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Alternative Splicing of Ryanodine Receptors Modulates Cardiomyocyte Ca\textsuperscript{2+} Signaling and Susceptibility to Apoptosis

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Abstract—Ca\textsuperscript{2+} release via type 2 ryanodine receptors (RyR2) regulates cardiac function. Molecular cloning of human RyR2 identified 2 alternatively spliced variants, comprising 30- and 24-bp sequence insertions; yet their role in shaping cardiomyocyte Ca\textsuperscript{2+} signaling and cell phenotype is unknown. We profiled the developmental regulation and the tissue and species specificity of these variants and showed that their recombinant expression in HL-1 cardiomyocytes profoundly modulated nuclear and cytoplasmic Ca\textsuperscript{2+} release. All splice variants localized to the sarcoplasmic reticulum, perinuclear Golgi apparatus, and to finger-like invaginations of the nuclear envelope (nucleoplasmic reticulum). Strikingly, the 24-bp splice insertion that was present at low levels in embryonic and adult hearts was essential for targeting RyR2 to an intranuclear Golgi apparatus and promoted the intracellular segregation of this variant. The amplitude variability of nuclear and cytoplasmic Ca\textsuperscript{2+} fluxes were reduced in nonstimulated cardiomyocytes expressing both 30- and 24-bp splice variants and were associated with lower basal levels of apoptosis. Expression of RyR2 containing the 24-bp insertion also suppressed intracellular Ca\textsuperscript{2+} fluxes following prolonged caffeine exposure (1 mmol/L, 16 hours) that protected cells from apoptosis. The antiapoptotic effects of this variant were linked to increased levels of Bcl-2 phosphorylation. In contrast, RyR2 containing the 30-bp insertion, which was abundant in human embryonic heart but was decreased during cardiac development, did not protect cardiomyocytes from caffeine-evoked apoptosis. Thus, we provide the first evidence that RyR2 splice variants exquisitely modulate intracellular Ca\textsuperscript{2+} signaling and are key determinants of cardiomyocyte apoptotic susceptibility. (Circ Res. 2007;100:874-883.)

Key Words: ryanodine receptor ■ Ca\textsuperscript{2+} ■ alternative splicing ■ cardiomyocyte ■ apoptosis
opmentally regulated, disease-linked splice insertion exhibited distinct Ca\(^{2+}\)--releasing profiles in skeletal myotubes,\(^4\) and a smooth-muscle–specific deletion in RyR3 that did not form functional homotetrameric channels, inhibited Ca\(^{2+}\) release when expressed in heteromeric combination with RyR isoforms that lacked insertions\(^5,6\) (Figure 1A and supplemental Table I, variants b and k, respectively).

Two alternatively spliced variants of the human cardiac RyR channel (RyR2) corresponding to a 30-bp insertion (encoding FAIDSLCGFG) and a 24-bp insertion (encoding VTGSQRSK) (variants n and d', respectively; Figure 1A and supplemental Table I) have been identified.\(^7\) However, their roles in cardiac development and cell signaling have remained a mystery. Here, we present the first functional characterization of human RyR2 splice variants and show that cellular architecture and Ca\(^{2+}\) signaling are profoundly modulated following their expression in HL-1 cardiomyocytes. Our data highlight an important role for the 24-bp insertion in protecting cardiomyocytes from stimulation-induced apoptosis and thus identify RyR2 alternative splicing as a key determinant of cardiomyocyte susceptibility to apoptosis. Furthermore, we show that the expression profiles of RyR2 splice variants exhibits distinct species-, tissue-, and developmentally specific regulation, and we evaluate the implications of our findings in the context of cardiac development and future therapeutic approaches to cardiac disease.

