


COMMENTARY

A privileged role for neuronal Na⁺ channels in regulating ventricular [Ca²⁺] and arrhythmias

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In cardiac myocytes, electrical signaling and Ca²⁺ signaling are closely coupled. Electrical signals, in the form of action potentials, produce periodic increases and decreases in intracellular [Ca²⁺]—so-called “Ca²⁺ transients”—and these Ca²⁺ signals can, in turn, influence action potentials. More specifically, depolarization of the myocyte opens voltage-gated L-type Ca²⁺ channels (LTCCs) in the cell membrane, and Ca²⁺ entering the cell through these channels triggers release of additional Ca²⁺ from the SR. Intracellular [Ca²⁺], in turn, affects the cell’s membrane potential via numerous Ca²⁺-dependent ion transport pathways: LTCCs, which are inactivated by Ca²⁺ (Ben-Johny and Yue, 2014); Ca²⁺-sensitive K⁺ currents such as the slow delayed rectifier current (Bartos et al., 2017); and the electrogenic Na⁺–Ca²⁺ exchanger (NCX), whose usual role is to extrude one Ca²⁺ ion while importing three Na⁺ ions. Two general rules follow from these associations. One is that intracellular Ca²⁺ regulation and Na⁺ regulation are closely coupled because of the fact that NCX exchanges one ion for the other. The second is that spatial relationships between the relevant proteins are extremely important in determining how the ion transport pathways influence each other. In this issue of the *Journal of General Physiology*, Koleske et al. investigate the role of neuronal isoforms of voltage-gated Na⁺ (nNa_v) channels in ventricular myocytes. Their results emphasize the importance of spatial relationships between ion channels, pumps, and transporters and show how these relationships can produce pathological behavior under particular conditions.

Spatial relationships between proteins involved in cardiac Ca²⁺-voltage coupling

Tight regulation of membrane potential and Ca²⁺ dynamics in cardiac myocytes is achieved by the spatial relationships between the proteins involved. Because, for example, a Ca²⁺-dependent ion channel will respond more readily to Ca²⁺ passing through an adjacent channel than to one located a few micrometers away, ventricular myocytes arrange many of the critical proteins into microdomains, thereby enabling adequate coupling of these

processes. Transverse tubules (T-tubules)—protrusions of the sarcolemmal membrane into the cell interior—contain numerous microdomains known as “couplons” (Ríos et al., 2015). In these couplons, LTCCs are brought into close proximity with RyRs, the Ca²⁺ release channels of the SR, and additional relevant ion transport proteins.

The complexity of coupling between Ca²⁺ and membrane potential has important implications for the maintenance of stable cardiac electrical activity. In particular, dangerous and potentially lethal ventricular arrhythmia syndromes can result when ion transport is disrupted by mutations, drugs, changes in gene expression, or pathological posttranslational modifications. Indeed, two of the most well-studied congenital arrhythmia syndromes, long QT syndrome (LQTS) and catecholaminergic polymorphic ventricular tachycardia (CPVT), can result from mutations in a wide range of ion channels and Ca²⁺-handling proteins. At present, 15 forms of LQTS (Bohnen et al., 2017) and 5 forms of CPVT (Landstrom et al., 2017) have been described. These two disorders show clear differences in clinical presentation and, at the cellular level, different mechanisms are thought to underlie “triggered activity”—i.e., the inappropriate membrane depolarizations that initiate arrhythmias. Specifically, triggered activity in LQTS is often considered to be purely voltage driven (Weiss et al., 2010); prolonged repolarization allows LTCCs to recover from inactivation, and reactivation of these channels during the repolarization phase can cause a secondary action potential upstroke known as an early afterdepolarization (EAD). In contrast, arrhythmias in CPVT are thought to arise from a different form of triggered activity, namely, delayed afterdepolarizations (DADs). These events result from spontaneous, aberrant release of Ca²⁺ from the SR after the cell membrane has fully repolarized (Sobie et al., 2017).

