

# Multiple Loops of the Dihydropyridine Receptor Pore Subunit Are Required for Full-Scale Excitation-Contraction Coupling in Skeletal Muscle

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**ABSTRACT** Understanding which cytosolic domains of the dihydropyridine receptor participate in excitation-contraction (EC) coupling is critical to validate current structural models. Here we quantified the contribution to skeletal-type EC coupling of the  $\alpha 1S$  ( $Ca_v1.1$ ) II-III loop when alone or in combination with the rest of the cytosolic domains of  $\alpha 1S$ . Chimeras consisting of  $\alpha 1C$  ( $Ca_v1.2$ ) with  $\alpha 1S$  substitutions at each of the interrepeat loops (I-II, II-III, and III-IV loops) and N- and C-terminal domains were evaluated in dysgenic ( $\alpha 1S$ -null) myotubes for phenotypic expression of skeletal-type EC coupling. Myotubes were voltage-clamped, and  $Ca^{2+}$  transients were measured by confocal line-scan imaging of fluo-4 fluorescence. In agreement with previous results, the  $\alpha 1C/\alpha 1S$  II-III loop chimera, but none of the other single-loop chimeras, recovered a sigmoidal fluorescence-voltage curve indicative of skeletal-type EC coupling. To quantify  $Ca^{2+}$  transients in the absence of inward  $Ca^{2+}$  current, but without changing the external solution, a mutation, E736K, was introduced into the P-loop of repeat II of  $\alpha 1C$ . The  $Ca^{2+}$  transients expressed by the  $\alpha 1C(E736K)/\alpha 1S$  II-III loop chimera were  $\sim 70\%$  smaller than those expressed by the  $Ca^{2+}$ -conducting  $\alpha 1C/\alpha 1S$  II-III variant. The low skeletal-type EC coupling expressed by the  $\alpha 1C/\alpha 1S$  II-III loop chimera was confirmed in the  $Ca^{2+}$ -conducting  $\alpha 1C/\alpha 1S$  II-III loop variant using  $Cd^{2+}$  ( $10^{-4}$  M) as the  $Ca^{2+}$  current blocker. In contrast to the behavior of the II-III loop chimera,  $Ca^{2+}$  transients expressed by an  $\alpha 1C/\alpha 1S$  chimera carrying all tested skeletal  $\alpha 1S$  domains (all  $\alpha 1S$  interrepeat loops, N- and C-terminus) were similar in shape and amplitude to wild-type  $\alpha 1S$ , and did not change in the presence of the E736K mutation or in the presence of  $10^{-4}$  M  $Cd^{2+}$ . Controls indicated that similar dihydropyridine receptor charge movements were expressed by the non- $Ca^{2+}$  permeant  $\alpha 1S(E1014K)$  variant, the  $\alpha 1C(E736K)/\alpha 1S$  II-III loop chimera, and the  $\alpha 1C(E736K)/\alpha 1S$  chimera carrying all tested  $\alpha 1S$  domains. The data indicate that the functional recovery produced by the  $\alpha 1S$  II-III loop is incomplete and that multiple cytosolic domains of  $\alpha 1S$  are necessary for a quantitative recovery of the EC-coupling phenotype of skeletal myotubes. Thus, despite the importance of the II-III loop there may be other critical determinants in  $\alpha 1S$  that influence the efficiency of EC coupling.

## INTRODUCTION

$Ca^{2+}$  signals of skeletal muscle cells are controlled by the voltage-gated L-type  $Ca^{2+}$  channel formed by the dihydropyridine receptor (DHPR), and by the sarcoplasmic reticulum (SR)  $Ca^{2+}$  release channel formed by the ryanodine receptor type 1 (RyR1). The well-established paradigm is that in response to depolarization, the DHPR produces a signal that briefly opens the RyR1 channel, leading to the release of SR-stored  $Ca^{2+}$ . Signal transmission takes place at specialized junctions between transverse tubules and SR membranes. At these junctions, DHPRs in tetrad arrangement juxtapose a single tetrameric RyR1 channel (1–3). The narrow physical gap between the transverse tubule and the SR ( $\sim 12$  nm) (2), the large protrusion of foot structure of the RyR1 channel into the gap ( $\sim 7$  nm) (4), and the overall molecular dimensions of the DHPR and RyR1 complexes (5,6), all suggest that the DHPR and RyR1 channels must be in physical contact. Strong evidence for the formation of a DHPR-RyR1 complex in myotubes is provided by a recent

freeze-fracture analysis of the molecular determinants that specify the arrangement of DHPRs in arrays of tetrads opposite to RyR1 (7).

The  $\alpha 1S$  subunit ( $Ca_v1.1$ ) of the skeletal DHPR has the familiar topology of a four-repeat voltage-gated channel with five cytosolic domains adjoining the four repeats (N-terminus, I-II loop, II-III loop, III-IV loop, and C-terminus) (8–10). Reports made almost 15 years ago (11,12) and refined later (13–17), have suggested that the cytosolic loop linking repeats II and III, consisting of 132 residues, brings about the conformational change that opens the RyR1 channel under the influence of membrane depolarization. The II-III loop is commonly viewed as the cell's version of the mechanical plunger proposed by Chandler et al. (18), in which an element of the transverse tubule linked to the excitation-contraction (EC) -coupling voltage sensor exerts torque on the SR  $Ca^{2+}$  channel. The II-III loop model of EC coupling is simple, has intuitive appeal, and has received broad consideration. However, in reality, the signaling mechanism may be more complex. The prevailing evidence indicates that interactions between  $\alpha 1S$  and RyR1 are likely to involve the II-III loop, but also many other domains of  $\alpha 1S$  (7,19–24). Additional complexity is brought about by a deletion analysis showing that the II-III loop may not

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account entirely for the signaling function of the DHPR (25). Furthermore, the DHPR  $\beta$ 1a subunit is essential for skeletal-type EC coupling (26–28), and interactions between this subunit and RyR1 are almost certain (6,29). Hence, the molecular determinants of the voltage-dependent mechanism by which the DHPR activates RyR1 may be broader than initially anticipated by the II-III loop model and are still open to debate despite unrelenting efforts.

In light of the growing multiplicity of DHPR-RyR1 interactions, here we reinvestigated the contribution of the cytosolic domains of  $\alpha$ 1S to skeletal-type EC coupling in dysgenic ( $\alpha$ 1S null) myotubes. Previous studies have focused almost exclusively on the functional identity of regions within the skeletal II-III loop (14,16,17,25,30,31). However, a voltage-clamp analysis of the EC-coupling phenotype contributed by each of the  $\alpha$ 1S interrepeat loops, as well as by the N- and C-terminal domains, has not been previously conducted. Likewise, the phenotype contributed by all the cytosolic domains together, as they would be present in the intact subunit, has not been documented. Since  $\alpha$ 1C does not express skeletal-type EC coupling (14,32), we focused on chimeras consisting of  $\alpha$ 1C ( $\text{Ca}_v$ 1.2) with sequences from  $\alpha$ 1S ( $\text{Ca}_v$ 1.1), substituting the interrepeat loops (I-II, II-III, or III-IV) or the N- or C-terminus. We report that  $\text{Ca}^{2+}$  entry-independent  $\text{Ca}^{2+}$  transients of a magnitude and voltage dependence similar to those expressed by wild-type (WT)  $\alpha$ 1S required a chimera with multiple  $\alpha$ 1S domains, including the II-III loop. However, the chimera with the II-III loop alone was insufficient. Some of these results have been published in abstract form (33,34).

## MATERIALS AND METHODS

### Identification of genotypes

Dysgenic ( $\alpha$ 1S-null *mdg*) mice were screened for both wild-type and mutant alleles of the DHPR  $\alpha$ 1S gene. Digestion of tail samples and subsequent verification of genotypes by the polymerase chain reaction (PCR) were described previously (27).

### Primary cultures and cDNA transfection

Cultures of myotubes were prepared from hind limbs of E18 fetuses, as described previously (35). Cultures were grown at 37°C in 8%  $\text{CO}_2$  gas. After myoblast fusion (~5 days), the medium was replaced with FBS-free medium, and  $\text{CO}_2$  was decreased to 5%. cDNA transfection was performed during the myoblast fusion stage with the polyamine LT1 (Panvera, Madison, WI). In addition to the cDNA of interest, cells were cotransfected with a plasmid encoding the T-cell protein CD8, which is used as a transfection marker. Transfected myotubes expressing CD8 were recognized by surface binding of polystyrene beads coated with anti-CD8 antibody (DynaL ASA, Oslo, Norway). Whole-cell analysis of  $\text{Ca}^{2+}$  currents, charge movements, and  $\text{Ca}^{2+}$  transients was performed 3–5 days post-transfection. The numbers of separate myotube cultures that were transfected and from which data were collected were as follows for  $\text{Ca}^{2+}$  current,  $\text{Ca}^{2+}$  transient, and charge movements when applicable: for nontransfected *mdg*, 10, 27, and 2; for WT  $\alpha$ 1S, 7, 3, and none; for  $\alpha$ 1S(E1014K), 3, 4, and 2; for WT  $\alpha$ 1C, 5, 3, and none; for  $\alpha$ 1C(E736K), 3,

2, and 2; for  $\alpha$ 1C/ $\alpha$ 1S N, 3, 3, and none; for  $\alpha$ 1C/ $\alpha$ 1S I-II, 4, 4, and none; for  $\alpha$ 1C/ $\alpha$ 1S II-III, 6, 4, and none; for  $\alpha$ 1C(E736K)/ $\alpha$ 1S II-III, 3, 2, and 3; for  $\alpha$ 1C/ $\alpha$ 1S III-IV, 4, 3, and none; for  $\alpha$ 1C/ $\alpha$ 1S C, 3, 2, and none; for  $\alpha$ 1C/ $\alpha$ 1S all loop, 3, 3, and none; for  $\alpha$ 1C(E736K)/ $\alpha$ 1S all loop: 3, 3, and 3; for all cadmium experiments, 2, 2, and none.

### cDNA constructs

Chimeric variants were made by two-step PCR strategies using cDNAs for rabbit skeletal muscle  $\alpha$ 1S (residues 1–1873; Genbank No. M23919) and rabbit cardiac  $\alpha$ 1C (residues 1–2171; Genbank No. X15539). The PCR products were subcloned into pCR-Blunt vector (Invitrogen, Carlsbad, CA), excised by digestion with *AgeI/NotI*, and cloned into the pSG5 vector (Stratagene, San Diego, CA) in frame with the first 11 residues of the phage T7 gene 10 protein for antibody tagging. All constructs were sequenced twice or more at a campus facility.

### Domain boundaries and nomenclature

Alignment of  $\alpha$ 1S and  $\alpha$ 1C sequences was performed with DNASTAR (Madison, WI) using the Jotun-Hein method.  $\alpha$ 1S N corresponds to residues 1–51 and replaced  $\alpha$ 1C N residues 1–154;  $\alpha$ 1S I-II loop corresponds to residues 335–432 and replaced  $\alpha$ 1C I-II loop residues 436–554;  $\alpha$ 1S II-III loop corresponds to residues 667–799 and replaced  $\alpha$ 1C II-III loop residues 789–930;  $\alpha$ 1S III-IV loop corresponds to residues 1067–1120 and replaced  $\alpha$ 1C III-IV loop residues 1188–1241;  $\alpha$ 1S C corresponds to residues 1328–1873 and replaced  $\alpha$ 1C C residues 1507–2171.

