II (Ang-II), produce InsP₃ that activates Ca²⁺ release via InsP₃ receptors (IP₃RII), which cross talks with RyR2 to modify Ca²⁺-induced Ca²⁺ release (CICR). (2) Ca²⁺ release from InsP₃R2 present at the perinuclear SR and the nuclear envelope stimulates nuclear Ca²⁺ signaling pathways. (3) β-Adrenergic receptor (β-AR) activation leads to the activation of protein kinase A (PKA), which in turn enhances the activity of the CD38 enzyme. (4) CD38 produces nicotinic acid adenine dinucleotide phosphate (NAADP) that promotes Ca²⁺ leak via endolysosomal two-pore channels (TPCs). (5) Activation of CD38 also generates cyclic ADP-ribose (cADPR), which acts on the RyR2 to enhance its activity. (6) To refill the SR as well as affect cytosolic Ca²⁺ levels, the STIM/ORAI/TRP system may be engaged.

three isoforms of InsP₃Rs have been identified in the heart, the type 2 InsP₃R is predominant (Perez et al. 1997; Lipp et al. 2000). InsP₃R expression is required in cardiac development and contributes to heart function during the embryonic and neonatal stages (Rosemblit et al. 1999; Sasse et al. 2007; Kockskämper et al. 2008b). InsP₃R expression level declines during postnatal heart maturation, as the number of RyRs increases. Ca²⁺ release via InsP₃R is initiated by InsP₃ generated downstream to the activation of G_{\alphaq}-coupled GPCR signaling cascades, for example, by endothelin-1 and angiotensin II (Fig. 3; Berridge 1993). As for all InsP₃R isoforms, InsP₃R2 activity shows a bell-shaped dependency for Ca^{2+} , with high activity occurring at Ca^{2+} levels present at diastole (Foskett et al. 2007). Perhaps making this isoform most appropriate for its function in the heart, it shows the highest sensitivity to InsP₃ (Fig. 3(1); Mak and Foskett 2015; Vervloessem et al. 2015).

InsP₃R expression varies substantially across the chambers of the heart, with \sim 10-fold higher expression in the atria than ventricle (Lipp et al. 2000). Greater expression levels are also observed in cardiomyocytes of the SAN (Kapoor et al. 2015) and the Purkinje conduction fibers (Gorza et al. 1993; Hirose et al. 2008) in which ECC is not the primary function. In the adult ventricle, InsP₃R is reported to be expressed at a substantially lower level than RyRs (10- to 50-fold) (Moschella and Marks 1993) and owing to this lower expression, as well their lower conductance compared with RyRs, have not been considered to play a substantial role in regulation of ECC in this heart region. Despite this low expression, roles for InsP₃R in regulation of ECC, hypertrophic gene expression, Purkinje fiber function, and SAN activity are reported (Domeier et al. 2008; Hirose et al. 2008; Higazi et al. 2009; Nakayama et al. 2010; Kapoor et al. 2015). The ability of InsP₃Rs to influence cardiomyocyte function despite low expression is made possible through their localization to functionally relevant cellular subcompartments and local signaling events (Fig. 3(2); Wu et al. 2006; Higazi et al. 2009; Ljubojevic et al. 2014; Hohendanner et al. 2015a; Wullschleger et al. 2017). In atrial and ventricular cardiomyocytes, InsP₃Rs are colocalized with RyRs in the subsarcolemmal space or at dyads, respectively (Lipp et al. 2000; Harzheim et al. 2009). At these locations, Ca²⁺ released via InsP₃Rs modulates ECC by bringing proximal RyRs closer to the threshold for activation (Harzheim et al. 2009; Horn et al. 2013; Hohendanner et al. 2015b; Wullschleger et al. 2017) leading to sensitization of Ca^{2+} release during the transient. Depending on the model studied, this channel cross talk induces SR Ca²⁺ leak and elicits inotropic and/or pro-arrhythmic effects (Mackenzie et al. 2002; Zima and Blatter 2004; Proven et al. 2006; Bootman et al. 2007; Domeier et al. 2008; Kockskämper et al. 2008a; Namekata et al. 2008; Signore et al. 2013; Blanch and Egger 2018). Although positive inotropic effects of InsP₃Rs are observed in atrial cardiomyocytes, the impact of InsP₃ signaling on contractility in ventricular cardiomyocytes is less obvious with effects on cellular automaticity more often reported (Harzheim et al. 2009; Blanch and Egger 2018).

