J Muscle Res Cell Motil DOI 10.1007/s10974-017-9470-z

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# Physiology and pathophysiology of excitation–contraction coupling in skeletal muscle: the functional role of ryanodine receptor

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<sup>5</sup> Received: 7 February 2017 / Accepted: 6 April 2017

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Abstract Calcium (Ca<sup>2+</sup>) release from intracellular stores
plays a key role in the regulation of skeletal muscle contraction. The type 1 ryanodine receptors (RyR1) is the
major Ca<sup>2+</sup> release channel on the sarcoplasmic reticulum (SR) of myocytes in skeletal muscle and is required
for excitation-contraction (E-C) coupling. This article explores the role of RyR1 in the skeletal muscle physiology
and pathophysiology.

Keywords Calcium · Excitation-contraction coupling ·
 Muscular dystrophy · RyR1 · Skeletal muscle

# 17 Introduction

Ryanodine receptors (RyRs) are intracellular calcium 18 (Ca<sup>2+</sup>) release channels located on the endo/sarcoplasmic 19 reticulum (ER/SR) (Flucher et al. 1993), a heterogene-20 ous intracellular compartment consisting of a network of 21 tubules (Chen et al. 2013; Brochet et al. 2005) represent-22 ing the major  $Ca^{2+}$  reservoir within the cell. There are three 23 subtypes of RyRs in mammalian tissues: RyR1 and RyR2 24 are required for skeletal muscle and cardiac excitation-con-25 traction coupling (E-C coupling), respectively (Marks et al. 26

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1989; Otsu et al. 1990), and are also expressed in nonmuscle tissues (Awad et al. 1997); RyR3, originally identified in the brain (Nakashima et al. 1997), is also widely expressed (Zhang et al. 2011).

RyR1 facilitates the rapid and coordinated release of 31 Ca<sup>2+</sup> from SR stores to activate skeletal muscle contrac-32 tion. EC coupling is the process that converts electrical sig-33 nals and rising Ca<sup>2+</sup> levels into mechanical output (muscle 34 contraction). RyRs are highly regulated for precise control 35 and Ca<sup>2+</sup> plays the key signaling role in activating the chan-36 nel and amplifying the signal (Endo et al. 1970). In this 37 process, depolarization of the plasma membrane activates 38 L-type voltage-gated calcium channels (Ca<sub>v</sub>), which signal 39 RyRs located on the SR to gate open and release Ca<sup>2+</sup> to 40 activate muscle contraction (Rios and Brum 1987; Gor-41 don et al. 2000; Tobacman 1996; des Georges et al. 2016). 42 RyR is a 2.2 mega Dalton homotetramer, composed of four 43 ~5000 residue protomers (Marks et al. 1989; Santulli and 44 Marks 2015), making it the largest known ion channel (des 45 Georges et al. 2016; Santulli and Marks 2015; Zalk et al. 46 2015). The narrow transmembrane core and larger cyto-47 plasmic shell result in a mushroom shaped structure (des 48 Georges et al. 2016; Zalk et al. 2015; Hwang et al. 2012). 49 The large shell interacts with other receptors and forms 50 much of the regulatory mechanism for the channel, allow-51 ing a range of stimuli to exert precise control over opening 52 (Marks et al. 1989; des Georges et al. 2016; Santulli and 53 Marks 2015; Zalk et al. 2015; Brillantes et al. 1994; Marx 54 et al. 1998, 2000; Marks 2003; Reiken et al. 2003; Lehnart 55 et al. 2005; Huang et al. 2006; Bellinger et al. 2009; Kush-56 nir et al. 2010; Shan et al. 2010; Andersson et al. 2011; 57 Lanner et al. 2010). The core of RyR houses the approxi-58 mately 90 Å long pore responsible for passage of Ca<sup>2+</sup> from 59 the ER/SR to the cytoplasm (des Georges et al. 2016; Yan 60 et al. 2015). This cation channel is actually poorly selective 61