Although this general paradigm fits the majority of clinical and cellular observations, recent work suggests that, under some conditions, the picture may be more nuanced. In particular, arrhythmia susceptibility in LQTS might not always result

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from purely voltage-dependent mechanisms, but can sometimes depend on Ca^{2+} -voltage coupling (Terentyev et al., 2014). Along these lines, Koleske et al. (2018) provide important new insight. The results presented in this study show how the action potential prolongation seen in certain models of LQTS can lead to SR $[\text{Ca}^{2+}]$ overload and arrhythmogenic spontaneous Ca^{2+} release. The data also offer novel suggestions regarding the spatial relationships between ion transport proteins. Specifically, the authors suggest that nNa_V channels may have a privileged role that makes them attractive drug targets for these disorders.

Neuronal Na^+ channels can influence ventricular arrhythmic behavior

The current study builds on previously published results from the same research group. In 2016, many of the same investigators used a mouse model of RyR dysfunction to show that catecholamine-stimulated Na^+ influx through nNa_V s can trigger arrhythmias (Radwański et al., 2016). In the current study (Koleske et al., 2018), the authors expand on this finding in an effort to uncover the underlying mechanisms. One of the major strengths of this study is the comprehensive approach taken by the authors. Multiple combinations of pharmacological perturbations were performed, both membrane potential and intracellular $[\text{Ca}^{2+}]$ were simultaneously monitored, and cellular as well as organ-level physiology were assessed.

The following general experimental strategy was used: A cellular environment encouraging arrhythmic dynamics (through EADs and/or DADs) was created, then Na^+ channels were blocked systematically to pinpoint the key player(s) contributing to triggered activity. First, in WT mouse ventricular myocytes, the authors induced a proarrhythmic LQTS phenotype using 4-Aminopyridine (4AP), an inhibitor of transient outward current (I_{to}), accompanied by β -adrenergic stimulation with isoproterenol (ISO). Inhibition of I_{to} , the major repolarizing current in these cells, increases action potential duration (APD), leading to enhanced Ca^{2+} entry through LTCCs and elevated SR Ca^{2+} load (Devenyi and Sobie, 2016). ISO also augments Ca^{2+} entry through LTCCs and Ca^{2+} uptake into the SR, further elevating the SR load. The combination of these two perturbations by Koleske et al. (2018) caused the cells to exhibit frequent triggered activity and aberrant intracellular Ca^{2+} release. Three Na_V -blocking agents were then applied to assess the potential role of nNa_V s. Although the global Na^+ channel blocker lidocaine did not reduce the frequency of either triggered activity or aberrant Ca^{2+} release, the nNa_V -specific blockers riluzole and 4,9-anhydro-tetrodotoxin (4,9-ah-TTX) significantly reduced both. None of the three Na_V blockers reversed the action potential prolongation induced by 4AP+ISO treatment, indicating that the antiarrhythmic effects of the drugs do not simply result from changes in action potential shape.

After these initial results suggesting that nNa_V blockade can inhibit arrhythmic behaviors, the authors investigated two additional experimental models to obtain further support, with a particular focus on unstable intracellular Ca^{2+} dynamics in the form of DAD-inducing Ca^{2+} waves. In the first model, APD prolongation was induced by nonselective augmentation of Na^+ influx with Anemone toxin II. They found that riluzole or

4,9-ah-TTX treatment largely reduced the frequency of EADs and DADs, and abolished the LQT phenotype. This assessment was repeated for a model in which the LQT phenotype was induced with the LTCC-augmenting drug Bay K 8644, and consistent results were observed.

The last two sets of experiments were performed in myocytes from mice with cardiac-specific deletion of calsequestrin (*CASQ2*), the primary SR Ca^{2+} buffer. Mutations in *CASQ2* account for a recessive form of CPVT (Faggioni et al., 2012), and the *CASQ2*-null mouse has been a reliable CPVT model for more than a decade (Knollmann et al., 2006). Although the substantial action potential prolongation induced by the pharmacological treatments is not typical of the CPVT phenotype, these experiments may nevertheless help to provide insight into heart failure. This condition is associated with both action potential prolongation and unstable SR Ca^{2+} release (Bers et al., 2006), although many additional alterations contribute to the phenotype.

Overall, the study demonstrated a protective, antiarrhythmic effect of nNa_V blockade in three separate experimental models of mouse ventricular arrhythmia. These results suggest a privileged role of neuronal Na_V channels in mediating cellular triggered activity and arrhythmia via a mechanism that involves Ca^{2+} -voltage coupling.