**Materials and Methods**

**Construction, Expression, and Detection of Human RyR2 Splice Variants**

The recombinant human RyR2 routinely expressed in our laboratory lacks the 30-bp and 24-bp splice insertions and is subsequently referred to as RyR2\(^{-/-}\). The construction of enhanced green fluorescence protein (eGFP)-tagged RyR2 containing the 30-bp exon (RyR2\(^{30/-}\)), 24-bp exon (RyR2\(^{-/-24}\)), or both (RyR2\(^{30/24}\)) is shown in Figure 1B and the online data supplement. N-terminal tagging of RyR2\(^{-/-}\) with *Discosoma* sp red fluorescent protein (DsRed) was performed as described.\(^8\)

HL-1 cardiomyocytes were cultured and transfected with recombinant RyR2 as described.\(^8\) Cells expressing eGFP-tagged RyR2 were selected by G418-sulfate resistance (500 μg/mL) and were isolated using fluorescent-activated cell sorting (FACS) based on eGFP intensity.\(^9\) FACS-enriched cells were used as the background for DsRed-tagged RyR2\(^{-/-}\) expression. The intracellular localization of recombinant RyR2 was visualized using eGFP or DsRed fluorescence.\(^9\) FACS-enriched cells were used as the background for DsRed-tagged RyR2\(^{-/-}\) expression. The intracellular localization of recombinant RyR2 was visualized using eGFP or DsRed fluorescence.\(^10\) and pAb129 was used for immunodetection of endogenous and recombinant RyR2.\(^7\) Antibodies to eGFP, DsRed, calreticulin (an ER marker), and a Golgi matrix protein (GM130) are described in the online data supplement. Profiling the species, tissue, and developmental aspects of RyR2 splice variant expression are described in the online data supplement.

**Ca\(^{2+}\) Imaging and Signal/Noise Analysis**

Ca\(^{2+}\) release triggered by the acute addition of caffeine (10 mmol/L) or following tonic RyR2 activation by prolonged exposure to caffeine (1 mmol/L, 16 hours) was determined in single fluo3-loaded cells using confocal microscopy (RS2, Leica Microsystems).\(^11\) Analysis of the amplitude and temporal variability in resting and caffeine-activated Ca\(^{2+}\) fluxes in nuclear and cytoplasmic regions...
was performed as described (see the expanded Materials and Methods section in the online data supplement).9,11

Determination of Cell Viability and Mode of Cell Death
Cell viability, and the extent of apoptosis versus necrosis (where “necrosis” is used to describe a mode of cell death that is distinct from apoptosis12), was determined.11

Transcriptional and Protein Expression Analysis of Bcl-2
The levels of Bcl-2 mRNA transcripts in untreated cells or following their prolonged exposure to caffeine (1 mmol/L, 16 hours) were determined using quantitative PCR. The expression levels and phosphorylation status of the endogenous Bcl-2 protein was determined by immunoblotting. Detailed methods are included in the online data supplement.

Results
Alternative Splicing Determines the Cellular Localization of RyR2
Recombinant eGFP-tagged RyR2 splice variants were overexpressed to equivalent levels in FACS-enriched HL-1 cardiomyocytes (Figure 2A). Coincident fluorescent signals from N-terminal eGFP and C-terminal pAb129 immunodetection confirmed the expression of full-length recombinant RyR2. All RyR2 splice variants were localized to an extensive lattice-like network consistent with ER, the nodal aggregates of the nuclear envelope [NE], 13,14 and a perinuclear nucleoplasmic reticulum (NR) (finger-like invaginations of the extended lattice-like network consistent with ER, the Golgi apparatus (GA) (Figure 2B). The localization of recombinant RyR2 to these compartments was indistinguishable for the cellular distribution of endogenous RyR2 (supplemental Figure I). The localization of RyR2 splice variants to these compartments was confirmed by antibody mapping of ER and GA (using compartment-specific markers calreticulin and GM130, respectively), although the extensive colocalization of GA and ER in the perinuclear region of HL-1 cardiomyocytes precluded the unambiguous identification of all RyR2 splice variants to perinuclear GA (Figure 2C). However, we identified a subpopulation of HL-1 cells (comprising ~11% of the total cell population) that exhibited a remarkably distinct intranuclear GA organization (INGA) that accounted for 12.1 ± 4.3% of the total cellular GA content (Figure 2Ci). The different GA architecture in HL-1 populations did not affect cellular morphology (Figure 3), size (760 ± 92 μm² versus 830 ± 118 μm²), viability (89 ± 10% versus 86 ± 15%), or nuclear size (132 ± 24 μm² versus 153 ± 27 μm²), where data refer to INGA-negative versus INGA-positive HL-1 populations, respectively.