#### $\alpha$ 1C/ $\alpha$ 1S N

This chimera consists of  $\alpha$ 1S residues M1–K51 fused to the N-terminus of  $\alpha$ 1C residues P155–L2171. The N-terminus of  $\alpha$ 1S was amplified from full-length  $\alpha$ 1S and corresponds to residues 1–51. The second-step PCR product containing the  $\alpha$ 1S N-terminus and part of  $\alpha$ 1C domain I was fused to the pSG5  $\alpha$ 1C vector using *NheI/SacI* sites.

#### $\alpha$ 1C/ $\alpha$ 1S I-II

This chimera consists of  $\alpha$ 1C residues M1–S435 fused to the N-terminus of  $\alpha$ 1S residues G335–R432 fused to the N-terminus of  $\alpha$ 1C residues V555–L2171. The I-II loop of  $\alpha$ 1S was amplified from full-length  $\alpha$ 1S and corresponds to residues 335–432. The second-step PCR product containing the  $\alpha$ 1S I-II loop and part of  $\alpha$ 1C domains I and II was fused to the pSG5  $\alpha$ 1C vector using *BamHI/XhoI* sites.

#### $\alpha$ 1C/ $\alpha$ 1S II-III

This chimera consists of  $\alpha$ 1C residues M1–D788 fused to the N-terminus of  $\alpha$ 1S residues A667–T799 fused to the N-terminus of  $\alpha$ 1C residues I931–L2171. To replace the II-III loop, a *HindIII* site at nucleotide 2561 and a *SpeI* site at nucleotide 3203 were introduced into full-length  $\alpha$ 1C as silent mutations. The II-III loop of  $\alpha$ 1S was amplified from full-length  $\alpha$ 1S, and corresponds to residues 667–799. The second-step PCR product containing the  $\alpha$ 1S loop and part of  $\alpha$ 1C domain III was fused to the pSG5  $\alpha$ 1C vector using *HindIII/SpeI* sites.

#### $\alpha$ 1C/ $\alpha$ 1S III-IV

This chimera consists of  $\alpha$ 1C residues M1–V1187 fused to the N-terminus of  $\alpha$ 1S residues T1067–F1120 fused to the N-terminus of  $\alpha$ 1C residues E1242–L2171. The III-IV loop of  $\alpha$ 1S was amplified from full-length  $\alpha$ 1S and corresponds to residues 1067–1120. The second step PCR product

containing the  $\alpha$ 1S III-IV loop and part of  $\alpha$ 1C domains III and IV was fused to the pSG5  $\alpha$ 1C vector using *SpeI/SacII* sites.

### $\alpha$ 1C/ $\alpha$ 1S C

This chimera consists of  $\alpha$ 1C residues M1–M1506 fused to the N-terminus of  $\alpha$ 1S residues D1328–P1873. The C-terminus of  $\alpha$ 1S was amplified from full-length  $\alpha$ 1S using a forward primer containing a 5' overhang of the C-terminal end of  $\alpha$ 1C domain IV up to the *BclI* restriction site, and a reverse primer at the stop codon of  $\alpha$ 1S. The PCR product containing the  $\alpha$ 1S C-terminus and part of  $\alpha$ 1C domain IV was fused to the pSG5  $\alpha$ 1C vector using *BclI/NotI* sites.

### $\alpha$ 1C/ $\alpha$ 1S all loop (N, I-II, II-III, III-IV, C)

This chimera consists of fusions of the following peptide fragments in sequential order from N- to C-terminus:  $\alpha$ 1S(M1–K51)/ $\alpha$ 1C(P155–S435)/ $\alpha$ 1S(G335–R432)/ $\alpha$ 1C(V555–D788)/ $\alpha$ 1S(A667–T799)/ $\alpha$ 1C(I931–V1187)/ $\alpha$ 1S(T1067–F1120)/ $\alpha$ 1C(E1242–M1506)/ $\alpha$ 1S(D1382–P1873). This chimera was made by a cut-and-paste method using the chimeras and restriction sites indicated above.

### $\alpha$ 1C(E736K)

This domain II pore mutation was described elsewhere (36) and consists of a replacement of the glutamate residue at position 736 by lysine. We designed a 37-base antisense primer that introduced a mismatch at nucleotide 2397 (g2397a), and a sense primer that annealed before the *BamHI* site of  $\alpha$ 1C. The PCR product was cloned into the pSG5  $\alpha$ 1C vector at *BamHI/EcoRI* sites.

### $\alpha$ 1S(E1014K)

This domain III pore mutation consists of replacement of a glutamate residue at position 1014 by lysine, and was previously made and described elsewhere (25).

## Whole-cell voltage clamp

Whole-cell recordings were performed with an Axopatch 200B amplifier (Axon Instruments, Foster City, CA). Effective series resistance was compensated up to the point of amplifier oscillation with the Axopatch circuit. All experiments were performed at room temperature. Patch pipettes had a resistance of 1–3 M $\Omega$  when filled with the pipette solution. To obtain  $\text{Ca}^{2+}$  conductance curves, cells were maintained at a holding potential of  $-40$  mV, and depolarized in ascending order every 3 s. The pulse duration was 500 ms and was changed in 5-mV increments up to  $+85$  mV. To obtain  $\text{Ca}^{2+}$  transient curves, cells were maintained at  $-40$  mV and depolarized in descending order every 30 s to permit recovery of the resting fluorescence. The pulse duration was 200 ms and was changed in 20-mV decrements from  $+90$  mV to  $-30$  mV. To obtain charge movement curves, we used a P/4 protocol with a long prepulse to inactivate  $\text{Na}^+$ -channel ionic and gating currents (25). The pulse protocol was as follows. The command voltage was stepped from a holding potential of  $-80$  mV to  $-30$  mV for 698 ms, to  $-50$  mV for 5 ms, to the test potential for 50 ms, to  $-50$  mV for 50 ms, and then to the  $-80$  mV holding potential. Test potentials were applied in decreasing order every 10 mV from  $+100$  to  $-80$  mV. The waiting period between test pulses was 10 s.

## Confocal fluorescence microscopy

$\text{Ca}^{2+}$  transients were measured by confocal line scanning at room temperature. Cells were loaded with 5  $\mu\text{M}$  fluo-4 acetoxymethyl ester

(Molecular Probes, Eugene, OR) for  $\sim 1$  h at room temperature. Cells were viewed with an inverted IX20 Olympus microscope with a 20 $\times$  (NA 1.4) objective and a Fluoview confocal attachment (Olympus, Melville, NY). The 488 nm line provided by a 5 mW Argon laser was attenuated to 6% with neutral density filters. Line scans were acquired at a speed of 2.05 ms per line. All line scans consisted of 1000 lines at a width of 512 pixels. The spatial dimension of the line scan was 30–60  $\mu\text{m}$ , and covered the entire width of the myotube. Locations selected for line scans were devoid of nuclei and had a low resting fluorescence. Line scans were synchronized to start 100 ms before the onset of the depolarization for voltage-clamp experiments. The time course of the space-averaged fluorescence intensity change was estimated as described elsewhere (26,27) and is reported in  $\Delta F/F$  units. The peak-to-peak noise in the baseline fluorescence averaged  $\sim 0.1 \Delta F/F$  units. Image analyses were performed with NIH Image software (National Institutes of Health, Bethesda, MD).

## Solutions

For  $\text{Ca}^{2+}$  currents and  $\text{Ca}^{2+}$  transients, the external solution was (in mM) 130 TEA methanesulfonate, 10  $\text{CaCl}_2$ , 1  $\text{MgCl}_2$ ,  $10^{-3}$  TTX, and 10 HEPES titrated with TEA(OH) to pH 7.4. The pipette solution consisted of (in mM) 140 Cs aspartate, 5  $\text{MgCl}_2$ , 0.1 EGTA (when  $\text{Ca}^{2+}$  transients were recorded) or 5 EGTA (when only  $\text{Ca}^{2+}$  currents were recorded), and 10 MOPS titrated with CsOH to pH 7.2. For charge movements, the internal solution was (in mM) 120 NMG (*N*-methyl glucamine)-Glutamate, 10 HEPES-NMG, and 10 EGTA-NMG, pH 7.3. This solution produced a more reliable block of the outward ionic current than the internal solution used for  $\text{Ca}^{2+}$  currents. The external solution was supplemented with 0.5 mM  $\text{CdCl}_2$  to block background  $\text{Ca}^{2+}$  currents present in *mdg* myotubes, 0.5 mM  $\text{LaCl}_3$  to increase pipette seal resistance and 0.05 mM TTX to block residual  $\text{Na}^+$  current.

## Curve fitting

The voltage dependence of the  $\text{Ca}^{2+}$  conductance, charge movements, and sigmoidal fluorescence-voltage relationships were fitted with a standard Boltzmann equation:

$$A = A_{\max}/(1 + \exp(-(V - V_{1/2})/k)), \quad (1)$$

where  $V$  (in mV) is the test potential,  $A_{\max}$  is  $G_{\max}$ ,  $Q_{\max}$ , or  $\Delta F/F_{\max}$ ,  $V_{1/2}$  (in mV) is the midpoint potential, and  $k$  (in mV) is the slope factor. For bell-shaped fluorescence-voltage curves, the Boltzmann equation was modified as follows:

$$\Delta F/F = [(V - V_r)/k'] \times [\Delta F/F_{\max}/(1 + \exp((V - V_{1/2})/k))], \quad (2)$$

where  $V_r$  (in mV) is a constant that accounts for the decrease in  $\text{Ca}^{2+}$  transient amplitude at positive potentials, and  $k'$  (in mV) is an empirical scaling factor (26,27). Other parameters are the same as in Eq. 1. Parameters of a fit of averages of many cells (population average) are shown in the figures. Parameters of the fit of individual cells are shown in tables. Parameters of the fit of the population average differed slightly from the mean of the fit of individual cells. The latter parameters generated theoretical curves that were a better fit with the average data and, for that reason, were used in the figures. Analysis of variance (ANOVA) was performed with Analyze-it (Leeds, UK).

