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HIGHLIGHTS

- Voltage-gated calcium channels (VGCCs) are implicated in heart failure being the major source of calcium influx in cardiomyocytes.
- So far, data regarding the role of VGCCs in heart failure is divergent.
- VGCCs are modulated by β -adrenergic receptor (β AR) stimulation during fight and flight response.
- Over the last decade, it is shown that heart failure is also a structural disease where T-tubule microdomains are lost leading to functional and structural de-coupling of VGCCs and β ARs.
- Recently, using the combination of state of the art “scanning ion conductance microscopy” and FRET/patch-clamp, it is shown that both β ARs and VGCCs are dislocated from their native locations, which may partly explain the pathology of the disease.

ABSTRACT

Voltage-gated calcium channels (VGCCs) are the predominant source of calcium influx in the heart leading to calcium-induced calcium release and ultimately excitation-contraction coupling. In the heart, VGCCs are modulated by the β -adrenergic signaling. Signaling through β -adrenergic receptors (β ARs) and modulation of VGCCs by β -adrenergic signaling in the heart are critical signaling and changes to these have been significantly implicated in heart failure. However, data related to calcium channel dysfunction in heart failure is divergent and contradictory ranging from reduced function to no change in the calcium current. Many recent studies have highlighted the importance of functional and spatial microdomains in the heart and that may be the key to answer several puzzling questions. In this review, we have briefly discussed the types of VGCCs found in heart tissues, their structure, and significance in the normal and pathological condition of the heart. More importantly, we have reviewed the modulation of VGCCs by β ARs in normal and pathological conditions incorporating functional and structural aspects. There are different types of β ARs, each having their own significance in the functioning of the heart. Finally, we emphasize the importance of location of proteins as it relates to their function and modulation by co-signaling molecules. Its implication on the studies of heart failure is speculated.

Key words: Heart failure, voltage gated calcium channels, β -adrenergic receptors, microdomains, T-tubules, Crest

INTRODUCTION

Cardiomyocyte contraction depends upon synchronous movements of calcium into and out of the cell and fast cycling of calcium between the cytosol and sarcoplasmic reticulum (SR). The calcium influx is predominantly carried out by cardiac L-type calcium channels (LTCCs), a class of voltage-gated calcium channels (VGCCs). In the embryonic heart, contraction depends on the calcium ions that enter the cytoplasm through extracellular space whereas in the adult heart it also depends on the calcium ions released from intracellular stores such as SR. Initially, in response to depolarizing stimulus, calcium ions enter cardiac myocytes through the activated LTCCs causing a localized increase in the calcium concentration (Bers, 2008). Calcium influx through LTCCs continue till they are inactivated in a negative feedback manner due to resulting high calcium in dyadic cleft. These calcium ions then bind to ryanodine-sensitive calcium receptors, RyR2- calcium channels, located on SR and activate them to release calcium ions from the SR termed as “calcium-induced-calcium-release” (CICR) (Bers, 2008, Mukherjee and Spinale, 1998, Richard et al. , 2006). The calcium released from the SR rapidly increases the calcium concentration in the dyadic cleft, which within tens of milliseconds diffuses into the rest of the cytosol and leads to an increase in the cytosolic calcium. The calcium ions then bind to heart troponin C subunit, moving the troponin complex away from actin. It unmasks the myosin binding site on actin so that myosin head can now bind to actin utilizing ATP hydrolysis, forming a cross-bridge which pulls the actin filament towards the centre of the sarcomere, contracting the muscle. The whole process is termed as excitation-contraction coupling (EC-coupling) (Bers, 2002). Following influx and release from SR, calcium from the cytosol must be removed and cytosolic calcium concentration must return to its resting level to allow cardiomyocyte relaxation. Calcium removal from the cytosol is controlled by calcium transport by (1) the SR calcium ATPase (SERCA) 2) the sodium-calcium (Na-Ca) exchanger, and (3) slower systems

(including calcium transport by mitochondria and the sarcolemmal calcium-pump) (Aronsen et al. , 2016). As the increase in cytosolic calcium is predominantly due to calcium release from SR, recycling of calcium into the SR by SERCA is the principal determinant of cytosolic calcium removal. Its activity is also controlled by binding of the small inhibitory protein phospholamban. Phosphorylation of phospholamban relieves the inhibition causing an increase in SERCA activity (Kranias and Hajjar, 2012). To maintain steady state contraction and relaxation, the calcium removal from the sarcolemma must be equal to the calcium influx and also SR reuptake must be equal to the calcium released from the SR during CICR. There are two feedback mechanisms in place that lead to the maintenance of calcium concentrations during contraction and relaxation. First mechanism is calcium-dependent inactivation (CDI) of LTCCs. Due to the proximity of LTCCs to RyRs in the dyadic cleft, the release of calcium from RyRs during CICR rapidly increases the dyadic calcium concentration, triggering the inactivation of LTCCs. This works like a localized negative feedback loop whereby a large calcium release into the cytosol restricts further calcium influx through the LTCCs. Second is the balance between the activity of SERCA and Na-Ca exchanger. SERCA and Na-Ca exchanger mediated calcium removal from the cytosol together determines the amount of calcium uptake by the SR or extruded from the cell, respectively. High SERCA activity and low Na-Ca exchanger activity will increase SR calcium uptake and thus increase the calcium transient magnitude in the next heartbeat (Aronsen et al., 2016). However, Na-Ca exchanger activity is regulated by the cytosolic calcium, promoting high calcium extrusion when cytosolic calcium concentration is high. This tends to reduce SR calcium load. This mechanism also works like a negative feedback loop controlling steady state excitation-contraction coupling (for reviews see (Aronsen et al., 2016, Bers, 2008, Eisner et al. , 2013, Shannon and Bers, 2004). Both CICR and CDI are involved in the control of the duration of

an action potential and have a significant function in the remodelling of calcium signalling during the action potential.

Contraction and relaxation of the heart is tightly regulated by autonomic and hormonal control, which is caused by catecholamine binding to β -adrenergic receptors (β ARs), which are heteromeric GTP binding protein (G-protein) coupled receptors (GPCRs) that trigger GDP-GTP exchange at the stimulatory G-protein subunit $G\alpha_s$. All these processes of calcium release and contraction can be either enhanced or reduced by calcium channels and β AR agonists or calcium channel blockers respectively (Mukherjee and Spinale, 1998).

Given the importance of calcium signaling in the functioning of heart, several cardiovascular disorders have been characterized with accompanying changes in calcium homeostasis or changes in calcium handling proteins. Alterations in calcium handling proteins and/or calcium cycling processes have been extensively reviewed before (for reviews see (Aronsen et al., 2016, Davlourous et al. , 2016, Kho et al. , 2012, Lindner et al. , 2002, Yano et al. , 2005). As an example, congestive heart failure (CHF) and hypertrophy, which are characterized by the structural and functional impairment of ventricle to get filled with or eject blood, involves a reduction in the calcium entry, EC-coupling and myocyte sensitivity to calcium concomitant with myocyte hypertrophy, fibrosis, and increased cardiac cell death. This is accompanied by the activation of the sympathetic nervous system, renin-angiotensin system and chronic hyper-activation of the β ARs (Baker, 2014, Woo and Xiao, 2012). The importance of involvement of both VGCCs and β ARs is highlighted by the fact that blockers of both are used as therapeutic agents (Aronow, 2010, Pascual et al. , 2016). Modulation of cardiac LTCCs by β ARs has also been described using cells isolated from animal models. However, the extent of dysfunction of LTCCs in heart failure and up to what extent their modulation is modified in heart failure is debatable.

We have focussed this review on 1) Brief knowledge of cardiac VGCCs, β AR and their spatial location 2) Modulation of VGCCs by β ARs 3) Changes in the modulation of VGCCs by β ARs during pathological conditions 4) Modifiers of functional and structural coupling between VGCCs and β ARs. Of note, our review highlights the importance of spatial location of VGCCs and β ARs on the cardiomyocyte sarcolemma in the context of structural remodelling that occurs during heart failure.

