Disruption of the IS6-AID linker affects voltage-gated calcium channel inactivation and facilitation
Felix Findeisen and Daniel L. Minor Jr.

Please note that in the original Fig. 2, “10^x” was missing from the y axes. The correct figure appears below.

Figure 2. Glycine substitution in IS6-AID linker disrupts helical structure. (A) Mean residue ellipticity at 222 nm for IS6-AID linker peptide, and AAA and GGG mutant peptides as a function of TFE concentration. Peptide sequence is shown. Black highlights the site of the GGG and AAA mutations. (B) IS6-AID linker peptide CD spectra at a peptide concentration of 50 µM in 50% TFE.
Disruption of the IS6-AID Linker Affects Voltage-gated Calcium Channel Inactivation and Facilitation

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Two processes dominate voltage-gated calcium channel (CaV) inactivation: voltage-dependent inactivation (VDI) and calcium-dependent inactivation (CDI). The CaVβ/CaVα-|I-II loop and Ca2+/calmodulin (CaM)/CaVα–C-terminal tail complexes have been shown to modulate each, respectively. Nevertheless, each complex couples to the pore and whether each affects inactivation independently have remained unresolved. Here, we demonstrate that the IS6–α-interaction domain (AID) linker provides a rigid connection between the pore and CaVβ/|I-II loop complex by showing that IS6-AID linker polyglycine mutations accelerate CaV1.2 (L-type) and CaV2.1 (P/Q-type) VDI. Remarkably, mutations that either break the rigid IS6-AID linker connection or disrupt CaVβ/|I-II association sharply decelerate CDI and reduce a second Ca2+/CaM/CaVα–C-terminal-mediated process known as calcium-dependent facilitation. Collectively, the data strongly suggest that components traditionally associated solely with VDI, CaVβ and the IS6-AID linker, are essential for calcium-dependent modulation, and that both CaVβ-dependent and CaM-dependent components couple to the pore by a common mechanism requiring CaVβ and an intact IS6-AID linker.

INTRODUCTION

Voltage-gated calcium channels (CaVs) serve as a major source of calcium influx in excitable cells (Hille, 2001). Calcium ions have a unique biological role in that they act as both charge carriers and as chemical messengers (Clapham, 2007). Thus, CaV activity provides a vital link between membrane potential charges and stimulation of calcium-driven intracellular signaling cascades that directly affect processes such as excitation–contraction coupling, neurotransmitter release, and gene regulation (Catterall, 2000). High voltage–activated channels consist of four essential components (Van Petegem and Minor, 2006): a pore-forming CaVα1 subunit from either CaV1 or CaV2 isoforms (Catterall, 2000), a cytoplasmic CaVβ subunit (Dolphin, 2003), the transmembrane CaVα2β subunit (Davies et al., 2007), and calmodulin (CaM) (Pitt, 2007). Two intracellular components of the complex, CaVβ and CaM, play central roles in channel modulation processes that affect calcium influx. In particular, both affect channel inactivation, a generalized term for phenomena that limit channel conduction and calcium influx under conditions in which the channel would otherwise remain open.

The two principal CaV inactivation processes are voltage-dependent inactivation (VDI) (Stotz et al., 2004; Cens et al., 2006) and calcium-dependent inactivation (CDI) (Cens et al., 2006; Halling et al., 2006). The molecular origins of VDI are complex and have remained imperfectly understood (Stotz et al., 2004). The predominant contributions appear to arise from the CaVβ subunit (Olcese et al., 1994; Stea et al., 1994; De Waard and Campbell, 1995), CaVα transmembrane segment IS6 (Zhang et al., 1994; Raybaud et al., 2006), and the CaVα1 intracellular I-II loop (Herlitze et al., 1997; Sokolov et al., 1999; Stotz et al., 2000; Berrou et al., 2001; Geib et al., 2002), although mutations in other transmembrane segments (Stotz et al., 2000; Berjukow et al., 2001; Shi and Soldatov, 2002; Raybaud et al., 2006, 2007), the cytoplasmic N-terminal domain (Kobrinsky et al., 2005; Kanevsky and Dascal, 2006), the C-terminal EF-hand region (Bernatchez et al., 1998), and the CaM-interaction domain (Li et al., 2003; Kim et al., 2004; Barrett and Tsien, 2008) have also been shown to affect VDI. The central role of CaVβ in VDI is evident from the diverse VDI rates bestowed upon CaV1 and CaV2 CaVα1 subunits through association with particular CaVβ isoforms. CaVβ2 slows VDI considerably (Olcese et al., 1994; Stea et al., 1994; De Waard and Campbell, 1995), a consequence of the anchoring of its N terminus to the membrane by palmitoylation (Chien et al., 1996; Qin et al., 1998). In contrast, CaVβ1, CaVβ2, and CaVβ3, which lack
the palmitoylation site found in Ca\(_{\alpha}\)\(\beta\)\textsubscript{2a}, support fast VDI (Olcense et al., 1994; Stea et al., 1994; De Waard and Campbell, 1995). The discovery that IS6 mutations that drastically reduce Ca\(_{\alpha}\)1.2 VDI cause a multisytem disorder involving lethal heart arrhythmias, cognitive abnormalities, and immune deficiencies, known as Timothy syndrome (Splawski et al., 2004, 2005), provides further evidence for the importance of IS6 in channel gating and a compelling example of the physiological relevance of VDI.

Structural studies have revealed that the high affinity Ca\(_{\alpha}\)\(\beta\)-binding site present on the I-II loop, the \(\alpha\)-interaction domain (AID), forms an \(\alpha\)-helix that interacts extensively with a deep pocket on Ca\(_{\alpha}\)\(\beta\), the \(\alpha\)-binding pocket (Chen et al., 2004; Opatowsky et al., 2004; Van Petegem et al., 2004). Although absent from the crystal structures, the 22 residues that bridge the C-terminal cytoplasmic end of the pore-lining IS6 helix and N-terminal end of the AID \(\alpha\)-helix, the IS6-AID linker, have been noted to have a high \(\alpha\)-helix propensity (Opatowsky et al., 2004; Van Petegem et al., 2004). This observation raises the possibility that the IS6-AID linker forms a continuous helix between IS6 and AID that acts as a rigid rod through which Ca\(_{\alpha}\)\(\beta\) affects channel gating (Opatowsky et al., 2004; Van Petegem et al., 2004). Partial support for this idea comes from functional studies of chimera between the low voltage-activated Ca\(_{\alpha}\)3.1, a Ca\(_{\alpha}\)4.1 subunit that lacks Ca\(_{\alpha}\)\(\beta\) modulation, and the Ca\(_{\alpha}\)2.2 I-II loop (Arias et al., 2005). Fusion of the Ca\(_{\alpha}\)2.2 I-II loop to the end of Ca\(_{\alpha}\)3.1 IS6 endowed the chimeric channel with Ca\(_{\alpha}\)\(\beta\)-dependent modulation that could be eliminated by hexaglycine mutations in the IS6-AID linker. Nevertheless, a detailed investigation of the role of the IS6-AID linker in the context of channels that are natively modulated by Ca\(_{\alpha}\)\(\beta\) has not been reported.

Ca\(_{\alpha}^{2+}\)/CaM binding to the IQ domain, which is located in the Ca\(_{\alpha}\)4.1 subunit cytoplasmic C-terminal tail, drives CDI (Zühlke et al., 1999; Erickson et al., 2003; Halling et al., 2006) as well as calcium-dependent facilitation (CDF), an increase in peak current upon repetitive stimuli (Zühlke et al., 1999; DeMaria et al., 2001; Van Petegem et al., 2005; Lee et al., 2006). The IQ domain is \(\sim\)200 residues C terminal to the last transmembrane segment IVS6. Although crystallographic studies have revealed the nature of the Ca\(_{\alpha}^{2+}\)/CaM-IQ domain interaction (Fallon et al., 2005; Van Petegem et al., 2005), it is not known how the binding of Ca\(_{\alpha}^{2+}\)/CaM to a site seemingly distant from the transmembrane pore affects gating.