## RESULTS

### Recovery of voltage- or $\text{Ca}^{2+}$ entry-dependent EC coupling in dysgenic myotubes

Studies have shown that  $\alpha$ 1C is targeted to EC-coupling junctions in cultured skeletal myotubes, and that the  $\text{Ca}^{2+}$

current generated by  $\alpha 1C$  can trigger  $Ca^{2+}$  transients by  $Ca^{2+}$ -dependent activation of RyR1 (31,32). Chimeras with  $\alpha 1C$  in the backbone also activate  $Ca^{2+}$  transients by a similar mechanism when expressed in skeletal myotubes (11,14). Hence,  $Ca^{2+}$  release induced by the  $Ca^{2+}$  current is inherent to chimeras of  $\alpha 1C$ , and this component needs to be carefully separated from the release of interest triggered by mechanical DHPR-RyR1 coupling. To exclude the component of the  $Ca^{2+}$  transient triggered by the  $Ca^{2+}$  current without changing the external solution, we mutated the conserved glutamate E736 in the P-loop of repeat II of  $\alpha 1C$ , previously shown to be critical for  $Ca^{2+}$  permeation (36). Fig. 1 shows the EC coupling and  $Ca^{2+}$  current characteristics of  $\alpha 1C(E736K)$  and  $\alpha 1S(E1014K)$ , localized in the P-loop of repeat III of  $\alpha 1S$  (25,37). The top traces show representative  $Ca^{2+}$  transients and  $Ca^{2+}$  currents at +30 mV, with the pore mutants depicted by shaded traces. In this and other figures, the displayed  $Ca^{2+}$  transients and  $Ca^{2+}$  currents were obtained with different protocols and different internal solutions (see Materials and Methods). For  $Ca^{2+}$  currents, we used 500-ms depolarizations in a highly buffered internal solution (5 mM EGTA). These conditions

permitted the determination of the time course of inactivation while maintaining a low cytosolic  $Ca^{2+}$  at all potentials. For  $Ca^{2+}$  transients, we used 200-ms depolarizations in a lightly buffered internal  $Ca^{2+}$  solution (0.1 mM EGTA). These conditions limited SR  $Ca^{2+}$  release, increased the rate of resting  $Ca^{2+}$  recovery, and increased the intensity of the fluorescence signal. In all cases, the external  $Ca^{2+}$  concentration was 10 mM. WT  $\alpha 1S$  expressed slow-activating/noninactivating  $Ca^{2+}$  currents typical of cultured normal primary myotubes (35). In contrast, WT  $\alpha 1C$  expressed fast-activating/slow-inactivating  $Ca^{2+}$  currents, in agreement with previous results in *mdg* myotubes (11,32,38). The degree of inactivation of  $\alpha 1C$  was variable, and to some extent varied with the  $Ca^{2+}$  current density, consistent with  $Ca^{2+}$ -entry-dependent inactivation of  $\alpha 1C$  investigated by others in myotubes (16). Both  $\alpha 1C$  and  $\alpha 1S$  recovered a  $Ca^{2+}$  current density close to that of normal myotubes reported elsewhere (35). Inward currents expressed by the pore mutants were drastically reduced. In the case of  $\alpha 1S(E1014K)$ , inward current was undetectable ( $<0.1$  pA/pF), consistent with previous results (25). In the case of  $\alpha 1C(E736K)$ , the inward current at +30 mV was reduced  $\sim 180$ -fold compared to WT  $\alpha 1C$ , consistent

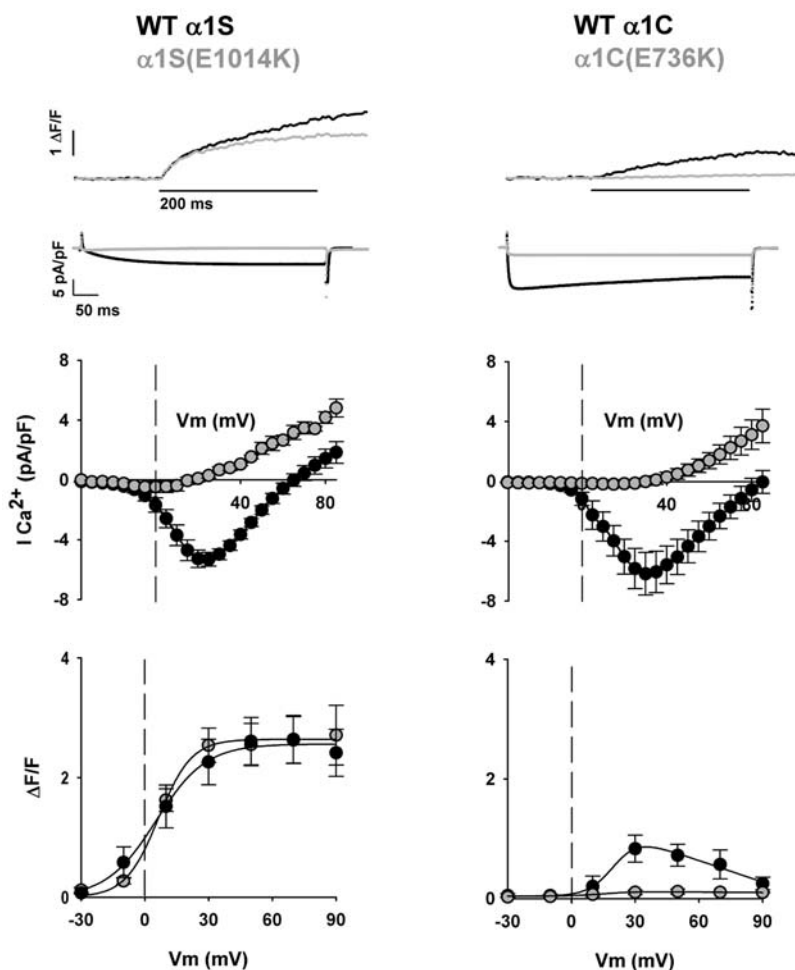


FIGURE 1  $Ca^{2+}$  currents and  $Ca^{2+}$  transients expressed by  $\alpha 1S$  and  $\alpha 1C$  variants. Columns show representative *mdg* myotubes transfected with WT  $\alpha 1S$ , WT  $\alpha 1C$ , and variants carrying pore mutations, namely  $\alpha 1S$  (E1014K) and  $\alpha 1C$  (E736K). Shaded traces and shaded symbols correspond to the pore mutant form of the variant indicated above each column. The top trace corresponds to the spatial integral of the confocal  $Ca^{2+}$  transient in  $\Delta F/F$  units in response to a 200-ms depolarization to +30 mV from a holding potential of -40 mV. The second row of traces corresponds to the  $Ca^{2+}$  current elicited during a 500-ms depolarization from a holding potential of -40 mV to +30 mV. The  $Ca^{2+}$  transients and  $Ca^{2+}$  currents shown in this and other figures were obtained with different protocols (see text, especially Materials and Methods). Population averages of the  $Ca^{2+}$  current-voltage curves are located centrally. These were obtained by depolarizing transfected myotubes in 5-mV increments from a holding potential of -40 mV for 500 ms. At the bottom are  $Ca^{2+}$  transient-voltage curves for population averages in response to a 200-ms depolarization from -40 mV to the indicated potentials. The population averaged fluorescence-voltage curves for  $\alpha 1S$  and  $\alpha 1S(E1014K)$  were fit with Eq. 1, and those obtained in myotubes expressing  $\alpha 1C$  and  $\alpha 1C(E736K)$  were fit with Eq. 2. Curves were fit with the following parameters ( $\Delta F/F_{max}$  in  $\Delta F/F$  units,  $V_{1/2}$  in mV, and  $k$  in mV, respectively): for  $\alpha 1S$ : 2.6, 5.3, and 11.7; for  $\alpha 1S(E1014K)$ , 2.6, 6.4, and 7.8; for  $\alpha 1C$ , 1.2, 20.6, and 6.1; for  $\alpha 1C(E736K)$ , 0, -19.7, and 20. For a fit of parameters by cell and number of cells included in the fit, see Table 1.

with determinations in oocytes (36). The reduction was less pronounced if calculations are based on the maximum  $\text{Ca}^{2+}$  conductance,  $G_{\text{max}}$ , expressed by the conducting and non-conducting variants (see Tables 1 and 2). This is because the  $G_{\text{max}}$  of  $\alpha$ 1S(E1014K) and  $\alpha$ 1C(E736K) is dominated by the conductance of the outward current (Fig. 1, *middle panels*). The latter is a mixture of outward current through the mutant  $\text{Ca}^{2+}$  channel and background outward currents unaffected by the mutation.

$\text{Ca}^{2+}$  transients expressed by the conducting and non-conducting variants were obtained by line-scan integration of confocal fluo-4 fluorescence in myotubes held under voltage-clamp conditions. As indicated by the superimposed traces at the top of Fig. 1, the pore mutation  $\alpha$ 1S(E1014K) had a minimal effect on the time course of the  $\text{Ca}^{2+}$  transient compared to WT  $\alpha$ 1S. This result is in agreement with previous observations (25,37), and confirms expression of a bona fide skeletal-type EC-coupling phenotype. In contrast, the amplitude of the  $\text{Ca}^{2+}$  transient evoked by  $\alpha$ 1C(E736K) was severely depressed compared to WT  $\alpha$ 1C. The bottom graphs of Fig. 1 show the relationship between the amplitude of the  $\text{Ca}^{2+}$  transient and the magnitude of the depolarization, in the presence and absence of pore mutations. The  $\text{Ca}^{2+}$  transient amplitude in these plots was measured just before the end of a 200-ms depolarization, and thus excluded  $\text{Ca}^{2+}$  release triggered by the tail current, which was prominent in some myotubes. For  $\alpha$ 1S and  $\alpha$ 1S(E1014K), the expressed  $\text{Ca}^{2+}$  transients had a sigmoidal voltage-dependence with saturation at potentials more positive than +30 mV. Furthermore, there was good agreement between the two sets of data. We interpreted this result as an indication that the EC coupling expressed by  $\alpha$ 1S or  $\alpha$ 1S(E1014K) was entirely  $\text{Ca}^{2+}$ -entry-independent. In contrast,  $\text{Ca}^{2+}$  transients recovered by  $\alpha$ 1C were smaller in magnitude, reached a maximum at  $\sim$ +30 mV, and decreased at more positive potentials. This biphasic behavior gives rise to a bell-shaped fluorescence-voltage curve that mirrors the bell-shaped dependence of the  $\text{Ca}^{2+}$  current-voltage curve (see Fig. 1, *middle panel*). This result agrees with previous

determinations in dysgenic myotubes (32), and suggests that  $\text{Ca}^{2+}$  transients may be triggered by the  $\text{Ca}^{2+}$  current via a  $\text{Ca}^{2+}$ -dependent mechanism. Consistent with this interpretation, the pore mutant  $\alpha$ 1C(E736K) failed to express a detectable  $\text{Ca}^{2+}$  transient. The changes in fluorescence in myotubes expressing WT  $\alpha$ 1C may also reflect changes in cytosolic  $\text{Ca}^{2+}$  produced directly by the  $\text{Ca}^{2+}$  current. The contribution of the  $\text{Ca}^{2+}$  current to the cell fluorescence was determined previously in myotubes treated with ryanodine (27). For cells with a comparable  $\text{Ca}^{2+}$  current density, we found that the contribution was  $<0.25 \Delta F/F$  at +30 mV (27). In this study, the  $\text{Ca}^{2+}$  transient expressed by WT  $\alpha$ 1C at +30 mV was  $\sim 1.3 \Delta F/F$  (Table 1). For this reason, we believe that the  $\text{Ca}^{2+}$  current expressed by WT  $\alpha$ 1C contributed only modestly to the overall cell fluorescence.