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Journal: Large 109/4 Article No: 94/0 Pages: 9 MS Code: JUKE-D-17-00004 Dispatch: 9-4-2017	Journal : Large 10974         Article No : 9470         Pages : 9         MS Code : JURE-D-17-00004         Dispatch : 9
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for  $Ca^{2+}$  (~7-fold selective for  $Ca^{2+}$  vs K<sup>+</sup>) and displays an 62 exceptionally large single channel conductance (Santulli 63 and Marks 2015). 64

We recently solved the high-resolution structure of 65 RyR1 using cryogenic electron microscopy (cryo-EM) (des 66 Georges et al. 2016; Zalk et al. 2015), confirming that it 67 adopts a fourfold symmetric mushroom-like superstructure, 68 with the large 'cap' (about 80% of the mass) located in the 69 cytosol and the 'stalk' embedded in the ER/SR membrane, 70 with six transmembrane helices (S1-S6) per protomer sur-71 rounding the central pore (des Georges et al. 2016). Each 72 protomer is built around an extended scaffold of alpha-sole-73 noid repeats which include an aminoterminal, a bridging, 74 and a core solenoid (des Georges et al. 2016; Zalk et al. 75 2015). At the extreme outer corners of the tetramer there 76 are three SPRY domains and two pairs of RyR repeats, 77 RY12 and RY34, the latter containing a regulatory protein 78 kinase A (PKA) phosphorylation site (Marx et al. 2000). 79 The RyR1 pore domain most closely resembles that of the 80 voltage-gated sodium channel (NavAB) and presents a sin-81 gle cytosolic constriction in the ion conduction pathway, at 82 the S6 bundle crossing (Zalk et al. 2015). Glycine residues 83

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in the pore-lining helices may operate as "hinges" to facili-84 tate the orientation of the cytoplasmatic extension of S6 in 85 order to modulate the aperture of the channel. In particular, 86 Gly<sup>4934</sup> is conserved in all RyR isoforms and in the IP3R. 87

### **RvR** macromolecular complex

The ER/SR of most cell types contains two types of 89 intracellular Ca<sup>2+</sup> release channels: the ryanodine receptors (RyRs) and the inositol 1,4,5-trisphosphate recep-91 tors (IP3Rs) (Santulli and Marks 2015; Go et al. 1995; 92 Yuan et al. 2016; Santulli 2017). There is ~40% homol-93 ogy between the RyR and IP3R in the putative transmem-94 brane regions (Marks et al. 1989, 1990; Santulli 2017), a 95 sequence similarity sufficient to indicate that these two 96 channels evolved from a common ancestral cation release 97 channel in unicellular species. The structural homology 98 between RyR1 and IP3R1 is depicted in Fig. 1. 99

RyR was named based on its purification using the high 100 affinity plant alkaloid ryanodine (Rogers et al. 1948), an 101 agent known to profoundly alter intracellular Ca<sup>2+</sup> handling 102 (Fairhurst and Hasselbach 1970). Indeed, when bound to 103



Fig. 1 Structural homology between the intracellular Ca<sup>2+</sup> release channels IP3R1 (top) and RyR1 (bottom). In a, c channels are viewed from the ER/SR lumen: in c. arrowheads indicate Calstabin

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RyR at low concentrations ryanodine locks the channel in a 104 half open state, thereby resulting in depletion of Ca<sup>2+</sup> from 105 the SR and subsequent interruption of E-C coupling. This 106 explains the historical use of extracts from the Ryania plant 107 family by natives of South and Central America as poison 108 for blow darts: the release of SR Ca<sup>2+</sup> via the locked open 109 RyRs causes tetany, and at high concentrations ryanodine 110 blocks the channel (Rogers et al. 1948). RyR is normally 111 closed at low cytosolic [Ca<sup>2+</sup>] (~100-200 nM); at sub-112 micromolar cytosolic [Ca<sup>2+</sup>] Ca<sup>2+</sup> binds to high-affinity 113 binding sites on RyR increasing the open probability  $(P_{o})$ 114 of the channel (Bezprozvanny et al. 1993). Channel activ-115 ity is maximal at cytosolic  $[Ca^{2+}] \sim 10 \ \mu M$  while elevating 116 cytosolic  $[Ca^{2+}]$  beyond this point leads to a reduction in P<sub>o</sub> 117 (Bezprozvanny et al. 1993; Copello et al. 1997; Laver et al. 118 1995). 119