Even though many models have been proposed, it is unclear how VDI and CDI proceed and whether they use separate (Barrett and Tsien, 2008) or common mechanisms (Cens et al., 1999; Kim et al., 2004). Here, we show that both the Ca\(_{\alpha}\) subunit and the integrity of the IS6-AID linker affect VDI, CDI, and CDF profoundly, and that an intact IS6-AID linker is required for both the Ca\(_{\alpha}\)\(\beta\) and Ca\(_{\alpha}^{2+}\)/CaM-IQ domain cytoplasmic elements to modulate the activity of the transmembrane pore. These results provide strong evidence for a model in which VDI, CDI, and CDF act through mediation of the protein–protein complex formed by Ca\(_{\alpha}\)\(\beta\) and the IS6-AID linker.

### MATERIALS AND METHODS

**Molecular Biology**

Constructors for electrophysiology consisted of human Ca\(_{\alpha}1.2\) (\(\alpha\)-C77; GenBank accession no. CAA84340) in pcDNA3.1 (Invitrogen), rabbit Ca\(_{\alpha}2.1\) (GenBank accession no. X57477) in pGEMHE, rabbit Ca\(_{\alpha}1.4\) (GenBank accession no. M25514) in pSp65, rat Ca\(_{\alpha}2.3\) (GenBank accession no. NP_445303) in pGEMHE, rabbit Ca\(_{\alpha}2.2\) (GenBank accession no. X04228) in pSPORT1 (Promega), and rabbit Ca\(_{\alpha}\)\(\alpha\)\(\beta\)-1 (GenBank accession no. NM_001082276) in pcDNA3.1. ssCa\(_{\alpha}2.3\) is a double mutant (C3S and C4S) of rat Ca\(_{\alpha}2.3\). To facilitate mutagenesis of the I-II loop region of Ca\(_{\alpha}1.2\), a silent HpaI site was added at nucleotide positions 1,114–1,119 to create an excisable fragment framed by the HpaI site and a naturally occurring PpuMI site at nucleotide positions 2,759–2,765. This fragment was excised and ligated into a pGEMHE backbone to serve as a template for mutagenesis. Similarly, for Ca\(_{\alpha}2.1\) I-II loop mutagenesis, a ClaI site from the vector N terminal to the Ca\(_{\alpha}2.1\) coding region and the naturally occurring XhoI site at nucleotide positions 1,395–1,400 framed a fragment that was excised and ligated into a pGEMHE backbone to serve as a cloning cassette. Mutations were introduced in the cloning cassette using QuikChange (Agilent Technologies), and mutated fragments were religated into their parent vector. Each mutant was sequenced in the final vector across either the entire channel coding sequence or the mutated fragment and points of reinsertion only, as appropriate.

**Electrophysiological Recordings and Data Analysis**

After overnight linearization of the vector (pcDNA3 with XhoI, pGEMHE with NotI, pSPORT1 with NotI, and pSP65 with XbaI), capped mRNA was synthesized with the T7 or SP6 Messenger kit (Applied Biosystems), as appropriate. 50 nl of equimolar Ca\(_{\alpha}\)\(\alpha\)\(\beta\), Ca\(_{\alpha}\)\(\beta\), and Ca\(_{\alpha}\)\(\alpha\)\(\beta\)-1 mRNA at final concentrations of 33–100 nM were injected into de-folliculated Xenopus oocytes prepared as described previously (Van Petegem et al., 2005). Two-electrode voltage clamp experiments were performed 2–5 d after injection using a GeneClamp 500B (MDS Analytical Technologies) amplifier controlled by a 1,200-MHz processor computer (Celeron; Gateway) running CLAMPLEX 8.2.0.244 and digitized at 1 kHz with a Digidata 1332A (MDS Analytical Technologies). Immediately before recording, oocytes were injected with 50 nl of 100 mM BAPTA to minimize Ca\(_{\alpha}^{2+}\)-activated Cl\(^{-}\) current. Recording solutions contained either 40 mM Ba(OH)\(_2\) or 40 mM Ca(NO\(_3\))\(_2\), 50 mM NaOH, 1 mM KOH, and 10 mM HEPES. Both solutions were adjusted to pH 7.4 using HNO\(_3\). Electrodes were filled with 3M KC\(_1\) and had resistances of 0.3–2.0 MO. Leak currents were subtracted using a P/4 protocol. Currents were analyzed with Clampfit 8.2 (MDS Analytical Technologies). During recordings, oocytes were superfused using a Valvelink 16 controller (Automate Scientific). All results are from at least two independent oocyte batches. \(G_{\text{max}}\), \(V_{\text{50}}\), and \(K_0\) were calculated by recording a series of 450-ms pulses from −50 to +70 mV from a resting potential of −90 mV and fitting them to the equation: \(I = G_{\text{max}} \times \left( \frac{V_m - V_{\text{rev}}}{1 + \exp \left( \frac{V_m - V_{\text{50}}}{K_0} \right) } \right)\), where \(I\) is the measured peak current at each \(V_m\), \(G_{\text{max}}\) is the maximal conductance, \(V_m\) is the test potential, \(V_{\text{50}}\) is the reversal potential, \(V_{\text{50}}\) is the midpoint of activation, and \(K_0\) is the slope factor (Kanovsky and Dascal, 2006). The \(t_{\text{300}}\) and \(t_{\text{2400}}\)
values were calculated from normalized currents at +20 mV and represent the percentage inactivation after 300 and 2,400 ms, respectively. CaV1.2 currents recorded with calcium as charge carrier show inactivation resulting from two inactivation processes, VDI and CDI. netCDI was determined by dividing the normalized calcium current by the normalized barium current (Barrett and Tsien, 2008). Inactivation \( t_\text{I300} \) values were calculated at a test potential of +20 mV using the formula \( I = A_1 \exp(-t/t_\text{I300}) + A_2 \exp(-t/t_\text{I300}) + C \), where \( I \) is the recorded current, \( A_1 \) is the amplitude of the current component, and \( C \) is the residual current at steady state. Isochronal inactivation data were obtained using a protocol modified from Berrou et al. (2001) in which a +20-mV control pulse was followed by a +20-mV prepulse to variable potentials and a test pulse to +20 mV. Inactivation in both barium and calcium were measured from the same oocyte and calculated as:

\[
\text{Inactivation}_{(Ba \ or \ Ca)} = 1 - \left( \frac{I_{\text{test}}}{I_{\text{control}}} \right)
\]

VDI and CDI. netCDI was determined by dividing the normalized current component, and C is the residual current at

\[
\text{Inactivation (Ba \ or \ Ca)} = 1 - \left( \frac{I_{\text{test}}}{I_{\text{control}}} \right)
\]

Cutoff of 2 kD (Vivascience) to 0.05 mM as determined by absorbance. Pellets were stored frozen at 4 °C for 30 min, the soluble fraction was isolated after sonication for 20 min at 4°C. Pellets were stored frozen at 4°C until further use. Thawed cells were lysed by sonication in 250 mM KCl and 10 mM KH2PO4/KHPO4, pH 7.3 (Buffer A). After centrifugation at 15,000 g at 4°C for 30 min, the soluble fraction was loaded on a nickel-charged Poros20MC column (Applied Biosystems), washed in Buffer A, and eluted using step elution of Buffer A plus 500 mM imidazole, pH 8.0. After overnight cleavage with TEV protease (Kapust et al., 2001) at room temperature, the peptides retained an N-terminal tripeptide sequence of Gly-His-Met derived from the TEV cleavage site, and a C-terminal tripeptide sequence of Gly-Gly-Trp to allow determination of the peptide concentration. Pure peptide was eluted in Buffer A as the flow-through from an amylase column (New England Biolabs, Inc.) and a Poros20MC column connected in sequence. Aggregated peptide was separated from soluble material using a Superdex75 HR10/30 gel filtration column (GE Healthcare) in Buffer A. The peptide was concentrated using a Vivaspin 15R with a molecular weight cutoff of 2 kD (Vivasave) to 0.05 mM as determined by absorbance (Edelhoch, 1967).