CARDIAC VOLTAGE-GATED CALCIUM CHANNELS

Two types of VGCCs are expressed on the sarcolemma of cardiomyocytes- LTCCs and T-type voltage-gated calcium channels (TTCCs). They are distinguished based on their gating properties and their differential sensitivity to pharmacological agents (Hess et al. , 1986). LTCCs express throughout the lifespan and have a main role in maintaining the plateau phase of the action potential by allowing calcium influx for EC-coupling in the heart (Bers, 2002). On the other hand, functional roles of TTCCs are diverse depending on the mammalian species, heart region, age and various cardio pathology (Ono and Iijima, 2010).

L-type voltage-gated calcium channels

LTCC derives its name from the slow kinetics of current decay (L for long-lasting, current: ICaL) and it belongs to the category of high voltage-activated channels. It is also called by the name dihydropyridine receptor in cardiac biology. The LTCC activates at potentials positive to -40 mV, peaks at 0 to $+10$ mV, and tends to reverse at $+60$ to $+70$ mV, following a bell-shaped current–voltage relationship (Reuter, 1979, Reuter et al. , 1988, Wang et al. , 2004). LTCCs are located in the T-tubules where they are in close proximity to RyR2 channels on SR (Jaleel et al. , 2008, Treinys and Jurevicius, 2008, Weiss et al. , 2013). There are several isoforms of LTCCs out of which, isoform $Ca_v1.2$ conducts the primary calcium current in cardiac myocytes (Dolphin, 2006, Fu et al. , 2014, Hulme et al. , 2006). Upon

activation, calcium enters through these channels and stimulates the release of calcium by RyR2 channels by the process of CICR (Bers, 2002).

The sympathetic nervous system releases catecholamines such as epinephrine and norepinephrine during the fight-or-flight response and increases I_{CaL} through Ca_v1.2 isoform leading to enhanced cardiac performance (Baker, 2014, Hulme et al., 2006). However excess calcium influx through Ca_v1.2 has been linked to necrotic myocyte death, cardiac dysfunction and premature death (Jaleel et al., 2008).

Structurally, LTCCs are heteromeric proteins with four subunits- α_1 , $\alpha_2\delta$, β and γ (Dolphin, 2006, Treinys and Jurevicius, 2008, Van Petegem and Minor, 2006). But, cardiac Ca_v1.2 consists only of three subunits- α_1 , $\alpha_2\delta$, and β (Hofmann et al., 2014, Mukherjee and Spinale, 1998, Treinys and Jurevicius, 2008). α_1 is the pore-forming subunit which also determines the important characteristics such as channel selectivity for calcium, voltage-dependent activation and the sensitivity to agonists and antagonists (Hofmann et al., 2014). It consists of four covalently linked homologous domains (I-IV) and cytoplasmic N-terminus and C-terminus. Each domain consists of six transmembrane helices (S1 to S6) linked by variable cytoplasmic loops. S4 transmembrane helix in each domain consists of positively charged amino acids lysine and arginine which collectively form voltage sensor. Voltage sensor induces voltage dependent conformational changes in the channel for activation. The P loops between S5 and S6 helices line the pore of the channel (Dolphin, 2006, Hofmann et al., 2014). α_1 is 242 kDa in its full-length, but *in vivo*, it is 210 kDa due to the proteolytic processing of the distal C-terminus (dCT) at Ala1800. This processed dCT remains non-covalently associated with the truncated α_1 subunit at the proximal C-terminus (pCT) and exhibits an autoinhibitory role on channel function. Auxiliary subunits i.e $\alpha_2\delta$, and β are associated with the subunit and are involved in anchorage, trafficking, and regulatory functions. β -subunit can modulate the expression of Ca_v1.2 at the cell surface (Fu et al.,

2011, Hofmann et al., 2014, Hulme et al., 2006, Oz et al. , 2017, Stolting et al. , 2015). Using co-sedimentation assays and FRET experiments Stölting et al. have shown a direct interaction of β -subunit and actin in mouse cardiomyocyte HL-1 cell line. Actin interacts with Src homology 3 domain on β -subunit. This association facilitates the forward trafficking of the $Ca_v1.2$, hence leading to increased calcium current density on the plasma membrane (Stolting et al., 2015). Further, upregulation of β -subunit is reported to be associated with heart failure (Hullin et al. , 2007). Detailed reports on the expression and function of LTCCs in the heart and cardiovascular disorders have been published before (for reviews see (Benitah et al. , 2010, Benitah et al. , 2002, Bodi et al. , 2005, Hess et al., 1986, Mukherjee and Spinale, 1998, Treinys and Jurevicius, 2008). Overall, most of the studies have shown that while the amplitude of I_{CaL} is increased in hypertrophied and failing myocytes, its density on the cell surface (normalized to cell capacitance, as an indirect measure of cell surface) is similar to the control myocytes (Benitah et al., 2002, Loyer et al. , 2008, Song et al. , 2005).

Structural location of LTCCs in cardiomyocytes

The questions of the fate of LTCCs in heart failure, their regulation by β ARs in heart failure and inconsistent data across researchers have puzzled the scientific community for a long time. This field has upto a certain extent advanced through the use of scanning ion conductance microscopy (SICM) and patch clamp to address this question. SICM is a non-contact and non-optical microscopy method which uses a glass pipette as a scanning probe (Hansma et al. , 1989) for visualization of the three-dimensional topography of live cells (Korchev et al. , 2000, Novak et al. , 2009). It is based on measuring the changes in the ion flow through the pipette (pipette similar to glass pipette used in patch-clamp) positioned at the cell surface and allows resolution of the structural features of cardiomyocytes, such as Z-grooves, cell crests located between them and T-tubules. The SICM pattern of T-tubule distribution co-localizes well with the T-tubular marker di-8-ANEPPS, a voltage sensitive

dye (Nikolaev et al. , 2010). The technique of combined SICM and patch clamp called as “super-resolution scanning patch-clamp” developed and validated by Gorelik and colleagues can provide a map of functional ion channels on the cell surface with nanoscale resolution (Bhargava et al. , 2013). With this technique, it was possible to locate ion channels within T-tubule and crest microdomains. Using “super-resolution scanning patch-clamp” it was recently shown that functional LTCCs (through which currents could be recorded) predominantly reside in T-tubules. In this method, first the topography of cardiomyocyte is obtained and then the patch-pipette is lowered at a precise location on the sarcolemma, in this case, either T-tubule or crest. Though the location of LTCCs on the sarcolemma was described before as membrane localization, super-resolution scanning patch-clamp for the first time gave direct evidence of physical location of clusters of functional LTCCs in T-tubules and very little functional LTCCs on the crest sarcolemma (Bhargava et al., 2013) (Fig. 1). Deduction of information of spatial location of functional LTCCs was not possible with conventional microscopy or convention patch clamp techniques. The T-tubular structural location of LTCCs is of prime importance in light of the fact that, in heart failure, structural abnormalities accompany a number of functional changes in cardiomyocytes. Overall, there is a clear evidence of T-tubule loss and disorganization during pathological alterations in the heart ((Nikolaev et al., 2010, Swift et al. , 2012), for reviews see (Crossman et al. , 2017, Crossman et al. , 2011, Gorelik et al. , 2013, Guo et al. , 2013, Ibrahim et al. , 2011)) (Fig. 2). This T-tubule loss and disorganization is consistently observed in isolated cardiomyocytes from different animal models of heart failure of different species including human cardiomyocytes (Guo et al., 2013). In the beginning, the T-tubule remodelling was probed using microscopy in fixed and stained cells. Gorelik group from Imperial College London, for the first time, obtained topography of live, unfixed and unstained cardiomyocytes using SICM. They also confirmed the loss of T-tubule openings on the

surface of human cardiomyocytes (Lyon et al. , 2009) which was consistent with the disorganization seen in a rat model of heart failure (Lyon et al., 2009).