Two-Pore Channels and Nicotinic Acid Adenine Dinucleotide Phosphate

Nicotinic acid adenine dinucleotide phosphate (NAADP) is an intracellular signaling messen-

ger that stimulates Ca²⁺ release via transient receptor potential (TRP) channels and two-pore channels (TPCs) from the endo/lysosome (Calcraft et al. 2009; Pitt et al. 2010; Grimm et al. 2012). NAADP is a potent second messenger, which acts at nanomolar levels to trigger micromolar release of Ca²⁺ from TPCs. Several lines of evidence support a role for NAADP signaling in cardiomyocyte ECC. Specifically, NAADP triggers Ca²⁺ release from microsomes prepared from SR; it activates single RyR2 incorporated into bilayer lipid membranes and direct application of NAADP increases the amplitude of Ca²⁺ transient and frequency/amplitude of Ca2+ sparks in intact guinea pig cardiomyocytes (Bak et al. 2001; Mojzisova et al. 2001; Macgregor et al. 2007a; Collins et al. 2011). Although a role for NAADP as a physiologically relevant messenger in the heart was for a long time not clear, the identification of its production downstream of β -adrenergic stimulation makes it an important regulator of cardiomyocyte function (Macgregor et al. 2007a; Lewis et al. 2012). NAADP is produced following β -adrenergic stimulation through activation of the enzyme CD38, an ADP-ribosyl cyclase, and is thereby proposed to contribute to both the inotropic and arrhythmogenic effects of this signaling pathway (Macgregor et al. 2007a; Lewis et al. 2012; Nebel et al. 2013; Warszta et al. 2014; Lin et al. 2017). To elicit its inotropic effect, NAADP is proposed to enhance Ca^{2+} loading of the SR (Macgregor et al. 2007a; Collins et al. 2011). A requirement for CaMKII in mediating this effect of NAADP has been shown (Capel et al. 2015). Reminiscent of the cross talk between InsP₃Rs and RyRs, Ca²⁺ release from the NAADP-sensitive stores sensitizes RyR2 at lysosomal-endoplasmic reticulum nanojunctions leading to spontaneous diastolic Ca²⁺ release events (Fig. 2(4); Macgregor et al. 2007a; Nebel et al. 2013; Warszta et al. 2014).

RyRs and cADPR

Cyclic ADP-ribose (cADPR) is a second messenger that is also produced by ADP-ribosyl cyclase (CD38) in mammalian cardiomyocytes after sympathetic or angiotensin II stimulation (Galione et al. 1998; Higashida et al. 1999, 2000; Xie et al. 2005). cADPR modulates the peak amplitude of Ca²⁺ transients and hence cardiomyocyte contractility (Rakovic et al. 1996; Cui et al. 1999; Macgregor et al. 2007a). Mechanisms involved in mediating this action of cADPR include increased RyR activity and greater SR Ca²⁺ load (Rakovic et al. 1999; Lukyanenko et al. 2001; Macgregor et al. 2007b; Zhang et al. 2009). Consistent with this hypothesis, a higher frequency of Ca²⁺ sparks is observed in response to increased cADPR. However, the relatively slow kinetics for the development of the full effect of cADPR on Ca²⁺ release, and evidence for a cADPR-responsive component independent of RyR2 is suggestive of a more complex mechanism (Cui et al. 1999; Prakash et al. 2000). Apart from the role in Ca²⁺ homeostasis, the ADPRcyclase and hence cADPR are implicated in the development of angiotensin II-induced hypertrophic responses (Gul et al. 2008, 2009) and in cellular toxicity following ischemia/reperfusion injury (Fig. 3(5); Xie et al. 2005).

Ca²⁺ Influx and STIM/Orai

A functional store-operated Ca²⁺ entry (SOCE) pathway is described in cardiomyocytes (Voelkers et al. 2010; Bootman and Rietdorf 2017). As in other cellular systems, in cardiomyocytes this pathway is activated in response to Ca²⁺ depletion of the SR, for example by treatment with SERCA inhibitors (cyclopiazonic acid or thapsigargin) and/or GPCR agonists (for review, see Hunton et al. 2002, 2004; Uehara et al. 2002; Kojima et al. 2012; Luo et al. 2012; Avila-Medina et al. 2018). The molecular components of SOCE, including the ER/SR Ca²⁺ sensors STIM1 and STIM2 and the plasma membrane channel ORAI are also all expressed in cardiomyocytes, further supporting the presence of this pathway in this cell type (Correll et al. 2015; Zhao et al. 2015). Although the role of SOCE in cardiomyocytes is not fully resolved, it has been shown to participate in regulation of gene transcription and Ca²⁺ homeostasis (Ohba et al. 2007; Voelkers et al. 2010; Hulot et al. 2011). SOCE activity is developmentally regulated, being readily detectible in fetal and neonatal cardiomyocytes, but is thereafter down-regulated, with low-to-nondetectable activity in healthy adult cardiomyocytes (Uehara et al. 2002). As such, it does not significantly contribute to ECC in healthy adult cardiomyocytes (Fig. 3(6)).

