


TOPICAL REVIEW

Neuronal sodium channels: emerging components of the nano-machinery of cardiac calcium cycling

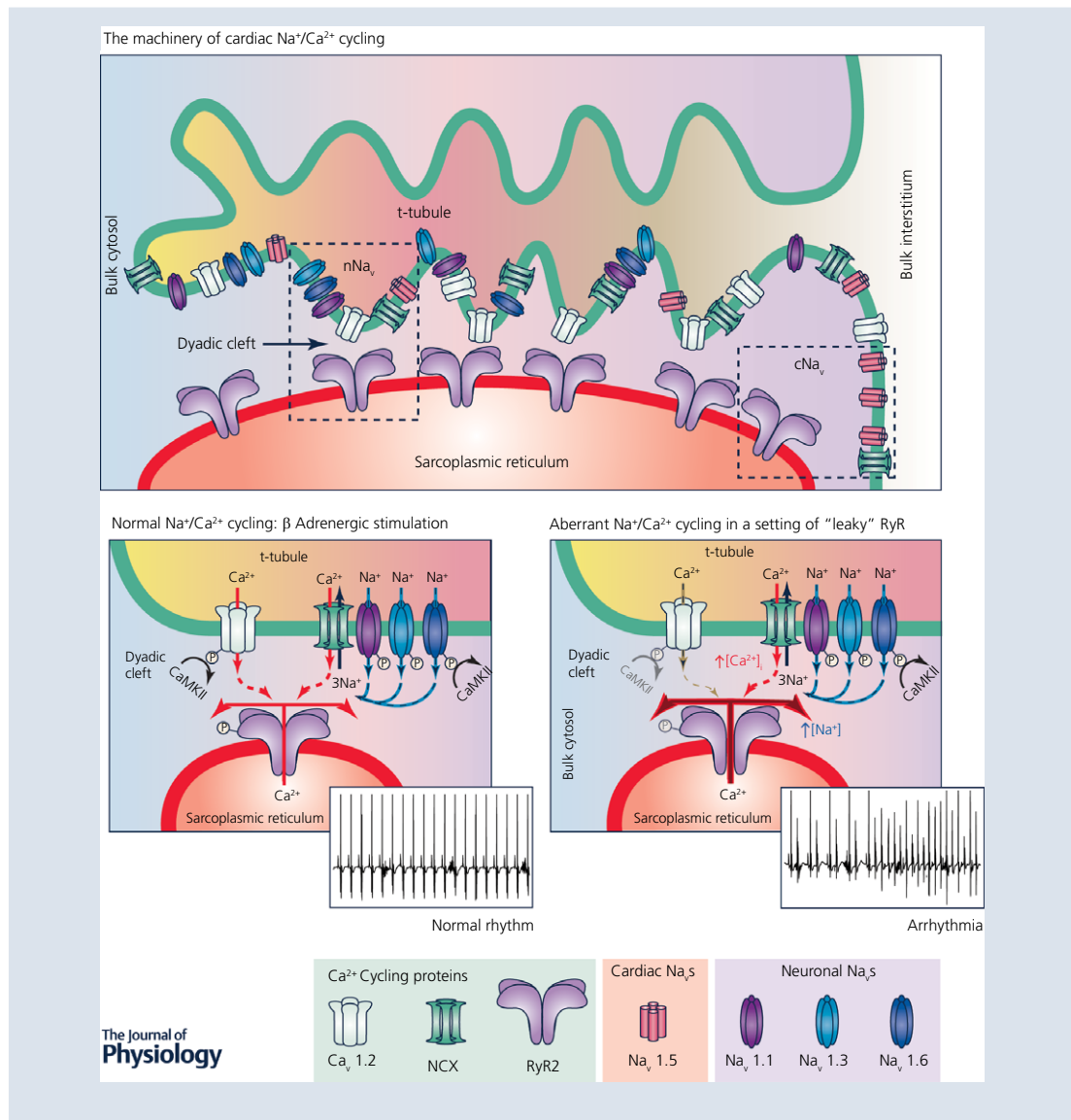
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Abstract Excitation–contraction coupling is the bridge between cardiac electrical activation and mechanical contraction. It is driven by the influx of Ca^{2+} across the sarcolemma triggering Ca^{2+} release from the sarcoplasmic reticulum (SR) – a process termed Ca^{2+} -induced Ca^{2+} release (CICR) – followed by re-sequestration of Ca^{2+} into the SR. The $\text{Na}^+/\text{Ca}^{2+}$ exchanger inextricably couples the cycling of Ca^{2+} and Na^+ in cardiac myocytes. Thus, influx of Na^+ via voltage-gated Na^+ channels (Na_V) has emerged as an important regulator of CICR both in health and in disease. Recent insights into the subcellular distribution of cardiac and neuronal Na_V isoforms and their ultrastructural milieu have important implications for the roles of these channels in mediating Ca^{2+} -driven arrhythmias. This review will discuss functional insights into the role of neuronal Na_V isoforms vis-à-vis cardiac Na_V s in triggering such arrhythmias and their potential as therapeutic targets in the context of the aforementioned structural observations.