The large and complex structure of RyR contains func-120 tion-modifying phosphorylation sites and protein-binding 121 domains, providing an attractive target for disease inter-122 vention (des Georges et al. 2016; Santulli and Marks 2015; 123 Zalk et al. 2015; Brillantes et al. 1994; Marx et al. 1998, 124 2000; 2001; Marks 2003; Lehnart et al. 2005; Kushnir et al. 125 2010; Marks et al. 2002). RyRs are macromolecular signal-126 ing complexes, in which multiple proteins bind to a domain 127 of the channel modulating its function (Marks et al. 1989, 128 2002). The Ca<sup>2+</sup> stabilizing proteins calstabin1 (Calcium 129 channel stabilizing binding protein, previously known as 130 FKBP12) and calstabin2 (FKBP12.6) are peptidyl-pro-131 pyl-cis-trans isomerases that associate via amphiphilic 132  $\beta$ -sheet structures with RyR1 and RyR2, respectively, such 133 that one calstabin protein is bound to each RyR monomer 134 (des Georges et al. 2016; Zalk et al. 2015; Jayaraman et al. 135 1992; Timerman et al. 1993; Xin et al. 1995; Yuan et al. 136 2014), in order to modulate the channel gating through pro-137 tein-protein interactions (Brillantes et al. 1994) and pre-138 vent pathological intracellular Ca<sup>2+</sup> leak that cause diseases 139 (Marks 2003; Huang et al. 2006). Calstabin1 and calstabin2 140 differ at only 18 positions out of 108 residues. We identi-141 fied the calstabin-binding loop as part of the aminotermi-142 nal subdomain of the bridging solenoid (Zalk et al. 2015). 143 Calstabin binding may rigidify the interface between such 144 a subdomain with SPRY1-2, thereby stabilizing the con-145 nection with the cytosolic regulatory domains and eventu-146 ally altering the relative orientation of these domains (Zalk 147 et al. 2015). Highly conserved leucine-isoleucine zipper 148 motifs in RyR2 form binding sites for adaptor proteins 149 that mediate binding of other proteins (Marx et al. 2001; 150 Marks et al. 2002), including kinases (e.g. PKA) (Reiken 151 et al. 2003; Shan et al. 2010) CaMKIIdelta (Kushnir et al. 152 2010) and phosphatases (e.g. PP1 and PP2A). Specifi-153 cally, the adaptor protein mAKAP mediates the binding 154 of PKA and phosphodiesterase PDE43, whereas PP1 and 155 PP2A are targeted to RyR2 via spinophilin and PR130, 156

respectively (Marx et al. 2000; Lehnart et al. 2005). All of 157 the above mentioned proteins regulate the phosphorylation-158 dephosphorylation of RyR2 in Ser<sup>2808</sup> (Shan et al. 2010) in 159 response to stress (Andersson et al. 2011; Shan et al. 2010; 160 Liu et al. 2012; Tester et al. 2007). Other channels are also 161 regulated by stress signals including the voltage-gated Ca<sup>2+</sup> 162 channels (Maki et al. 1996). RyRs are also regulated by 163 oxidation and nitrosylation (Shan et al. 2010; Andersson 164 et al. 2011; Santulli 2017; Fauconnier et al. 2010). Other 165 modulatory proteins complex directly and indirectly with 166 RyR, including sorcin (Farrell et al. 2004), calmodulin 167 (Meissner and Henderson 1987), homer (Feng et al. 2002), 168 histidine-rich Ca<sup>2+</sup> binding protein (Lee et al. 2001), triadin 169 (Rossi et al. 2014), junctin (Zhang et al. 1997), and calse-170 questrin (Ohkura et al. 1998). 171