Recombinant RyR2 containing the 24-bp insertion (RyR2-24 and RyR230/24) exhibited striking intranuclear distribution, localizing to fibrillar-like structures that were distinct from the NR, yet were indistinguishable from the INGA morphology identified using anti-GA antibodies (Figure 2B and 2C). Analysis of fluorescent signal intensity revealed that INGA-localized RyR2-1+ and RyR2-1/+ accounted for 9.3 ± 3.6% and 11.4 ± 4.6% of the total cellular content of recombinant RyR2, respectively, entirely consistent with the proportion of cellular GA that comprises INGA (11.3%). Costaining of GA and RyR2 splice variants revealed that INGA localization was restricted to RyR2-24/ and RyR230/24 and that the number INGA-positive cells was increased by more than 4-fold following RyR2-24/ and RyR230/24 expression (Figure 2D). Analysis of discrete FACS-isolated cell populations ex-
RyR2 coexpressing eGFP-tagged splice variants and DsRed-tagged (supplemental Figure II). Although RyR2 tagged RyR2 splice variants (black bars) and DsRed-tagged eGFP-tagged RyR2 splice variants and DsRed-fluorescence.15 eGFP-tagged RyR2 splice variants and DsRed-tagged obligate tetramerization required for DsRed fluorescence to this intranuclear compartment. Moreover, the proportion of INGA-localized eGFP-tagged RyR2−/− and RyR230/24 in these coexpression experiments was similar to those in which these were the only variants expressed (RyR2−/−, 11.9±2.8% and RyR230/24, 9.6±3.7% of the total cellular recombinant protein), indicating that coexpression of DsRed-tagged RyR2 did not inhibit the INGA localization of RyR2 containing the 24-bp splice insertion (Figure 3C). These data strongly suggested that although all RyR2 splice variants exhibited limited nuclear localization by virtue of NR invaginations (Figures 2B and 3B), the 24-bp insertion was necessary for RyR2 localization in INGA, thereby conferring subcellular segregation of RyR2 variants.

RyR2 Splice Variants Modulate Cardiomyocyte Ca2+ Signaling and Susceptibility to Apoptosis

Using caffeine as a quasiphysiological activator of Ca2+-dependent RyR2 Ca2+ release, we investigated the role of differential cellular localization of RyR2 splice variants on cardiomyocyte Ca2+ signaling. Cytoplasmic and nuclear Ca2+ levels were comparable in nonstimulated cells expressing all RyR2 variants (Figure 4C), but only cells expressing RyR2 containing the 30-bp or 24-bp exons exhibited suppressed cytoplasmic Ca2+ transients in response to acute caffeine stimulation (Figure 4B and 4C), possibly reflecting reduced Ca2+ release from the ER and the perinuclear GA. In contrast, nuclear Ca2+ mobilization (comprising Ca2+ release from the NE, NR, and inward diffusion of Ca2+ from the cytosol) was markedly augmented only in RyR2−/− and RyR230/24 cells (Figure 4B and 4C). The amplitude of caffeine-evoked cytoplasmic and nuclear Ca2+ mobilization was not an index of the cellular Ca2+ content because the total cellular Ca2+ content in this compartment was not an artifact of cellular overexpression (supplemental Figure II). Although RyR2−/− and RyR230/24 were found in the NR invaginations, we did not detect these variants in INGA-like structures, suggesting that the 24-bp insertion was a key determinant of RyR2 localization to this intranuclear compartment.

To further investigate these observations, we used the obligate tetramerization required for DsRed fluorescence.15 eGFP-tagged RyR2 splice variants and DsRed-tagged RyR2−/− were coexpressed to equivalent levels (Figure 3A). eGFP-tagged RyR2−/− and RyR230/24 extensively colocalized with DsRed-tagged RyR2−/− in the ER network, NR projections, and perinuclear regions (Figure 3B, arrowheads), but we did not detect these variants in INGA. Coexpression of eGFP-tagged RyR2−/− or RyR230/24 with DsRed-tagged RyR2−/− also resulted in significant colocalization in extranuclear and NR compartments (Figure 3B). Importantly, we determined a striking intracellular segregation of RyR2 splice variants, because INGA localization was exclusively restricted to eGFP-tagged RyR2−/− and RyR230/24 and there was a marked absence of homotetrameric DsRed-tagged RyR2−/− in this compartment (Figure 3B and 3C, “green only” intranuclear fluorescence). Consequently, the altered caffeine-induced nuclear and cytoplasmic Ca2+ mobilization in this compartment was not an index of the total cellular Ca2+ content because the total cellular Ca2+ content (see Discussion).