Most interestingly, using the same rat model of heart failure, it is now shown that, not only the function of LTCCs, but their spatial location is also altered in heart failure. Normally LTCCs are found deep inside the T-tubules, but during heart failure, LTCCs are not only present in T-tubules but also at crest locations where they are rarely present in control cells (Sanchez-Alonso et al. , 2016) (Fig. 2). Moreover, open probability of only those LTCCs was increased which were moved from their native locations (Sanchez-Alonso et al., 2016). Using computational models and calcium imaging it was demonstrated that this relocated LTCC current could contribute to early-after depolarizations and initiate re-entrant arrhythmias (Sanchez-Alonso et al., 2016). This observation is of prime importance in light of the fact that early studies on failing human cells also suggested that open probability of LTCC increases in heart failure but in the absence of spatial location nothing could be said about the changing location of those dysfunctional channels. This also provides answer to various studies where no change was detected in the LTCC channel activity during heart failure. It could be due to the masking of microdomain readout in the whole cell recording conditions.

T-type voltage-gated calcium channels

TTCCs (T for transient, current: I_{CaT}) are distinguished from LTCCs on the basis of their kinetics of activation and inactivation. They are low voltage activated with activation threshold for I_{CaT} being -70 to -60 mV. I_{CaT} is fully activated at -30 to -10 mV at physiological calcium concentration. I_{CaT} is completely inactivated at membrane potentials more positive than -40 mV (Ono and Iijima, 2010). Earlier, TTCC was considered to play a minor functional role in cardiomyocytes. However, after the discovery of TTCC antagonists and cloning of its isoforms- Ca_v3.1, Ca_v3.2, and Ca_v3.3 in the early 90s, its importance was acknowledged. TTCCs show significant contribution in cardiac automaticity, development

and EC-coupling in normal cardiac myocytes (Ono and Iijima, 2010, Zhou and January, 1998). TTCCs also play a major role in the pacemaker activity of adult sinus node. This property is attributed to their low threshold of voltage activation which allows them to get activated with even a slight change in the membrane potential from the resting potential (Katz, 1996, Yasui et al. , 2005). This was supported by a number of studies that reported high expression of TTCCs in SA node (Bohn et al. , 2000, Hagiwara et al. , 1988, Ono and Iijima, 2005). Knock out mouse models of TTCCs further emphasized the role of T-type channel isoforms in cardiac pacemaking and impulse conduction (Chen et al. , 2003, Mangoni et al. , 2006, Thuesen et al. , 2014). Along the same lines, isoform specific $Ca_v3.1$ knockout mice shows bradycardia and slowing of the atrioventricular conduction (Mangoni et al., 2006).

Electrophysiological and immunostaining techniques have shown that TTCCs are highly concentrated on cardiomyocytes surface than in T-tubules (Jaleel et al., 2008). Hence, calcium entering through TTCCs is not taken up by the SR to the same extent as the calcium entering through LTCCs. This explains why calcium influx from TTCCs induces only little calcium release from SR (Jaleel et al., 2008). It is also reported that calcium influx through TTCCs doesn't cause increased myocyte contractility, calcium mediated pathologies and death (Jaleel et al., 2008, Katz, 1996). $Ca_v3.1$ and $Ca_v3.2$ are the major isoforms expressed in cardiomyocytes of an embryo, although $Ca_v3.3$ mRNA was also reported to be expressed in Purkinje fibers. During fetal period, current density and expression of TTCCs changes and they contribute to electrical activity in the early embryonic stages. $Ca_v3.1$ has been reported to be functional in mouse hearts at the middle embryonic stage and both $Ca_v3.1$ and $Ca_v3.2$ in rat hearts at the middle embryonic to perinatal stages (Ono and Iijima, 2010, Yasui et al., 2005). With age, their expression is lost, almost undetectable in ventricular myocytes of the adult heart. But they are prevalent in the sinoatrial node, facilitating pacemaker

depolarization. In pathological conditions such as cardiac hypertrophy and heart failure, TTCCs have been found to be re-expressed in atrial and ventricular myocytes, contributing abnormal electrical activity and excitation-contraction coupling through a small contribution of calcium release from SR (Ono and Iijima, 2010, Vassort et al. , 2006, Wang et al. , 2013, Yasui et al., 2005). This increased I_{CaT} has relatively high sensitivity towards Ni²⁺ suggesting that Ca_v3.2 is the re-expressed TTCC under pathological conditions (Vassort et al., 2006, Yasui et al., 2005). It has been shown that increased calcium influx through Ca_v3.2 induces calcineurin/NFAT (nuclear factor of activated T-cell) hypertrophic signaling (Houser, 2009, Houser and Molkenin, 2008, Ono and Iijima, 2010, Yasui et al., 2005). Various studies have investigated the role of TTCCs in the pathology of heart disorders. For details on TTCCs in the heart and pathological disorders, please refer to the detailed reviews published before (Ono and Iijima, 2010, Yasui et al., 2005). Spatial location of functional TTCCs on the cardiomyocyte sarcolemma has not been investigated so far. This is limited by the fact that there is no/little expression of TTCCs in healthy adult ventricular cardiomyocytes and that the TTCCs have a tiny conductance. However, it would be interesting to investigate the spatial location of TTCCs in heart failure where they are re-/overexpressed.

Unlike LTCCs, TTCCs are found to consist only of α_1 subunit (Ono and Iijima, 2010). Electrophysiological studies have shown that recombinant LTCC requires auxiliary subunits for normal gating behaviour, but in the case of recombinant Ca_v3.1 and Ca_v3.2, currents similar to native I_{CaT} was seen without auxiliary subunits (Zhang et al. , 2013). It's not yet clear whether auxiliary subunits for native TTCCs exist or not.

β -ADRENERGIC RECEPTOR IN CARDIAC MYOCYTE

The β ARs are G-protein-coupled receptors (GPCRs) found on the membrane of cardiac myocytes. The sympathetic nervous system modulates cardiac function (such as heart rate

and contractility) by activating β ARs during fight or flight response. Acute β AR stimulation regulates cardiac output in the fight-or-flight response, whereas chronic β AR stimulation plays an important role in physiological and pathological cardiac remodelling (Woo and Xiao, 2012). Due to insufficient cardiac function in pathological conditions, the sympathetic system releases norepinephrine which initiates the chronic activation of β AR (Baker, 2014, Davidson and Koch, 2001, Engelhardt et al. , 1999, Nikolaev et al., 2010, Woo and Xiao, 2012). When catecholamines bind to β ARs, conformational changes occur in the receptor enabling its coupling to heterotrimeric G-proteins. This results in the substitution of the GDP on the $G\alpha$ subunit of G-proteins by GTP and subsequent dissociation of the heterotrimer into active $G\alpha$ -GTP and $G\beta\gamma$ subunits to mediate downstream signalling (Wess, 1997). $G\alpha$ -GTP then stimulates adenylyl cyclase (AC) which results in the formation of cyclic AMP (cAMP). Increased cAMP levels regulate a wide variety of cellular processes activating a number of downstream signaling molecules. One such pathway involves the activation of cAMP dependent protein kinase A (PKA) by the dissociation of regulatory subunits (PKA-RS) from the catalytic subunits (PKA-CS). This activated PKA then phosphorylates further targets including cardiac calcium channels (An et al. , 1996, Baker, 2014, Bernstein et al. , 2011, Davidson and Koch, 2001, Fujita and Ishikawa, 2011, Kamp and Hell, 2000, Lohse et al. , 2003, Madamanchi, 2007, Marsh, 1989, Oz et al., 2017, Weiss et al., 2013, Woo and Xiao, 2012). Calcium channel modulation by PKA is described in detail in the next section. There are extensive changes in the downstream cAMP signaling in heart failure which include decreased cellular levels of cAMP due to increased activity of protein phosphatase 1 (PP1) (Movsesian, 2004) and due to desensitization of β ARs (Perera and Nikolaev, 2013). Rat models of heart failure showed a dramatic decrease in the expression and activity of phosphodiesterases (PDEs) in the heart (Perera and Nikolaev, 2013). Therefore, it is proposed

that this decrease in cAMP-hydrolyzing PDE activity could be a short-term adaptive mechanism to counterbalance the reduction in cAMP production by desensitized β ARs.