Mitochondrial Calcium in Cardiomyocytes

Cardiomyocyte Ca²⁺ dynamics are also influenced by mitochondria. They constitute about one-third of the volume of cardiomyocytes being arranged as bricks spanning the sarcomere (Bossen et al. 1978). Via the tricarboxylic acid (TCA) cycle and oxidative phosphorylation, mitochondria are responsible for ~90% of ATP generated in cardiomyocytes. Although mitochondria take up Ca²⁺ from the cytosol during ECC and show a high capacity for Ca²⁺ accumulation (Wei et al. 2012, 2015), their influence on Ca²⁺ dynamics is more subtle, especially under physiological conditions (Drago et al. 2012; Williams et al. 2013; Boyman et al. 2014). Ca²⁺ uptake into mitochondria is, however, an important regulator of mitochondrial metabolism. It augments the activity of pyruvate dehydrogenase, isocitrate dehydrogenase, and α -ketoglutarate dehydrogenase, which are key enzymes of the TCA cycle as well as the activity of cytochrome c oxidase and F₀-F₁-ATPase, which are components of the electron transport chain (ETC) (Denton et al. 1988; Balaban 2009). By augmenting mitochondrial ATP generation, Ca²⁺ thus coordinates cellular metabolism, and the dynamic changes in the energy requirements of the cardiac myocyte, including for Ca²⁺ clearance mechanisms and actomyosin-mediated contraction that are enhanced during the fightor-flight response (Balaban 2009; Kwong et al. 2015). During pathology such as following ischemia, excessive mitochondrial Ca²⁺ uptake is toxic, resulting in increased reactive oxygen species generation and permeability transition pore opening associated with cell death mechanisms (Santulli et al. 2015).

Cardiomyocyte mitochondrial Ca^{2+} has been reported to either mirror changes in cytosolic Ca^{2+} showing short-lived transients (Robert et al. 2001; Kettlewell et al. 2009) or to show steady-state Ca²⁺ changes that increase according to the frequency of cytosolic Ca²⁺ transients (Paillard et al. 2017). Reasons for these different models are not clear but are in part proposed to be methodological (Dedkova and Blatter 2013). The mitochondrial Ca^{2+} uptake mechanism has a low affinity, in the tens of µM, precluding its activation by bulk cytosolic Ca²⁺ elevations generated during ECC and in response to hormonal stimulation that do not reach this level (Collins et al. 2002; Kirichok et al. 2004; Kettlewell et al. 2009; Dedkova and Blatter 2013). Mitochondrial Ca²⁺ uptake sites are, however, localized to within tens of nm of Ca²⁺ release channels on the SR/ER, exposing them to a microdomain of Ca^{2+} in the tens of µM, which is sufficiently high to activate the lowaffinity Ca²⁺ uniporter (Hajnóczky et al. 1995; Csordás et al. 1999, 2010). These ER/SR mitochondrial uptake sites are known as "hotspots" and structurally as mitochondrial-associated membranes (MAMs) (Rizzuto et al. 2004). Supporting colocalization of sites for mitochondrial Ca²⁺ uptake and SR Ca²⁺ release in cardiomyocytes, cardiomyocyte mitochondria show a gradient in Ca²⁺ from the Ca²⁺ release sites at the junctional SR to the center of the sarcomere (Lu et al. 2013).