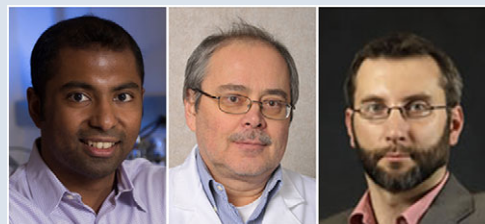
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Abstract figure legend Top: Schematic diagram showing the protein machinery of cardiac $\text{Na}^+/\text{Ca}^{2+}$ cycling showing a t-tubule and associated junctional SR. Microfolds in t-tubule are depicted based on recent findings. (Hong *et al.* 2014; Lavorato *et al.* 2015) Note the close proximity of neuronal sodium channels (nNaVs) to ryanodine receptor channels (RyRs) and the $\text{Na}^+/\text{Ca}^{2+}$ exchanger (NCX). Differential shading of the interstitial space within the t-tubule and the cytoplasm within the dyadic cleft indicates local differences in ionic concentrations, particularly with respect to the bulk interstitium and cytosol respectively. Bottom left: During β -adrenergic stimulation in healthy hearts, Na^+ influx is enhanced secondary to CaMKII-mediated phosphorylation of nNaVs. This augments Ca^{2+} influx via reverse mode NCX, and in turn, to enhanced SR Ca^{2+} release via RyRs. Inset shows normal electrocardiogram resulting from normal $\text{Na}^+/\text{Ca}^{2+}$ cycling. Bottom right: In diseased hearts, pathologically elevated Na^+ influx via nNaVs results in a larger Ca^{2+} influx via reverse mode NCX. This, particularly in the presence of elevated diastolic Ca^{2+} levels or RyR leak, can trigger arrhythmogenic diastolic Ca^{2+} release. Inset electrocardiogram shows premature beats and arrhythmias triggered by diastolic Ca^{2+} releases.

Abbreviations BIN1, bridging integrator 1; CaMKII, Ca^{2+} /calmodulin-dependent protein kinase II; CICR, Ca^{2+} -induced Ca^{2+} release; cNa_V , cardiac sodium channel; CPVT, catecholaminergic polymorphic ventricular tachycardia; ECC, excitation–contraction coupling; HF, heart failure; LCC, L-type Ca^{2+} channel; Na_V , voltage-gated Na^+ channel; NCX, sodium–calcium exchanger; nNaV, neuronal sodium channel; RyR, ryanodine receptor; SR, sarcoplasmic reticulum; t-tubule, transverse tubule; TTX, tetrodotoxin; WT, wild-type.

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Cardiac calcium (Ca^{2+}) cycling involves the release of Ca^{2+} from intracellular stores, i.e. the sarcoplasmic reticulum (SR), prompted by Ca^{2+} influx across the sarcolemma – a process termed Ca^{2+} -induced Ca^{2+} release (CICR), and its re-sequestration into the SR. The interaction of the Ca^{2+} released from the SR with contractile proteins links the

heart's electrical activity with mechanical contraction and is termed excitation–contraction coupling (ECC); as such, it is a vital process for cardiac function. Abnormalities in ECC underlie life-threatening arrhythmias in several pathologies ranging from catecholaminergic polymorphic ventricular tachycardia (CPVT) to heart failure (HF)

(Belevych *et al.* 2013; Radwanski *et al.* 2013a). That Ca^{2+} cycling within cardiac myocytes is inextricably intertwined with the regulation of intracellular sodium (Na^+) is well established (Bers *et al.* 2003; Murphy & Eisner, 2009). Voltage-gated Na^+ channels (Na_Vs) permit Na^+ into the cell, resulting in electrical excitation, thereby initiating ECC. The Na^+ – Ca^{2+} exchanger (NCX), on the other hand, electrogenically exchanges 1 Ca^{2+} ion for 3 Na^+ ions (Blaustein & Lederer, 1999; Philipson & Nicoll, 2000), creating a direct link between Na^+ influx into the myocytes and Ca^{2+} cycling. This review will focus on the roles of Na_V isoforms, the principal pathways for Na^+ influx into cardiomyocytes, in modulating cardiac Ca^{2+} cycling in health and in disease, with particular emphasis on the spatial integration of Na_Vs with Ca^{2+} cycling proteins to form a larger macromolecular machine.

The interplay between sodium and calcium

Classically, the NCX's role in the cardiac cycle was viewed as the extrusion, from the cardiac myocyte, of all Ca^{2+} entering the cell during ECC. However, since ion transport via NCX is governed by the concentration gradients of Na^+ and Ca^{2+} as well as the membrane potential, it can operate in both forward (3 Na^+ in: 1 Ca^{2+} out) and reverse modes (3 Na^+ out: 1 Ca^{2+} in; reversal potential according to the Nernst equation). As early as 1990, Leblanc and Hume demonstrated that, in the absence of Ca^{2+} entry via voltage-dependent Ca^{2+} channels, Ca^{2+} entry via reverse mode NCX could elicit Ca^{2+} release from the SR (Leblanc & Hume, 1990). Using tetrodotoxin (TTX; 5 μM) to block Na_Vs , they further demonstrated that this Ca^{2+} entry via reverse mode NCX was dependent upon Na^+ entry via Na_Vs : Na^+ entry through Na_Vs elevates subsarcolemmal Na^+ levels, causing NCX to reverse (3 Na^+ out: 1 Ca^{2+} in) and bring in Ca^{2+} , eliciting Ca^{2+} release from the SR. Shortly thereafter, Lipp and Niggli demonstrated Na^+ current (I_{Na})-induced Ca^{2+} transients in guinea pig ventricular myocytes, which were mediated by reverse mode NCX (Lipp & Niggli, 1994). These investigators concluded that Na^+ influx via Na_Vs resulted in a rapid rise in subsarcolemmal $[\text{Na}^+]$, causing NCX to operate in reverse mode.