Three subtypes of β ARs have been cloned (β_1 AR, β_2 AR, β_3 AR). β_1 AR is found primarily in the heart and comprises 75-80% of the β ARs found in the heart. The β_2 AR is expressed in various tissues including heart and comprises 20-25% of cardiac β ARs. β_1 ARs and β_2 ARs are expressed in the ratio of 70-80%:30-20% in the human ventricle and 60-70%:40-30% in human atrium (Baker, 2014, Biolo et al., 2006, Gorelik et al., 2013, Lohse et al., 2003, Madamanchi, 2007, Wallukat, 2002, Woo and Xiao, 2012). The β_3 AR is found in the adipose tissue, and only minimally in the heart. Another subtype, β_4 AR is also known which is considered as a low affinity state of β_1 AR, which awaits genetic and pharmacologic characterization (Madamanchi, 2007). There are significant differences in the signaling pathways and cellular responses of the different β AR subtypes as described below (Baker, 2014, Bernstein et al., 2011, Biolo et al., 2006, Gorelik et al., 2013, Woo and Xiao, 2012). The different signaling pathways used by the β_1 ARs and the β_2 ARs also suggest that these proteins may be physically separated in the cardiomyocyte membrane providing evidence for spatial and functional signaling microdomains. Signaling through β_1 ARs and β_2 ARs is described below in brief highlighting the differences in the signaling.

Signaling through β_1 ARs

When stimulated, cardiomyocyte β_1 ARs primarily binds to the G stimulatory (Gs) protein. The $G\alpha$ subunit of the Gs protein ($G\alpha_s$) activates AC and PKA. Through β_1 AR signaling, PKA phosphorylates a number of key proteins such as LTCCs, RyR2 receptors, phospholamban and cardiac contractile proteins, generating a positive inotropic and lusitropic effect. During heart failure β_1 AR levels reduce up to 50% reflecting severely diminished β_1 AR signaling likely due to sustained elevated catecholamine levels (Freedman and Lefkowitz, 2004). β_1 AR knockout mice showed no response to catecholamine stimulation

despite the presence of β_2 ARs (Rohrer et al. , 1996). On the other hand, cardiomyocyte-targeted β_1 AR overexpressing mice developed dilated cardiomyopathy and heart failure at young age. This is similar to the pathology caused by chronic catecholamine overstimulation (Engelhardt et al., 1999) which reinforces the view that increased β AR signaling that may happen in chronic stimulation plays an important role in pathological cardiac remodelling.

Signaling through β_2 ARs

β_2 ARs can activate PKA in the same manner as described above for β_1 ARs. However, through β_2 AR signaling, only LTCCs are phosphorylated with smaller inotropic and no lusitropic effects (Gorelik et al., 2013). In addition to Gs, the β_2 ARs can couple to pertussis toxin - sensitive G inhibitory (Gi) protein upon sustained activation opposing the positive inotropic effect (Baker, 2014, Bernstein et al., 2011, Lohse et al., 2003, Madamanchi, 2007, Steinberg, 1999). Gi coupling releases the activated $G_i\alpha$ subunit, which inhibits AC activity, which causes downstream activation of the mitogen-activated protein kinases (MAPK). Of note, $G_i\alpha$ coupling also activates the cytosolic effector molecule phospholipase A2 (cPLA2), which causes cAMP-independent enhancement of calcium signaling and cardiac contraction. This β_2 AR-cPLA2 pathway is reported to operate during inefficient activation of β_1 AR-Gs-cAMP pathway thus supplementing defective β_1 AR signalling (Pavoine and Defer, 2005). Due to the dual capability of β_2 ARs to couple either to Gs or Gi, the effect of their activation varies depending on the species, and the developmental or pathophysiological state of the heart. Of note, β_2 AR levels are reported to remain constant during heart failure (Madamanchi, 2007). The β_2 AR knockout mice did not suffer from developmental defects and showed no significant differences in the cardiovascular phenotype which is in sharp contrast to β_1 AR knockouts. The β_2 AR knockout mice also showed typical response to catecholamine stimulation which indicates that β_1 AR is the signaling pathway for the catecholamine-induced changes in cardiac physiology. Interestingly, mice with cardiac-specific overexpression of

β_2 ARs displayed enhanced basal contractility and cardiac function with minimal pathology (Milano et al. , 1994). This led to many studies probing the potential of β_2 AR overexpression as a therapeutic approach (Akhter et al. , 1997, Dorn et al. , 1999), however this line of research is hampered by many conflicting studies (Du et al. , 2000, Freeman et al. , 2001).

Termination of β AR signaling following stimulation

To prevent the overstimulation of β AR receptors, which can be detrimental, there are several regulatory mechanisms in place (Ferguson, 2001). These processes involve receptor desensitization which acts as a negative feedback to the adrenergic signal, under conditions of prolonged agonist stimulation. The first of these processes is the deactivation of G-proteins. Soon after the dissociation of the coupled G-protein into active $G\alpha$ and $G\beta\gamma$ subunits, conformational changes occur that again causes formation of inactive G-protein. This process is rapid and ensures dose dependent nature of β AR signal propagation. Prolonged catecholamine stimulation overthrows the short-term active/inactive cycling of the G-protein and triggers further negative feedback regulation of β AR activity. Second, upon activation β ARs undergo homologous desensitization which occurs within minutes of agonist stimulation (Barak et al. , 1999a, Barak et al. , 1999b). Homologous desensitization begins when the dissociated $G\beta\gamma$ subunit binds with the active form of a β AR kinase 1 (β ARK1). β ARK1 is translocated to the activated receptor after binding with the activated $G\beta\gamma$ subunit, where it phosphorylates the agonist-occupied β AR (Freedman and Lefkowitz, 2004). β ARK1 is the most prominent cardiac G-protein coupled receptor kinase. Phosphorylation of the receptor occurs at the C-terminus and targets it for arrestin-induced uncoupling from the G-protein. β ARs can also undergo heterologous desensitization which occurs when the β ARs are phosphorylated through PKA (Freedman et al. , 1995). Decreased density of β ARs on the cell surface was also demonstrated in cultured neonatal cardiomyocytes upon agonist exposure leading to the attenuation of β AR signal (Sibley and Lefkowitz, 1985). In both

desensitization cases, β AR phosphorylation allows for β -arrestin to bind and interfere with future association with G-proteins, functionally uncoupling the receptor (Perry et al. , 2002). Binding to β -arrestin increases β AR's affinity for adaptor protein (AP)-2 and clathrin (Claing et al. , 2002). The receptors are then internalized via clathrin-coated vesicles, within minutes of stimulation (Zhang et al. , 1996). Following internalization, receptors are transported to endosomes where they can be recycled back to the plasma membrane for the next cycle of activation (Claing et al., 2002). In response to prolonged receptor stimulation, the internalized receptor can instead be degraded in the liposomes. This down-regulation process lowers the total number of receptors in the cell to relieve chronic overstimulation. Down-regulation is initiated within hours to days after consistent receptor internalization. Of note, down-regulation is reported to occur in the early development of the heart disease, but slowly than uncoupling, taking hours to days (Biolo et al., 2006, El-Armouche et al. , 2007, Engelhardt et al., 1999, Ungerer et al. , 1993, Ungerer et al. , 1994, Wallukat, 2002).