### Incomplete recovery of skeletal-type EC coupling by the $\alpha$ 1S II-III loop revealed by pore mutations that eliminate inward $\text{Ca}^{2+}$ current

$\text{Ca}^{2+}$  currents and transients expressed by chimeras consisting of  $\alpha$ 1C carrying each of the cytosolic domains of  $\alpha$ 1S, namely the N-terminal, I-II loop, II-III loop, III-IV loop, or C-terminal domains, are shown in Fig. 2. Coordinates of skeletal domains donated to  $\alpha$ 1C, and of homologous regions removed from  $\alpha$ 1C, are described in Materials and Methods. The top traces correspond to inward  $\text{Ca}^{2+}$  currents for depolarizations to  $-30$  mV and  $+30$  mV in dysgenic myotubes expressing each of the five indicated chimeras. All chimeras expressed high-density, fast-activating, and slow-inactivating  $\text{Ca}^{2+}$  currents typical of WT  $\alpha$ 1C when expressed in myotubes. Furthermore, the fitted  $G_{\text{max}}$  was statistically similar to that of  $\alpha$ 1C or  $\alpha$ 1S (Table 1). Two chimeras, that carrying the N-terminal domain (labeled  $\alpha$ 1C N) and that carrying the II-III loop (labeled  $\alpha$ 1C/ $\alpha$ 1S II-III), expressed  $\text{Ca}^{2+}$  current at a density higher than that of WT  $\alpha$ 1C, although the difference was not significant. Representative  $\text{Ca}^{2+}$  transients at +30 mV, and the voltage dependence of the  $\text{Ca}^{2+}$  transient amplitude measured at the

**TABLE 1**  $\text{Ca}^{2+}$  conductance and  $\text{Ca}^{2+}$  transients expressed by  $\alpha$ 1C/ $\alpha$ 1S chimeras in dysgenic (*mdg*) skeletal myotubes

	$G_{\text{max}}$ (pS/pF)	$V_{1/2}$ (mV)	$k$ (mV)	$\Delta F/F_{\text{max}}$	$V_{1/2}$ (mV)	$k$ (mV)
NT <i>mdg</i>	$20 \pm 3^*$ (27)	$4 \pm 5^*$	$19.5 \pm 7.1^*$	—(25)	—	—
WT $\alpha$ 1S	$163 \pm 13$ (14)	$38 \pm 2$	$6.5 \pm 0.7$	$2.7 \pm 0.4$ (5)	$7 \pm 2$	$8.6 \pm 1.1$
WT $\alpha$ 1C	$152 \pm 27$ (10)	$19 \pm 3$	$7.1 \pm 0.7$	$1.3 \pm 0.4^*$ (6)	$24 \pm 3^*$	$5.9 \pm 1.1$
$\alpha$ 1C/ $\alpha$ 1S N	$213 \pm 50$ (7)	$18 \pm 3$	$6.3 \pm 1.2$	$0.7 \pm 0.2^*$ (7)	$26 \pm 10$	$11.0 \pm 3.0$
$\alpha$ 1C/ $\alpha$ 1S I-II	$140 \pm 35$ (10)	$21 \pm 2$	$9.6 \pm 0.5$	$1.1 \pm 0.3^*$ (8)	$19 \pm 4$	$7.1 \pm 1.0$
$\alpha$ 1C/ $\alpha$ 1S II-III	$208 \pm 29$ (15)	$11 \pm 2$	$5.4 \pm 0.7$	$2.5 \pm 0.9$ (7)	$1 \pm 3$	$3.3 \pm 1.0^*$
$\alpha$ 1C/ $\alpha$ 1S III-IV	$153 \pm 27$ (9)	$9 \pm 3$	$6.8 \pm 0.8$	$1.3 \pm 0.4^*$ (6)	$2 \pm 2$	$4.8 \pm 0.8^*$
$\alpha$ 1C/ $\alpha$ 1S C	$151 \pm 26$ (12)	$13 \pm 2$	$6.3 \pm 0.5$	$1.0 \pm 0.3^*$ (5)	$7 \pm 7$	$3.1 \pm 1.5^*$
$\alpha$ 1C/ $\alpha$ 1S all loop	$121 \pm 25$ (5)	$11 \pm 4$	$6.2 \pm 1.0$	$2.2 \pm 0.6$ (8)	$9 \pm 5$	$8.7 \pm 1.9$

Values are mean  $\pm$  SE of Boltzmann parameters fitted to each cell, with the number of cells indicated in parentheses.  $\Delta F/F_{\text{max}}$ ,  $V_{1/2}$ , and  $k$  are parameters of the Boltzmann fit to each cell with either Eq. 1 or Eq. 2, as indicated in the text. Changes in fluo-4 fluorescence were not detected at any test potential ( $-30$  to  $+90$  mV) in nontransfected dysgenic myotubes (NT *mdg*).

\*Parameters with one-way ANOVA significance  $p < 0.05$  compared to myotubes expressing WT  $\alpha$ 1S.

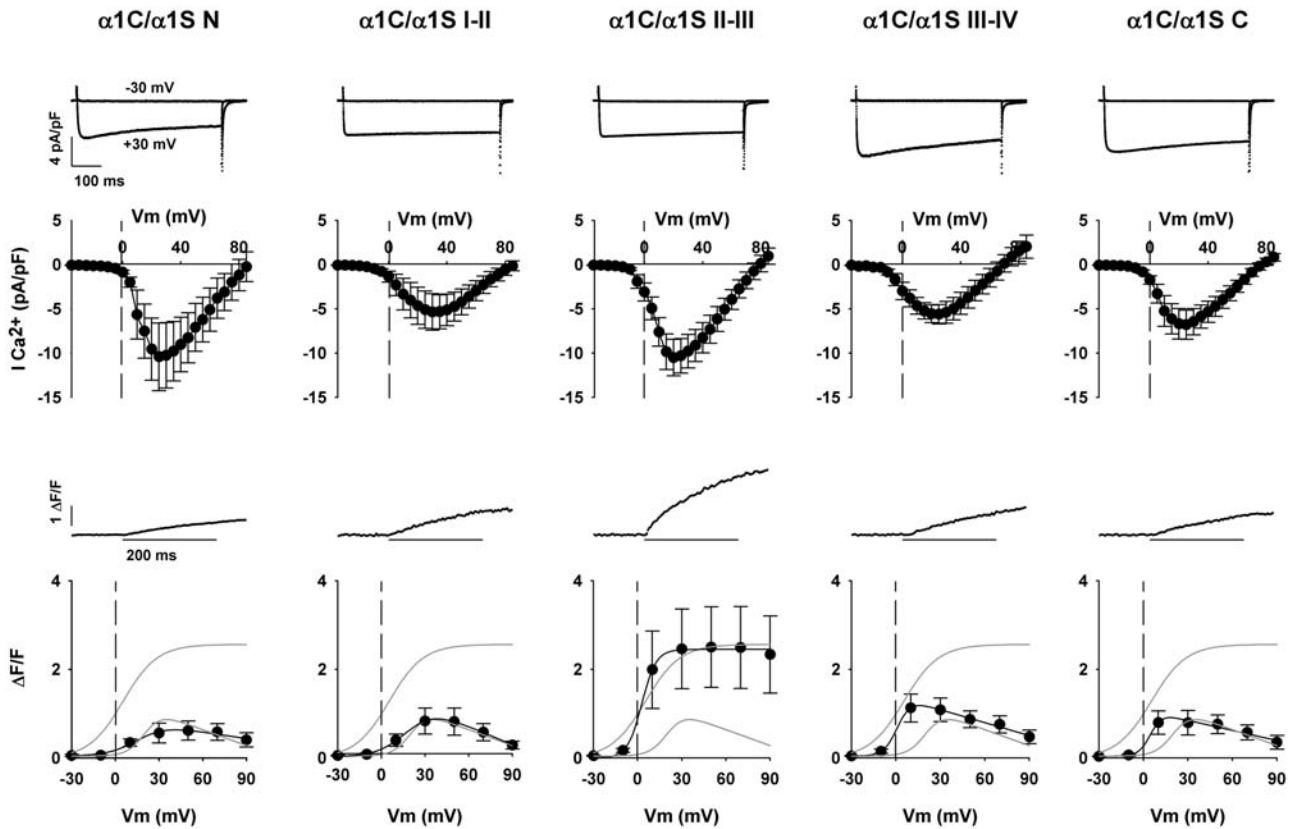


FIGURE 2  $\text{Ca}^{2+}$  currents and  $\text{Ca}^{2+}$  transients expressed by  $\alpha 1\text{C}/\alpha 1\text{S}$  chimeras. Columns show representative *mdg* myotubes transfected with the identified  $\alpha 1\text{C}/\alpha 1\text{S}$  chimeras. Nomenclature and domain boundaries for the chimeras are described in Materials and Methods. The top traces correspond to  $\text{Ca}^{2+}$  currents from the same cell in response to a 500-ms depolarization from a holding potential of  $-40$  mV to  $-30$  mV (no current) and to  $+30$  mV (near maximum inward current). Population averages of the  $\text{Ca}^{2+}$  current-voltage curves are located centrally. These were obtained by depolarizing transfected myotubes in 5-mV increments from a holding potential of  $-40$  mV for 500 ms. The traces in the middle correspond to confocal  $\text{Ca}^{2+}$  transients in *mdg* myotubes expressing each of the chimeras in  $\Delta F/F$  units in response to a 200-ms depolarization to  $+30$  mV from a holding potential of  $-40$  mV. At the bottom are  $\text{Ca}^{2+}$  transient-voltage curves for population averages in response to a 200-ms depolarization from  $-40$  mV to the indicated potentials. The shaded traces without data in each graph correspond to the fitted voltage dependence of WT  $\alpha 1\text{S}$  and WT  $\alpha 1\text{C}$  from Fig. 1. The fluorescence-voltage curves for all  $\alpha 1\text{C}/\alpha 1\text{S}$  chimeras were fit with Eq. 2, except that obtained in myotubes expressing  $\alpha 1\text{C}/\alpha 1\text{S}$  II-III, which was fit with Eq. 1. Curves (black) were fit with the following parameters ( $\Delta F/F_{\text{max}}$  in  $\Delta F/F$  units,  $V_{1/2}$  in mV, and  $k$  in mV, respectively): for  $\alpha 1\text{C}/\alpha 1\text{S}$  N, 0.5, 16.7, and 10.0; for  $\alpha 1\text{C}/\alpha 1\text{S}$  I-II, 1.3, 20.0, and 9.9; for  $\alpha 1\text{C}/\alpha 1\text{S}$  II-III, 2.4, 2.8, and 4.9. For  $\alpha 1\text{C}/\alpha 1\text{S}$  III-IV, 1.0, 1.2, and 4.5; and for  $\alpha 1\text{C}/\alpha 1\text{S}$  C, 0.8, 4.9, and 3.9.

end of a 200-ms depolarization, are shown in the bottom graphs of Fig. 2. For reference, the shaded lines in the plots indicate the fitted fluorescence-voltage relationship of myotubes expressing WT  $\alpha 1\text{S}$  and WT  $\alpha 1\text{C}$  described above. The II-III loop chimera consistently expressed  $\text{Ca}^{2+}$  transients that were much larger in amplitude than those expressed by the other chimeras. Furthermore, only the II-III loop chimera expressed a fluorescence-voltage relationship that was sigmoidal like that of WT  $\alpha 1\text{S}$ . All other chimeras expressed fluorescence-voltage relationships that were bell-shaped like that of WT  $\alpha 1\text{C}$ , indicative of a  $\text{Ca}^{2+}$ -dependent mechanism. The bell-shaped voltage dependence is particularly prominent for the III-IV loop and the C-terminal domain chimeras. Furthermore, in these cases there was a significant negative shift in midpoint potential compared to WT  $\alpha 1\text{C}$ . The shifts were consistent with differences in midpoint potential found for the  $\text{Ca}^{2+}$  conductance

described in Table 1. In summary, only the  $\alpha 1\text{C}/\alpha 1\text{S}$  II-III loop chimera expressed  $\text{Ca}^{2+}$  transients with a sigmoidal fluorescence-voltage curve indicative of skeletal-type EC coupling. This result is consistent with previous observations, which have suggested that the II-III loop is a critical domain for skeletal-type EC coupling (11,13–17,30,32). Other domains of  $\alpha 1\text{S}$ , namely the III-IV loop and the C-terminal domain, affected channel gating by shifting  $\text{Ca}^{2+}$  current activation to more negative potentials, resulting in a concurrent shift in the voltage dependence of the  $\text{Ca}^{2+}$  transient. Furthermore, the skeletal N-terminal domain and the I-II loop do not appear to influence the  $\text{Ca}^{2+}$ -dependent EC-coupling phenotype in a significant manner.