Although these studies demonstrated a link between Na^+ influx via Na_Vs and SR Ca^{2+} release, the question remained as to the physiological role of I_{Na} -induced Ca^{2+} release. Larbig *et al.* (2010) determined that blockade of I_{Na} with 10 μM TTX decreased the influx of trigger Ca^{2+} resulting in a lower rate of Ca^{2+} release from the SR and a reduced Ca^{2+} transient amplitude in myocytes isolated from wild-type (WT) mice but not in those isolated from NCX knockout mice. These results suggested that Ca^{2+} entry via reverse mode NCX secondary to Na^+ entry via Na_Vs does indeed contribute to activation of SR Ca^{2+} release.

The identity of Na_Vs responsible for the enhanced Ca^{2+} release in the heart is the subject of ongoing research. The predominant Na_V isoform identified in the heart is $\text{Na}_V1.5$ (Chen-Izu *et al.* 2015), which is sensitive to micromolar concentrations of TTX and is therefore, categorized as a TTX-resistant cardiac-type Na_V (cNa_V) (Satin *et al.* 1992). Recent work in the heart (Dhar Malhotra *et al.* 2001; Maier *et al.* 2002, 2004; Westenbroek *et al.* 2013; Radwanski *et al.* 2015), however, has identified the presence of neuronal Na_V isoforms (nNa_Vs), so called because they were first identified in neurons. Unlike cNa_Vs ($\text{Na}_V1.5$), nNa_Vs ($\text{Na}_V1.1$, 1.3, 1.6) are sensitive to nanomolar concentrations of TTX (Ritchie & Rogart, 1977; Renaud *et al.* 1983). In subsequent work, the groups of Goldhaber and Bridge demonstrated that 100 nM TTX suppressed SR Ca^{2+} release flux and Ca^{2+} transient amplitude in rabbit ventricular myocytes, pointing to a role for TTX-sensitive nNa_Vs in triggering SR Ca^{2+} release (Torres *et al.* 2010). In this vein, our group recently obtained similar findings with 100 nM TTX using optical mapping in intact guinea pig ventricles (Radwanski *et al.* 2013b). These results underscore the importance of Na_Vs as modulators of cardiac Ca^{2+} cycling and complement the structural observations that nNa_Vs in cardiac myocytes are localized to invaginations of the surface membrane known as the transverse tubules (t-tubules; Fig. 1; Dhar Malhotra *et al.* 2001; Maier *et al.* 2002, 2004; Westenbroek *et al.* 2013; Radwanski *et al.* 2015) – where Ca^{2+} cycling proteins are also localized. Thus, it has been postulated that, at the beginning of an action potential, they admit Na^+ into areas of closest proximity between the t-tubule sarcolemma and SR. This Na^+ is then extruded out of the cell by the NCX in exchange for Ca^{2+} , 'priming' this nanodomain with Ca^{2+} . This, in conjunction with Ca^{2+} that enters the cell through the L-type Ca^{2+} channels (LCCs), facilitates opening of SR Ca^{2+} release channels, ryanodine receptors (RyRs), resulting in a robust Ca^{2+} release and contraction.

Compartmentation of cardiac sodium–calcium cycling: neuronal Na^+ channels in the t-tubules

In both skeletal and cardiac muscle, the dynamics of Ca^{2+} cycling are heavily influenced by the spatial organization of the RyRs, relative to the primary source of trigger Ca^{2+} , LCCs (Fabiato, 1983). Whereas in skeletal muscle, sarcolemmal Ca^{2+} channels ($\text{Ca}_V1.1$) are mechanically linked to RyRs (RyR1), in cardiac muscle, LCCs ($\text{Ca}_V1.2$) and RyRs (RyR2) are closely associated in space without any known direct mechanical linkage. Therefore, the 10–12 nm wide dyadic cleft separating the SR membrane containing the RyRs and the sarcolemma at the t-tubule, containing the LCCs, is of critical importance in determining the functional properties of cardiac Ca^{2+} cycling (Greenstein *et al.* 2006; Koh *et al.* 2006; Cannell