Spatial location of β ARs

After successful application of SICM to image normal and failing cardiomyocyte topography, Gorelik group for the first time combined SICM with fluorescence resonance energy transfer (FRET) imaging to probe the structural location of β ARs. Non-specific agonist isoproterenol was applied together with the specific inhibitor of either β_1 ARs (CGP) or β_2 ARs (ICI) to record specific signaling through either β_2 ARs or β_1 ARs respectively (Nikolaev et al., 2010). Interesting results were obtained when the drugs were applied either to T-tubules or crest. The results suggested that functional β_1 ARs are located across the entire surface of cardiomyocytes whereas β_2 ARs are located exclusively in the deep T-tubules (Nikolaev et al., 2010) (Fig. 1). And hence, cAMP signaling via β_2 ARs gives a fine control on LTCC modulation which also resides deep within T-tubules. Using a rat model of chronic heart failure and using the same combination of SICM-FRET technique they further showed that

during heart failure, β_2 ARs were redistributed from the T-tubules to the cell crests (Fig. 2.). This redistribution lead to the diffused receptor-mediated cAMP-signaling. cAMP generated by activation of β_2 ARs, usually confined to smaller microdomains, was generated globally in heart failure (Nikolaev et al., 2010). It is possible that this redistribution of β_2 ARs in heart failure changes compartmentation of cAMP and contributes to the failing myocardial phenotype.

MODULATION OF LTCC ACTIVITY IN THE HEART BY β -ADRENERGIC RECEPTOR SIGNALING

$Ca_v1.2$ channels are modulated by β ARs/cAMP signaling pathway in the heart. In the fight-or-flight response, sympathetic system activates β ARs transiently. This transient stimulation of β ARs has different functional consequences as against sustained β AR activation which occurs in pathological states as described in the previous section. Both β_1 and β_2 ARs couple to AC via Gs proteins, thus ensuring the cascade: activation of AC, increase in cAMP, activation of protein kinase A (PKA) and calcium channel phosphorylation. Many different receptors can stimulate cAMP synthesis in the heart but only β ARs can produce cAMP-dependent stimulation of the LTCCs in cardiomyocytes (Warrier et al. , 2007). This difference is due to the compartmentation of generated cAMP. β ARs can stimulate cAMP production in both cytosolic and caveolar compartments as opposed to other receptors which only stimulate cAMP production in the cytosolic compartment. Caveolar compartments are associated with β AR regulation of LTCC function and this is the reason why receptors which can stimulate cAMP in caveolar compartments can modulate LTCCs (Warrier et al., 2007). At the molecular level, dCT of LTCCs contains a leucine zipper motif that interacts with A-kinase anchoring protein (AKAP15). PKA anchors dCT through AKAP15, this complex interacts directly with the β subunit of LTCCs through pCT and phosphorylates LTCC $Ca_v1.2$. Phosphorylation leads to 3- to 4-fold increase in ICa_L in the cell and increased

cardiac contractile force (Catterall, 2015, Fu et al. , 2013, Fu et al., 2014, Fuller et al. , 2010, Hofmann et al., 2014, Hulme et al. , 2003, Hulme et al., 2006, Mukherjee and Spinale, 1998, Oz et al., 2017, Treinys and Jurevicius, 2008, Yang et al. , 2016). Voltage dependence of I_{CaL} also shifts to more hyperpolarized potentials (Benitah et al., 2010, Chen et al. , 2002, Collis et al. , 2007) resulting in a gain of function. This shift has only been reported by few groups and has not been reproduced in many studies (Reuter, 1987). Also upon β AR stimulation, inactivation of LTCC is mainly due to calcium (calcium dependent inactivation, CDI), due to a slow-down of VDI (Findlay et al. , 2008) . The fast inactivation time constant of I_{CaL} of rat ventricular cardiomyocytes was “unexpectedly” slowed down after I_{CaL} was increased by β AR stimulation (Alvarez et al. , 2004, Haase et al. , 2005) which would also result in increased calcium influx. At the level of single channel activity, β AR stimulation leads to an increase in the channel's open probability shifting to Mode 2 (Reuter, 1987, Reuter et al. , 1986, Tsien et al. , 1986, Yue et al. , 1990). It is important to note that cardiac LTCCs have multiple gating modes: mode 0 in which channels do not open or open very rarely, mode 1 in which the open probability is low, and mode 2 in which the open probability is higher and the openings are long-lasting (Reuter et al., 1986, van der Heyden et al. , 2005). Early studies by Maki et al. have shown that in cultured rat neonatal ventricular myocytes, exposure to norepinephrine, results in increased mRNA levels of α_1 subunit and number of functional VGCCs on the membrane (Maki et al. , 1996). However, there is no further evidence in literature supporting this.

Multiple LTCC sites for phosphorylation by PKA have been identified in α_1 subunit *in vitro*, but most of them are not required for β AR regulation *in vivo* (Fu et al., 2014, Hulme et al., 2006, Yang et al., 2016). Hulme et al. showed in dissociated rat ventricular myocytes that on isoproterenol treatment, a non-selective activator of β AR, there was an increased phosphorylation of S1928 in dCT. A similar result was seen with forskolin, a direct activator

of AC, indicating the role of cAMP and PKA in the phosphorylation (Hulme et al., 2006). In embryonic heart, deletion of dCT resulted in the loss of β AR regulation of ICaL thereby causing the death of embryo due to heart failure (which model which system). This result showed that autoinhibitory signaling complex formed with $\text{Ca}_v1.2$ and dCT anchored with PKA via AKAP15 is a modulatory substrate for β AR regulation and its disruption leads to heart failure (Fu et al., 2014, Fu et al., 2011, Yang et al., 2016). On pre-treatment with selective β_1 AR and β_2 AR antagonists, there was a reduction in phosphorylation of S1928 by 79% and 42% respectively. When both the antagonists were used together, there was a complete blockage of phosphorylation. In presence of 1,2-bis(2-aminophenoxy) ethane- N -, N - tetraacetic acid (BAPTA)-acetoxymethyl ester to buffer intracellular calcium, only phosphorylation by β_1 AR stimulation was seen. Whole-cell patch clamp in presence of BAPTA showed 98% increase in current through β_1 AR stimulation. This indicated that the phosphorylation of S1928 occurs via both β_1 AR and β_2 AR stimulation at an elevated level of calcium, but at basal calcium levels only β_1 AR was responsible for phosphorylation (Hulme et al., 2006).

Interestingly, calcium current through $\text{Ca}_v1.2$ channels with S1928 mutated to Ala (S1928A) could still be regulated by β AR stimulation but the level of stimulation was 70-80% compared to that of wild-type $\text{Ca}_v1.2$, indicating that S1928 is responsible only for 20-30% of total response and not required for significant β AR stimulation (Benitah et al., 2010, Ganesan et al., 2006, Hulme et al., 2003, Hulme et al., 2006). By reconstitution studies and *in vivo* proteomics analysis Fu et al. had revealed S1700 to be the key amino acid for phosphorylation, located at the interface between the pCT and dCT, mediating the fight-or-flight response, cardiac homeostasis and normal physiological regulation (Fu et al., 2014). Mutation of S1700 to Ala (S1700A/SA) in mice eliminated the phosphorylation by PKA. This reduced the basal ICaL in neonatal as well as adult cardiomyocytes by ~37% of WT