Analysis of the temporal aspects of caffeine-evoked Ca2+ mobilization revealed that the rate of cytoplasmic Ca2+ increase following caffeine addition was comparable in cells expressing all RyR2 variants, although RyR2−/− and RyR230/24 exhibited a significantly faster recovery of resting cytoplasmic Ca2+ levels (Figure 4C). In contrast, the augmented nuclear Ca2+ transients mediated by RyR2−/− and RyR230/24 (Figure 4B and 4C) exhibited more rapid rise times and recovery to basal levels than cytoplasmic Ca2+ transients (Figure 4C).
Normal cardiomyocyte function occurs against a background of large cytoplasmic Ca\(^{2+}\) fluctuations, and normal cell phenotype is maintained following acute caffeine-induced Ca\(^{2+}\) mobilization. However, small but persistent perturbations in Ca\(^{2+}\) homeostasis arising from chronic exposure to caffeine (1 mmol/L) promoted cardiomyocyte dysfunction. Thus, we investigated the functional impact of RyR2 splice variants on cellular Ca\(^{2+}\) signaling and phenotype in response to prolonged exposure to caffeine (1 mmol/L). Under nonstimulated conditions, nuclear and cytoplasmic Ca\(^{2+}\) amplitude variation (Ca\(^{2+}\) "flux") was suppressed in all cells expressing RyR2 containing 30/24 insertions when compared with that occurring in cells expressing RyR2/24 (Figure 5A and 5B), indicating that reduced basal Ca\(^{2+}\) fluxes were independent of the distinct subcellular localization of RyR2\(^{30/24}\), RyR2\(^{24}\), and RyR2\(^{30/24}\) (Figure 2). The reduced Ca\(^{2+}\) fluxes were probably caused by altered basal activity of RyR2 splice variants, because a comparable reduction in the magnitude of Ca\(^{2+}\) flux through RyR2\(^{-/-}\) channels was achieved following ryanodine inhibition (Figure 5A and 5B). However, tonic activation of RyR2 following prolonged caffeine exposure (1 mmol/L, 16 hours), manifested as persistently increased nuclear and cytoplasmic Ca\(^{2+}\) fluxes in RyR2\(^{-/-}\) and RyR2\(^{24}\) cells (Figure 5A and 5C). In contrast, caffeine-triggered Ca\(^{2+}\) fluxes were significantly reduced in RyR2\(^{30/24}\) and RyR2\(^{30/24}\) cells (Figure 5A and 5C).

We next investigated the phenotypic consequences of differential suppression of Ca\(^{2+}\) fluxes by distinct RyR2 splice variants. The extent of cell death (occurring via necrosis and apoptosis) within HL-1 populations is typically 8% to 10%, and this is not affected by the expression of RyR2\(^{-/-}\) or other splice variants (Figure 6A). However, the reduced "resting" nuclear and cytoplasmic Ca\(^{2+}\) flux in nonstimulated cardiomyocytes expressing RyR2 contain-
increased nuclear and cytoplasmic Ca\textsuperscript{2+} fluxes during prolonged caffeine exposure. A, Ca\textsuperscript{2+} traces from nuclear and cytoplasmic regions in untreated cells or those exposed to caffeine (1 mmol/L, 16 hours). The effect of ryanodine (1 mmol/L) on RyR2\textsuperscript{30/24} is shown (ry). B, The amplitude and temporal variability ("noise") in Ca\textsuperscript{2+} signal fluxes obtained from nuclear and cytoplasmic regions (white and black bars, respectively) in nonstimulated cells was normalized to the signal variability in nontransfected HL-1 cells (assigned 1). The increased nuclear and cytoplasmic Ca\textsuperscript{2+} signal variability following prolonged exposure to caffeine (1 mmol/L, 16 hours) was calculated. Data are given as the mean±SEM (n=4 experiments, 20 cells per experiment). *P<0.05 when compared with nuclear Ca\textsuperscript{2+} signal variability in HL-1 cells and those expressing RyR2\textsuperscript{24/24}.