Circular Dichroism (CD)

CD spectra were measured in a 2-mm path-length quartz cuvette (Hellma), 50 mM KCl, and 10 mM KH2PO4/KHPO4, pH 7.3, and varying trifluoroethanol (TFE) concentrations using an Aviv Model 215 spectropolarimeter (Aviv Biomedical) equipped with a pellic temperature controller. Wavelength scans from 320 to 190 nm were taken at 4°C. Each point was determined in triplicate from the same sample and subtracted by the average of a triplicate buffer scan. Each sample was checked for purity by HPLC. Molar ellipticity was calculated as follows: \( \theta = 100(\Delta M)/Cn \)), where \( Cn \) is the CD signal in millidegrees after buffer subtraction, \( C \) is the peptide concentration in millimoles, \( n \) is the number of residues in the peptide, and \( I \) is the cuvette path length in centimeters. Fraction helix was calculated as \( \theta_{\text{helix}} = (\theta_{\text{obs}} - \theta_{\text{coil}})/(\theta_{\text{helix}} - \theta_{\text{coil}}) \), where \( \theta_{\text{helix}} \) and \( \theta_{\text{coil}} \) signify the mean residue ellipticity that is +640 for random coil and -42,500°(1-3/n) for complete helix, respectively (Rohl et al., 1996).

Online Supplemental Material

Fig. S1 shows the effects of the GGG mutation on CaV1.2 in the absence of Ca\(\beta\). Fig. S2 shows the influence of Ca\(\beta\)\(\beta\) on CaV1.2 \(V_{50}\). Fig. S3 displays the averaged \(V_{50}\) values of CaV1.2 mutations in barium- and calcium-containing buffers. Fig. S4 shows the effect of Ca\(\beta\) titration on CaV1.2 and CaV1.2 GGG \(G_{\text{max}}\) values. Fig. S5 compares calcium currents for CaV1.2 6G, CaV1.2 GGG/HotA, and wild-type CaV1.2 expressed at similar levels. Table S1 lists the inactivation parameters in calcium-containing buffer for all CaV1.2/Ca\(\beta\) combinations tested. Table S2 presents the current ranges recorded for the channels used in this study. The online supplemental material is available at http://www.jgp.org/cgi/content/full/jgp.200810143/DC1.

RESULTS

Glycine Substitution in the IS6-AID Linker Affects VDI

As noted previously (Opatskowsky et al., 2004; Van Petegem et al., 2004), the IS6-AID linker has a high probability to form an \( \alpha \)-helical structure (Fig. 1 A). To disrupt the integrity of this putative helix, we mutated three consecutive residues in the middle of the CaV1.2 IS6-AID linker, residues 415–417, to glycine (denoted as GGG) (Fig. 1 A). Due to the extremely low helix propensity of glycine (O’Neil and DeGrado, 1990; Blaber et al., 1993), the GGG mutation is expected to cause substantial disruption of any helical structure present in the IS6-AID linker, as it should incur an \( \sim 3\)–kcal mol\(^{-1}\) destabilization of the helical conformation. As a control for effects resulting from side chain deletion, we also made a mutant that converts CaV1.2 residues 415–417 into a triple-alanine sequence, denoted as AAA. Based on the high helix–forming propensity of alanine, this substitution should leave the IS6-AID helix intact.

We used two-electrode voltage clamp recording in \( \text{Xenopus} \) oocytes under conditions in which barium was the charge carrier to examine the consequences of IS6-AID linker mutations in the presence or absence of Ca\(\beta\)\(\beta\) modulation. When coexpressed with Ca\(\beta\)\(\beta\), GGG channels inactivated \( \sim 7\)-fold faster than wild-type CaV1.2 channels (\(t_{\text{i300}} = 489 \pm 130\) ms vs. 3,730 \pm 670 ms, respectively) and to a sixfold greater extent at 300 ms after activation (\(t_{500} = 13.2 \pm 2.5\%\) and 2.2 \pm 1.3\%, respectively) (Fig. 1, B and C, and Table I). In contrast, AAA mutant channels displayed VDI \(t\) and \(t_{500}\) values similar to wild-type CaV1.2 (\(t_{500} = 3,290 \pm 160\) ms; \(t_{500} = 1.1 \pm 0.6\)). This result indicates that the functional effects caused by the GGG substitution do not result from the loss of key side chain interactions, but rather from the likely loss of structure in the IS6-AID linker. Further disruption of the IS6-AID linker by a hexa-glycine mutant (CaV1.2 6G) (Fig. 1 A) resulted in channels having VDI properties that were indistinguishable from CaV1.2 GGG channels (\(t_{500} = 485 \pm 155\) ms; \(t_{500} = 13.0 \pm 5.6\%\)) (Fig. 1, B and C, and Table I). In contrast, the corresponding hexa-alanine mutation (CaV1.2 6A) had properties similar to wild-type channels (Table I). Thus, additional disruption of the...
IS6-AID linker had no further functional consequences on VDI beyond what was observed for the GGG mutant.

Cav1.2 GGG expressed without Cavβ2a shows VDI that is 1.8-fold faster than Cav1.2 expressed without Cavβ2a (Table I and Fig. S1), a difference that could indicate that the GGG mutation is able to affect the Cavα1 subunit VDI response in the absence of Cavβ modulation. Xenopus oocytes are known to express Cavβ3 (Tareilus et al., 1997), a subunit that accelerates VDI and whose presence could confound interpretation of experiments in which Cavα1 subunits are expressed in the absence of Cavβ coinjection. To get a cleaner assessment regarding whether the GGG mutation affects Cavα1 subunit VDI properties, we examined the effect of the GGG mutant in the context of Cavα1 subunits that bear a triple mutant in the Cavβ high affinity binding site, denoted as HotA, which renders the channels incapable of binding Cavβ (Van Petegem et al., 2008). The inactivation properties Cav1.2 HotA and Cav1.2 GGG/HotA (Fig. S1) are indistinguishable (τ = 601 ± 211 ms and 607 ± 277 ms, respectively; P = 0.99). Further, the VDI τ values are similar to Cav1.2 alone. (τ1 = 455 ± 99 ms) (Fig. 1, B and C, and Table I). These results indicate that the VDI properties of the Cav1.2 α1 subunit in the absence of Cavβ modulation are unaffected by the GGG mutation. The VDI τ values and extent of inactivation for the HotA channels were not significantly different from GGG and 6G channels coexpressed with Cavβ2a (Table I) (one-way ANOVA for VDI τ values, P = 0.45; t300, P = 0.28). Thus, the effects of the glycine mutants on VDI appear to arise from the loss of the influence of Cavβ2a modulation and indicate that the intact IS6-AID linker is required for functional modulation of VDI by Cavβ2a.

In addition to the faster τ values and increased extent of inactivation, Cav1.2 GGG channels lacked the characteristic hyperpolarizing shift in the G-V relationship caused by Cavβ2a coexpression (Perez-Reyes et al., 1992; Neely et al., 1993; Yamaguchi et al., 2000) (Fig. 1 D, Figs. S2 and S3 A, and Table II) and were not significantly different from channels expressed in the absence of Cavβ2a or from Cav1.2 HotA. In contrast, AAA channels had biophysical properties that

![Figure 1](image_url)
were indistinguishable from wild-type Ca V 1.2 (Fig. 1 D, Fig. S3 A, and Table II).

Even though the GGG mutant does not affect any residues that are important for the AID-Ca β high affinity interaction (Van Petegem et al., 2008), it was important to test whether the loss of modulation in the GGG background arose from an unexpected effect on Ca β2a coexpression with the pore-forming subunit. Ca β2a coexpression potently stimulates the total macroscopic current on wild-type Ca V 1.2 channels (Perez-Reyes et al., 1992; Neely et al., 1993), an effect that was retained for Ca β2a, coexpression with Ca V 1.2 GGG (Fig. S4). Thus, the changes in both VDI and G-V modulation resulting from glycine mutations in the IS6-AID linker must arise from a loss of functional coupling and not from a loss of the physical interaction between Ca β2a and the Ca α1 subunit.