To examine the extent of recovery of the skeletal phenotype by the II-III loop chimera, we investigated  $\text{Ca}^{2+}$  transients elicited by the II-III loop chimera in the presence

of the  $\alpha$ 1C(E736K) pore mutation. For the sake of clarity, we refer to this mutation as E736K in all cases even though the actual coordinate will differ for some chimeras. The left panel of Fig. 3 shows representative  $\text{Ca}^{2+}$  transients and  $\text{Ca}^{2+}$  currents expressed by the  $\alpha$ 1C(E736K)/ $\alpha$ 1S II-III loop chimera compared to the  $\text{Ca}^{2+}$  conducting variant at +30 mV. Current-voltage relationships and fluorescence-voltage relationships are shown immediately below. Shaded areas are reserved for the pore mutant. Inward  $\text{Ca}^{2+}$  currents were severely curtailed in the  $\alpha$ 1C(E736K)/ $\alpha$ 1S II-III chimera compared to the  $\text{Ca}^{2+}$ -conducting variant. Furthermore, inward current was blocked to the same extent as with  $\alpha$ 1C(E736K). This can be readily appreciated by comparing current-voltage curves in Figs. 1 and 3, and by the parameters of the conductance fit. Table 1 shows data for WT  $\alpha$ 1C and  $\alpha$ 1C/ $\alpha$ 1S II-III, and Table 2 for  $\alpha$ 1C(E736K) and  $\alpha$ 1C(E736K)/ $\alpha$ 1S II-III. Based on these results, the mutation was deemed useful for removing a component of the  $\text{Ca}^{2+}$  transient of the II-III loop chimera triggered by the  $\text{Ca}^{2+}$  current, if such a component was present. Quite surprisingly,  $\text{Ca}^{2+}$  transients expressed by the  $\alpha$ 1C(E736K)/ $\alpha$ 1S II-III loop chimera were severely depressed relative to those

expressed by the  $\text{Ca}^{2+}$ -conducting  $\alpha$ 1C/ $\alpha$ 1S II-III loop variant. This can be appreciated in the noticeably small  $\text{Ca}^{2+}$  transient shown at the top of Fig. 3 for a representative myotube expressing  $\alpha$ 1C(E736K)/ $\alpha$ 1S II-III, and by the fluorescence-voltage relationship at the bottom of Fig. 3. At face value, the data suggests that the II-III loop chimera relies heavily on external  $\text{Ca}^{2+}$  for activation of SR  $\text{Ca}^{2+}$  release, and that the voltage-dependent skeletal-type component is minor. However, other explanations must be considered also. It is possible that  $\alpha$ 1C/ $\alpha$ 1S chimeras are only partially functional, and, as a consequence, none of them are able to rescue the skeletal phenotype to the same extent as WT  $\alpha$ 1S. Also, the charge movement density expressed by the II-III chimera may be inherently low, and hence unable to rescue a substantial skeletal-type component. Finally, the E736K mutation in repeat II may have adversely affected skeletal-type EC coupling. The latter is troublesome since it is known that the E1014K charge reversal eliminates high-affinity  $\text{Ca}^{2+}$  binding to the  $\alpha$ 1S subunit (39). The  $\text{Ca}^{2+}$ -binding site in the pore region could be the  $\text{Ca}^{2+}$ -binding site identified as critical for the DHPR voltage sensor (40,41). In what follows, we tested these alternatives.

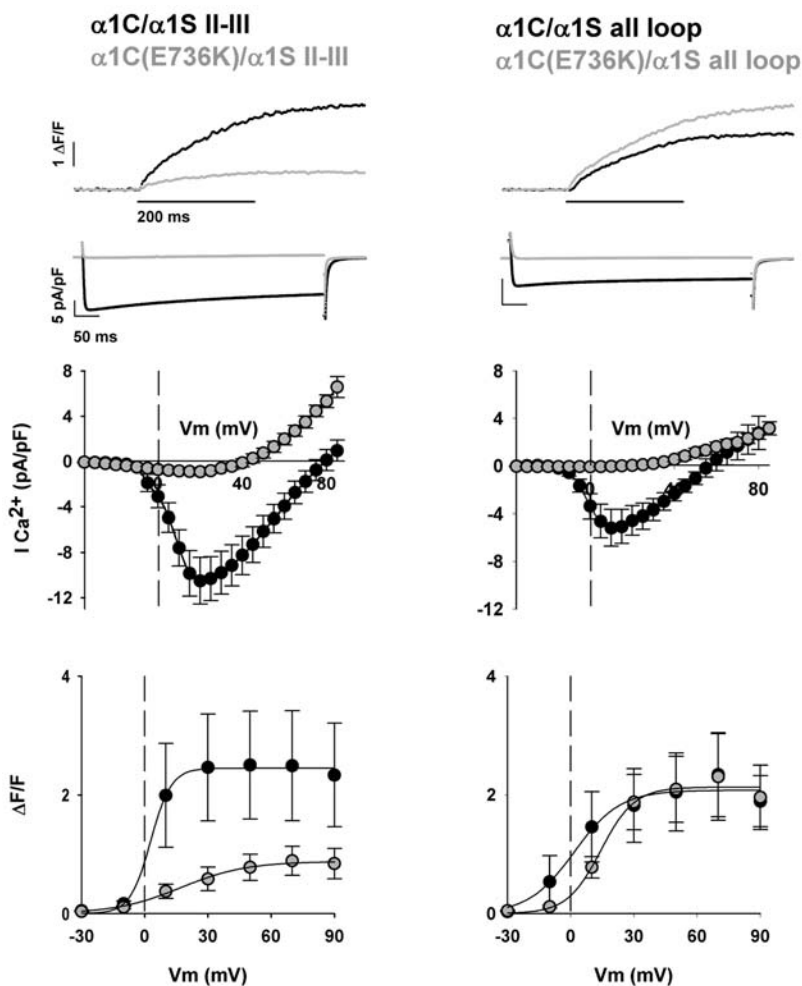


FIGURE 3 Full restoration of skeletal-type EC coupling by the all loop chimera and partial restoration by the II-III loop chimera. Columns show representative *mdg* myotubes transfected with the  $\alpha$ 1C/ $\alpha$ 1S II-III loop chimera and  $\alpha$ 1C/ $\alpha$ 1S all loop chimera, both in the presence and absence of the pore mutation E736K. Shaded traces and shaded symbols correspond to pore mutants. The top traces correspond to the spatial integral of the confocal  $\text{Ca}^{2+}$  transient in  $\Delta F/F$  units in response to a 200-ms depolarization to +30 mV from a holding potential of  $-40$  mV. The second row of traces corresponds to the  $\text{Ca}^{2+}$  current elicited during a 500-ms depolarization from  $-40$  mV to +30 mV. Population averages of the  $\text{Ca}^{2+}$  current-voltage curves are located centrally. These were obtained by depolarizing transfected myotubes in 5-mV increments from a holding potential of  $-40$  mV for 500 ms. At the bottom are  $\text{Ca}^{2+}$  transient-voltage curves for population averages in response to a 200-ms depolarization from  $-40$  mV to the indicated potentials. All fluorescence-voltage curves were fit with Eq. 1. Curves were fit with the following parameters ( $\Delta F/F_{\text{max}}$  in  $\Delta F/F$  units,  $V_{1/2}$  in mV, and  $k$  in mV, respectively): for  $\alpha$ 1C/ $\alpha$ 1S II-III, 2.4, 2.8, and 4.9; for  $\alpha$ 1C(E736K)/ $\alpha$ 1S II-III, 0.9, 17.1, and 15.5; for  $\alpha$ 1C/ $\alpha$ 1S all loop, 2.1, 1.7, and 10.9; for  $\alpha$ 1C(E736K)/ $\alpha$ 1S all loop, 2.1, 14.3, and 8.

**TABLE 2** Ca<sup>2+</sup> conductance, Ca<sup>2+</sup> transients, and charge density expressed by pore mutants in dysgenic (*mdg*) skeletal myotubes

	$G_{\max}$ (pS/pF)	$V_{1/2}$ (mV)	$k$ (mV)	$\Delta F/F_{\max}$	$V_{1/2}$ (mV)	$K$ (mV)	$Q_{\max}$ (fC/pF)	$V_{1/2}$ (mV)	$k$ (mV)
NT <i>mdg</i>	20 ± 3 (27)	4 ± 5	19.5 ± 7.1	— (25)	—	—	1.4 ± 0.1* (10)	-5 ± 4	12.0 ± 1.2
$\alpha 1S$ (E1014K)	48 ± 12 (7)	23 ± 14	16.2 ± 3.9	2.6 ± 0.4 (11)	7 ± 4	9.3 ± 1.0	4.7 ± 0.8 (9)	10 ± 2	17.8 ± 0.8
$\alpha 1C$ (E736K)	25 ± 6 (7)	21 ± 3	13.2 ± 1.9	— (5)	—	—	5.9 ± 1.3(4)	5 ± 4	18.1 ± 0.8
$\alpha 1C$ (E736K)/ $\alpha 1S$ II-III	43 ± 7 (7)	6 ± 3	10.7 ± 1.5	0.9 ± 0.2* (7)	20 ± 7	12.9 ± 2.7	5.8 ± 0.9 (7)	12 ± 4	21.2 ± 1.9
$\alpha 1C$ (E736K)/ $\alpha 1S$ all loop	44 ± 9 (8)	44 ± 14	18.7 ± 3.8	2.2 ± 0.6 (8)	11 ± 5	9.0 ± 2.1	4.5 ± 0.6 (4)	12 ± 6	17.4 ± 1.8

Values are mean ± SEM of Boltzmann parameters fitted to each cell, with the number of cells indicated in parenthesis.  $G_{\max}$ ,  $\Delta F/F_{\max}$  or  $Q_{\max}$ ,  $V_{1/2}$ , and  $k$  are parameters of the Boltzmann fit to each cell with Eq. 1. Changes in fluo-4 fluorescence were not detected at any test potential in NT *mdg* and  $\alpha 1C$ (E736K)-expressing myotubes. Parameters for conductance and fluorescence of NT *mdg* myotubes are the same as in Table 1.

\*Parameters with one-way ANOVA significance  $p < 0.05$  compared to myotubes expressing  $\alpha 1S$ (E1014K). Using the mean  $Q_{\max}$  provided in the table, the ratio ( $\Delta F/F_{\max}$ )/ $Q_{\max}$  was 0.55 ± 0.08 for  $\alpha 1S$ (E1014K) ( $n = 11$ ); 0.16 ± 0.04 for  $\alpha 1C$ (E736K)/ $\alpha 1S$  II-III ( $n = 7$ ); and 0.45 ± 0.13 for  $\alpha 1C$ / $\alpha 1S$  all loop ( $n = 8$ ). The ratio for  $\alpha 1C$ (E736K)/ $\alpha 1S$  II-III was significantly lower ( $t$ -test significance  $p < 0.05$ ) than that of  $\alpha 1S$ (E1014K) or that of  $\alpha 1C$ (E736K)/ $\alpha 1S$  all loop.