Subcellular microdomains enable nNa_V s to influence Ca^{2+} -voltage coupling

How can we understand the results presented by Koleske et al. (2018), which suggest that Na^+ influx through nNa_V s plays a particularly important role in determining arrhythmic behavior? A straightforward potential explanation is illustrated schematically in Fig. 1 A, which shows the subcellular location of nNa_V s at an influential position near the couplon. Classical cardiac Na^+ channels, cNa_V s (i.e., $\text{Na}_V1.5$), are for simplicity shown in the T-tubule membrane but distant from the couplon, although localization and functional data suggest that these channels cluster in the intercalated disk regions between adjacent myocytes (Lin et al., 2011; Westenbroek et al., 2013). The arrangements illustrated in Fig. 1 A imply that augmentation of either nNa_V s or cNa_V s would lead to action potential prolongation, which would then increase Ca^{2+} influx and diastolic SR $[\text{Ca}^{2+}]$ load. However, selective augmentation of nNa_V s would be predicted to cause more pronounced effects than selective augmentation of cNa_V s, as illustrated by the hypothetical action potential, intracellular $[\text{Ca}^{2+}]$, and SR $[\text{Ca}^{2+}]$ time courses shown in Fig. 1 B. Because nNa_V s are located in much closer proximity to the couplon than cNa_V s, a local increase in $[\text{Na}^+]$ near the couplon would reduce the efflux of Ca^{2+} through NCX. This would allow more local Ca^{2+} to be taken into the SR by the SR Ca^{2+} ATPase pump, leading to a greater increase in SR $[\text{Ca}^{2+}]$ load than would occur in the absence of elevated local $[\text{Na}^+]$. Elevated SR $[\text{Ca}^{2+}]$ load caused by nNa_V augmentation would increase the risk of spontaneous SR Ca^{2+} release and DADs. This model can also explain why, when SR $[\text{Ca}^{2+}]$ is increased through various interventions, selective blockade of nNa_V s (as in the experiments of Koleske et al., 2018) reduce the frequency of both Ca^{2+} waves and triggered activity. In contrast, nonspecific Na^+ channel blockade using lidocaine did not correct triggered activity, suggesting that local increases