Mitochondrial Ca²⁺ uptake primarily occurs via the voltage-dependent anion channel (VDAC) of the outer mitochondrial membrane (OMM) (Shimizu et al. 2015) and a low affinity mitochondrial Ca²⁺ uniporter (MCU) of the inner mitochondrial membrane (IMM) (Kirichok et al. 2004). Other mechanisms of mitochondrial Ca²⁺ uptake have been described, including a rapid mode of mitochondrial uptake (RaM) (Buntinas et al. 2001) via mitochondrial RyR1 (Beutner et al. 2005) and connexin 43 (Gadicherla et al. 2017). The molecular identification of the MCU in the last decade (Baughman et al. 2011; De Stefani et al. 2011) has led to new insights into its role in mitochondrial Ca²⁺ sequestration in the heart (Pan et al. 2013; Kwong et al. 2015; Wu et al. 2015). A common finding of these studies is that MCU function is not required for baseline function but is necessary for adaptive responses of the heart to stress or work. This is illustrated by results of loss-offunction studies, which showed that MCU was required for heart rate acceleration at the level of pacemaker cells and inotropy of ventricular cardiomyocytes (Kwong et al. 2015; Rasmussen et al. 2015; Wu et al. 2015). The greatest contribution of these effects of loss of MCU function was to limit increases in ATP generation during periods of greater stress/workload and not on Ca²⁺ buffering (Drago et al. 2012). As a consequence of insufficient ATP, the increase in SERCA function required to bring about chronotropic and inotropic responses is prevented (Kwong et al. 2015; Rasmussen et al. 2015; Wu et al. 2015). MCU is associated with a number of regulatory proteins, including MICU1 and MICU2 and EMRE (Perocchi et al. 2010; Vais et al. 2016). Of particular importance in the context of the cardiomyocyte is MICU1, which sets the threshold of activation and properties of Ca²⁺ uptake via MCU (Csordás et al. 2013). Notably, whereas MCU and MICU1 interact in a stoichiometric manner in liver, a reduced proportion of MCU is associated with MICU1 in cardiomyocytes (Paillard et al. 2017). Through this decreased interaction with MICU1, cardiomyocyte mitochondrial Ca²⁺ uptake shows a higher affinity and lower cooperativity than in nonmuscle tissues such as liver (Paillard et al. 2017). Whereas MCU is positioned close to RyR to facilitate mitochondrial Ca²⁺ uptake (De La Fuente et al. 2016), Ca²⁺ extrusion mechanisms, including the Na⁺/Ca²⁺/Li⁺ exchanger NCXL (Palty et al. 2010; Luongo et al. 2017), are localized to regions of the mitochondria distinct from the Ca²⁺ uptake route (De La Fuente et al. 2018). Furthermore, an electrogenic $Ca^{2+}/$ 2H⁺ exchanger (potentially the leucine zipper EF-hand-containing transmembrane protein 1 [LETM1]) has also been proposed to extrude Ca^{2+} out of the mitochondria (Jiang et al. 2009; Haumann et al. 2018).

REMODELING OF ECC IN DISEASE

Given its fundamental role in regulation of cardiac function, it is not surprising that disturbances in the organization and regulation of Ca^{2+} signals result in cardiac dysfunction (Hasenfuss and Pieske 2002; Wehrens et al. 2005;

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Luo and Anderson 2013; Marks 2013). Indeed, altered Ca²⁺ handling is observed during hypertrophic remodeling and heart failure, as well as during diseases associated with rhythmic disturbances, including atrial fibrillation (Berridge et al. 2003; Fearnley et al. 2011; Mozaffarian et al. 2015; Denham et al. 2018). Perturbations in Ca²⁺ handling are also apparent in hearts remodeled because of mutations in myofilament proteins (hypertrophic as well as dilated cardiomyopathies). Further, mutations in Ca²⁺-handling proteins, including RyRs (e.g., during catecholaminergic polymorphic ventricular tachycardia [CPVT]) and PLB are described to have a direct effect on cardiomyocyte function (Wehrens et al. 2005; Liu et al. 2015).

Cardiac remodeling (i.e., changes in structure and function), including altered Ca²⁺ handling, is seen in diseases with different etiologies, and is often the first step in progression to frank heart failure (Marks 2013; Schirone et al. 2017). Despite variability in the disease phenotype, some general features and patterns are common. They have been characterized in detail in animal models (e.g., during pressure overload). In the early stages of pathological remodeling, the change of ECC is adaptive, with augmented ECC observed (Ohkusa et al. 1997; Lymperopoulos et al. 2013). This is characterized by enhanced Ca²⁺ transient amplitude, greater contraction, and more effective relaxation (SR Ca²⁺ sequestration). As remodeling progresses to failure, ECC capacity decreases, eventually reaching a point that effective contraction is no longer possible (Gomez et al. 1997; Marks 2013; Høydal et al. 2018; Munro et al. 2018). Under these conditions, intracellular Ca2+ release becomes less homogenous, the kinetics of Ca²⁺ release and reuptake are slower, Ca²⁺ transient amplitude is lower, and ultimately these maladaptations combine to decrease contractile function (Fig. 4; Gomez et al. 1997; Mozaffarian et al. 2015; Høydal et al. 2018). This decline in ECC is brought about through a combined alteration in membrane architecture and Ca²⁺-handling machinery. The Ca²⁺ influx through LTCC is generally unchanged, but because of changes in cytoarchitecture, it may have a different mi-