To test if the importance of the IS6-AID linker for VDI generalized to other high voltage–activated Ca V s, we made the analogous substitutions in the IS6-AID linker of a Ca V 2 α1-subunit, Ca V 2.1 (Fig. 1 A). Similar to the effects of the triple-glycine substitution in Ca V 1.2, coexpression of Ca V 2.1 GGG with Ca β2a results in channels having greatly increased VDI compared with wild type (Fig. 1 E and Table I). The Ca V 2.1 GGG mutation caused a new fast inactivation component (τ2 = 17.8 ± 2.2 ms), increased the extent of the main inactivation component by approximately sixfold relative to wild type (A1 = 10.0 ± 1.3% vs. A1 = 59.3 ± 8.6%, respectively), and brought

### TABLE I

<table>
<thead>
<tr>
<th>Construct</th>
<th>t i300 (%)</th>
<th>t i2400 (%)</th>
<th>A1 (%)</th>
<th>τ1 (ms)</th>
<th>A2 (%)</th>
<th>τ2 (ms)</th>
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<tr>
<td>Ca V 1.2, β2a</td>
<td>2.2 ± 1.3</td>
<td>10.9 ± 2.6</td>
<td>20.9 ± 3.6</td>
<td>3,730 ± 670</td>
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<td>Ca V 1.2 AAA, β2a</td>
<td>1.1 ± 0.6</td>
<td>11.9 ± 5.2</td>
<td>18.5 ± 7.5</td>
<td>3,290 ± 160</td>
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<td>Ca V 1.2 6A, β2a</td>
<td>1.8 ± 0.6</td>
<td>16.1 ± 3.1</td>
<td>16.9 ± 1.6</td>
<td>1,880 ± 160</td>
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<td>—</td>
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</tr>
<tr>
<td>Ca V 1.2, β1</td>
<td>22.3 ± 1.8</td>
<td>62.4 ± 5.2</td>
<td>73.0 ± 5.7</td>
<td>1,150 ± 80</td>
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<td>Ca V 1.2, βn</td>
<td>4.8 ± 1.5</td>
<td>25.2 ± 2.1</td>
<td>44.5 ± 4.9</td>
<td>2,840 ± 630</td>
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<td>Ca V 1.2, ssβ2a</td>
<td>7.1 ± 2.9</td>
<td>35.7 ± 7.7</td>
<td>43.3 ± 11.3</td>
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<td>Ca V 1.2</td>
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<td>ND</td>
<td>22.7 ± 3.9</td>
<td>455 ± 99</td>
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<td>Ca V 1.2 HotA, β2a</td>
<td>8.9 ± 4.1</td>
<td>ND</td>
<td>23.6 ± 7.2</td>
<td>601 ± 211</td>
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<td>Ca V 1.2 GGG, β2a</td>
<td>13.2 ± 2.5</td>
<td>ND</td>
<td>30.0 ± 6.6</td>
<td>489 ± 150</td>
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<td>Ca V 1.2 6G, β2a</td>
<td>13.0 ± 5.6</td>
<td>ND</td>
<td>34.2 ± 3.4</td>
<td>485 ± 155</td>
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<td>Ca V 1.2 GGG/HotA, β2a</td>
<td>8.9 ± 5.6</td>
<td>ND</td>
<td>21.7 ± 7.6</td>
<td>607 ± 277</td>
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<td>Ca V 1.2 GGG</td>
<td>28.1 ± 3.6</td>
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<td>41.9 ± 3.8</td>
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<td>Ca V 1.2 GGG, β1</td>
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<td>ND</td>
<td>79.2 ± 3.7</td>
<td>292 ± 12</td>
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<td>Ca V 1.2 GGG, βn</td>
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<td>66.0 ± 1.7</td>
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<td>72.0 ± 5.6</td>
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<td>Ca V 2.1, β2a</td>
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<td>308 ± 80</td>
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<td>—</td>
<td>10</td>
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<tr>
<td>Ca V 2.1 GGG, β2a</td>
<td>36.9 ± 4.1</td>
<td>ND</td>
<td>59.3 ± 8.6</td>
<td>439 ± 42</td>
<td>9.2 ± 1.9</td>
<td>17.8 ± 2.2</td>
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<tr>
<td>Ca V 2.1 6G, β2a</td>
<td>39.5 ± 9.8</td>
<td>ND</td>
<td>45.3 ± 8.0</td>
<td>326 ± 31</td>
<td>14.5 ± 4.1</td>
<td>13.0 ± 2.3</td>
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<tr>
<td>Ca V 2.1 AAA, β2a</td>
<td>8.2 ± 1.2</td>
<td>ND</td>
<td>11.9 ± 1.6</td>
<td>283 ± 53</td>
<td>—</td>
<td>—</td>
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<tr>
<td>Ca V 2.1 6A, β2a</td>
<td>9.6 ± 1.5</td>
<td>ND</td>
<td>14.2 ± 2.2</td>
<td>311 ± 79</td>
<td>—</td>
<td>—</td>
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<tr>
<td>Ca V 2.1, β1</td>
<td>57.3 ± 4.3</td>
<td>ND</td>
<td>77.1 ± 7.1</td>
<td>340 ± 55</td>
<td>13.7 ± 2.9</td>
<td>43.9 ± 7.3</td>
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<tr>
<td>Ca V 2.1 GGG, β1</td>
<td>98.0 ± 5.1</td>
<td>ND</td>
<td>63.3 ± 2.3</td>
<td>101.2 ± 1.2</td>
<td>36.9 ± 4.1</td>
<td>94.1 ± 10.2</td>
<td>7</td>
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</table>

Data are expressed as mean values ± SD. τ values were determined at a holding potential of +20 mV (see Materials and methods). t i300 and t i2400 denote percent inactivation at 300 and 2,400 ms, respectively. ND, a value not determined.
about an approximately sixfold increase in \( t_{300} \) (36.9 ± 4.1% vs. 6.5 ± 1.3%, respectively), a comparable effect relative to that observed in \( \text{Ca}^{2+}_1 \) \( \text{GGG} \). Substitution of six glycines, denoted as \( \text{Ca}^{2+}_1 \) \( 6G \), gave rise to channels with VDI properties similar to \( \text{Ca}^{2+}_1 \) \( \text{GGG} \), indicating that as in the \( \text{Ca}^{2+}_1 \) case, an IS6-AID linker triple-glycine substitution is sufficient for uncoupling the VDI modulatory effects of \( \text{Ca}^{2+}_1 \beta_{2\alpha} \), from the pore-forming subunit. Alanine substitution at the same positions, \( \text{Ca}^{2+}_1 \) \( \text{AAA} \) and \( \text{Ca}^{2+}_1 \) \( 6A \), only had marginal effects on VDI, suggesting that none of the side chains deleted by the multiple glycine substitutions was responsible for the VDI acceleration. Collectively, the data indicate that an intact IS6-AID linker helix is essential for \( \text{Ca}^{2+}_1 \beta_{2\alpha} \)-dependent modulation of \( \text{Ca}^{2+}_1 \) and \( \text{Ca}^{2+}_2 \) VDI.