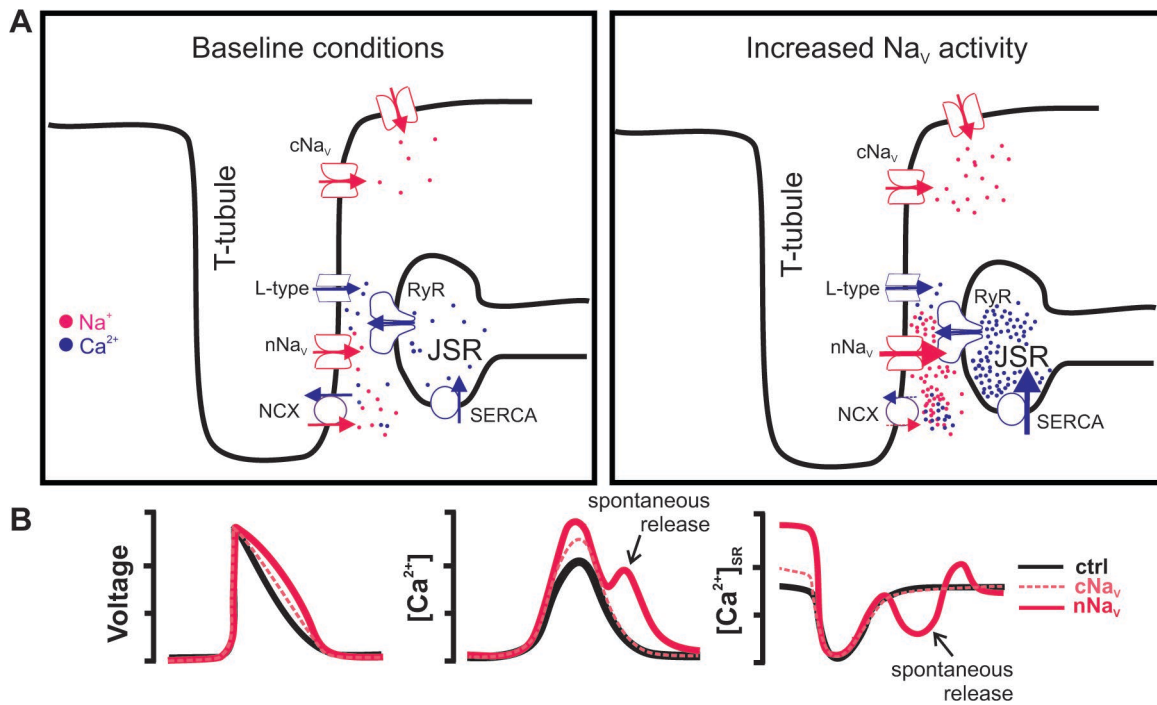


Figure 1. The proximity of nNavs to the excitation–contraction coupling machinery can be proarrhythmic. (A) Inferred locations of proteins important in excitation–contraction coupling are shown under control conditions (left) and after augmentation of flux through Navs (right). Compared with cNavs, nNavs appear to be located closer to the excitation–contraction coupling machinery, including LTCCs and NCX in the T-tubule membrane and RyRs and SERCA in the local SR membrane. An increase in Na⁺ influx through nNavs will lead to increased local [Na⁺] (red dots), reduced Ca²⁺ removal via NCX, and increased SR [Ca²⁺] (blue dots). (B) Hypothetical action potentials (left), intracellular [Ca²⁺] (middle), and SR [Ca²⁺] (right) under control conditions (solid black lines), after augmentation of cNavs (dashed red lines), and after augmentation of nNavs (solid red lines). Increased flux through either cNavs or nNavs will prolong the AP and increase SR [Ca²⁺] load. When this occurs through nNavs, however, the local signaling means that the increase in SR [Ca²⁺] will be greater, increasing the risk of spontaneous, arrhythmogenic Ca²⁺ release.

in Na⁺ near other Na⁺ channels, i.e., cNavs, do not significantly affect Ca²⁺ efflux through NCX.

A potentially important protein that is not depicted in Fig. 1A is Ca²⁺/calmodulin-dependent protein kinase II (CaMKII). This kinase can phosphorylate both RyRs and nNavs, increasing their open probability (Wehrens et al., 2004) and augmenting the current through these channels (Radwański et al., 2016), respectively. Prior studies have suggested that a deleterious feedback loop involving elevated intracellular [Na⁺], intracellular [Ca²⁺], and CaMKII can be proarrhythmic in mouse myocytes (Morotti et al., 2014). Because agonists such as isoproterenol lead to activation of CaMKII in addition to the classical downstream effector protein kinase A (Curran et al., 2007; Gutierrez et al., 2013; Poláková et al., 2015), the proarrhythmic state seen during β-adrenergic stimulation is likely to involve CaMKII activation in addition to the steps outlined above. Indeed, Radwański et al. (2016) previously showed that CaMKII inhibition can be beneficial during conditions associated with increased Na⁺ flux through nNavs.

Neuronal Na⁺ channels in close proximity to excitation–contraction coupling machinery: an emerging theme

In addition to supporting the findings of the present study, the conceptual model shown in Fig. 1A is consistent with recent work by other groups. For instance, when the cell membrane is depolarized and intracellular [Ca²⁺] is low, NCX operates in reverse mode to import Ca²⁺ and export Na⁺. Although early studies

showed that this Ca²⁺ entry pathway is inefficient at triggering SR Ca²⁺ release when operating in isolation (Sipido et al., 1997), more recent investigations have demonstrated that LTCCs, NCXs, and nNavs can interact to boost the trigger for SR Ca²⁺ release (Sobie et al., 2008; Larbig et al., 2010; Chu et al., 2016). Indeed, selective blockade of nNavs with nanomolar concentrations of TTX can inhibit SR Ca²⁺ release, suggesting involvement of these isoforms (Torres et al., 2010). This can only occur if these ion transport pathways are in reasonably close proximity, as also suggested by Koleske et al. (2018).