# Intracellular Ca<sup>2+</sup> leak

Ca<sup>2+</sup> finely regulates innumerable events as muscle con-173 traction, secretion, and gene transcription (Santulli and 174 Marks 2015; Santulli 2017; Ringer 1883; Zetterstrom and 175 Arnhold 1958; Javaraman and Marks 2000). Cytosolic Ca<sup>2+</sup> 176 signals are produced by rapidly increasing the concentra-177 tion of free Ca<sup>2+</sup> ions (Blaustein 1993) by opening channels 178 permeable to Ca<sup>2+</sup> either in the surface cell membrane or in 179 the membranes of intracellular organelles containing high 180 Ca<sup>2+</sup> concentrations. Amplification of external stimuli by 181 triggering the release of intracellular Ca<sup>2+</sup> stores represents 182 a common signaling mechanism in the cell. The key role of 183 RyRs in the rapid and voluminous release of  $Ca^{2+}$  from the 184 SR during E-C coupling is well known. Importantly, RyRs 185 are also crucially involved in maintaining Ca<sup>2+</sup> homeostasis 186 in the cell under resting conditions. Stress-induced remod-187 eling of RyRs results in leaky channels and the inappro-188 priate release of  $Ca^{2+}$  from the intracellular stores into the 189 cytosol, contributing to the pathophysiology of diverse dis-190 orders including heart failure, cardiac arrhythmias, muscu-191 lar dystrophy, diabetes, and cognitive dysfunction (Brillan-192 tes et al. 1994; Marx et al. 1998, 2000, 2001; Marks 2003; 193 Reiken et al. 2003; Lehnart et al. 2005; Huang et al. 2006; 194 Bellinger et al. 2008, 2009; Kushnir et al. 2010; Shan et al. 195 2010; Andersson et al. 2011, 2012; Santulli 2017; Marks 196 et al. 2002; Liu et al. 2012; Tester et al. 2007; Faucon-197 nier et al. 2010; Ward et al. 2003; Umanskaya et al. 198 2014; Matecki et al. 2016; Santulli et al. 2015a, 2015b; 199 Xie et al. 2013, 2015). 200

# **Skeletal muscle**

E–C coupling is similar in skeletal and cardiac muscle 202 but there are important differences (Santulli 2017). 203 Briefly, whereas in the heart a depolarizing Na<sup>+</sup> current 204 activates  $Ca^{2+}$  influx via the L-type  $Ca^{2+}$  channel 205 (LCC,  $Ca_v 1.2$ ),

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which in turn activates the RyR2 isoform via Ca<sup>2+</sup>-induced 206  $Ca^{2+}$  release (Fabiato and Fabiato 1975), the depolariza-207 tion of skeletal myocytes involves a protein-protein inter-208 action (Rios and Brum 1987) across the junctional cleft 209 between the dihydropyridine receptor (Ca, 1.1) on special-210 ized invaginations of the sarcolemma (transverse tubules) 211 and RyR1 on the SR membrane (terminal cisternae), lead-212 ing to  $Ca^{2+}$  release (Nelson et al. 2013). Both morphologic 213 and electrophysiological data are consistent with the con-214 cept that four Ca<sub>2</sub>1.1s interact with a single RyR1 tetramer 215 (one Ca, 1.1 binding to each RyR1 subunit). However, Fran-216 zini-Armstrong and Kish determined that a cluster of four 217 Ca<sub>v</sub>1.1 overlie only every other RyR1 tetramer (Franzini-218 Armstrong and Kish 1995). Reconciling those findings, 219 we have demonstrated coupled gating of RyR1 (Marx et al. 220 1998), which provides a mechanism by which RyR1 chan-221 nels that are not associated with Ca<sub>v</sub>1.1 can be regulated. 222 RyRs were initially observed in skeletal muscle, visualized 223 in electron micrographs as large electron-dense masses 224 located along the face of the SR terminal cisternae, which 225 is closely apposed to transverse tubule membranes to form 226 a structure named triad junction (Santulli 2017; Block et al. 227 1988). Therefore, the RyRs were initially termed triad junc-228 tional foot proteins (Wagenknecht et al. 1989; Brandt et al. 229 1990). Noda and colleagues provided the in vivo evidence 230 for a functional role of RyR1 in E-C coupling, engineer-231 ing a mouse lacking exon 2 of RyR1 and demonstrating that 232 such a mouse exhibits severe skeletal muscle abnormalities 233 and dies perinatally due to respiratory failure (Takeshima 234 et al. 1994). Subsequent ultrastructural studies of hind 235 limb and diaphragm muscles demonstrated the absence of 236 RyR1-Cav1.1 complexes (Takekura et al. 1995), which are 237 essential for a proper E-C coupling in the skeletal muscle 238 (Nakai et al. 1996). 239