Figure 5. The 24-bp insertion suppresses intracellular Ca\textsuperscript{2+} fluxes during prolonged caffeine exposure. A, Ca\textsuperscript{2+} traces from untreated cells or those exposed to caffeine (1 mmol/L, 16 hours). The effect of ryanodine (1 mmol/L) on RyR2\textsuperscript{30/24} is shown (ry). B, The amplitude and temporal variability ("noise") in Ca\textsuperscript{2+} signal fluxes obtained from nuclear and cytoplasmic regions (white and black bars, respectively) in nonstimulated cells was normalized to the signal variability in nontransfected HL-1 cells (assigned 1). C, The increased nuclear and cytoplasmic Ca\textsuperscript{2+} signal variability following prolonged exposure to caffeine (1 mmol/L, 16 hours) was calculated. Data are given as the mean±SEM (n=4 experiments, 20 cells per experiment). *P<0.05 when compared with nuclear Ca\textsuperscript{2+} signal variability in HL-1 cells and those expressing RyR2\textsuperscript{24/24}.

Apoptosis was markedly increased in caffeine-activated cells expressing RyR2\textsuperscript{30/24} (Figure 6A). Notably, although RyR2\textsuperscript{30/24} reduced nuclear and cytoplasmic Ca\textsuperscript{2+} fluxes in nonstimulated cells, and reduced the basal levels of apoptosis (Figure 6A), RyR2\textsuperscript{30/24} did not protect cells from apoptosis following prolonged caffeine exposure (Figure 6A). In contrast, apoptosis was dramatically reduced in cells expressing RyR2\textsuperscript{24/24} following caffeine stimulation (Figure 6A). Thus our data reveal a clear link between the magnitude of RyR2-dependent nuclear and cytoplasmic Ca\textsuperscript{2+} fluxes and the extent of apoptosis (Figure 6B), a finding that was reinforced by the pronounced anti-apoptotic effects of channel inhibition using ryanodine (Figures 5C and 6).

These data established a clear functional consequence of 24-bp exon insertion, namely a markedly reduced caffeine-induced Ca\textsuperscript{2+} flux that was innately linked to a reduced apoptotic propensity. Because the Bcl-2 family of proteins have been shown to be involved in the signaling of apoptosis following agonist-triggered RyR2-dependent Ca\textsuperscript{2+} release,\textsuperscript{17} we investigated whether the antiapoptotic effects of 24-bp splice insertion following prolonged caffeine exposure was linked to alterations in the expression or posttranslational modification of Bcl-2. We did not detect significant changes in Bcl-2 transcription or in the cellular levels of Bcl-2 protein in cells expressing RyR2 splice variants (Figure 7A and 7B). However, we determined significantly increased levels of Bcl-2 phosphorylation in RyR2\textsuperscript{30/24} and RyR2\textsuperscript{24/24} cells. These data suggest that the protection from apoptosis conferred by expression of RyR2 containing the 24-bp splice insertion may be linked to an alteration in the phosphorylation status of Bcl-2.

**RyR2 Alternative Splicing Exhibits Developmental Regulation and Tissue and Species Specificity**

We determined the species, tissue, and developmental profile of RyR2 alternative splicing. In human cardiac tissue, we identified pronounced developmental regulation of 30-bp–containing mRNA transcripts, and this insertion was far more abundant in embryonic heart (>90%) than in adult heart tissue, where it accounted for <20% of the total RyR2 (Figure 7A). The disparate relative abundance of the 30-bp insertion in human and mouse embryos strongly indicated a species-dependent regulation of this variant in developing mammalian heart (Figure 7C and 7D). We did not detect the 30-bp insertion in mRNA transcripts derived from adult rat, rabbit, and mouse hearts, and thus the exclusive detection of this variant in adult human heart may represent an intriguing feature of human cardiac regulation (Figure 7D). RyR2 is also the predominant isofrom in brain, and, in stark, contrast to its profile in adult heart, the 30-bp insertion was abundant in adult human hippocampus, suggesting that, in humans, alternative splicing of the 30-bp exon exhibits tissue-specific regulation (Figure 7B). In contrast, mRNA transcripts containing the 24-bp splice variant were detected at comparable levels in all species investigated (≈15% to 25% of total RyR2) (Figure 7D), and we found no evidence of its developmental regulation (Figure 7C). Our screening strategy did not resolve the abundance of RyR2 containing both 30-bp and 24-bp insertions (RyR2\textsuperscript{30/24}) in mammalian tissues, although our functional characterization suggests that channels formed from RyR2\textsuperscript{30/24} are indistinguishable from those of RyR2\textsuperscript{24/24}.