To determine if the tested  $\alpha 1C$ / $\alpha 1S$  chimeras were broadly EC-coupling-defective, we investigated the behavior of  $\alpha 1C$ / $\alpha 1S$  all loop, a chimera consisting of  $\alpha 1C$  and all the cytoplasmic elements of  $\alpha 1S$  characterized in Fig. 2, namely the N-terminal, I-II loop, II-III loop, III-IV loop, and C-terminal domains. If chimeras are defective in general, such a defect should also be present in a chimera containing the II-III loop and the rest of the skeletal cytoplasmic elements. Alternatively, if the  $\alpha 1C$ / $\alpha 1S$  II-III loop chimera was partially defective due to the absence of critical skeletal elements, the  $\alpha 1C$ / $\alpha 1S$  all loop chimera should recover the skeletal phenotype more effectively. These results are shown in the right panel of Fig. 3. The  $\alpha 1C$ / $\alpha 1S$  all loop chimera expressed Ca<sup>2+</sup> currents with a fast activation and slow inactivation, typical of WT  $\alpha 1C$  and all tested  $\alpha 1C$ / $\alpha 1S$  chimeras. Furthermore, the Ca<sup>2+</sup> current density was not significantly different from that of the other chimeras (Table 2), and as shown by the current-voltage curves, the E736K pore mutation curtailed the bulk of the inward Ca<sup>2+</sup> current. Significantly, the voltage dependence of the Ca<sup>2+</sup> transients was sigmoidal for both the Ca<sup>2+</sup>-conducting  $\alpha 1C$ / $\alpha 1S$  all loop and for the poorly conducting  $\alpha 1C$ (E736K)/ $\alpha 1S$  all loop chimeras. The maximum fluorescence at large positive potentials was also the same. This is indicated by the traces of cell fluorescence at +30 mV in separate representative myotubes shown at the top of Fig. 3, and by the fluorescence-voltage relationships at the bottom of Fig. 3. The fitted Boltzmann parameters indicated a small difference in mid-point potential; however, the difference was not significant. Parameters of the fit of the voltage dependence of Ca<sup>2+</sup> transients are shown in Table 1 for  $\alpha 1C$ / $\alpha 1S$  all loop and in Table 2 for  $\alpha 1C$ (E736K)/ $\alpha 1S$  all loop. From the similarity in shape and maximum Ca<sup>2+</sup> fluorescence at large potentials, we concluded that this pair of chimeras recapitulated well the behavior of WT  $\alpha 1S$  and  $\alpha 1S$ (E1014K) described above. To determine effectiveness of recovery of the skeletal-type EC-coupling components by the II-III loop and all loop chimeras, we compared the behavior of  $\alpha 1C$ (E736K)/ $\alpha 1S$  all loop and  $\alpha 1C$ (E736K)/ $\alpha 1S$  II-III loop in terms of the maximum amplitude of the Ca<sup>2+</sup> transients elicited at large

positive potentials (Table 2). The all-skeletal loop chimera recovered a  $\Delta F/F_{\max}$  statistically similar to that of  $\alpha 1S$ (E1014K), and ~2.4-fold higher than that of the II-III loop chimera ( $t$ -test significance <0.05). Hence the all loop chimera was more effective than the II-III loop chimera in recovery of a skeletal EC-coupling component. The results show that it is possible to design an  $\alpha 1C$ / $\alpha 1S$  chimera with a phenotype similar to WT  $\alpha 1S$ , and that  $\alpha 1C$ / $\alpha 1S$  chimeras are not inherently EC-coupling-defective. Evidently, several cytoplasmic loops of  $\alpha 1S$ , not only the II-III loop, are required for a quantitative recovery of the EC-coupling phenotype.

Fig. 4 shows normalized charge movement density (fC/pF) expressed by the II-III loop chimera, the all loop chimera, and the two WT constructs. We carried out a standard gating current protocol (25) in myotubes expressing variants carrying the pore mutation. This reduced the ionic current, and hence increased the success of the measurement. The traces in the insets show the transient outward ON current at the start of a 50-ms test voltage step to +60 mV followed by inward OFF current at the end of the voltage step as charges return to the original position. The complete pulse protocol (see Materials and Methods) included a 698-ms prepulse depolarization to -30 mV to remove immobilization-sensitive components of the gating current unrelated to the DHPR, and pretest P/4 pulses to eliminate linear components unrelated to voltage sensors. The graphs show normalized charge density-voltage relationships obtained by integration of the OFF component which, in our hands, was less contaminated by residual ionic current than the ON component. The main contaminant of the ON component was an outward current, presumably from a K<sup>+</sup> channel, that was not always blocked by the pipette solution. In all cases, the OFF charge increased in a sigmoidal fashion starting at ~-40 mV and saturated at potentials more positive than +60 mV. Data were adequately fit by a Boltzmann equation (Eq. 1). In nontransfected myotubes, we detected a small background charge with a maximum density of ~1 fC/pF, similar to that reported previously (25). The average charge movement density of nontransfected cells is shown



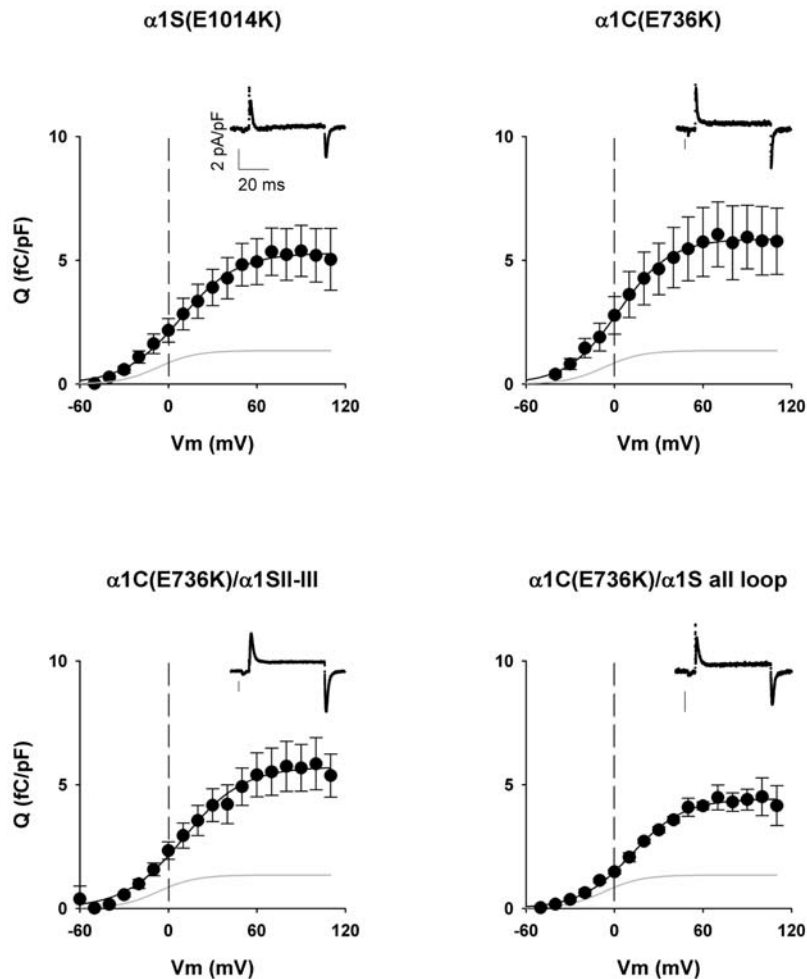


FIGURE 4 Charge movement density expressed  $\alpha$ 1C/ $\alpha$ 1S chimeras carrying pore mutations. Graphs show the population-averaged voltage dependence of the OFF charge in femto-Coulombs normalized to the linear membrane capacitance of each cell in pico-Farads. The OFF charge was obtained by integration of the OFF charge movement current at the end of a 50-ms test pulse after on-line subtraction of the linear component. Measurements were made in *mdg* myotubes transfected with the indicated constructs using a pulse protocol and external and pipette solutions described in Materials and Methods. The shaded trace in each graph corresponds to the fit of the population averaged charge movement of nontransfected dysgenic myotubes. Insets are representative traces of charge movement currents during the test-pulse phase of the pulse protocol elicited from a holding potential of  $-80$  mV to a test potential of  $+60$  mV for 50 ms. Charge movement versus voltage curves were fit with Eq. 1 with the following parameters ( $Q_{\max}$  in fC/pF,  $V_{1/2}$  in mV, and  $k$  in mV, respectively); for  $\alpha$ 1S(E1014K), 5.3, 8.2, and 19.1; for  $\alpha$ 1C(E736K), 5.9, 2.7, and 17.6; for  $\alpha$ 1C(E736K)/ $\alpha$ 1S II-III, 5.7, 10.6, and 20.1; for  $\alpha$ 1C(E736K)/ $\alpha$ 1S all loop, 4.4, 12.0, and 17.6; and for nontransfected dysgenic myotubes (shaded traces): 1.4,  $-7.0$ , and 12.9. For a fit of parameters by cell and number of cells included in the fit, see Table 2.

by the line without data, and the parameters of the fit are shown in Table 2. The maximum charge-movement densities expressed by the  $\alpha$ 1C(E736K)/ $\alpha$ 1S II-III loop chimera, the  $\alpha$ 1C(E736K)/ $\alpha$ 1S all loop chimera,  $\alpha$ 1C(E736K), and  $\alpha$ 1S(E1014K) were statistically similar (Table 2). These values agreed with previous determinations in dysgenic myotubes expressing WT  $\alpha$ 1C and WT  $\alpha$ 1S (12,25). The results show that DHPR voltage-sensor density was not a confounding factor in our studies.