RyR1 dysfunction has been described in both inher-240 ited and acquired muscle disorders (Bellinger et al. 2008; 241 Andersson et al. 2012). Central core disease (CCD) and 242 malignant hyperthermia (MH) represent the best examples 243 of RyR1 channelopathies in the skeletal muscle. 244

#### Central core disease (CCD) 245

CCD is a congenital myopathy first described in 1956 246 (Magee and Shy 1956), characterized by the presence 247 of tissue cores with reduced oxidative activity in type I 248 myofibers, which results in progressive muscle weakness 249 (Sewry et al. 2002). Common symptoms include hypoto-250 nia, delayed motor milestones, and skeletal abnormalities 251 including congenital hip dislocation and scoliosis. Over 60 252 different RyR1 mutations have been linked to CCD, which 253 presents during infancy as delayed motor development 254 and hypotonia. CCD occurs in 1:100,000 live births, and 255

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comprises 16% of total congenital myopathies (Jungbluth 2007).

We now know that RyR1 mutations cause the disorder 258 which should be reclassified as RyR1 myopathies. There 259 are no established therapeutics for RvR1 myopathies 260 (Witherspoon and Meilleur 2016). The phenotypic presen-261 tation is quite variable ranging from near normal to neona-262 tal death. 263

The histopathological appearance of CCD is most 264 closely linked to dominant RyR1 mutations (often mis-265 sense) clustered (Fig. 2) in disease causing "hot spots" in 266 RyR1 (Quane et al. 1993; Zhang et al. 1993; Lynch et al. 267 1999; Monnier et al. 2000; Scacheri et al. 2000), whereas 268 RyR1 mutations (often truncating) causing recessive RyR1-269 related myopathies, including multi-minicore disease, cen-270 tronuclear myopathies, and congenital fiber-type disproportion, are evenly distributed throughout the entire RYR1 272 coding sequence (Amburgey et al. 2013; Klein et al. 2012). 273

# Malignant hyperthermia (MH)

MH is a pharmacogenetic disorder, inherited in an auto-275 somal dominant fashion and causes inhaled anesthetic-276 induced deaths in otherwise healthy individuals (Censier 277 et al. 1998). MH episodes are typically rapid and severe, 278 reaching core body temperatures of 43 °C, leading to organ 279 failure and death if not rapidly treated. Susceptibility can be 280 determined in vitro by measuring the contractile response 281 to caffeine or halothane in biopsied muscle fibers. Over 100 282 RyR1 mutations have been associated with MH, involving 283 inappropriate activation of RyR1, which causes uncon-284 trolled release of SR Ca<sup>2+</sup> and muscle contractions. MH 285 occurs at a rate of 1:50,000-100,000 adults and 1:15,000 286 children undergoing anesthesia; some studies have sug-287 gested a much more frequent rate of 1:5000 adults with MH 288 susceptible mutations occurring at 1:3000 (Rosenberg et al. 289 2007; Monnier et al. 2002). The exact prevalence of MH 290 susceptibility is difficult to determine since the syndrome 291 only becomes apparent after exposure to triggering agents 292 including volatile anesthetic agents such as halothane, iso-293 flurane, sevoflurane, desflurane, enflurane and the neuro-294 muscular blocking agent succinylcholine (Larach 2007). 295 A related syndrome referred to as porcine stress syndrome 296 is found in certain lines of domestic swine where stressed 297 pigs undergo stress-induced hyperthermia (Nelson and 298 Bee 1979). Alterations in <sup>3</sup>H-ryanodine binding properties 299 in porcine MH samples provided evidence linking RyR1 300 dysfunction to the disease (Mickelson et al. 1988), which 301 was later confirmed by biophysical experiments (Fill et al. 302 1990). 303

