conduction and QT prolongation observed in SUDEP and that TTX-sensitive channels play an important role in these changes. Our results suggest a new paradigm by which some of the arrhythmias observed during epilepsy are not centrally mediated but also occur as a consequence of electrical remodeling of the heart.

Voltage-gated Ca Channels II

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Profiling Mechanisms of RGK Inhibition Across the Family of High-Voltage-Activated Cav1/Cav2 Calcium Channels

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Rad/Rem/Rem2/Gem (RGK) proteins are Ras-like monomeric G-proteins that powerfully potently inhibit all high-voltage-activated Ca_V1 and Ca_V2 calcium channels. Since all RGKs bind auxiliary Ca_Vβs it was generally assumed that the RGK-β interaction is essential for Ca_V channel inhibition. Recently, using a mutated β (β_{TM}) which), which selectively loses the ability to interact with RGKs, we reported that Rem inhibits Ca_V1.2 channels using both β-bindingdependent and direct α₁-binding-dependent mechanisms (Yang et al, 2013, PLoS One, 7:e37079). Our aims here were twofold: (1) to identify determinants and mechanisms underlying direct Rem binding to, and inhibition of, Cav1.2 pore-forming α_{1C} subunit;; (2) to profile the relative prevalence of β -binding-dependent and -independent mechanisms of inhibition across the RGK and Ca_V1/Ca_V2 channel families. Using a combination of FRET, coimmunoprecipitation assays, systematic truncations, and whole-cell electrophysiology we found that Rem C-terminus interacts with α_{1C} N-terminus to inhibit Ca_V1.2 current (I_{Ca,L}) and gating charge. For profiling, we compared the impact of the four RGKs on currents through recombinant channels (Ca_V1.3, Ca_V2.1, Ca_V2.2) reconstituted with either wt β_{2a} or $\beta_{2a,TM}$, respectively. When reconstituted with wt $\beta_{2a},\, \text{all}$ three channel types were strongly inhibited by each RGK. By contrast, when reconstituted with $\beta_{2a,TM}$, $Ca_V1.3$ and Ca_V2.1 were completely refractory to all four RGKs indicating these channels display only $Ca_V\beta$ -binding-dependent mechanisms of inhibition. $Ca_V2.2$ channels reconstituted with $\beta_{2a,TM}$ displayed a strong inhibition solely to Rad, identifying a second example of $\text{Ca}_V\beta$ -binding-independent regulation of a Cav channel by an RGK protein. The results reveal latent capabilities of distinct RGKs to selectively inhibit particular Ca_V1/Ca_V2 channels in an isoform-specific manner. These dormant capabilities may be exploitable to develop novel genetically-encoded isoform-selective Ca_V1/Ca_V2 channel inhibitors

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Leucine-Rich Repeat Containing 10 (Lrrc10) Protein is a Novel Regulator of Cardiac Cav1.2 L-Type Calcium Channels

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¹Medicine, University of Wisconsin, Madison, WI, USA, ²Cell and Regenerative Biology, University of Wisconsin, Madison, WI, USA. Leucine-rich repeat containing 10 (LRRC10) is a cardiac-specific protein that plays a critical role in cardiac function. We have demonstrated that the Lrrc10null (*Lrrc10*^{-/-}) mice develop dilated cardiomyopathy. Our recent data indicate that *Lrrc10*^{-/-} cardiomyocytes exhibit reduced L-type Ca²⁺ channel (LTCC) current (I_{Ca,L}). However, it is unclear how LRRC10 regulates I_{Ca,L} in the heart. To investigate the role of LRRC10 in the regulation of LTCCs, we coexpressed the Myc tagged LRRC10 (LRRC10-Myc), heamagglutinin tagged $Ca_v 1.2$ ($Ca_v 1.2$ -HA) and the auxiliary $Ca_v \beta_{2C}$ subunit in HEK293 cells and performed co-immunoprecipitation (co-IP) on lysates using either anti-HA, anti-Myc antibody or control IgG. Western blot analysis demonstrated that Ca_v1.2 and LRRC10 associated with one another without the co-expression of $Ca_{\nu}\beta_{2C}$ subunit. Also, the $Ca_{\nu}\beta_{2C}$ and LRRC10 did not co-IP with one another suggesting that the LRRC10 may directly interact with Ca_v1.2 subunit. We then tested if a single point mutation H150A or triple point mutations Y104A, W127A and H150A would alter putative functional interaction sites in the LRRC10 and investigated if these mutations disrupt LRRC10 association with Cav1.2. Both LRRC10 mutants did not associate with Cav1.2. Additionally, co-IP analysis using mouse ventricular homogenates demonstrated that LRRC10 and Ca_v1.2 subunit are associated with one another. Finally, wholecell patch clamp experiments performed in ventricular myocytes from $Lrrc10^{-/-}$ mice demonstrated a significant reduction in the $I_{Ca,L}$ density (-2.5) 0.2 pA/pF) and delayed inactivation, compared to WT myocytes (-6 0.6 pA/ pF). In summary, we demonstrate that the LRRC10 and Ca_v1.2 subunit of LTCC may directly interact with one another and that mutations in LRRC10 residues, likely important for protein-protein interactions, disrupts this association. We conclude that LRRC10 is a novel and essential regulator of the LTCC function in ventricular myocytes.