### Incomplete recovery of skeletal-type EC coupling by the $\alpha$ 1S II-III loop revealed by $\text{Cd}^{2+}$ block of inward $\text{Ca}^{2+}$ current

Is the reduced activity of the  $\alpha$ 1C(E736K)/ $\alpha$ 1S II-III loop chimera a consequence of the E736K mutation? To answer this critical question, in Fig. 5 we compared  $\text{Ca}^{2+}$  transients expressed by WT  $\alpha$ 1S and the  $\text{Ca}^{2+}$ -conducting II-III loop and all loop chimeras in the presence of external  $\text{Cd}^{2+}$  to block the inward  $\text{Ca}^{2+}$  current. Titrations indicated that  $10^{-4}$  M, but not  $10^{-6}$  M  $\text{Cd}^{2+}$ , blocked the  $\text{Ca}^{2+}$  conductance to the same extent as the pore mutations. This is shown in Table

3, with control data in the absence of  $\text{Cd}^{2+}$  in Table 1.  $\text{Ca}^{2+}$  currents and  $\text{Ca}^{2+}$  transients in control external solution and in external solution supplemented with  $10^{-4}$  M  $\text{Cd}^{2+}$  are shown for WT  $\alpha$ 1S,  $\alpha$ 1C/ $\alpha$ 1S II-III loop and  $\alpha$ 1C/ $\alpha$ 1S all loop in left, center, and right panels as indicated. Shaded traces and symbols are reserved for myotubes in external solution containing  $\text{Cd}^{2+}$ . Inward  $\text{Ca}^{2+}$  currents were severely curtailed by  $10^{-4}$  M  $\text{Cd}^{2+}$  in all cases. This can be readily appreciated from the insets of  $\text{Ca}^{2+}$  currents at  $+30$  mV, and by comparing current-voltage curves in the presence and absence of the blocker. It is significant to observe that  $\text{Ca}^{2+}$  transients in the presence of  $\text{Cd}^{2+}$  reproduced the same phenotype as those seen in the presence of the pore mutations. The  $\text{Ca}^{2+}$  transients expressed by the  $\alpha$ 1C/ $\alpha$ 1S II-III loop chimera were severely depressed in the presence of the  $\text{Ca}^{2+}$  current blocker. However, the  $\text{Ca}^{2+}$  transients expressed by WT  $\alpha$ 1S and the  $\alpha$ 1C/ $\alpha$ 1S all loop chimera were not depressed by  $10^{-4}$  M  $\text{Cd}^{2+}$ . This can be appreciated in the  $\text{Ca}^{2+}$  transients shown as insets for a representative myotube expressing the indicated construct, and by the fluorescence-voltage relationship in the center of each panel in Fig. 5. The results are further confirmed by the correlation

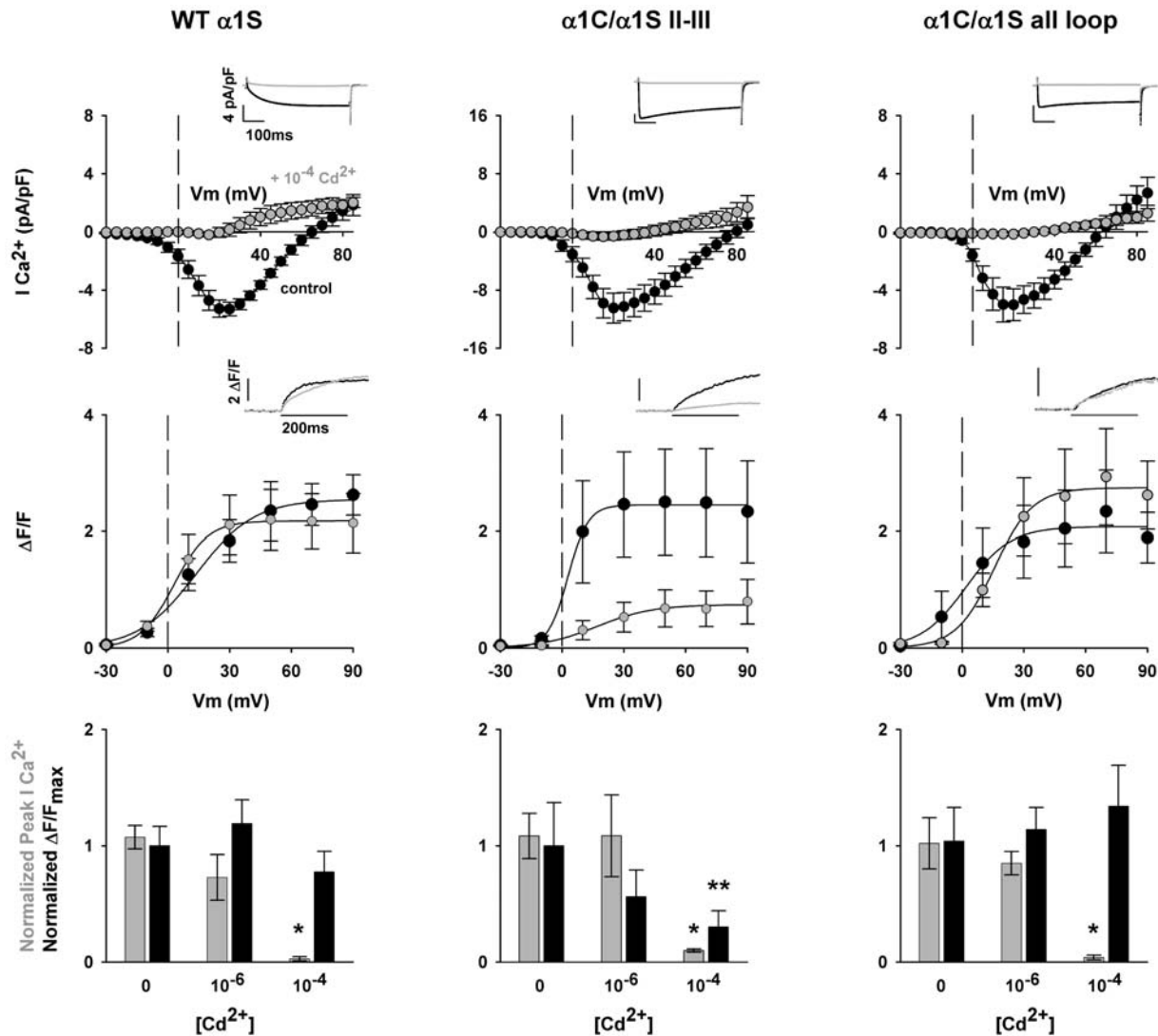


FIGURE 5  $Cd^{2+}$  block of  $Ca^{2+}$ -dependent EC coupling promoted by the II-III loop chimera. Columns show representative *mdg* myotubes expressing the II-III loop and all loop chimeras. The left panel shows myotubes expressing WT  $\alpha 1S$  used as control. The top graphs correspond to population average current-voltage curves for depolarizations of 500 ms from a holding potential of  $-40$  mV. Insets show representative  $Ca^{2+}$  currents elicited at  $+30$  mV from a holding potential of  $-40$  mV. With the exception of the bar graphs at the bottom, all shaded traces and shaded symbols are in  $10^{-4}$  M  $CdCl_2$  added to the bath solution. The middle graphs show population-averaged  $Ca^{2+}$  transient-voltage relationships for depolarizations of 200 ms from a holding potential of  $-40$  mV. Insets correspond to the spatial integral of the confocal fluorescence in  $\Delta F/F$  units in response to a 200-ms depolarization to  $+30$  mV from a holding potential of  $-40$  mV. Fluorescence-voltage curves were fit with Eq. 1. Curves were fit with the following parameters ( $F_{max}$  in  $\Delta F/F$  units,  $V_{1/2}$  in mV, and  $k$  in mV, respectively): for WT  $\alpha 1S$  in 0  $Cd^{2+}$ , 2.5, 13.7, and 14.1; for WT  $\alpha 1S$  in  $10^{-4}$   $Cd^{2+}$ , 2.2, 3.0, and 8.2; for  $\alpha 1C/\alpha 1S$  II-III in 0  $Cd^{2+}$ , 2.8, 2.8, and 4.7; for  $\alpha 1C/\alpha 1S$  II-III in  $10^{-4}$   $Cd^{2+}$ , 0.7, 17.0, and 13.5; for  $\alpha 1C/\alpha 1S$  all loop in 0  $Cd^{2+}$ , 2.1, 1.7, and 10.9; for  $\alpha 1C/\alpha 1S$  all loop in  $10^{-4}$   $Cd^{2+}$ , 2.7, 15.6, and 9.3. For a fit of parameters by cell and number of cells included in the fit, see Table 3. The bottom bar graphs correspond to normalized  $Ca^{2+}$  currents (shaded bars) and normalized  $\Delta F/F_{max}$  (black) in control solution without  $Cd^{2+}$ , external solution with  $10^{-6}$  M  $CdCl_2$ , and external solution with  $10^{-4}$  M  $CdCl_2$ .  $Ca^{2+}$  currents at  $+30$  mV were normalized to the population averaged  $Ca^{2+}$  current at  $+30$  mV in the absence of  $Cd^{2+}$ .  $\Delta F/F_{max}$  from a fit of individual cells was normalized to  $\Delta F/F_{max}$  from a fit of the population average in the absence of  $Cd^{2+}$ .

presented in the histograms at the bottom of each panel.  $Ca^{2+}$  current density and  $Ca^{2+}$  transient amplitude at  $+30$  mV, at two  $Cd^{2+}$  concentrations, were normalized to the mean  $Ca^{2+}$  current and  $Ca^{2+}$  transient amplitude in control solution. In all cases, there was a significant decrease in fractional  $Ca^{2+}$  current density at  $10^{-4}$  M  $Cd^{2+}$ . However, only in the case of the  $\alpha 1C/\alpha 1S$  II-III loop chimera did we observe a concomitant decrease in fractional  $Ca^{2+}$  transient

amplitude. This was not the case for WT  $\alpha 1S$  or the  $\alpha 1C/\alpha 1S$  all loop chimera. A statistical analysis of the parameters of  $Ca^{2+}$  conductance and cell fluorescence in the presence of  $Cd^{2+}$  are described in Table 3. The  $Ca^{2+}$  fluorescence data in Table 3 are in agreement with the statistical analysis of the data at a single potential presented in histogram form at the bottom of Fig. 5. The  $\Delta F/F_{max}$  fitted to cells expressing the II-III loop chimera in  $10^{-4}$  M  $Cd^{2+}$ , but not that of the

**TABLE 3**  $\text{Ca}^{2+}$  conductance and  $\text{Ca}^{2+}$  transients expressed by  $\alpha$ 1C/ $\alpha$ 1S chimeras in presence of extracellular cadmium

	$G_{\max}$ (pS/pF)	$V_{1/2}$ (mV)	$k$ (mV)	$\Delta F/F_{\max}$	$V_{1/2}$ (mV)	$k$ (mV)
WT $\alpha$ 1S + $10^{-4}$ $\text{Cd}^{2+}$	43 $\pm$ 4 (7)	18 $\pm$ 4	6.7 $\pm$ 2.0	2.2 $\pm$ 0.5 (9)	0 $\pm$ 3	6.9 $\pm$ 1.7
WT $\alpha$ 1S + $10^{-6}$ $\text{Cd}^{2+}$	158 $\pm$ 15* (6)	11 $\pm$ 2	3.8 $\pm$ 0.3	3.4 $\pm$ 0.6 (7)	3 $\pm$ 3	5.8 $\pm$ 0.4
$\alpha$ 1C/ $\alpha$ 1S II-III + $10^{-4}$ $\text{Cd}^{2+}$	53 $\pm$ 8 (5)	14 $\pm$ 4	10.1 $\pm$ 3.6	0.7 $\pm$ 0.3* (7)	16 $\pm$ 3*	13.0 $\pm$ 2.0*
$\alpha$ 1C/ $\alpha$ 1S II-III + $10^{-6}$ $\text{Cd}^{2+}$	211 $\pm$ 9* (4)	2 $\pm$ 6	5.4 $\pm$ 3.3	1.4 $\pm$ 0.6 (4)	13 $\pm$ 9	5.1 $\pm$ 0.7
$\alpha$ 1C/ $\alpha$ 1S all loop + $10^{-4}$ $\text{Cd}^{2+}$	29 $\pm$ 8 (6)	38 $\pm$ 14	20.1 $\pm$ 5.8*	2.8 $\pm$ 0.7 (6)	18 $\pm$ 4*	10.6 $\pm$ 2.2
$\alpha$ 1C/ $\alpha$ 1S all loop + $10^{-6}$ $\text{Cd}^{2+}$	104 $\pm$ 9* (5)	6 $\pm$ 3	5.2 $\pm$ 1.6	2.4 $\pm$ 0.4 (5)	5 $\pm$ 4	6.9 $\pm$ 1.9

Values are mean  $\pm$  SEM of Boltzmann parameters fitted to each cell, with the number of cells indicated in parentheses.  $G_{\max}$  or  $\Delta F/F_{\max}$ ,  $V_{1/2}$ , and  $k$  are parameters of the Boltzmann fit to each cell with Eq. 1.