Although dantrolene is an established therapeutic that 304 quickly resolves MH episodes, mortality from this event 305 remains at approximately 7% and a validated mechanism 306

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**Fig. 2** RyR1 with localization of the reported mutations for CCD (a-c) and MH (d-f). **a** and **d** are the full tetramer viewed top down from the cytosol, while **b** and **e** are rotated 90° to show the narrow transmembrane core and the larger cytoplasmic shell (an additional 45° rotation along the vertical axis was also performed). In **c**, **f** one

of action for dantrolene has yet to be reported (Paul-Pletzer 307 et al. 2002; Zhao et al. 2001). This remains a concern for 308 otherwise healthy individuals harboring these mutations 309 (Fill et al. 1990). Mutations causing MH are autosomal 310 dominant and typically seen (Fig. 2) in the central and 311 N-terminal clusters. Another MH mutation hotspot is at the 312 inter-protomer contacts between the N-terminal domains A 313 and B, which are disrupted in channel opening (Kimlicka 314 et al. 2013). 315

Notably, there is no clear division between MH and 316 RyR1 myopathies and some RyR1 mutations have been 317 linked to a combined MH and RyR1 myopathy phenotype 318 319 (Zhou et al. 2007). Importantly, the mutated codons giving rise to MH and RyR1 myopathies tend to cluster in three 320 specific regions of the RyR1 gene (Fig. 2) correspond-321 ing to the following domains in the amino acid sequence: 322 regions 1 (C35-R614) and 2 (D2129-R2458) reside in the 323 myoplasmic foot domain of the protein, whereas region 3 324 (I3916-G4942) is located in the transmembrane/luminal 325 region of the highly conserved carboxy-terminal domain, 326 important for allowing Ca<sup>2+</sup> flux through the channel 327 (Zalk et al. 2015). Mutations in RyR1 are also associ-328 ated with other rare RyR1 related congenital myopathies 329 including centronuclear myopathy, multi-minicore dis-330 ease, Samaritan myopathy, heat/exercise induced exertional 331

protomer is depicted (following a 60° rotation), demonstrating the high proportion of interprotomer mutation sites (in *pink*). Interestingly, CCD mutations typically occur in the pore forming C-terminal domain, while MH mutations occur in central and N-terminal clusters

rhabdomyolysis, congenital fiber-type disproportion, lateonset axial myopathy, and atypical periodic paralyses (Bharucha-Goebel et al. 2013; Zvaritch et al. 2009; Ferreiro et al. 2002; Capacchione et al. 2010; Zhou et al. 2010; Inui et al. 1987; Takeshima et al. 1989; Loseth et al. 2013). 336

# Intracellular Ca<sup>2+</sup> leak and muscular dystrophy

We recently demonstrated that intracellular Ca<sup>2+</sup> leak via 338 RyR1 represents an essential feature of different forms of 339 muscular dystrophy (MD), including Duchenne muscu-340 lar dystrophy (Bellinger et al. 2009) and limb-girdle (or 341 Erb's) MD (Andersson et al. 2012). Specifically, RyR1 342 from a Duchenne muscular dystrophy murine model (mdx 343 mouse) was excessively cysteine nitrosylated and the RyR1 344 complex was depleted of calstabin1, leading to increased 345 spontaneous RyR1 openings and reduced specific muscle 346 force (Bellinger et al. 2009). Similar findings were obtained 347 when evaluating RyR1 in  $\beta$ -sarcoglycan-deficient mice, 348 an established model of limb-girdle muscular dystrophy 349 (Andersson et al. 2012). Thus, we demonstrated common 350 mechanisms of stress-induced remodeling of RyR1, includ-351 ing post-translational modifications of the channel and dis-352 sociation of the stabilizing subunit calstabin1, in two major 353 disorders that weaken the muscular system hampering 354

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Journal : Large 10974	Article No : 9470	Pages : 9	MS Code : JURE-D-17-00004	Dispatch : 9-4-2017

locomotion and that remain without effective pharmacological treatment. We demonstrated in both cases that
stabilizing the RyR1-calstabin1 association using a novel
small molecule Rycal called S107 improved muscle function (Bellinger et al. 2009; Andersson et al. 2012), thereby
providing an innovative therapeutic target and potential
options for the treatment of muscular dystrophy.