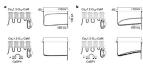
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A Unified Framework for Calcium Channel Modulation by Calcium Binding Proteins

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Biomedical Engineering, Johns Hopkins University, Baltimore, MD, USA. Distinguishing between allostery and competition among modulating ligands is challenging for large target molecules. One key example of such ambiguity concerns calcium-binding proteins (CaBPs) that tune signaling molecules regulated by calmodulin (CaM). In L-type Ca²⁺ channels, CaBPs can potently eliminate CaM-dependent inactivation (CDI). However, the mechanism for this modulation remains controversial. In past, using a live-cell holomolecule approach, we resolved a cyclical allosteric binding scheme for CaM and CaBP4 to Ca_V1.3 channels. In this scheme, both CaBP4 and CaM can simultaneously bind, resulting in strong inhibition of CDI despite the presence of a covalently attached CaM (a), supporting an allosteric regulatory mechanism. By contrast, Findeisen *et al* (*J Mol. Biol.* 425(17):3217-34) showed that fusion of CaM to Ca_V1.2 channels prevents CaBP1 modulation, thus arguing for a competitive regulatory mechanism. These results are confounded by limited delivery of CaBPs through pipet dialysis. Here, we show that the CDI of

Ca_V1.2 channels with a fused CaM is robustly inhibited by recombinantly expressed CaBP1 and CaBP4 (**b**). Thus, it appears that the cyclical allosteric scheme first resolved in Ca_V1.3 now stands as a common framework for CaBP modulation of L-type calcium channels.



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C-Terminal Modulation of Cav1.3 L-Type Calcium Channels Modifies their Gating Properties in Cochlear Inner Hair Cells

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The Ca^{2+} currents in inner hair cells (IHCs) are crucial for synaptic transmission and flow through voltage-gated calcium channels (VGCCs) formed by the $\alpha 1$ subunit $\text{Ca}_{\nu} 1.3$. VGCCs exhibit a calmodulin (CaM) mediated calcium-dependent inactivation (CDI), via binding CAM to the channel's C-terminus. In IHCs, $\text{Ca}_{\nu} 1.3$ exhibits unusually weak CDI, probably caused by calcium binding proteins (CaBP) competing with CaM. IHCs express long and short $\text{Ca}_{\nu} 1.3$ splice variants either including (long variant, $\text{Ca}_{\nu} 1.3 \text{L}$) or excluding (short variants) a C-terminal modulatory domain. In expression systems - lacking CaBPs - the C-terminal modulatory mechanism (CTM) functions via intramolecular interaction of a proximal (PCRD) and a distal C-terminal regulatory domain (DCRD) by inhibiting CaM binding near the PCRD, thereby inhibiting CaM-mediated CDI (Bock et al., JBC 2011). Here, the role of the CTM for IHC VGCCs was investigated in $\text{Ca}_{\nu} 1.3 \text{L}$ -DCRDHA/HA mice in which CTM was disrupted by partial replacement of the DCRD with an HA tag.

Localization of HA-tagged $\mathrm{Ca_v}1.3$ channels in IHCs was determined by immunohistochemistry. Channel properties were investigated by whole-cell patch-clamp recordings. Hearing was assessed using auditory brainstem responses (ABR) and distortion products of otoacoustic emissions (DPOAE).

Anti-HA immunolabeling was present at all IHC ribbons. Patch-clamp recordings revealed significantly reduced CDI and increased amplitudes of $\mathrm{Ca^{2+}}$ and $\mathrm{Ba^{2+}}$ currents in $\mathrm{Ca_v1.3L\text{-}DCRDHA/HA}$ IHCs. Non-stationary fluctuation analysis showed unchanged numbers of $\mathrm{Ca_v1.3}$ channels and single channel currents. Voltage dependence and activation kinetics of $\mathrm{I_{Ca}}$ and $\mathrm{I_{Ba}}$, ABR thresholds and DPOAEs were unaffected.

Our data demonstrate that the long $Ca_v1.3$ isoform is an intrinsic component of $Ca_v1.3$ clusters at *all* IHC ribbon synapses and that its DCRD is required for normal CDI and I_{Ca} amplitude.

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