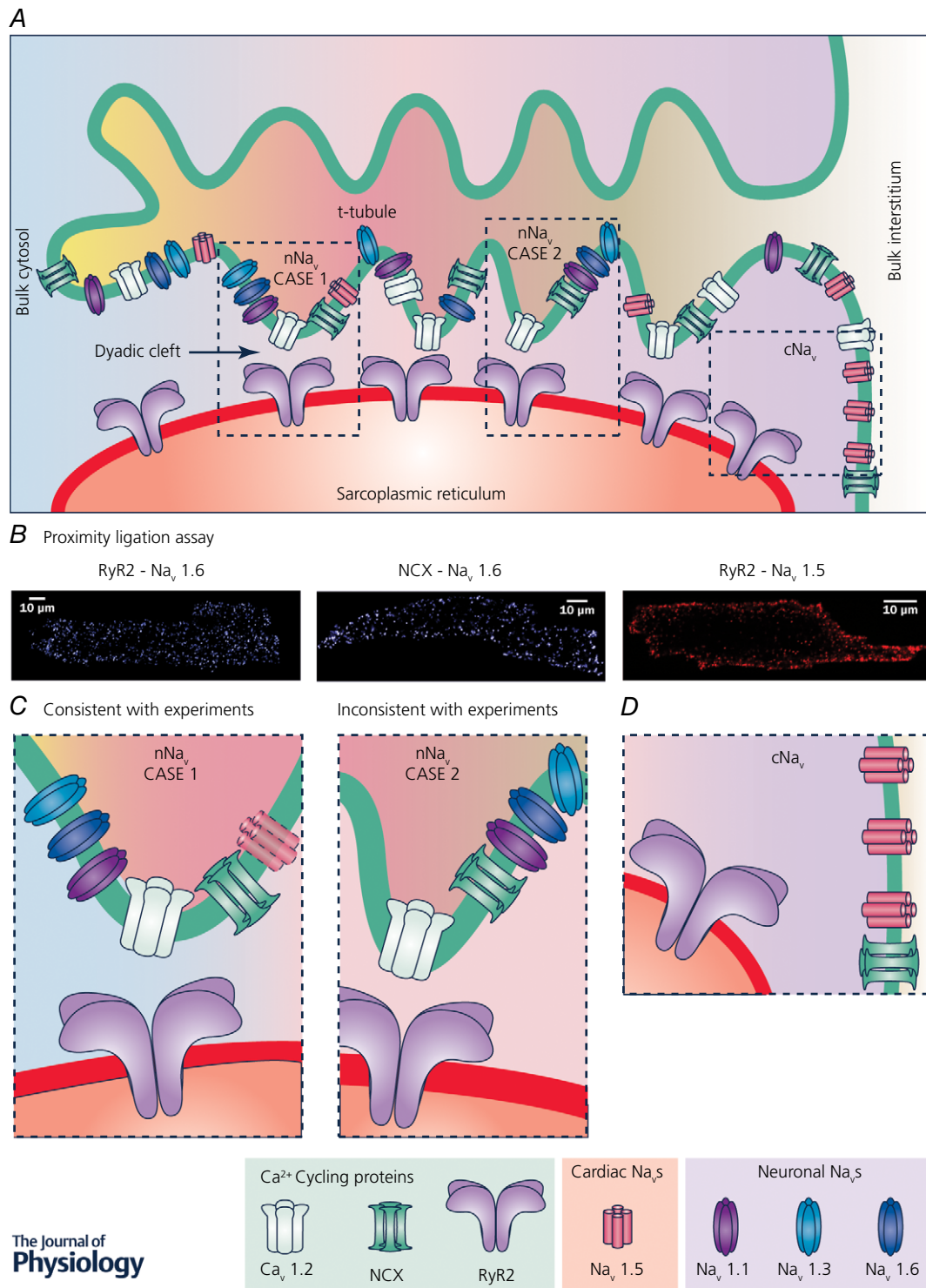


Figure 1. Schematic diagram showing the protein machinery of cardiac Na⁺-Ca²⁺ cycling

A, schematic diagram of a t-tubule and associated junctional SR. Microfolds in t-tubule are depicted based on recent findings (Hong *et al.* 2014; Lavorato *et al.* 2015). Different arrangements of Ca²⁺ cycling proteins and sodium channels are depicted along the t-tubule. Regions highlighted by the dashed boxes are presented at higher magnification in C and D. Note that differential shading of the interstitial space within the t-tubule and the cytoplasm within the dyadic cleft indicates local differences in ionic concentrations within these spaces due to their diffusional isolation from the bulk interstitial space and cytoplasm, respectively. B, results from Duolink proximity ligation assays (PLAs) show close association of nNaV isoform Na_v1.6 with both RyR2 and NCX throughout murine

myocytes, consistent with enrichment of nNa_vs in t-tubules. In contrast, PLA signal corresponding to association between cNa_v (Na_v1.5) and RyR2 is only observed at the periphery of the cell, consistent with cNa_v localization at the lateral membrane. Adapted from Radwański *et al.* (2016). C, higher magnification views of regions from A showing two possible scenarios of nNa_v localization within t-tubules. Left, case 1, very close association between nNa_vs and RyRs, which is consistent with PLA results. A cNa_v is depicted faded since experimental results including PLA results argue against cNa_v enrichment in t-tubules. Right, case 2, nNa_vs localized to t-tubules but not very closely associated with RyRs, which is *not* consistent with PLA results. D, higher magnification view of region from A showing cNa_v (Na_v1.5) localization at the lateral membrane.

et al. 2013). In consequence, the spatial organization of Na_vs and NCX relative to RyRs and LCCs is likely to be a critical modulator of Na⁺–Ca²⁺ cycling. Further underscoring the importance of the spatial organization of Na⁺ and Ca²⁺ cycling proteins relative to each other, Sobie and colleagues demonstrated that LCCs allosterically activate NCX in rabbit cardiomyocytes at positive membrane potentials, thereby enabling further augmentation of trigger Ca²⁺ for SR Ca²⁺ release by Na⁺ influx (Sobie *et al.* 2008).