**Glycine Substitutions Disrupt the Ability of the IS6-AID Linker to Form an \( \alpha \)-Helix**

To determine the structural consequences of our substitutions in the IS6-AID linker, we examined the secondary structure content of peptides corresponding to \( \text{Ca}^{2+}_1 \) 6G, gave rise to channels with VDI properties similar to \( \text{Ca}^{2+}_1 \) \( \text{GGG} \), indicating that as in the \( \text{Ca}^{2+}_1 \) case, an IS6-AID linker triple-glycine substitution is sufficient for uncoupling the VDI modulatory effects of \( \text{Ca}^{2+}_1 \beta_{2\alpha} \), from the pore-forming subunit. Alanine substitution at the same positions, \( \text{Ca}^{2+}_1 \) \( \text{AAA} \) and \( \text{Ca}^{2+}_1 \) \( 6A \), only had marginal effects on VDI, suggesting that none of the side chains deleted by the multiple glycine substitutions was responsible for the VDI acceleration. Collectively, the data indicate that an intact IS6-AID linker helix is essential for \( \text{Ca}^{2+}_1 \beta_{2\alpha} \)-dependent modulation of \( \text{Ca}^{2+}_1 \) and \( \text{Ca}^{2+}_2 \) VDI.

Figure 2. Glycine substitution in IS6-AID linker disrupts helical structure. (A) Mean residue ellipticity at 222 nm for IS6-AID linker peptide, and AAA and GGG mutant peptides as a function of TFE concentration. Peptide sequence is shown. Black highlights the site of the GGG and AAA mutations. (B) IS6-AID linker peptide CD spectra at a peptide concentration of 50 \( \mu \)M in 50% TFE.
Rank Order Effects of Caβ Isotypes Remain in the Presence of Disrupted IS6-AID Linker

Prior studies of VDI rates imparted to Caβα1 subunits by various Caβ isoforms demonstrated a stereotyped rank order: fastest to slowest, Caβ1 > Caβ2b > Caβ2a (Olcese et al., 1994; Stea et al., 1994; De Waard and Campbell, 1995; Yasuda et al., 2004). Coexpression of Caβ1.2 with Caββ1, Caββ2b, or Caββ2a results in VDI that is 3.2- and 1.3-fold faster for Caββ1 and Caββ2a relative to Caββ2a (Fig. 3 A and Table I). Additionally, the mutant subunit ssCaβ2a (Chien et al., 1996), which lacks the N-terminal palmitoylation that causes Caβ2a to retard VDI (Chien and Hosey, 1998; Qin et al., 1998; Restituito et al., 2000), displays VDI that is 1.8-fold faster than Caβ2a and similar to Caβ2a.

Having established that different Caβ subunits impart stereotyped VDI differences to Caβ1.2, and that GGG causes a clear acceleration of Caβ1.2 VDI in the presence of Caββ2a (Fig. 1 B), we investigated how the GGG mutation affected the VDI modulation of Caβ1.2 by the different Caβ isoforms. Caβ1.2 GGG channels coexpressed with Caββ1, Caββ2b, or ssCaββ2a all have greatly accelerated VDI compared with wild-type Caβ1.2 coexpressed with the same isoforms (VDI τ value increases of 5.6-, 10.7-, and 7.8-fold for Caββ1, Caββ2b, and ssCaββ2a, respectively) (Fig. 3 A and B, and Table I). Interestingly, the rank order VDI effects relative to Caββ2a are retained (2.4-, 1.8-, and 1.9-fold faster for Caββ1, Caββ2b, and ssCaββ2a relative to Caββ2a). Similar experiments using wild-type Caβ2.1, Caβ2.1 GGG, Caββ1, and Caββ2a show that the GGG substitution causes Caβ2.1 channels to inactivate considerably faster regardless of the Caβ isoform while also maintaining the isoform-specific rank order (Fig. 3 C). The retention of the relative VDI rank order in the context of disrupted Caβ1 and Caβ2 IS6-AID linkers suggests the existence of conserved secondary interaction sites between Caββ and yet to be defined regions of the pore-forming subunits. The observation that Caβ1.2 GGG and Caβ2.1 GGG channels both inactivate faster than wild type regardless of the Caβ isoform provides further support for the idea that the IS6-AID linker forms a rigid connection that couples Caββ to the pore. Thus, the importance of the integrity of the IS6-AID linker for Caββ modulation of VDI is a common element of high voltage-activated Caβα1 architecture.

Disruption of IS6-AID Linker or Caβ Binding Reduces CDI

Given the clear effects of IS6-AID linker disruption on VDI, we investigated whether disruption of the IS6-AID linker affected the other prominent mode of Caβ inactivation, CDI. When calcium ions are used as the charge carriers, the time-dependent decay of Caβ currents arises from two processes: CDI and VDI, which is calcium independent. As long as CDI is much faster than VDI, apparent changes in inactivation of Caβ calcium currents caused by the presence of different subunits or resulting from mutations should reflect alteration of the actual extent of inactivation driven by calcium-dependent feedback modulation. However, when CDI and VDI occur on similar timescales, the observed inactivation represents contributions from both processes and can confound the analysis. Measurement of the ratio of I_{Ca} and I_{Ba} from the same cell permits one to separate CDI
and VDI contributions. Division of normalized $I_{Ca}$, which measures inactivation by CDI and VDI, by normalized $I_{Ba}$, which reflects the fraction of channels available to undergo inactivation, yields a ratio that isolates the contribution of calcium-dependent processes to the overall observed inactivation (Barrett and Tsien, 2008). The more common practice of taking the simple difference between CDI and VDI can underestimate effects on CDI when VDI is accelerated, a problem that the normalized $I_{Ca}/I_{Ba}$ metric avoids. Because many of our manipulations accelerate VDI, we used the normalized $I_{Ca}/I_{Ba}$ metric, which we denote as netCDI, to analyze the inactivation properties of the mutant channels.

A previous study of wild-type CaV1.2 channels expressed in a mammalian cell line suggested that in some cases, $I_{Ba}$ may also undergo current-dependent inactivation (Ferreira et al., 1997), a condition that if present to a substantial degree would complicate the netCDI analysis. To test whether such a phenomenon occurred in our Xenopus oocyte experimental setup, we examined the inactivation properties of $I_{Ba}$ using a double-pulse protocol (Fig. 4 C). Comparison of the $I_{Ba}$ prepulse and test pulse amplitudes does not reveal a U-shaped dependence that would be a signature of VDI current-dependent inactivation (Fig. 4 C) and supports the use of netCDI as a means for parsing inactivation into effects from CDI and VDI.

In striking contrast to the VDI acceleration caused by the IS6-AID linker GGG mutation, two-electrode voltage clamp experiments in Xenopus oocytes in which calcium ions were used as the charge carrier showed that the GGG mutation unexpectedly decreased netCDI (Fig. 4 A and Table I). The triple-glycine mutation caused drastic reductions relative to wild type in both the main inactivating component ($\tau_1 = 217 \pm 16$ ms vs. $20.3 \pm 4.2$ ms, respectively) and extent of inactivation, $t_{i300}$ ($43.7 \pm 3.6\%$ vs. $69.5 \pm 2.6\%$) (Fig. 4, A and B, and Table I). Unlike the VDI case in which GGG and 6G substitutions had equivalent effects on inactivation, CaV1.2 6G showed a further reduction in netCDI extent ($t_{i300} = 19.8 \pm 5.4\%$), although the time constant of the main inactivating component was not changed. A similarly strong reduction of netCDI

Figure 4. IS6-AID linker disruption reduces CDI. (A) Representative netCDI ($I_{Ca}/I_{Ba}$) at a test potential of +20 mV for the combinations of the indicated CaV1.2 subunits and CaV2.2. (B) $t_{i300}$ values from A. Results of unpaired $t$ tests are indicated as follows: N.S., $P > 0.05$, not significant; ***, $P < 0.001$. (C) Isochronal inactivation of CaV1.2 ($n = 4$, black X's, netCDI; $n = 4$, black open squares, VDI), CaV1.2 GGG netCDI ($n = 4$, gray), and CaV1.2 GGG/HotA netCDI ($n = 5$, orange). Inactivation extent comparing the ratio of prepulse and test pulse current amplitudes plotted as a function of the test voltage. The pulse protocol is shown at the top. (D) G-V relationships in calcium for the indicated combinations of CaV1.2 subunits and CaV2.2.
extent was seen in the GGG/HotA mutant (Fig. 4 A). In contrast to the potent changes elicited by the glycine substitutions, CaV1.2 AAA and CaV1.2 6A netCDI were very similar to wild type (Fig. 4 A and Table I). The CaV1.2 6G and CaV1.2 GGG/HotA mutants expressed at lower levels than most other mutant channels (Table S2). To test the possibility that the additional reduction in netCDI observed in these cases was due to an indirect effect caused by the low current amplitudes, we recorded wild-type CaV1.2 currents at comparable expression levels (Fig. S3). Comparison of these currents showed no change in netCDI. Thus, the changes in netCDI can be confidently attributed to direct effects on the channel that arise from the mutations and not from differences in current amplitudes.