**Discussion**

We investigated the role of RyR2 splice variants in cardiomyocytes and present the first evidence that developmentally regulated, tissue-specific splice variants of RyR2 have profound effects on organelle structure, Ca\textsuperscript{2+} signaling, and susceptibility to apoptosis. In skeletal myotubes, nuclear Ca\textsuperscript{2+} signaling is shaped via RyR1 localized to NR projections deep into the nucleus,\textsuperscript{14} and nuclear and cytoplasmic Ca\textsuperscript{2+} release events in cardiomyocytes are markedly different.\textsuperscript{18} We now demonstrate that in HL-1 cardiomyocytes, all RyR2 variants exhibited NR localization, although the 24-bp inser-
tion was essential for the localization of this RyR2 splice variant to a distinct intranuclear structure that was morphologically identical to an intranuclear GA, presently termed INGA (Figures 2 and 3). Nuclear Golgi “tendrils” have been previously identified in atrial cardiomyocytes, and tubular transnuclear structures that modulate intracellular Ca\(^{2+}\) signaling have been reported, suggesting that INGA is not an idiosyncratic feature of HL-1 cells (supplemental Figure III). However, our data suggest that currently unknown molecular mechanisms may act as “gate-keepers” to selectively incorporate RyR2 channels containing the 24-bp insertion into this compartment. Consequently, an important conclusion of the present study is that alternative splicing contributes to the intracellular segregation of RyR2 variants. The role of alternative splicing in determining RyR targeting to other cellular compartments including mitochondria, cytoplasmic GA, and plasma membrane is unknown. The protein sequences encoded by the 30- and 24-bp insertions do not represent known organelle targeting motifs, but they do exhibit limited sequence homology with domains present within K\(^{+}\) channels and ankyrin (Figure IV). The 30-bp insertion deletes a putative protein kinase C phosphorylation site found at 1479Ser-Ile-Lys1481, although the functional significance of this remains to be determined.

The present study provides evidence that RyR2 splice variants fundamentally contribute to shaping nuclear and cytoplasmic events, a significant finding given that spatially distinct Ca\(^{2+}\) release events underpin altered gene transcription. Consequently, our data suggest that the precise control of cardiomyocyte Ca\(^{2+}\) handling via differential RyR2 splice variant expression may play an important role in modulating diverse aspects of cardiac cell signaling, rather than in simply controlling the mechanics of heart muscle contraction. We do not yet know the precise basis for the differential Ca\(^{2+}\) release mediated by the distinct RyR2 splice variants, although we interpret our results to suggest that cell-compartment–specific regulation by currently unknown nuclear and/or cytoplasmic factors (including the relative contribution of ER-, NR-, GA-, and INGA-derived Ca\(^{2+}\) sources, the differences in subcellular architecture, and differential nuclear and cytoplasmic protein–protein interactions) may contribute to the distinct Ca\(^{2+}\) modulation.

We reveal a strong link between reduced RyR2-dependent Ca\(^{2+}\) fluxes following 24-bp insertion and the protection from caffeine-induced apoptosis (Figures 5 and 6). This important finding is entirely consistent with the reduced channel activity determined in some 1,4,5-trisphosphate receptor and RyR3 splice variants, although further work is needed to conclusively determine whether the INGA localization of the 24-bp–containing splice variant is a critical determinant of the observed antiapoptotic effects. Importantly, our data show that the suppression of caffeine-evoked Ca\(^{2+}\) fluxes mediated by RyR2 containing the 24-bp splice insertion was associated with altered Bcl-2 phosphorylation. This new evidence indicates that the interplay between Ca\(^{2+}\) flux, Bcl-2 phosphorylation, and apoptosis can be modulated by the specific expression of distinct RyR2 splice variants. The precise mechanisms through which Bcl-2 family proteins transduce RyR2-dependent Ca\(^{2+}\) fluxes in apoptotic signaling remain to be determined, and one should consider that caffeine-evoked apoptosis may be attributable to other mechanisms, in addition to perturbations in Ca\(^{2+}\) fluxes,