While the presence of Na_vs within t-tubules is widely accepted, there remains some debate regarding which isoforms are localized there. This question has important implications given the biophysical differences between cNa_vs and nNa_vs: the TTX-sensitive nNa_vs exhibit more positive voltage dependence of gating, i.e. greater channel availability at positive potentials, as well as more rapid activation and inactivation compared to the TTX-resistant cNa_vs (Fozzard & Hanck, 1996; Maier *et al.* 2004). In a 2000 study, Moore and colleagues, using wide-field microscopy, observed no close association between cNa_vs and RyRs (Scriven *et al.* 2000). In subsequent work using confocal microscopy, cNa_vs (Na_v1.5) were found to be enriched at the intercalated disk whereas nNa_vs (Na_v1.1, Na_v1.3 and Na_v1.6) and skeletal muscle Na_vs (Na_v1.4) were enriched within t-tubules (Dhar Malhotra *et al.* 2001; Maier *et al.* 2002, 2004; Westenbroek *et al.* 2013; Radwański *et al.* 2015). In this context, the aforementioned results highlighting the role of TTX-sensitive Na⁺ current in modulating Ca²⁺ release (Larbig *et al.* 2010; Torres *et al.* 2010; Gershon *et al.* 2011; Radwański *et al.* 2013b) argue in favour of nNa_vs rather than cNa_vs being a part of the Na⁺–Ca²⁺ cycling machinery. However, when interpreting these findings, it is important to bear in mind that the resolution of these microscopy techniques is limited by diffraction to 200–300 nm resolution. Some functional validation was provided by measurements made by Brette and Orchard – these investigators examined Na⁺ current densities in both intact and detubulated rat ventricular myocytes and determined that TTX-resistant cNa_vs (Na_v1.5) are predominantly located at the lateral sarcolemma whereas TTX-sensitive nNa_vs are preferentially localized to the t-tubules (Brette & Orchard, 2006). Furthermore, Lin *et al.* (2011) using cell-attached macropatch demonstrated that cNa_vs were distributed between the intercalated disk

and the midsection of myocytes whereas nNa_vs were only observed at the latter location. Interestingly, these investigators also observed functional differences in cNa_vs based on their subcellular location highlighting the role of subcellular location in modulating ion channel function: TTX-resistant Na_vs (likely to be Na_v1.5) along the lateral sarcolemma activated at more positive potentials than those at the intercalated disk suggesting that cellular excitability at physiological resting potentials is largely governed by Na_v1.5 at the intercalated disk. A related approach to this problem was reported by Bhargava *et al.* (2013) who combined scanning ion conductance microscopy and cell-attached patch clamp to record currents from LCCs as well as clusters of Na_vs located within t-tubules. However, these investigators used sensitivity to 30 μM TTX to confirm the identity of Na_vs in their experiments; thus, they did not discriminate between cardiac and neuronal isoforms. It is important to note here that RyRs in cardiac muscle are distributed between the junctional and corbular SR, organized into clusters with uneven gaps (Cabra *et al.* 2016; Franzini-Armstrong, 2016). Thus, it is possible that neuronal and/or cardiac Na_vs may be present in sufficient density at or near the dyadic cleft interspersed with RyRs to significantly influence Ca²⁺ cycling.

In the context of characterizing t-tubular Na_vs, novel experimental techniques have proved to be of great value. One such technique is the proximity ligation assay (PLA), which identifies proteins located within 40 nm of each other with extremely high sensitivity (Gullberg & Andersson, 2010). Using PLA in conjunction with confocal immunofluorescence, we recently demonstrated that primarily nNa_vs (Na_v1.1, Na_v1.3 and Na_v1.6) and, to a lesser extent, cNa_vs (Na_v1.5) are closely associated with RyR2 and NCX in t-tubules in ventricular myocytes isolated from murine hearts (Fig. 1; Radwański *et al.* 2016). Notably, PLA signal is only generated when colabelled proteins are within ~40 nm of each other (Gullberg & Andersson, 2010) suggesting very close association between nNa_vs and Ca²⁺ cycling proteins (Fig. 1C – case 1). And, among the nNa_vs, Na_v1.6 demonstrated the greatest degree of association with Ca²⁺ handling proteins. Overall, these results highlight nNa_vs and Na_v1.6 as potentially important components of nanodomains which comprise the machinery of ECC. However, data from animal models with cardiac-specific

gene-targeted deletion of nNa_Vs is necessary to confirm this hypothesis.

Physiological modulation of neuronal Na⁺ channels

Like cNa_Vs, nNa_Vs possess consensus Ca²⁺/calmodulin-dependent protein kinase II (CaMKII) phosphorylation sites that correspond to DI–II linker (Marionneau *et al.* 2012). Therefore, phosphorylation of nNa_V by CaMKII may account for synergistic interaction between reverse mode NCX and LCC at positive membrane potentials during β-adrenergic stimulation (Viatchenko-Karpinski *et al.* 2005). In fact, recently, we demonstrated CaMKII augmentation of TTX-sensitive nNa_Vs during β-adrenergic stimulation result in an increased intracellular Na⁺ influx (Fig. 2A, bottom panel) (Radwański *et al.* 2016). The notion of CaMKII regulation of Na⁺ influx is consistent with work in genetic models where CaMKII is either rendered constitutively active (Wagner *et al.* 2006) or knocked out (Dybikova *et al.* 2014). Further, there is evidence that augmentation of Na⁺ influx through nNa_V in WT murine hearts may be potentially inotropic by increasing Ca²⁺ transient amplitude (Kirchhof *et al.* 2015; Radwanski *et al.* 2015). However, in a setting of altered RyR2 function, augmentation of nNa_V activity may in fact be proarrhythmic (Radwański *et al.* 2016).