ICaL value. It also reduced the up-regulation of Ca_v1.2 channel current via β AR/PKA pathway. Still, SA mice have shown to be regulated by PKA phosphorylation (Fu et al., 2014). This regulation might be due to the additional phosphorylation sites, residing either in α_1 or β subunits. Phosphorylation at another conserved phosphorylation site Thr-1704 (T1704) has been shown to be involved in normal β AR regulation of LTCCs. Mutation of T1704 to Ala (T1704A) had shown similar results as SA (Fu et al., 2013, 2014). When both the mutations were present together i.e. S1700A and T1704A (STAA) there was also a reduction in basal ICaL, cellular contractility, impaired exercise capacity and sensitivity to β AR agonists, but complete elimination of β AR stimulation was not seen (Fu et al., 2013). Effect of this double mutation was greater at low levels of β AR stimulation, which shows that effective phosphorylation of S1700 is enhanced by the phosphorylation of T1704, diminishing autoinhibition with an increase in channel activity (Fu et al., 2013). Notably, Thr1704 is phosphorylated by casein kinase II, implicating this constitutively active protein kinase in the control of basal Ca_v1.2 channel activity as well (Emrick et al., 2010, Fuller et al., 2010). Casein kinase II conserved phosphorylation site was originally found in skeletal muscle Ca_v1.1 channels (Emrick et al., 2010). However, Fuller et al. have shown that stimulation of Ca_v1.2 activity through the phosphorylation by PKA requires only S1700 (Fuller et al., 2010). All these studies indicate that multiple phosphorylation sites are responsible for the increase in LTCC current upon phosphorylation by PKA and oppose the long-standing belief that S1928 is the key phosphorylation site.

Phosphorylation of the regulatory β_2 subunit also plays a crucial role in the PKA-mediated up-regulation of ICaL. In dog cardiomyocytes, after phosphorylation of calcium channels by PKA, followed by immunoprecipitation using a polyclonal antibody against C-terminal of β_2 subunit, Haase et al. found that 62kDa β_2 subunit was the major PKA-substrate in the immunoprecipitate and hence suggested that the phosphorylation of β_2 subunit has a major

role in the β AR upregulation of cardiac LTCCs (Haase et al. , 1993). In 1999, using phosphopeptide mapping and micro sequencing, Gerhardstein et al. identified the phosphorylation sites of PKA in β 2 subunit as serine478 (S478) and serine479 (S479) (Gerhardstein et al. , 1999). To confirm the significance of β 2 subunit phosphorylation by PKA, Bunemann et al. used a truncated α_1 subunit lacking S1928 ($\alpha_{1C}\Delta 1905$) which is a PKA-substrate and WT β 2 subunit. Using the truncated channel in HEK cells, they found some barium currents on depolarization of cells. To confirm that this current was due to the phosphorylation of β 2 subunit, they mutated S478 and S479 to alanine (S478A, S479A) and added PKA in the cell system. They observed no current augmentation with $\alpha_{1C}\Delta 1905$ and S478A/S479A β 2 subunit. These results showed that β 2 subunit has a major role in the upregulation of LTCC current upon phosphorylation by PKA (Bunemann et al. , 1999).

The underlying molecular mechanisms of how phosphorylation of sites located either on $Ca_v1.2$ or β 2 results in increased channel opening probability are not completely understood. This could be due to the fact that several other players of calcium handling are also involved.

Modifiers of β AR modulation of LTCCs (functional coupling)

So far, a few other proteins have been identified that modify β -adrenergic regulation of LTCCs (Fig. 1).

A) Sphingosine-1-phosphate (S1P): S1P is a circulating bioactive sphingolipid and has been identified as an important signaling mediator implicated in the regulation of several cellular processes including cardiac calcium handling (Means and Brown, 2009). Early evidence suggested an important regulatory role of S1P in regulating electrophysiological and contractile properties of cardiac myocytes under both basal and β AR stimulation conditions (Landein et al. , 2008, Means and Brown, 2009). Only recently, Egom and colleagues reported that S1P partially reverses the effect of the β AR activation on LTCC current through signalling pathway that involves Pak1 (P21-activated kinase 1) - PP2A (protein phosphatase

2A) interaction. The basal LTCC current, however, was unaffected by S1P (Egom et al. , 2016). Which subtype of β AR signalling was involved was not investigated. More studies are needed to elucidate the role of S1P in cardiovascular disorders although currently available data indicates that that S1P can produce beneficial effects in disease models of cardiac hypertrophy, although it may induce cardiac hypertrophy in normal condition (Li and Zhang, 2016).

B) Ahnak: Another modifier of LTCC- β AR coupling is an important protein “ahnak” that is tightly bound to the LTCC β 2 subunit in cardiomyocytes. Ahnak was originally identified in 1992 as tumour-related gene by Shtivelman and co-workers (Shtivelman et al. , 1992). Ahnak derives its name due to its large size which is approximately 700kDa. β 2 Subunit interaction with ahnak was identified in several cardiac preparations derived from rodent to human heart (Haase, 2007). In humans, polymorphism is identified in the gene loci encoding ahnak. One such ahnak polymorphism, I5236T, interferes with adrenergic stimulation of ICaL (Haase, 2007). Ahnak requires the conserved β subunit modules, SH3 and/or GK, for efficient ahnak/ $Ca_v1.2$ channel interaction. Ahnak’s role as a modifier of LTCC- β AR coupling can be summarised as: ahnak acts as a repressor of ICaL by β 2 subunit sequestration. PKA phosphorylation relieves the inhibition imposed by ahnak. PKA phosphorylation can be mimicked by ahnak-derived fragments carrying a naturally occurring missense mutation Ile5236Thr. Therefore, ahnak-derived peptides are emerging as potent modulators of LTCC current in the adult mammalian heart (Haase, 2007). Ahnak’s interaction with LTCC β 2 subunit during heart failure remains to be determined. Also which subtype of β ARs is involved is not known, though ahnak is expressed throughout the sarcolemma (Hohaus et al. , 2002).

C) Rem GTPase: Rem GTPase is a member of Rad/Rem/Rem2/Gem/Kir (RGK) GTPases that belong to the Ras superfamily of monomeric G-proteins (Colicelli, 2004). Like Ras,

RGK proteins contain a nucleotide binding domain (NBD) that can cycle between GTP- and GDP-bound states. However, these proteins also have long N- and C-terminus extensions, and non-conservative substitutions of residues important for nucleotide binding and hydrolysis compared to Ras (Colicelli, 2004, Finlin and Andres, 1997, Finlin et al. , 2000). Rem GTPase inhibits LTCCs in the heart cells by arresting LTCCs in a low open probability state, without changing the number of channels at the cell surface (Xu et al. , 2010) by binding to the LTCC β 2 subunit (Finlin et al. , 2003). More importantly, the Rem-inhibited calcium channels can be rescued by LTCC activators such as BayK8644, but not by the β AR stimulation (Xu et al., 2010). This indicates that Rem completely eliminated β AR stimulation of LTCCs when overexpressed. Rem proteins are found in heart, and their levels are up/down regulated in cardiac diseases (Chang et al. , 2007, Finlin and Andres, 1997, Tan et al. , 2002). Therefore, they present as important drug targets modulating LTCCs.

Potential modifiers of β AR modulation of LTCCs (structural coupling)

A) **Bridging integrator 1 (BIN1):** BIN1 is essential for localization of LTCCs to T-tubules. This was demonstrated using human and mouse adult cardiomyocytes and using complementary immunocytochemistry, electron microscopy with dual immunogold labeling, and co-immunoprecipitation techniques. BIN1 is a member of the BAR domain protein superfamily which is involved in membrane invagination and endocytosis (Hong et al. , 2010). BIN1 is also known to initiate T-tubule genesis in skeletal muscle cells (Hong et al., 2010). The delivery of LTCCs to BIN1 structures is not a specific property of cardiomyocytes as it also occurs in non-myocyte cell lines. This indicates that other myocyte-specific structures are not essential for this trafficking and that there is an intrinsic relationship between LTCC delivery and its BIN1 scaffold. Therefore up/down regulation of BIN1 may significantly affect LTCC localization to T-tubules and therefore its regulation by β ARs.