The results of this study (Koleske et al., 2018) also improve our understanding of cellular arrhythmia initiation mechanisms under pathological conditions. As mentioned above, studies into LQTS have generally focused on arrhythmias initiated by EADs (Weiss et al., 2010), a process that can be understood without considering SR Ca²⁺ release. However, a series of recent investigations have suggested that, at least under some conditions, Ca²⁺ overload and spontaneous SR Ca²⁺ release can contribute to the arrhythmic phenotype in various forms of LQTS. This can take the form of triggered activity initiated by spontaneous Ca²⁺ waves and DADs, as reported here. However, this unstable Ca²⁺ release can be proarrhythmic in other ways. Secondary spontaneous Ca²⁺ releases during the action potential can prolong the repolarization phase, thereby making EADs caused by LTCC reactivation more likely (Edwards et al., 2014; Terentyev et al., 2014). Additionally, unstable spontaneous Ca²⁺ release can encourage

the formation of spatially discordant alternans, patterns of voltage and $[Ca^{2+}]$ at the tissue level that can predispose hearts to arrhythmias (Liu et al., 2018). Overall, these recent studies paint a picture that spontaneous SR Ca^{2+} release is a critical proarrhythmic signal not only in CPVT, as is well established, but also in LQTS, where its role has been less appreciated. The current study (Koleske et al., 2018) makes a significant addition to this emerging paradigm, emphasizing the importance of SR Ca^{2+} release in LQTS and drawing additional mechanistic links between the two arrhythmia disorders.

Future research on nNa_vs and cardiac arrhythmias

As with all important investigations, the study by Koleske et al. (2018) suggests avenues for future research. One will be to determine the precise roles played by different nNa_v isoforms in promoting proarrhythmia. The schematic in Fig. 1 groups all nNa_vs into a single category because most of the results presented by Koleske et al. (2018) were not aimed at distinguishing between nNa_v isoforms. However, the antiarrhythmic effectiveness of 4,9-ah-TTX, which preferentially blocks Na_v1.6, suggests a critical role for this isoform. This is consistent with prior studies (Noujaim et al., 2012; Westenbroek et al., 2013), including one by the same group (Radwański et al., 2016), indicating that Na_v1.6 may be more important in ventricular pathophysiology than other neuronal isoforms such as Na_v1.1 and Na_v1.3. Additional studies will be required, perhaps with cardiac-specific knockout mice (Noujaim et al., 2012), to fully elucidate the roles of the various isoforms.

A second issue to address in future work concerns the applicability of the results, obtained using mice, to arrhythmias in humans and larger animals. The mouse action potential is not only much shorter, but has a fundamentally different shape compared with action potentials seen in larger mammals. Repolarization in mouse myocytes depends primarily on transient outward current (I_{to}), whereas the rapid and slow delayed rectifier currents, I_{Kr} and I_{Ks} , are critical in humans, dogs, and rabbits. In contrast, the primary depolarizing currents, I_{Na} (carried by Na_v1.5) and I_{CaL} (carried by LTCCs), are similar in mice and humans. This means that mouse myocytes can serve as reasonable experimental models for LQT3 (caused by mutations in Na_v1.5) or LQT8 (caused by mutations in LTCCs), whether these models are genetic (Fredj et al., 2006; Drum et al., 2014) or pharmacological, as used here. Mice are much less useful for investigations of LQT1 or LQT2, caused by mutations in the genes responsible for I_{Ks} and I_{Kr} , respectively. Future studies using larger animals should address whether the proarrhythmic Na⁺-Ca²⁺ signaling described in this paper plays an important role in LQT1 and/or LQT2. For such studies that compare results obtained in different experimental models, novel computational approaches to translate perturbation responses across cell types are likely to be extremely useful (Gong and Sobie, 2018).

Overall, the study by Koleske et al. (2018) provides important novel insight into the role played by nNa_vs in creating proarrhythmic conditions in ventricular myocytes. The results emphasize the importance of spatial microdomains, in which ion channels, pumps, and transporters can closely interact, and they improve our understanding of the potential proarrhythmic

consequences of Ca^{2+} -voltage coupling. The study is sure to inspire future investigations and may provide a roadmap for the development of novel antiarrhythmic therapeutics.

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