Role of neuronal Na⁺ channels in cardiac arrhythmias

Abnormal Na_V function underlies arrhythmias in several pathologies (Ruan *et al.* 2009). Over-active Na_Vs in neurons precipitate seizures, whereas in the heart, they can precipitate triggered arrhythmias. As noted above, nNa_V activity is increased during β-adrenergic stimulation in a CaMKII-dependent manner (Radwański *et al.* 2016). Pathologically elevated Na⁺ influx into the confined space of the t-tubular junction during late phase 3 of an action potential or during rest (diastole) can precipitate arrhythmias by modulating RyR function via Na⁺-dependent signalling mechanisms. For instance, in inherited ryanopathies such as CPVT where RyRs are 'leaky' and the junctional cleft is primed with Ca²⁺, physiological enhancement of nNa_V activity by isoproterenol precipitated aberrant diastolic Ca²⁺ releases and consequent arrhythmias *in vivo* via an NCX-mediated mechanism (Radwanski *et al.* 2015, 2016). *In silico* studies suggest that pathological accumulation of cytosolic Na⁺ and Ca²⁺ facilitate NCX reversal (Armoundas *et al.* 2003; Radwanski & Poelzing, 2011), thereby facilitating aberrant SR Ca²⁺ releases. Such Na⁺-mediated signalling increases Ca²⁺ spark frequency through sensitized RyR2 (Radwanski *et al.* 2015). Likewise, in CPVT cardiomyocytes with enhanced SR Ca²⁺ load (via acute, conditional overexpression of SERCA2a), selectively slowing nNa_V inactivation with β-pompilidotoxin

increased Na⁺ influx, which in turn, through NCX, triggered aberrant Ca²⁺ releases and arrhythmias *in vivo* (Radwanski *et al.* 2015, 2016). Overall, these results point to nNa_Vs as important regulators of aberrant Ca²⁺ release events in such disease states.

Several further examples exist of the arrhythmogenic impact of pathologically increased Na⁺ influx via nNa_Vs. In mice lacking the Na⁺ channel auxiliary subunit β1, a compensatory upregulation of a nNa_V isoform, Na_V1.3, results in higher rates of aberrant diastolic Ca²⁺ releases in β1-knockout mice than in their WT littermates (Lin *et al.* 2014). Likewise, a rat pilocarpine-induced epilepsy model evidenced increased persistent Na⁺ current secondary to an upregulation of Na_V1.1 (Biet *et al.* 2015). This enhanced persistent Na⁺ current, in turn, precipitated cardiac arrhythmias *in vivo*. In yet another model of epileptic encephalopathy, gain of function mutation in Na_V1.6 resulted in frequent aberrant diastolic Ca²⁺ releases and ventricular arrhythmias upon catecholamine challenge (Frasier *et al.* 2016). Taken together, these results strongly support a role of enhanced persistent Na⁺ influx via nNa_Vs, particularly within Na⁺–Ca²⁺ cycling nanodomains in precipitating aberrant diastolic Ca²⁺ releases and thereby cardiac arrhythmias (Fig. 2B) in multiple pathologies where intracellular (and particularly dyadic) Na⁺ and Ca²⁺ is elevated.

Role of neuronal Na⁺ channels in the failing heart

Enhanced persistent Na⁺ influx is widely acknowledged as a contributor to arrhythmogenesis in acquired forms of ryanopathy, such as heart failure (Valdivia *et al.* 2005; Undrovinas & Maltsev, 2008; Undrovinas *et al.* 2010; Sossalla & Maier, 2012; Antzelevitch *et al.* 2014; Makielski, 2016). Undrovinas and colleagues identified Na_V1.1 as a significant contributor to persistent Na⁺ influx in a coronary artery embolization-mediated canine model of HF (Mishra *et al.* 2014), highlighting the role of nNa_Vs in this phenomenon. Likewise, NCX function is pathologically enhanced in failing hearts (Pogwizd & Bers, 2002). Taken together, these findings suggest that arrhythmogenic SR Ca²⁺ releases in failing hearts may be triggered by Na⁺-driven Ca²⁺ entry. Interestingly, despite the enhanced Na⁺ influx and NCX function, failing rat hearts do not demonstrate a synergistic interaction between NCX and LCCs to increase ECC as part of CICR during β-adrenergic stimulation (Viatchenko-Karpinski *et al.* 2005). This may reflect the severe disruption of t-tubules in failing hearts (Li *et al.* 2015), which contributes to compromised mechanical function and reduced functional reserve. Despite this disruption of the t-tubular network in failing hearts, the remaining t-tubules host abnormal functional nanodomains composed of nNa_Vs, NCX and hyper-sensitive RyRs that facilitate temporal synchronization of