B) **Caveolin-3**: In ventricular cardiomyocytes a subpopulation of LTCCs localize to caveolae. Caveolae are specialized microdomains of the plasmamembrane rich in signaling molecules and supported by the structural protein caveolin-3. Of note, caveolin protein expression decreases with age and studies on caveolin knock out (KO) mice support the hypothesis that the loss of caveolin protein causes an aged phenotype (Kawabe et al. , 2001, Ratajczak et al. , 2003). Immunofluorescence studies have shown that LTCCs colocalize with caveolin-3 (the abundant isoform of caveolin in heart) in caveolae microdomains present in the cardiomyocyte sarcolemma as a part of a macromolecular signaling complex necessary for β_2 AR regulation of LTCC current (Balijepalli et al. , 2006, Makarewich et al. , 2012). This is evidenced by the fact that the stimulation of LTCC current by β_2 AR stimulation was eliminated by disruption of caveolae or by small interfering RNA directed against caveolin-3, whereas β_1 AR stimulation of LTCC current remained unaltered (Balijepalli et al., 2006). This means that there is a specific coupling of LTCCs with β_2 ARs within caveolae and also suggests that LTCCs coupled to β_1 AR signaling may be located outside of caveolar microdomains.

MODULATION OF T-TYPE VOLTAGE-GATED CALCIUM CHANNEL ACTIVITY IN THE HEART BY β -ADRENERGIC RECEPTOR SIGNALING

Various neurotransmitters and hormones such as endothelin, bradykinin, ATP, β -adrenergic agonists etc, are known to affect the activity of TTCCs (Vassort et al., 2006). In the literature, β AR modulation of ICaT is less reported. It could be due to the fact that TTCCs are rarely expressed in adult cardiomyocytes. There is some evidence of an increase of ICaT by β AR stimulation and G-proteins as early as 1992, under more physiological conditions (Vassort et al., 2006). In guinea pig ventricular myocytes, isoproterenol increased ICaT (25–100% increase) only at high concentrations (1M) while ICaL was increased at much lower concentration (10 nM) (Mitra and Morad, 1986). Modulation of ICaT is also reported in atrial

myocytes of frog where almost 100% increase was seen in 50% of the cells (Alvarez et al. , 1996, Alvarez and Vassort, 1992). However, the general consensus is that TTCCs are resistant to stimulation by β AR stimulation (Vassort et al., 2006). Presence of TTCCs in adult human cardiomyocytes is never reported. Because TTCCs reappear during cardiovascular disorders, it would be interesting to investigate the modulation of TTCCs by β AR signaling in those pathological conditions, if any?

CHANGES IN β -ADRENERGIC REGULATION OF CARDIAC VOLTAGE-GATED CALCIUM CHANNELS IN HEART FAILURE

During heart failure pathology, there is an inconsistent change in the basal I_{CaL} and Ca_v1.2 becomes consistently less responsive to β AR stimulation and PKA activation, resulting in diminished contractile force and fight-or-flight response (Mukherjee and Spinale, 1998, Nikolaev et al., 2010, Saraiva et al. , 2003, Wallukat, 2002, Zheng et al. , 2013). Reduced responsiveness of Ca_v1.2 to β AR stimulation can be attributed to the greater basal Ca_v1.2 availability and open probability as compared to the normal heart, studied in ventricular myocytes from patients with heart failure. This increased basal Ca_v1.2 availability and open probability is likely because of the hyper-phosphorylation or persistent phosphorylation of the channel by PKA which limits the channel stimulation by β AR agonists (Chen et al., 2002, Zheng et al., 2013) and increases calcium influx causing cardiac hypertrophy and pathological remodelling of the ventricles as seen in both animal models and human patients. In hypertrophied rat myocytes (Scamps et al. , 1990), dogs (Kaab et al. , 1996) and rabbits (Rozanski et al. , 1997) with pacing-induced left-ventricular dysfunction, a significant lowering of β AR augmentation of I_{CaL} was reported. In hypertensive rat myocytes, I_{CaL} was augmented with β AR stimulation as compared to controls (Xiao and McArdle, 1994). In human patients with CHF, reduction in the number of β ARs was found in association with increased plasma catecholamine concentrations and hence I_{CaL} augmentation was reduced

by β AR stimulation with the development of CHF (Brodde et al. , 1995). It is also reported that prolonged β AR stimulation also internalizes LTCC in a macromolecular complex together with β -arrestin into clathrin-coated vesicles (Lipsky et al. , 2008). However, there are also studies which suggest that there are no changes in the expression and function of LTCCs per se in heart failure. Studies by Yang et al. have shown that in SA mice (described in the previous section) there is a reduced β AR regulation, causing reduced contractile function, cardiac hypertrophy and heart failure without changing expression, location or function of $Ca_v1.2$ (Yang et al., 2016). The immunocytochemical technique was used by them to identify the location of $Ca_v1.2$ (Yang et al., 2016). This indicates the higher sensitivity of the heart to even partial disruption of the normal upregulation of $Ca_v1.2$ by the mutation at S1700. STAA mice showed accelerated hypertrophy, heart failure, and death (Yang et al., 2016). Cardiac hypertrophy increased with voluntary wheel-running exercise and β AR stimulation in SA mice. Exercised SA mice showed an increase in heart weight (HW)/ body weight (BW) ratio compared to non-exercised SA mice of the same age. While exercised wild-type (WT) mice had similar HW/BW ratio as non-exercised WT mice. It shows that SA mice are more sensitive to exercise-induced cardiac hypertrophy, than WT mice (Yang et al., 2016).

Structurally, in heart failure (Fig. 2), LTCCs are dislocated from their localization in T-tubules and so are β_2 ARs. LTCCs and β_2 ARs reside in T-tubule signaling microdomain together with a number of other proteins, a few of which maintain the structure of T-tubules. Since T-tubule structure is lost in heart failure, these proteins were investigated. Any change in the expression of these structural proteins will not only affect the structure of T-tubules, but also the coupling between β_2 ARs and LTCCs. In this context, BIN1 transcription is reported to be reduced in the heart failure which leads to intracellular localization of LTCCs (Hong et al. , 2012). These intracellular channels can neither participate in calcium influx nor

β AR regulation. Therefore one can speculate that in failing myocytes where BIN1 transcription is reduced, LTCC current upon β AR stimulation may not show an increase due to channels not being targeted to T-tubule microdomains. Similarly, caveolin-3 expression is reduced in human heart failure and rodent models of heart failure (Feiner et al. , 2011) and overexpression of caveolin-3 is cardioprotective (Horikawa et al. , 2011, Tsutsumi et al. , 2008). Mice lacking caveolin-3 showed no presence of caveolae (Galbiati et al. , 2001) and developed hypertrophy (Woodman et al. , 2002), indicating that absence of caveolar microdomains is detrimental. This knock out mice possibly lacks of β_2 AR modulation of LTCCs and thus contributing to cardiac pathological phenotype. Microdomain (T-tubule or crest) specific changes in the β AR modulation of LTCCs is yet to be investigated. Also β AR modulation of over/re-expressed TTCCs remains to be determined.