\*Parameters with one-way ANOVA significance  $p < 0.05$  compared to WT  $\alpha$ 1S +  $10^{-4}$   $\text{Cd}^{2+}$ .

all loop chimera, was significantly lower relative to controls in external solution with  $10^{-6}$  M  $\text{Ca}^{2+}$  or external solution without  $\text{Cd}^{2+}$ . The results confirmed that the E736K mutation was not responsible for the weak EC coupling recovered by the II-III loop chimera. Rather, the behavior of the all loop chimera emphasized that a quantitative recovery of the skeletal phenotype could not be achieved unless all the cytosolic elements of  $\alpha$ 1S were present. It remains to be determined in future work which cytosolic domains in addition to the II-III loop are required for a quantitative functional recovery.

## DISCUSSION

Studies in *mdg* myotubes designed to investigate the contribution of  $\alpha$ 1S to skeletal-type EC coupling have concluded that the II-III loop is functionally unique (11,12,14,16,17,25,30,32). Our results confirmed this observation. However, it was not previously known if the functional recovery produced by the  $\alpha$ 1S II-III loop was comparable to that produced by WT  $\alpha$ 1S, or if multiple cytosolic domains of  $\alpha$ 1S were necessary for a quantitative recovery of the EC-coupling phenotype. Earlier studies (11) did not provide a voltage-clamp analysis of the contribution of the skeletal loops alone or in combination, and the more recent studies have focused exclusively on domains within the  $\alpha$ 1S II-III loop (16,17,25). The efficiency of EC-coupling recovery by the  $\alpha$ 1S II-III loop is a significant issue since structural models suggest that the area of juxtaposition between the  $\alpha$ 1S subunit and RyR1 is large, and therefore the number of interaction sites is potentially large (5,6). The EC-coupling triggering mechanism could thus be much more complex than a single DHPR loop orchestrating SR  $\text{Ca}^{2+}$  release. Sequence divergence between  $\alpha$ 1S and  $\alpha$ 1C is mostly confined to the long cytoplasmic domains rather than the transmembrane repeats. Hence, it was reasonable to expect that a  $\alpha$ 1C/ $\alpha$ 1S chimera carrying all the cytosolic domains of  $\alpha$ 1S could recover the skeletal EC-coupling phenotype quantitatively. We found that a large fraction of the  $\text{Ca}^{2+}$  transient expressed by the  $\alpha$ 1C/ $\alpha$ 1S II-III loop chimera was eliminated when the pore mutation  $\alpha$ 1C(E736K) was introduced to reduce the inward  $\text{Ca}^{2+}$  current. This was not the case for the  $\alpha$ 1C/ $\alpha$ 1S chimera

carrying all the cytosolic domains of  $\alpha$ 1S. Furthermore, the results were confirmed using  $\text{Ca}^{2+}$ -conducting variants of the same chimeras in which the inward  $\text{Ca}^{2+}$  current was blocked by a low concentration of  $\text{Cd}^{2+}$ . The  $\alpha$ 1C/ $\alpha$ 1S all loop chimera, unlike the  $\alpha$ 1C/ $\alpha$ 1S II-III loop chimera, rescued  $\text{Ca}^{2+}$  transients of the same  $\Delta F/F_{\max}$  regardless of the presence of the pore mutation. When normalized by the DHPR charge movement and compared to  $\alpha$ 1C/ $\alpha$ 1S all loop and WT  $\alpha$ 1S (see Table 2 legend), the maximum  $\text{Ca}^{2+}$  fluorescence expressed by the II-III loop chimera was  $0.16 \pm 0.04 F_{\max}/Q_{\max}$ , compared to  $0.45 \pm 0.13 F_{\max}/Q_{\max}$  for  $\alpha$ 1C/ $\alpha$ 1S all loop, and  $0.55 \pm 0.08 F_{\max}/Q_{\max}$  for  $\alpha$ 1S(E1014K), or  $\sim 3$ -fold lower (*t*-test significance,  $p < 0.05$ ). These ratios only have comparative value since it is unlikely that all the DHPR charge movement is involved in EC coupling (42). The observations lend themselves to the conclusion that a conglomerate of cytoplasmic domains, rather than the II-III loop alone, is necessary to restore normal EC-coupling function.

The  $\text{Ca}^{2+}$  transient expressed by CSk3, the  $\alpha$ 1C/ $\alpha$ 1S II-III loop chimera described by Tanabe et al. (11) was substantially reduced in the presence of inorganic blockers of the inward  $\text{Ca}^{2+}$  current.  $\text{Ca}^{2+}$  fluorescence-voltage relationships for CSk3 have not been described (11,14); therefore, it is difficult to compare the two sets of results. However, qualitatively the results are similar and indicate that both II-III loop chimeras have a sizable EC-coupling component unrelated to the skeletal phenotype. CSk3 consists of  $\alpha$ 1C(1–787)/ $\alpha$ 1S(666–791)/ $\alpha$ 1C(923–2171), whereas our chimera included eight additional residues, namely  $\alpha$ 1S(1–788)/ $\alpha$ 1S(667–799)/ $\alpha$ 1C(931–2171). These differences may not be significant since critical determinants within the  $\alpha$ 1S II-III loop have been mapped to the segment of residues 671–690 and 720–765 present in both chimeras (14,25). Furthermore, charge movements expressed by both chimeras in dysgenic myotubes are comparable (12) (Table 2). Hence, possible differences in voltage-sensor densities, which could conceivably affect the density of mechanically coupled RyR1 channels, are nonexistent. Interestingly,  $\text{Ca}^{2+}$  fluorescence-voltage relationships have been published for GFP-CSk53, an  $\alpha$ 1C/ $\alpha$ 1S chimera carrying the  $\alpha$ 1S II-III loop residues 720–765 deemed critical for skeletal-type EC coupling. This chimera also has an N-terminal fusion of the green

fluorescent protein (GFP). The  $F_{\max}$  expressed by GFP-CSk53 was considerably lower than that expressed by the GFP-WT  $\alpha 1S$  fusion even in external solution containing the standard 10 mM  $Ca^{2+}$  (31). Thus, the low  $F_{\max}$  of a II-III loop chimera may not be related in all instances to the presence of an enlarged  $Ca^{2+}$ -dependent EC-coupling component, which is removed when the inward  $Ca^{2+}$  current is blocked. It could be that in this case, the GFP moiety hinders EC coupling in the CSk53 chimera, or that residues 720–765 are insufficient for a quantitative EC-coupling recovery comparable to that of WT  $\alpha 1S$ . In support of the latter, it is important to note that the identification of critical  $\alpha 1S$  II-III loop residues 720–765 in chimeras without GFP was achieved at the expense of a substantial loss in  $Ca^{2+}$  transient amplitude relative to the  $Ca^{2+}$  transient expressed by the parent CSk3 chimera carrying the complete  $\alpha 1S$  II-III loop (14). Thus, an appropriate structural context is essential for a quantitative recovery of EC-coupling function.

It was intriguing to find that, on average, the shape of the fluorescence-voltage curve for the  $Ca^{2+}$ -conducting and pore-mutant variants of the  $\alpha 1C/\alpha 1S$  II-III loop chimera were both sigmoidal (Fig. 3). A somewhat bell-shaped curve was expected for the former based on the significant dependence on the  $Ca^{2+}$  current for triggering release. We considered the possibility that the reduction in  $\Delta F/F_{\max}$  observed in the pore-mutant variant of the II-III loop chimera reflected inactivation of the voltage sensor due to the elimination of a critical  $Ca^{2+}$ -binding site (41). Several reasons argue against this possibility. First, the pore mutation  $\alpha 1S(E1014K)$  was shown to eliminate high-affinity  $Ca^{2+}$  binding to the subunit (39). Yet, WT  $\alpha 1S$  and  $\alpha 1S(E1014K)$  had fluorescence-voltage characteristics that were superimposable (Fig. 1). Second, the  $Ca^{2+}$ -conducting and pore-mutant variants of the  $\alpha 1C/\alpha 1S$  all loop chimera expressed skeletal-type EC coupling with a similar  $\Delta F/F_{\max}$  (Tables 1 and 2). This was not expected under the assumption that the pore mutation inactivated the voltage sensor. Finally, and most significantly, a reduction in  $\Delta F/F_{\max}$  was observed in the  $Ca^{2+}$ -conducting  $\alpha 1C/\alpha 1S$  II-III loop chimera when the  $Ca^{2+}$  current was blocked by  $Cd^{2+}$ . This was not observed for WT  $\alpha 1S$ , nor for the  $\alpha 1C/\alpha 1S$  all loop chimera (Fig. 5). Hence, it could not be argued that  $Cd^{2+}$  block limited access of  $Ca^{2+}$  to the binding site on the voltage sensor. We further searched for an explanation in the data itself. A cell-by-cell fit of the fluorescence-voltage curve indicated that some cells expressing the  $Ca^{2+}$ -conducting II-III loop chimera displayed a slight bell-shaped voltage dependence (three out of seven) whereas others did not (four out of seven). This heterogeneity contributed to the much larger variance of the data collected for the II-III loop chimera relative to other single-loop chimeras (see Fig. 2). A freeze-fracture analysis of *mdg* myotubes expressing the CSk3 chimera revealed that only a few of the chimeric DHPR particles present at a DHPR-RyR1 junction were arranged as tetrads (43). DHPR tetrad formation is a precondition for skeletal-type EC

coupling (1). Hence, junctions with tetrads are more likely to trigger  $Ca^{2+}$  release by a skeletal-type mechanism whereas junctions without tetrads, or with “incomplete” tetrads, are more likely to trigger  $Ca^{2+}$  release via the  $Ca^{2+}$  current. We suggest that in myotubes expressing the II-III loop chimera, the EC-coupling mechanism itself may be heterogeneous due to a variable density of tetrads in each DHPR-RyR1 junction. The voltage dependence of the  $Ca^{2+}$  transient may approximate a sigmoidal relationship when the number of skeletal-like junctions in a muscle cell is high and bell-shaped when it is low. In addition, it is necessary to realize that the  $Ca^{2+}$ -entry dependent component, in the best of circumstances, is small. This can be appreciated by comparing the maximum  $Ca^{2+}$  transient amplitudes expressed by WT  $\alpha 1S$  and WT  $\alpha 1C$  in Fig. 1. Such a component may not be always possible to detect, particularly when the voltage-dependent component is much larger.

The presence of a  $Ca^{2+}$ -entry-dependent EC-coupling component in the  $\alpha 1S$  II-III loop chimera and not in the chimera carrying all the cytosolic domains of  $\alpha 1S$ , strongly suggests that structural determinants unknown at this point contribute to the stability of the DHPR-RyR1 complex. The mechanism by which the II-III loop in combination with other cytoplasmic domains of  $\alpha 1S$  enable the formation of a stable DHPR-RyR1 complex remains to be understood.

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