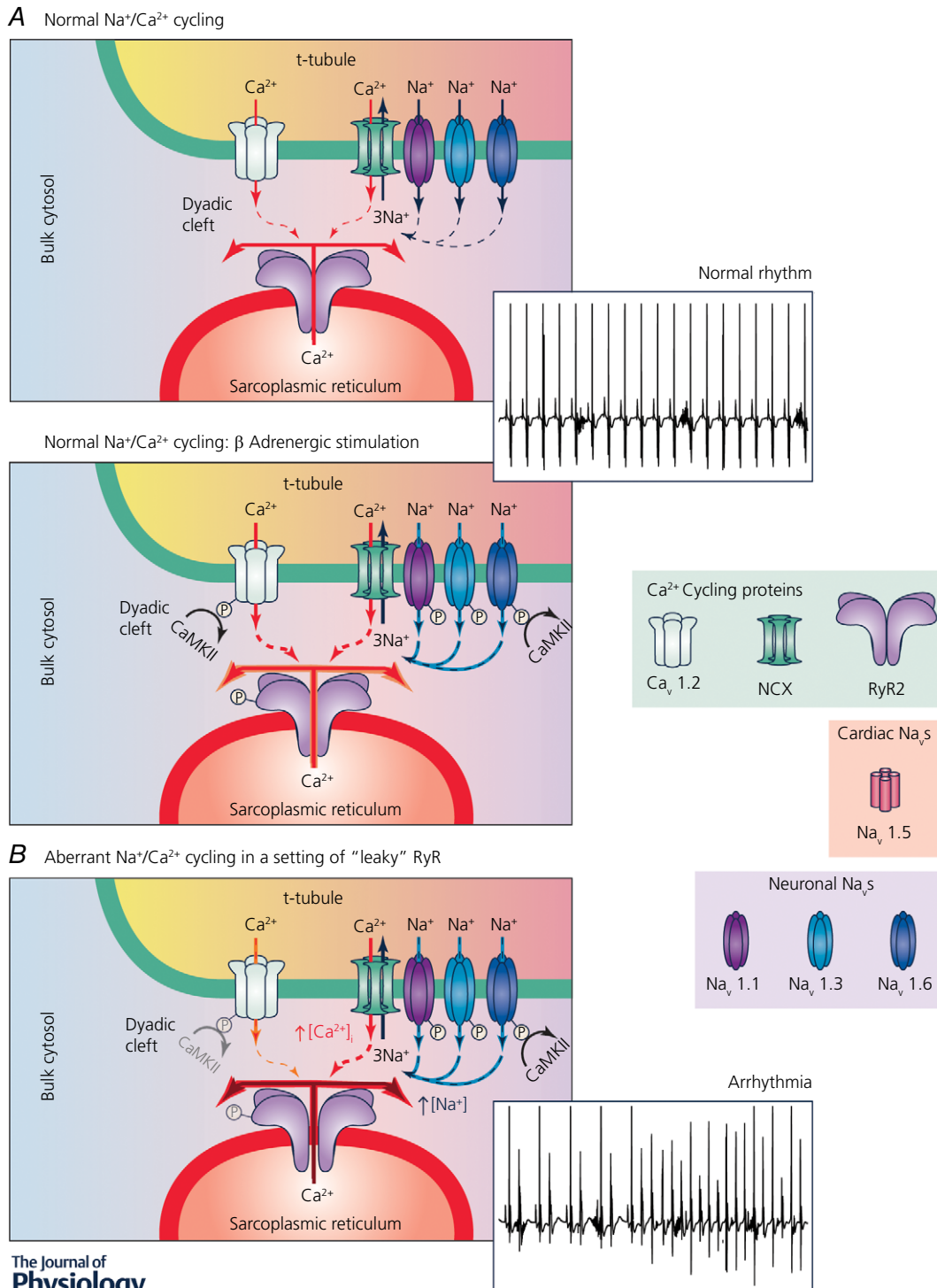


Figure 2. Schematic diagram showing normal and aberrant Na⁺-Ca²⁺ cycling
 A, top, during normal Na⁺-Ca²⁺ cycling, Na⁺ influx via nNa_vs early in the action potential leads to Ca²⁺ influx via reverse mode NCX, which in turn, in conjunction with Ca²⁺ influx via LCCs, leads to SR Ca²⁺ release via RyRs. Inset shows normal electrocardiogram resulting from normal Na⁺-Ca²⁺ cycling. Bottom, during β-adrenergic stimulation, Na⁺ influx is enhanced secondary to CaMKII-mediated phosphorylation of nNa_vs. This leads to augmented Ca²⁺ influx via reverse mode NCX, which in turn leads to enhanced SR Ca²⁺ release via RyRs. C, pathological elevated Na⁺ influx via nNa_vs results in a larger Ca²⁺ influx via reverse mode NCX. This, particularly in the presence of elevated diastolic Ca²⁺ levels or RyR leak, can trigger arrhythmogenic diastolic Ca²⁺ release. Inset electrocardiogram shows premature beats and arrhythmias triggered by diastolic Ca²⁺ releases.

aberrant Ca^{2+} release (Belevych *et al.* 2012), thereby precipitating cardiac arrhythmias.

An important debate in this context has been about whether the interplay between Na^+ and Ca^{2+} cycling in the failing heart is mediated by Na^+ -driven Ca^{2+} entry via NCX directly triggering SR Ca^{2+} release or by means of this enhanced Ca^{2+} influx being taken up into the SR, thereby enhancing SR Ca^{2+} load. SR Ca^{2+} load in the failing heart is reduced compared to non-failing hearts. This is in line with observations that SR Ca^{2+} load was lowered even when Na^+ entry was enhanced through cardiac glycoside treatment (Ho *et al.* 2011), pointing to Na^+ -driven Ca^{2+} entry via NCX directly triggering SR Ca^{2+} release as the likely arrhythmia mechanism. However, this does not exclude a role for elevated SR Ca^{2+} load under other conditions. Thus, structural characterization of Na^+ - Ca^{2+} cycling nanodomains in this complex disease state will be crucial to fully understanding this arrhythmia mechanism. Equally, the contribution of nNa_V s to arrhythmias needs to be investigated in mathematical models incorporating nano-scale structural organization as well as in experimental heart failure models.