CONCLUSIONS AND FUTURE PROSPECTS: LESSONS FROM MICRODOMAINS

Contradictory data obtained from different cellular and animal models regarding functioning and regulation of cardiac VGCCs in cardiovascular pathology suggests that the information is still not complete. However, the amelioration of pathological symptoms by calcium channel blockers suggest an unequivocal causal role of cardiac calcium channels. The recently developed technique of super-resolution scanning-patch clamp (Bhargava et al., 2013) provides some missing answers. This technique developed and validated by Gorelik and colleagues provided a map of functional ion channels on the cardiomyocyte surface with nanoscale resolution (Bhargava et al., 2013). Their investigation concluded that not only function, but location of LTCCs is disturbed in heart failure (Sanchez-Alonso et al., 2016). Since heart failure is a structural disease where T-tubules are reduced and disorganized, using the combination of SICM and FRET, Nikolaev et al. showed that β_2 ARs also change locations (Nikolaev et al., 2010). Similar to LTCC, β_2 ARs are usually restricted to T-tubules but redistribute to crest locations in heart failure (Nikolaev et al., 2010). How this change

affects the modulation of LTCCs by β ARs in T-tubule and crest microdomains is yet to be investigated. To investigate this, perhaps a triple combination of SICM-FRET-patch clamp would be required. It is certainly challenging but worth exploiting. One could include the β AR agonist in the glass pipette used for SICM and patch clamp or an additional pipette may be used to deliver agonist locally. This would give critical insights on the outcome of β -blockers and calcium channels blocker (CCBs) therapy. The spatial concept underscores the fact that not all LTCCs are dysfunctional and by using CCBs, the therapy is targeted towards blocking all LTCCs which may not be beneficial in the long term.

FIGURE LEGENDS

Figure 1. Healthy Cardiomyocyte. In healthy cardiomyocytes, LTCCs, β 2ARs, AHNAK, REM and Bin1 colocalize in T-tubule scaffolds. REM inhibits LTCCs and eliminates its modulation by β ARs (2). AHNAK inhibits LTCCs but this inhibition can be relieved by β AR modulation of LTCCs (3). SIP modulates the β AR regulation of LTCCs via Pak-PP2A pathway (4). A subset of LTCCs also colocalize with β 2ARs in caveolae. TTCCs are present in sarcolemma only.

Figure 2. Failing cardiomyocyte. In failing cardiomyocytes, T-tubule scaffolds are disorganised with reduced expression of BIN1 and caveolin-3 (Cav3). The proximity between LTCCs and RyRs is reduced. LTCCs and β 2ARs redistribute to sarcolemma. TTCCs are overexpressed on the sarcolemma. Regulation of these overexpressed channels by β ARs is not defined. Also, regulation of coupling between LTCCs and β ARs by REM, AHNAK and SIP is not defined in heart failure.

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DISCLOSURE STATEMENT

The authors declare having no financial competing interest.

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L-type Calcium Channels

(Current increase in Heart)

Functional

(T-tubules and Sarcolemma)

Modifiers:

AHANAK, SIP1,
REM GTPases

Structural

(T-tubules and Caveolae)

Facilitators:

Bin1, Caveolin 3

Coupling

β -Adrenergic Receptors

(Heart)

Catecholamine

(Epinephrine,
Norepinephrine)

Activation

Graphics Abstract

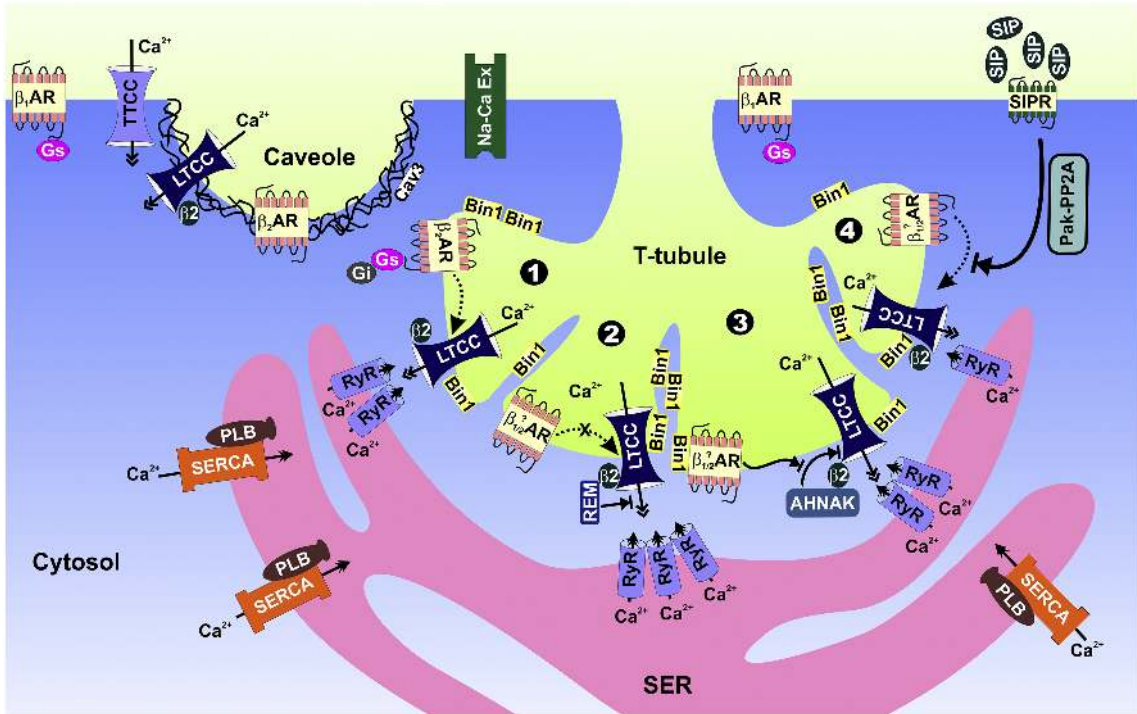


Figure 1

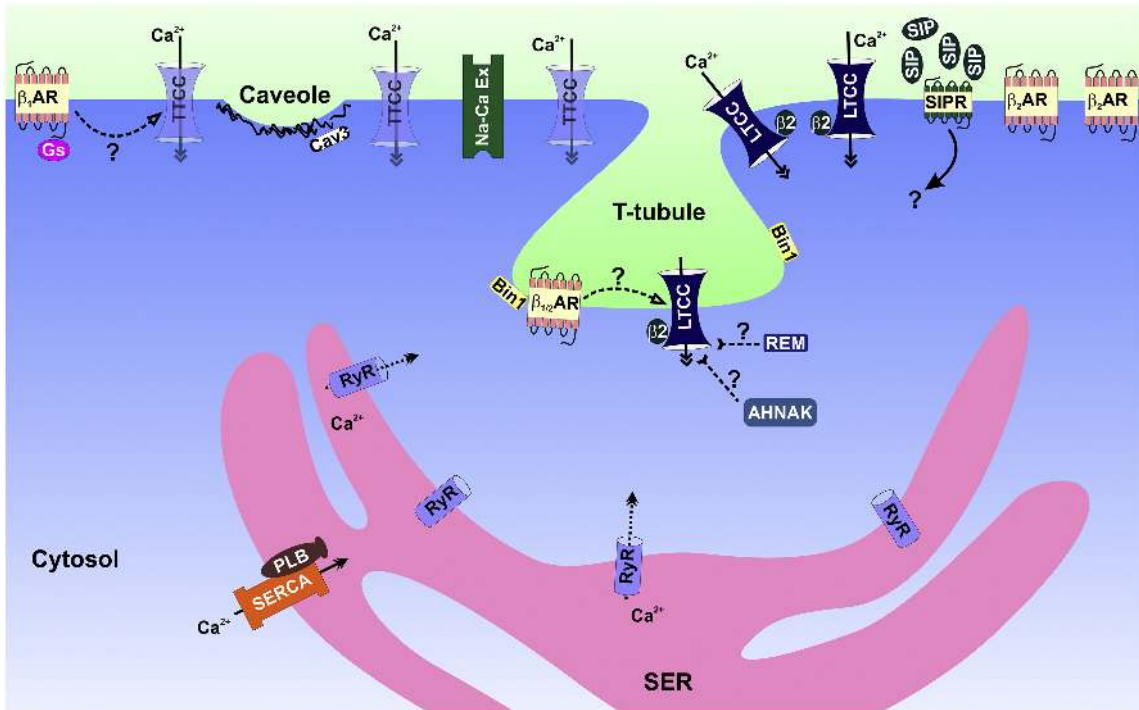


Figure 2