To examine the changes to netCDI over a broad voltage range, we measured netCDI using a multi-pulse protocol in which the extent of inactivation was measured following a variable voltage pulse and compared with a control prepulse (Fig. 4 C). Under this protocol, wild-type CaV1.2 netCDI displays the typical inverted U-shape dependence expected of a calcium-dependent modulatory process. This dependence is markedly reduced for both CaV1.2 GGG and CaV1.2 GGG/HotA (Fig. 4 C). The drastic reduction in the U-shape dependence of inactivation in the mutant channels adds further support for the idea that the IS6-AID linker and Caβ have a role in CDI.

Comparison of netCDI measured from CaV1.2 co-expressed with Caβ2a, CaV1.2 expressed without Caβ, and CaV1.2 HotA, which cannot bind Caβ, revealed an unexpected effect of Caβ2a. Caβ2a causes a dramatic, ~10-fold increase in netCDI (τ1 = 20.3 ± 4.2 ms, 216 ± 55 ms, and 239 ± 42 ms, respectively) (Fig. 4 A and Table I). This netCDI acceleration stands in stark disparity to the approximately eightfold retardation Caβ2a imparts to VDI relative to channels lacking Caβ. Hence, Caβ2a has the opposite functional effects on CDI and VDI. This paradoxical effect has not been noted previously. netCDI for CaV1.2 GGG channels coexpressed with Caβ2a is indistinguishable from CaV1.2 channels expressed in the absence of a Caβ subunit and HotA channels that cannot bind Caβ (τ1 = 217 ± 16 ms, 216 ± 55 ms, and, 239 ± 42 ms, respectively). Thus, even though the GGG mutation has opposite effects on Caβ2a-mediated VDI and CDI, accelerating the former while decelerating the latter, the net effect is the same. The CaV1.2 GGG channels inactivate with τ values equivalent to channels lacking Caβ2a modulation.

Figure 5. Effects of Caβ isoforms on calcium inactivation stem from underlying effects on VDI. Normalized inactivation curves measured at +20 mV for (A) CaV1.2 and (B) CaV1.2 GGG subunits coexpressed with Caβ1, Caβ2a, Caβ2b, or in the absence of Caβ. (Left) VDI is shown and is reproduced for comparison from the first 300 ms of Fig. 3 (A and B). (Middle) Inactivation in calcium. (Right) netCDI.
Similar to the effect seen using barium as a charge carrier, the use of calcium as the charge carrier reveals that CaV1.2 GGG lacks the hyperpolarizing shift in the G-V relationship caused by Caβ2a (Fig. 4 D, Fig. S3 B, and Table II). Further, the CaV1.2 GGG/Caβ2a channels show similar G-V relationships to wild-type CaV1.2 expressed in the absence of Caβ and to CaV1.2 HotA. In contrast, CaV1.2 AAA coexpressed with Caβ2a behaves like wild-type CaV1.2 (Fig. 4 D). Therefore, disruption of the IS6-AID linker shows similar abrogation of effects on voltage activation caused by Caβ2a, regardless of the valent charge carrier.

Together with the data from the studies of IS6-AID linker peptides, the results strongly suggest that the observed reduction in netCDI for CaV1.2 GGG and CaV1.2 6G is the consequence of the disruption of the IS6-AID linker. These data provide compelling evidence that both Caβ and an intact IS6-AID linker are required for netCDI and suggest that there is an intimate dependence between elements that drive CDI, namely the Ca²⁺-CaM-IQ domain complex (Halling et al., 2006), and components that control VDI.

Caβ Isoform Identity Has Little Influence on CaV1.2 netCDI
In light of the clear rank order effects that different Caβ isoforms have on VDI, we asked whether there were similar differences in netCDI when different Caβs were present. Wild-type CaV1.2 channels coexpressed with Caβ1, Caβ2a, or Caβ2b show small differences in CDI but no real difference when netCDI is considered (τ values of 20–30 ms) (Fig. 5 A and Table I). Incorporation of the triple-glycine mutant in the CaV1.2 IS6-AID linker causes a reduction in CDI in the presence of Caβ1, Caβ2b, and Caβ2a (τ1 = 200–350 ms; Table I). Even though there appear to be differences between the Caβ isoforms with respect to inactivation in calcium (Fig. 5 B, middle, and Table S1), these distinctions are due almost exclusively to the underlying VDI differences (Fig. 5 B, left) and vanish when one considers netCDI (Fig. 5 B, right, and Table I). Together with the HotA CDI results, these data suggest that although a Caβ subunit is required for CDI, all Caβ isoforms support netCDI equally. Thus, the primary route for coupling CDI components to the pore would appear to be through the IS6-AID linker and not through secondary interaction sites that contribute to isoform-specific VDI modulation differences.

CDF Is Reduced by Disruption of Either IS6-AID Linker or Caβ Association
CaV1.2 channels display a phenomenon known as CDF, which is unmasked in the context of a point mutation, I1624A, in the C-terminal tail IQ domain that comprises the primary Ca²⁺/CaM binding site (Zühlke et al., 1999, 2000; Hudmon et al., 2005; Van Petegem et al., 2005). Given the pronounced effects of the IS6-AID linker GGG mutation and the importance of Caβ for both VDI and CDI, we tested whether CDF might also rely upon an intact IS6-AID linker or the Caβ subunit. Under conditions of similar current amplitude, the GGG mutation causes a reduction in CaV1.2 I1624A CDF of almost two thirds (13.8 ± 8.2% GGG/I1624A vs. 38.9 ± 12.3% I1624A, respectively). In contrast, the corresponding AAA mutant

Figure 6. CDF is reduced by disruption of the IS6-AID linker and loss of Caβ binding. (A) Relative current increase between the last (40th) and first +20-mV pulses at 3 Hz for CaV1.2 and the indicated mutants. Parentheses indicate the number of oocytes tested. Results of unpaired t tests are indicated as follows: N.S., P > 0.05, not significant; ***, P < 0.001. (B) Exemplar current traces for CaV1.2 I1624A, CaV1.2 GGG/I1624A, and CaV1.2 HotA/I1624A in a 3-Hz 40-pulse train normalized to the peak of the first pulse.
did not alter CDF significantly (37.5 ± 12.1%). \( \text{CaV}_{1.2} \) I1624A channels incapable of binding \( \text{CaV}_{\beta} \) through the incorporation of the HotA mutations show a complete absence of CDF (Fig. 6). This result agrees with the observation that \( \text{CaV}_{\beta} \) is central to the CDF mechanism (Grueter et al., 2006). Collectively, these data suggest that CDF requires both an intact IS6-AID linker and a \( \text{CaV}_{\beta} \) subunit, and that both \( \text{CaV}_{1.2} \) netCDI and CDF use the same components, including the IS6-AID linker and \( \text{CaV}_{\beta} \) for communicating with the transmembrane pore.

**DISCUSSION**

The process of inactivation is critical for \( \text{CaV} \) function and forge important connections between electrical signaling, activity-dependent feedback modulation of the channel, and activation of other calcium-dependent signaling cascades. Although a definitive molecular mechanism has yet to emerge, several models have been forwarded for how the components that govern the two principal inactivation processes, VDI and CDI, communicate with the transmembrane pore to regulate inactivation. The models fall into two distinct classes: those that assert that VDI and CDI use the same physical components to regulate the open state of the transmembrane pore (Cens et al., 1999; Stotz and Zamponi, 2001; Soldatov, 2003; Findlay, 2004; Kim et al., 2004), and those that maintain VDI and CDI use distinct physical components (Lee et al., 1985; Hadley and Lederer, 1991; Barrett and Tsien, 2008).