Neuronal Na^+ channels as targets for anti-arrhythmic therapy

Given that aberrant diastolic Ca^{2+} releases resulting from altered RyR2 function underlie arrhythmias in a wide range of pathologies, including CPVT (Radwanski *et al.* 2015, 2016) and ischaemic and non-ischaemic cardiomyopathy (Belevych *et al.* 2013), nNa_V inhibition may have wide-ranging therapeutic applications. Such a strategy would also avoid a major pitfall of non-isoform-selective Na_V inhibition: although initially beneficial in managing Ca^{2+} -mediated arrhythmias following myocardial infarction (The CAPS investigators, 1986), the loss of excitability resulting from blunting of peak Na^+ current proved pro-arrhythmic, increasing the incidence of sudden arrhythmic death in patients with structural heart disease (Echt *et al.* 1991; Starmer *et al.* 1991). Since TTX-resistant cardiac Na_V s ($\text{Na}_V1.5$) are primarily responsible for cardiac excitability, selectively targeting nNa_V could beneficially lower pathological persistent Na^+ influx without any detrimental effects on excitability. Indeed, in mice with CPVT, selective inhibition of nNa_V s with riluzole or 4,9-anhydro-TTX, a TTX analogue, desynchronized pathological diastolic Ca^{2+} releases in both isolated myocytes and in intact tissue, and proved potentially antiarrhythmic *in vivo* (Radwanski *et al.* 2015, 2016). Last but not least, selective silencing of $\text{Na}_V1.6$ recapitulated this antiarrhythmic effect *in vivo*, suggesting that the therapeutic strategy of inhibiting nNa_V s could even be further refined to target specific Na^+ channel isoforms.

Future directions: the subcellular milieu of Na^+ channels

The development of novel, selective therapeutic strategies to prevent Ca^{2+} -mediated arrhythmias by targeting nNa_V s depends on understanding the relationship between structure – the subcellular organization of different nNa_V isoforms and their milieu at the nano-scale, and function – the interplay between Na^+ and Ca^{2+} cycling in the heart. In recent years, we have learned a great deal about the subcellular localization of cNa_V s. In an elegant 2011 study, Petitprez and colleagues identified two distinct pools of $\text{Na}_V1.5$ within cardiac myocytes, one located at the intercalated disk scaffolded by SAP97, and the other located at the lateral sarcolemma scaffolded by the syntrophin–dystrophin complex (Petitprez *et al.* 2011). More recently, we used super-resolution microscopy techniques to identify a subpopulation of intercalated disk-localized $\text{Na}_V1.5$ located within 200 nm of connexin43 gap junctions (Veeraghavan *et al.* 2015; Veeraghavan & Gourdie, 2016). Importantly, the ultrastructural properties of this juxta-gap junctional membrane region, where the extracellular cleft is just 5–10 nm wide, were shown to be an important modulator of cardiac conduction dependence on the sodium current (Veeraghavan *et al.* 2015). Likewise, Delmar and colleagues have utilized super-resolution microscopy correlated with electron microscopy to identify yet another subpopulation of intercalated disk-localized $\text{Na}_V1.5$ localized to N-cadherin-rich sites, where the membranes of adjacent cells are 50–75 nm apart (Agullo-Pascual *et al.* 2014; Leo-Macias *et al.* 2016). The techniques developed by these investigators could prove very useful in future investigation of the ultrastructural milieu of nNa_V s in cardiac myocytes. Perhaps more importantly, the identification of these $\text{Na}_V1.5$ -rich nano-domains suggests that nNa_V s may also be similarly organized into nano-domains with distinct ultrastructural properties and therefore behave in a location-dependent manner. The hypothesis that the nano-scale milieu of t-tubule-localized Na_V s may modulate their function is supported by the work of Hong and colleagues: having previously identified a role for the t-tubule protein bridging integrator 1 (BIN1) in Ca^{2+} channel trafficking and clustering at the t-tubule surface (Hong *et al.* 2010, 2012), these investigators recently demonstrated that BIN1 promotes micro-folding of the t-tubular membrane (Hong *et al.* 2014; Fu & Hong, 2016). These microfolds in the t-tubular membrane can trap extracellular ions, thus diffusively isolating the t-tubular extracellular clefts from bulk extracellular space (Forssmann & Girardier, 1970; Hong *et al.* 2014; Lavorato *et al.* 2015). Importantly, loss of these t-tubular microfolds in heart failure is associated with impaired contractile function secondary to desynchronized ECC as well as elevated risk of ventricular arrhythmias. Not

only will any nNa_vs co-distributed with Ca²⁺ handling proteins be subject to intra- and extra-cellular ionic concentrations modulated by local ultrastructure, but studies have also demonstrated that Na_vs are directly regulated in a Ca²⁺-dependent manner (Van Petegem *et al.* 2012; Wang *et al.* 2014; Gabelli *et al.* 2016). Therefore, studies of nNa_v localization relative to Ca²⁺-handling proteins and their local ultrastructural milieu will be critical in understanding the interplay between Na⁺ and Ca²⁺ cycling in health and in disease. Further, both the nNa_vs themselves and the structural proteins that generate their ultrastructural niches could represent valuable therapeutic targets in a wide array of disease states.

Conclusions

In summary, the available evidence suggests that Na⁺ influx through Na⁺ channels, in particular neuronal Na⁺ channels (nNa_vs), contributes both to the triggering of CICR in normal physiology and to arrhythmogenic diastolic Ca²⁺ release during disease states as diverse as CPVT and heart failure. Importantly, selective inhibition of nNa_vs shows promise as a therapeutic strategy in such pathologies, further underscoring the importance of the interplay between cardiac Na⁺ and Ca²⁺ cycling. Going forward, understanding the subcellular organization of nNa_vs, particularly in relation to Ca²⁺ handling proteins, will be vital to elucidating the mechanisms underlying this phenomenon as well as to the development of effective therapies against Ca²⁺-induced arrhythmias.

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Additional information

Competing interests

None.

Author contributions

R.V., S.G. and P.B.R. contributed equally to the conceptualization of this article. The text was written by R.V. and P.B.R., and revised

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