![Figure 6](image_url)

**Figure 6.** Expression of RyR2 containing the 24-bp splice insertion protects cells from caffeine-induced apoptosis. A, The extent of apoptosis vs necrosis in resting and caffeine-activated cells is shown. *P<0.05 and #P<0.001, respectively, when compared with nontransfected HL-1 cardiomyocytes. B, The mode of cell death was plotted against the Ca\(^{2+}\) signal flux (see Figure 5) in nuclear and cytoplasmic compartments in nonstimulated (−) and caffeine-activated (1 mmol/L, 16 hours) (+) cells expressing RyR2 splice variants (color coded as shown). Data are plotted as the mean±SEM (n=4, >20 cells per experiment), and R\(^2\) values are given. In A and B, the effects of ryanodine inhibition of RyR2 \(^{-}\) is given (ry).
including the activation of a number of cAMP-dependent pathways.

Although we show that developmentally regulated RyR2 splicing occurs in human heart (Figure 7), the relative abundances of 30-bp and 24-bp insertions identified in embryonic and adult transcripts do not provide an accurate insight into the channel subunit stoichiometry occurring in vivo. The adult human heart is a highly heterogeneous tissue composed of numerous cell types tailored for specialized function. It is possible that the 2 RyR2 splice variants can be coexpressed in the same cells, or differentially distributed in distinct cell types within the myocardium. Furthermore, we do not know the precise stoichiometric arrangement of the RyR2 tetramers generated in our experiments, although the approximate 4-fold overexpression of recombinant RyR2 would predict that most recombinant RyR2 channels exist in homotetrameric combina
tion. Notably, the 24-bp insertion appeared to be “dominant,” because the functional characteristics of RyR2 containing both 24- and 30-bp splice insertions were indistinguishable from RyR2 containing only the 24-bp insertion.

The Therapeutic Potential of Manipulating Cardiac Phenotype by Alternative Splicing

During development, cell-specific regulatory pathways dictate the intrinsic susceptibility of the cells to die. Embryonic human hearts were characterized by very high levels of 30-bp–containing transcripts, splice variants that do not protect cells from increased Ca\(^{2+}\) fluxes and apoptosis. The abundance of this variant in embryonic heart (Figure 8) may limit the incorporation of antiapoptotic RyR2 containing the 24-bp insertion into functional tetramers, and we speculate that the high levels of RyR2 containing the 30-bp splice insertion may indirectly confer apoptotic susceptibility during cardiac development. Apoptosis is a critical determinant of embryonic myocardial architecture, but it may also be important in normal adult heart remodeling. The long-term adaptive value of apoptosis in the adult myocardium, and its place as a target for therapeutic intervention, remains to be determined. The adult heart can be repaired by gene-based reprogramming of embryonic signaling patterns, and thus our demonstration that cardiomyocyte Ca\(^{2+}\) signaling and phenotype can be fine-tuned by the expression of functionally distinct RyR2 splice variants potentially represents a novel approach to future cardiac therapies.

Limitations of Study

We have not succeeded in generating antibodies that specifically recognize the distinct RyR2 splice variants, and it is not currently possible to investigate the developmental profiles and intracellular localization of these variants in native cardiac tissue, or primary cell cultures at the protein level. Accordingly, at the present time, a functional characterization of RyR2 splice variants is restricted to heterologous expression systems. Despite this, HL-1 cardiomyocytes retain the contractile and phenotypic properties of adult cardiomyocytes and express recombinant RyR2 that, in our hands, is indistinguishable from the endogenous protein. Thus HL-1 cells represent the best heterologous system currently available for evaluating the role of RyR2 splice variants in cardiomyocyte Ca\(^{2+}\) signaling. Analysis of HL-1–derived mRNA transcripts (at passage nos. 37, 55, and 87) showed that endogenous RyR2 lacked the 30- and 24-bp insertions (0/18 and 0/25 transcripts, respectively), and although this is entirely consistent with the progressive loss of RyR1 splice insertions during skeletal myotube culture, HL-1 cells may not reflect the RyR2 splicing events that occur in the myocardium in vivo.

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Disclosures

None.

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