Identification of elements that affect VDI is relatively straightforward. Examination of the consequences of mutational manipulations or changes in subunit composition for inactivation when barium is the permeant ion provides an unambiguous VDI metric. Consequently, characterization of mutations in various elements of the \( \text{CaV}_{1.2} \) C terminus including the IQ domain, which has a prominent role in CDI (Zühlke et al., 1999; Barrett and Tsien, 2008), putative EF-hand, and sequences between IQ domain and EF-hand (Zühlke and Reuter, 1998; Kim et al., 2004), have indicated that many components that are thought to be important for CDI also affect VDI.

On the contrary, delineation of the extent to which components that are thought to dominate VDI, such as the \( \text{CaV}_{\beta} \)-/I-II loop complex (Olcese et al., 1994; Stea et al., 1994; De Waard and Campbell, 1995), contribute to inactivation under conditions when calcium is the permeant ion can be problematic. In the regime where VDI and CDI occur on the same timescale, perturbation to elements that contribute to VDI may also alter apparent CDI rates. Such changes might lead one to mistakenly conclude that VDI components have a role in CDI and that perhaps both inactivation processes use common elements. This point has been clearly articulated recently by Barrett and Tsien (2008), who present a new and important means of analyzing \( \text{CaV} \) inactivation that allows for a dissection of the relative contributions of VDI and CDI to the overall inactivation process. The calculation of the normalized \( I_{\text{Ca}}/I_{\text{Ba}} \) ratio (Barrett and Tsien, 2008), a parameter we call netCDI, allows the isolation of the inactivation component that is specifically conferred by calcium and avoids complications that could be caused by acceleration of VDI. This type of analysis indicates that prior evidence used to support the idea of a shared role for \( \text{CaV}_{\beta} \) action in VDI and CDI (Cens et al., 1999) can be explained entirely by differences in how the different \( \text{CaV}_{\beta} \)s act on VDI (Barrett and Tsien, 2008) (compare Fig. 5 A). Thus, whether CDI requires the VDI components or proceeds via an independent mechanism has remained an open question.

**Structural Integrity of the IS6-AID Linker Is Essential for VDI and CDI**

Our experiments testing the importance of the structural integrity of the IS6-AID linker support the idea that in \( \text{CaV}_{1} \) and \( \text{CaV}_{2} \) channels, the IS6-AID linker is a helix that functions as a rigid rod connecting \( \text{CaV}_{\beta} \) to the pore domain (Opatowsky et al., 2004; Van Petegem et al., 2004; Arias et al., 2005) (Fig. 7 A). This structural connection appears to be responsible for a large fraction of the VDI modulation that any \( \text{CaV}_{\beta} \) isoform imparts on \( \text{CaV}_{\alpha} \) subunits and for the effects \( \text{CaV}_{\beta} \) has on channel activation (compare Figs. 1 and 4).

X-ray crystallographic (Chen et al., 2004; Opatowsky et al., 2004; Van Petegem et al., 2004) and CD studies (Opatowsky et al., 2004; Van Petegem et al., 2008) indicate that the helical structure of the AID, which is integral to the \( \text{CaV}_{\alpha} \)–\( \text{CaV}_{\beta} \) interaction, is induced by formation of the AID–\( \text{CaV}_{\beta} \) complex. The presence of such a well-supported helix and consideration of the established importance of such a template for nucleating helix formation (Zimm and Bragg, 1959; Lifson and Roig, 1961; Wang et al., 2006; Patgiri et al., 2008) suggest that the AID helix can promote the propagation of \( \alpha \)-helical structure in the IS6-AID linker (Opatowsky et al., 2004; Van Petegem et al., 2004). In agreement with this hypothesis, we find that mutations that reduce the helical propensity of the IS6-AID linker and mutations that eliminate \( \text{CaV}_{\beta} \) binding to the AID have similar functional effects.

Remarkably, we find that disruption of the IS6-AID linker by the GGG mutation or the loss of \( \text{CaV}_{\beta} \) binding caused by the disruption of the AID-binding hotspot by the HotA mutations (Van Petegem et al., 2008) also causes large reductions (>10-fold) in the main inactivation component of netCDI. The remaining netCDI can be essentially eliminated by the introduction of additional flexibility into the IS6-AID linker (\( \text{CaV}_{1.2} \) 6G) or by the GGG/HotA combination (Fig. 4). These data constitute strong evidence that CDI relies on \( \text{CaV}_{\beta} \) and portions of the I-II loop, physical components that have been traditionally associated with VDI.

Interestingly, the disruption of the IS6-AID linker structural integrity affects VDI and CDI in opposite directions;
VDI is accelerated, while CDI is slowed down. By use of the netCDI analysis, we uncovered a previously unrecognized difference between how Ca\textsubscript{\textbeta}2a affects VDI and CDI. Ca\textsubscript{\textbeta}2a, which slows VDI relative to channels lacking a Ca\textsubscript{\textbeta} subunit (Olcese et al., 1994; Stea et al., 1994) (Fig. 1 B), accelerates netCDI (Fig. 4 A). These changes mirror the seemingly opposite effects of the GGG mutation on VDI and CDI in the presence of Ca\textsubscript{\textbeta}2a. Thus, the VDI and CDI results are both consistent with the same interpretation; a rigid IS6-AID linker is absolutely required to couple Ca\textsubscript{\textbeta} with the pore and indicate that Ca\textsubscript{\textbeta} has a centrally important role in CDI.

Our data support the hypothesis that VDI and CDI act through shared components (Cens et al., 1999; Stotz and Zamponi, 2001; Soldatov, 2003; Findlay, 2004; Kim et al., 2004) rather than through independent elements (Lee et al., 1985; Hadley and Lederer, 1991; Barrett and Tsien, 2008). The observation that VDI proceeds through a process that includes gating charge immobilization whereas CDI does not has given support to the idea that VDI and CDI are mediated by distinct effector mechanisms (Barrett and Tsien, 2008) and would seem at odds with the interpretation that both VDI and CDI act through a common element, namely Ca\textsubscript{\textbeta} and the IS6-AID linker. However, our discovery that Ca\textsubscript{\textbeta}2a has opposite effects on VDI and CDI may provide a way to reconcile this observation. It suggests that the underlying structural rearrangements that cause VDI and CDI are not equivalent, even though both rely upon the coupling of IS6-AID linker to the pore via a rigid IS6-AID linker. Further support for this idea comes from the observations that the different Ca\textsubscript{\textbeta} isoforms have dissimilar effects on VDI but not netCDI (Fig. 5), and that relative to the GGG mutation, GGG/HotA affects netCDI but not VDI (Fig. 4 and Table I).

How Do VDI and CDI Elements Communicate?

The functional evidence that the main VDI and CDI elements operate in an interdependent manner raises the question about the exact underlying molecular interactions that drive VDI and CDI. The simplest hypothesis is that, at least in one functional state, there is a direct physical interaction between the two major components of VDI and CDI, the Ca\textsubscript{\textbeta}/Ca\textsubscript{\textalpha}1.2-I-II loop and Ca\textsuperscript{2+}/CaM-C-terminal tail complexes. Unfortunately, robust evidence for such a direct physical interaction remains elusive. Pulldown experiments by Kim et al. (2004) have suggested that there could be an interaction between the isolated I-II loop and the Ca\textsubscript{\textbeta}2a-I-II loop; however, those experiments were done in the absence of Ca\textsubscript{\textbeta}, conditions under which the AID portion of the I-II loop is not folded (Opatowsky et al., 2004; Van Petegem et al., 2008). Therefore, whether the observed interaction reflects authentic binding between...
two natively folded components remains an open question. Using a similar assay, Zhang et al. (2005) reported the binding of Caβ to the CaV1.2 C terminus; however, this interaction was preserved even when a mutant construct that destroys Caβ structural integrity, the ΔBID mutant, was used. Thus, the observed Caβ–CaV1.2 C terminus interaction cannot reflect a functionally relevant interaction. Our attempts to establish robust complexes between biochemically well-behaved constructs that include Caβ, the I-II loop, and the C-terminal complex having defined stoichiometries have thus far been unsuccessful.