crodistribution (Sanchez-Alonso et al. 2016). A particular feature of the remodeling of membrane architecture is alteration in TATS (Song et al. 2006; Heinzel et al. 2008; Lenaerts et al. 2009; Lyon et al. 2009; Crossman et al. 2015, 2017; Crocini et al. 2016; Seidel et al. 2017; Dries et al. 2018; Høydal et al. 2018). During the early stages of pathological remodeling, the TATS becomes disorganized and membrane/SR distances increased (Xu et al. 2007; Wu et al. 2012; Jones et al. 2018). As disease progresses, together with cardiomyocyte hypertrophy, a further disorganization (seen in rodent models) and decrease in density (recorded in large mammals) of TATS is observed, resulting in an increase in the fraction of noncoupled RyRs (Song et al. 2006; Sachse et al. 2012; Seidel et al. 2017; Dries et al. 2018; Munro et al. 2018). Consequently, a lower proportion of RyRs is directly activated by Ca²⁺ influx during the initial phase of the AP. The noncoupled RyRs are activated, albeit with a delay, by Ca²⁺ diffusion from the coupled RyRs (Dries et al. 2018). Owing to decreased synchrony in RyR activation, the Ca²⁺ flux from the SR is lower, consequently reducing Ca²⁺ transient amplitude and contraction. The rate of Ca²⁺ clearance is also substantially reduced in disease (Fig. 4). This is manifest as a slower rate of decline of the Ca²⁺ transient/contraction and an increase in cytosolic Ca²⁺ during relaxation (Kubalova et al. 2005; Hohendanner et al. 2013). Poor cardiomyocyte relaxation contributes to the overall decrease in diastolic function and consequently poor filling of the ventricle. A reduction in SERCA expression and/or activity is primarily responsible for this reduced Ca²⁺ clearance (Røe et al. 2018). Notably, in vivo reexpression of SERCA reverses many of the features of disease-associated remodeling of Ca²⁺ handling raising its potential as a therapy (Lyon et al. 2011). Disappointingly, clinical trials have not shown a similar benefit, which is possibly related to methodological hurdles to reach the necessary increase in SERCA expression within failing cardiomyocytes. Further advances in this area may yet provide benefit (Greenberg et al. 2016).

Further adding to the perturbation of Ca²⁺ handling in disease is a dysregulation of SR Ca²⁺



Figure 4. Mitochondrial Ca^{2+} . Mitochondria are densely packed in the cardiomyocyte being aligned along the myofilaments as bricks. Their Ca^{2+} uptake sites are closely localized to the junctional sarcoplasmic reticulum (SR) and a microdomain of elevated Ca^{2+} generated by SR Ca^{2+} release via RyRs. Ca^{2+} enters the mitochondria through the voltage-gated anion channel (VDAC) of the outer mitochondrial membrane and the mitochondrial Ca^{2+} uniporter (MCU) of the inner mitochondrial membrane. Ca^{2+} acts at multiple sites in the electron transport chain and tricarboxylic acid (TCA) cycle to modulate mitochondrial metabolism and ATP production. Ca^{2+} is extruded from the mitochondria through a Na⁺/Li⁺/Ca²⁺ exchanger (NCXL) and/or a Ca^{2+}/H^+ exchanger (mHCX).

release. At the nanoscale, RyR clusters are reorganized in heart failure, which is associated with an increase in their activity (Kolstad et al. 2018). Atrial fibrillation is also associated with changes in RyR cluster size, distribution, and activity (Macquaide et al. 2015). Increased RyR channel activity in diastole, observed as increased spark frequency, is very often seen, including in latestage human heart failure (Fischer et al. 2014; Dries et al. 2018). Although RyR expression is not substantially altered in disease, posttranslational modifications including phosphorylation by PKA and CaMKII, oxidation, as well as remodeling of RyR clusters, contribute to the increase in spontaneous Ca²⁺ release events (Fischer et al. 2014; Ho et al. 2014; Grimm et al. 2015; Fu et al. 2016; Uchinoumi et al.