Even though the functional data indicate a codependency between the Caβ/I-II loop and the calcium-sensing elements of the channel, such a functional link does not demand a direct physical association of these components. Given the substantial amount of Caβ mass in the cytoplasm, ~150 kD (Van Petegem and Minor, 2006), and that the Caβ/Caα1/I-II loop and Ca2+/CaM/CaV1–C-terminal tail complexes comprise only a portion of this mass, it seems likely that interactions between the Caβ/Caα1–I-II loop and Ca2+/CaM/Caα1–C-terminal tail complexes involve other yet to be determined elements from the pore-forming subunit intracellular portions. One candidate is the N-terminal cytoplasmic domain (Ivanina et al., 2000; Dick et al., 2008; Tadross et al., 2008). Defining the exact arrangement of the channel intracellular components and the state dependence of interactions between the Caβ/I-II loop and CaM/C-terminal complexes remains an important goal. Further, it will be essential to determine how rearrangements within the channel cytoplasmic domains affect changes in the pore that may also participate in channel inactivation (Babich et al., 2007).

Effects of IS6–AID Linker Disruption on VDI and CDI Are Incompatible with a Hinged Lid Model

The details of the macromolecular conformational changes that cause CaV inactivation remain unknown. To account for the importance of the I-II linker in determining inactivation rates of CaV channels and chimaeras (Cens et al., 1999; Stotz et al., 2000), CaV inactivation has been suggested to occur via an inactivation particle or hinged lid analogous to voltage-gated sodium channels (Goldin, 2003; Ulbricht, 2005). The N-terminal portion of the AID helix has been suggested as a candidate for a CaV inactivation particle (Dafi et al., 2004) based on the influence that charged residues on the AID external face in the CaV–AID complex have on VDI kinetics (Herlitze et al., 1997; Berrou et al., 2001; Dafi et al., 2004).

From the homology and deep evolutionary relationship between Caβ and voltage-gated potassium channels (Hille, 2001), it is very likely that Caβ IS6 is a helical pore-lining segment similar to the homologous region of voltage-gated potassium channels (Long et al., 2005). Our data indicate that the IS6-AID linker forms a continuous helix that bridges the AID helix and IS6. To assess the impact of such a structural element on the probable location of the Caβ–AID complex relative to the pore, we modeled a helical IS6-AID linker onto the structure of the Kv1.2 transmembrane domains (Long et al., 2005). The resulting continuous helix places the Caβ–AID complex ~40 Å distant from the pore (Fig. 7). This structural arrangement is incompatible with a mechanism in which the Caβ–AID acts as an inactivation particle that approaches the pore. The glycine substitutions that we tested are situated midway between the pore and Caβ–AID complex and should impart increased flexibility to the IS6-AID linker. If the Caβ–AID complex acted like an inactivation particle that needed to approach the pore, these substitutions would be expected to show a minimal effect. In contrast, we see greatly increased inactivation τ values (Figs. 1 and 3). Further, the absence of effects on inactivation in the case where no Caβ is bound (e.g., Caβ1.2 GGG–Caβ2a vs. Caβ1.2 GGG/HoTA–Caβ1.2a), and where the helix propensity of the IS6-AID linker is increased by multiple alanine substitutions, also conflicts with the idea that there is some sort of inactivation particle formed by the Caβ–AID complex. Thus, it seems difficult to reconcile the functional effects of the IS6-AID linker mutations with the I-II linker acting as a hinged lid or inactivation particle. Rather, our results support the idea that inactivation involves some type of constriction of the pore involving the S6 segments from each domain (Zhang et al., 1994; Stotz et al., 2000; Cens et al., 2006).

A Second Interaction Site between Caβ and CaVα1 Is Important for VDI

The functional consequences of disrupting the helicity of the IS6-AID linker suggest that Caβ–βs modulate VDI through two different routes. The principal mechanism appears to be through the IS6-AID linker as the changes in τ values caused by the GGG substitution are of the same magnitude as that caused by the absence of a Caβ subunit (Table 1). The fact that the rank order VDI effects of different Caβ isoforms persists in the context of a disabled IS6-AID linker (Fig. 3) indicates that the IS6-AID linker is not the sole element involved. The palmitoylation of the N-terminal variable domain of Caβ2a remains an important factor that sets Caβ2a apart from the other Caβs. Additionally, there must be other functionally important sites of interaction between CaV and other portions of the pore-forming subunit that account for the remnant differences observed among the Caβs. One candidate for such interactions is the CaV V2 (or HOOK) domain, which connects the highly conserved SH3 and NK domains (Hanlon et al., 1999; Chen et al., 2004; Opatowsky et al., 2004; Van Petegem et al., 2004). Indeed, functional experiments support an important role for the V2 region in VDI. Chimeras that swap the V2 region between the core domains of Caβ1 and Caβ2a result in an exchange of VDI
properties (He et al., 2007), and deletion of the Caββ2 V2 domain causes acceleration of VDI (Richards et al., 2006). Our experiments show that ssCaββ2 and Caββ0 do not have identical effects on VDI (e.g., 1.4-fold difference in τ; Table 1), even though both share identical V2 domains. Thus, other Caβ variable regions must also play a role in VDI. These two isoforms have multiple differences in the V1 and V3 that must bear the elements that contribute to the differing effects on VDI. In contrast, Caβ subunit isoform identity has little effect on CDI (Fig. 5), suggesting that interactions between the Caβ-variable regions and pore-forming subunit are not critical for CDI. Although the importance of the variable regions with respect to isoform-specific modulation of VDI seems clear from the perspective of the Caβ subunit, the target sites on the pore-forming subunit remain unknown. Definition of the functionally relevant Caβ subunit points of contact on the pore-forming subunit remains an important unresolved issue.

CDF and CDI Share Requirement for Caβ and Intact IS6-AID Linker

Although the detailed mechanism for Ca1.2 CDF remains unresolved (Richard et al., 2006), three different macromolecular components appear to contribute: the complex of Ca2+/CaM and the Caα1 C-terminal tail IQ domain (Zühlke et al., 1999; Van Petegem et al., 2005), Ca2+/CaM-dependent kinase II (Anderson et al., 1994; Yuan and Bers, 1994; Hudmon et al., 2005; Grueter et al., 2006; Lee et al., 2006), and Caβ (Grueter et al., 2006). Our data support the critical role of Caβ in CDF. Incorporation of the HotA mutations that prevent Caβ binding (Van Petegem et al., 2008) eliminates the CDF that is unmasked by the I1624A IQ domain mutation (Fig. 6). Furthermore, we uncover a requirement for the IS6-AID linker. Disruption of the IS6-AID linker structure blunts CDF and provides new evidence that an intact rigid connection between the channel pore and Caβ is also essential for CDF (Fig. 6). Collectively, our data show clearly that CDF and CDI share the same requirements, the presence of a Caβ subunit and an intact IS6-AID linker, suggesting that these two processes use the same determinants to communicate with the pore.

Calcium influx into excitable cells is tightly regulated by a plethora of different processes. Our data strongly suggest that rearrangements of the intracellular Caβ domains have effects on inactivation that are mediated by Caβ through a rigid connection to the IS6 pore helix. Presently, very little is known about how Caβ intracellular domains interact with each other in open-, closed-, or inactivated-channel states. Development of a true molecular description of Caβ inactivation will require the definition of the physical intermolecular interactions present in each stage of the channel and how they rearrange. The definition of the central role of the Caβ subunit for VDI, CDI, and CDF should focus attention on defining how this centrally important channel element interacts with other intracellular domains to modulate activity-dependent feedback modulation of the channel.

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