2016; Walweel et al. 2017; Dries et al. 2018). The greater frequency of these spontaneous Ca²⁺ release events can lead to a leak of Ca²⁺ from the SR as well as an increase in the propensity of Ca²⁺ waves (Cheng et al. 1996; Venetucci et al. 2008; Curran et al. 2010; Dries et al. 2018). These Ca²⁺ waves stimulate NCX activity, which because of its electrogenic nature, leads to the generation of delayed after depolarizations (DADs), triggering APs that may propagate to neighboring cardiomyocytes and induce arrhythmia (Venetucci et al. 2008). A similar proarrhythmic phenotype arises because of CPVT-associated mutations in RyR2 (Priori and Chen 2011). These mutated forms of RyRs show enhanced sensitivity to luminal and/or cytosolic Ca²⁺ and show increased spontaneous openings. Although the heart can accommodate for these more active RyRs under normal conditions, during periods of increased catecholamine stimulation and associated increased SR store loading, large spontaneous Ca^{2+} release events induce NCX activity and AP generation. This can trigger arrhythmogenic events, ventricular tachycardia, and eventually sudden cardiac death. The identification of small molecules such as K201 and EL0 that stabilize the closed state of the RyR may reverse the pathological SR Ca^{2+} leak observed in heart failure as well as in CPVT (Li et al. 2017).

A re-expression of a gene program expressed in the fetus/neonate (the fetal gene program) characterized by atrial and brain natriuretic factors (NPPA and NPPB) is often described during hypertrophy. Notably this gene program includes a number of proteins involved in Ca^{2+} handling. Indeed, increases in expression of InsP₃R (Harzheim et al. 2010), proteins involved in SOCE (Correll et al. 2015), and of T-type Ca^{2+} channels are observed during cardiac pathology (Izumi et al. 2003). Moreover, the increase in the expression of these proteins contributes to pathological alterations of cardiomyocyte physiology (Izumi et al. 2003; Harzheim et al. 2010; Correll et al. 2015).

Increased InsP₃R expression, as well as the mechanisms responsible for InsP₃ generation, are observed in hypertrophy and heart failure, as well as in atrial fibrillation (Yamda et al. 2001; Harzheim et al. 2010; Drawnel et al. 2012; Signore et al. 2013). As a consequence, Ca²⁺ release independent of ECC is enhanced (Harzheim et al. 2009; Nakayama et al. 2010; Hohendanner et al. 2015b). Although InsP₃-mediated Ca^{2+} release remains of a low magnitude, through promoting Ca²⁺ release via neighboring Ca²⁺-sensitive RyRs, it leverages increased Ca²⁺ spark events that may lead to arrhythmogenic cell-wide Ca²⁺ activity (Hohendanner et al. 2015b). The summation of increased RyR sensitivity and greater InsP₃-mediated Ca²⁺ release may create a perfect storm in which the cardiomyocyte is sensitized to spontaneous release that, in turn, via activation of NCX, induces the generation of APs and tissue-wide arrhythmia.

SOCE is also increased in hypertrophied cardiomyocytes (Hulot et al. 2011; Luo et al. 2012). Remarkably, the overwhelming majority of studies showed that stress-induced overexpression of SOCE-associated proteins and, hence, the enhanced activity of SOCE in cardiomyocytes contribute to, and sustain, hypertrophic remodeling (Hunton et al. 2002, 2004; Ohba et al. 2007; Voelkers et al. 2010; Hulot et al. 2011). Attenuation of SOCE components suppresses this induction of hypertrophy in neonatal cardiac myocytes (Voelkers et al. 2010; Luo et al. 2012). Increased SOCE through transgenic STIM1 overexpression is also sufficient to induce hypertrophic remodeling of the heart, promoting enhanced CnA/NFAT and CaMKII signaling. Moreover, in advance of disease development, STIM1 overexpression induces spontaneous Ca²⁺ transients, increased LTCC current and Ca²⁺ sparks-effects that may underlie the sudden death observed in these mice (Correll et al. 2015). Together these combined roles of SOCE in cardiomyocytes would suggest that SOCE inhibition may be of therapeutic benefit (Kojima et al. 2012).

Ca²⁺ Triggering of Hypertrophic Remodeling

Alterations in Ca²⁺ handling are a cue for cardiac remodeling during disease. The connection between Ca²⁺ and cardiomyocyte growth-hypertrophy associated with disease-was first uncovered by examining the responses of neonatal cardiomyocytes to altered frequency of electrical stimulation (McDonough et al. 1994; Tavi et al. 2004). In vivo, tachypacing or catecholamine infusion is also sufficient to elicit a hypertrophic response (Kubalova et al. 2005). The absence of hypertrophy in mice deficient for PLB that show a constitutive inotropic state is not sufficient to trigger hypertrophy, and suggests that enhanced Ca^{2+} cycling per se is not, however, sufficient for the induction of hypertrophic gene expression (Kiriazis and Kranias 2000). Indeed, increases in nuclear Ca²⁺ are now considered to play an important role in activation/modulation of cardiomyocyte gene expression (Fig. 5; Wu et al. 2006; Guatimosim et al. 2008; Higazi et al.



Figure 5. Remodeling of excitation-contraction coupling (ECC) in disease. (1) The coupling between Ca^{2+} influx and Ca^{2+} release is compromised because of a loss of tight connections between the transverse and axial tubule system (TATS) and the sarcoplasmic reticulum (SR) with an atrophy and remodeling of the tubular network. (2) RyRs thus become uncoupled and are then activated with a delay by Ca^{2+} diffusion across the cell from coupled RyRs. (3) Consequently, activation of myofilaments is less homogeneous and contraction impaired. (4) SERCA expression is reduced leading to an elevation in diastolic Ca^{2+} and reduced SR Ca^{2+} , which in turn leads to a decrease in Ca^{2+} release via RyRs during each ECC cycle, thereby reducing contraction amplitude. (5) RyRs display spontaneous releases of Ca^{2+} , (6) generating Ca^{2+} waves. (7) This cytosolic Ca^{2+} overload leads to NCX activation, triggering after-depolarizations and potentially a spontaneous AP.

2009; Arantes et al. 2012). Moreover, in the absence of these nuclear Ca^{2+} changes, altered frequency of cytosolic Ca^{2+} oscillations may not be sufficient to increase hypertrophic gene expression (Higazi et al. 2009). In generating nuclear-specific Ca^{2+} changes, InsP₃Rs have been proposed to play a role (Wu et al. 2006; Guatimosim et al. 2008; Higazi et al. 2009; Arantes et al. 2012). Since InsP₃Rs are activated

downstream of $G_{\alpha q}$ -coupled receptors by circulating hormones or phospholipase C_{ε} (Zhang et al. 2013), this mechanism can be engaged independent of the Ca²⁺ changes associated with ECC (Fig. 5).

The role of Ca^{2+} in hypertrophic gene expression is further substantiated by gain- and loss-of-function studies involving downstream sensors and mediators of Ca^{2+} . Through a num-

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ber of studies, key roles for a pathway involving calmodulin (CaM) (Obata et al. 2005), the archetypal Ca²⁺ sensor, calcineurin (CnA) a calcium-dependent phosphatase and its downstream transcription factor-the nuclear factor of activated T-cells (NFAT) in hypertrophic gene expression has been identified (Fig. 5(5) and 5(6); Molkentin et al. 1998; Sussman et al. 1998; Bourajjaj et al. 2008). Nuclear Ca²⁺ changes have been invoked in regulation of this pathway through maintaining CnA in the nucleus and prolonging its dephosphorylation of NFAT (Higazi et al. 2009; Olivares-Florez et al. 2018). Indeed, nuclear translocation of CaM is important in the activity of nuclear CnA (Zhu and McKeon 1999; Oda et al. 2018). The involvement of this CnA/NFAT pathway in hypertrophy induced by a pathological tropomyosin mutation suggests a more general role for this pathway in cardiac pathology (Sussman et al. 1998). Ca²⁺ also elicits its hypertrophic effects via CaMKII. This kinase phosphorylates the type II histone deacetylase (HDAC) causing its translocation out of the nucleus and loss of inhibition of MEF2-dependent gene expression (Fig. 5(7) and 5(8); Zhang et al. 2002; Wu et al. 2006; Backs et al. 2008).

Ca²⁺ Handling and Hypertrophic Remodeling Are Interdependent

Notably, while ECC and the gene expression underlying hypertrophic remodeling are selectively controlled by Ca²⁺, these cell mechanisms are intimately linked. Indeed, at the same time that Ca²⁺ stimulates the induction of hypertrophy, the expression of Ca²⁺-handling proteins involved in ECC is altered during disease. Thus, the Ca²⁺ signals that stimulate hypertrophy are modified. As a consequence, the hypertrophic response is augmented and sustained. Clear examples of this feedback/feedforward system are illustrated by the roles of InsP₃Rs and SERCA2a. As indicated above, SERCA activity/expression is often decreased during heart failure contributing to the associated diminished contractility. Re-expression of SERCA leads, however, to a reversal of the hypertrophic phenotype: SR Ca²⁺ leak, β-adrenergic receptor distribution and ECC return to a healthy state

(Lyon et al. 2011). InsP₃R expression is increased and the nuclear membrane invaginations where it is localized decreased during disease (Ljubojevic et al. 2014). Nuclear InsP3 signaling is also a cue for the activation of CnA/NFAT and CaMKII/HDAC pathways and the induction of the hypertrophic response (Wu et al. 2006; Higazi et al. 2009; Plačkić et al. 2016). Notably, InsP₃ signaling suppresses the expression of microRNA miR-133 (Figs. 5(2), 5(3), and 6; Drawnel et al. 2012), which is not only an inhibitor of hypertrophy-related genes but also of InsP₃R expression (Li et al. 2018). Thus, enhanced InsP₃ signaling that may initiate hypertrophy, is self-augmenting and sustaining. Further, InsP₃R expression has also been reported to be under the control of NFAT (Sankar et al. 2014; Olivares-Florez et al. 2018), which is again sensitive to InsP₃ signaling independent of Ca²⁺ changes associated with ECC (Higazi et al. 2009). CnA/NFAT signaling also shows feedback regulation. In particular, NFAT stimulates induction of RCAN1.4 (regulator of CnA) also known as DCSR1 and calcipressin), which then directly inhibits the activity of CnA (Oh et al. 2010). These links between modifications in expression of certain Ca²⁺-handling proteins, in particular those that show disease-dependent changes, are particularly interesting targets for therapeutic intervention.

CONCLUSIONS AND PERSPECTIVES

Cardiomyocytes rely on Ca²⁺ signaling for their core task as contractile units in the heart, and Ca²⁺ dysregulation is one of the main contributors to failure of the heart as pump. Yet, Ca²⁺ signaling in cardiomyocytes is equally pivotal as a mechanism for regulating cardiomyocyte growth and physiological remodeling. Further, Ca²⁺-handling mechanisms are remodeled in disease, generating a unique link with contraction and arrhythmias in heart disease (Denham et al. 2018). Such feedback loops involving these dual roles of Ca²⁺ in the cardiomyocyte may represent ideal targets for therapy (Hulot et al. 2012; Gabisonia and Recchia 2018). To gain greater insight into these mechanisms and to develop strategies for their exploitation for



Figure 6. Excitation–transcription coupling. (1) $InsP_3R$ -mediated cytosolic Ca^{2+} increase induces activation of different signaling pathways: (2) Ca^{2+} activates cytosolic and nuclear CaMKII that phosphorylates the inhibitory transcription factor histone deacetylase (HDAC) and (3) induces its export out of the nucleus. (4) MEF2 is activated and this triggers hypertrophic genes expression. (5) Ca^{2+} increases, including via InsP₃Rs, activates calcineurin (CnA), leading to dephosphorylation of nuclear factor of activated T-cells (NFAT) and its translocation to the nucleus. (6) NFAT then activates the transcription of hypertrophic genes including fetal genes (InsP₃R, NPPA, NPPB, RCAN1) and can also repress miR-133. (7) Nuclear Ca^{2+} signals arising from InsP₃R can contribute to activation of nuclear CnA and trigger pathways for hypertrophy (9). (7) miR-133 suppresses expression of NFAT, CnA, and InsP₃R, which will inhibit the hypertrophic responses previously described (8).

therapeutic ends, novel approaches and methodologies are required. Further insights into cardiomyocyte physiology and mechanisms underlying ECC are expected to emerge with the development of new technologies including live cell imaging, superresolution microscopy, and in particular automated image analysis and artificial intelligence for high throughput and discovery (Sacconi et al. 2006; Jayasinghe et al. 2018a). Using multiomics approaches and single-cell analysis, new molecular targets and their interactions that determine the physiological status of the cardiomyocyte will be discovered (Barwari et al. 2016; Perrino et al. 2017; See et al. 2017; Thienpont et al. 2017; Gilsbach et al. 2018), for example, microRNAs, long noncoding RNAs, and epigenetic modifications that govern the expression of Ca²⁺-handling proteins. Notably, some of these microRNAs are found in the circulation in plasma (sometimes in exosomes) and act on the cardiomyocyte compartment as well as being biomarkers of disease progression (Hoefer et al. 2015; Devaux et al. 2017). As our understanding and methodology for physiological analysis of intact tissue develops, analysis of the interactions of the multiple cell types in the heart (e.g., fibroblasts with cardiac myocytes) and their heterogeneity will be made possible (Perbellini et al. 2018; Scardigli et al. 2018b). Through these means, a true picture of how Ca^{2+} signaling at the cellular level is regulated to control cardiac function will emerge.

COMPETING INTEREST STATEMENT

The authors declare no conflict of interest.

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