In conditions of strenuous muscular stress or in a dis-362 ease such as heart failure, both of which are characterized 363 by chronic activation of the sympathetic nervous system 364 and increased production of reactive oxygen and nitrogen 365 species (Santulli 2014; Dalla Libera et al. 2005; Santulli 366 and Iaccarino 2016), skeletal muscle function is impaired, 367 possibly due to remodeling of RyR1 and impaired E-C 368 coupling. We have shown in both an animal model as well 369 as in exercising humans that chronic BAR stimulation and 370 depletion of calstabin1 from RyR1 plays a role in contrac-371 tile failure and muscle fatigue, defined as a decline in abil-372 ity of a muscle to generate force during sustained exercise 373 (Bellinger et al. 2008). Consistent with these observations, 374 we have demonstrated that the remodeling of RyR1 plays a 375 role in sarcopenia or age-dependent loss of muscle function 376 (Andersson et al. 2011) and we were able to reduce RyR1 377 dysfunction and improve skeletal muscle function in aged 378 mice (2 years old) by genetically enhancing mitochondrial 379 antioxidant activity (Umanskaya et al. 2014). 380

Since skeletal muscle dysfunction, as observed in HF or 381 muscular disorders, remains without effective treatment, 382 drugs that restore RyR Ca2+ release function represent 383 promising candidates. In this sense, Rycal treatment could 384 be ideal in conditions that impair both cardiac and skeletal 385 muscle function. Indeed, as well as muscular RvR1 under-386 goes post-translational modifications in HF (Reiken et al. 387 2003; Ward et al. 2003), remodeling of the cardiac RyR2 388 has been also reported in murine models of Duchenne mus-389 cular dystrophy, triggering ventricular arrhythmias (Fau-390 connier et al. 2010). 391

# RyR1 mutations: clinical significance and structural effects

Over 300 mutations have been mapped to RyRs that are 394 implicated in human diseases and 200 more that do not 395 result in modified channel function. The disease causing 396 mutations are most often found in hotspots, including the 397 N-terminal ( $\sim$ 1–600), the central ( $\sim$ 2000–2600) and the 398 C-terminal (~4000-5000) regions. High-resolution cryo-399 EM reconstructions have recently become available making 400 it possible to see how these hotspots are localized, some in 401 the channel pore and others in the inter-protomer and inter-402 domain interfaces (Tung et al. 2010). The phosphorylation 403 domain is another hotspot for disease causing mutations 404 (Yuchi et al. 2012). 405

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Proper post-translational modifications and interac-406 tion with other proteins are also critical for RvR function. 407 Several human disorders are linked to improper phospho-408 rylation or oxidation of RyRs including ventilator-induced 409 diaphragmatic dysfunction (VIDD) and Duchenne mus-410 cular dystrophy (DMD). VIDD involves diaphragm mus-411 cle weakness after extended mechanical ventilation and 412 has been linked to oxidation of RyR (Matecki et al. 2016). 413 RyR1 cysteine-nitrosylation has been shown to have a 414 role in DMD (Bellinger et al. 2009). An age-dependent 415 increase in cysteine-nitrosylation occurs with dystrophic 416 changes in the muscle, depleting the RyR1 macromolecu-417 lar complex of calstabin1 resulting in Ca<sup>2+</sup> leak. This find-418 ing links muscle inflammation and Ca<sup>2+</sup> leak in the patho-419 genesis of DMD (Tidball and Villalta 2009). Indeed, in 420 inflamed tissues there is an increased expression of induc-421 ible nitric oxide synthase (iNOS), which binds to RyR1 422 leading to Ca<sup>2+</sup> leak and eventually to the activation of 423 Ca<sup>2+</sup>-dependent proteases (calpains) that promote muscle 424 damage and wasting. 425

These alterations affect the function of RyRs, but the 426 direct impact on the tetrameric assembly has yet to be 427 shown in structural studies. Due to the critical requirement 428 of the channel for proper muscle function, mutations that 429 severely destabilize or significantly alter the channel struc-430 ture most likely lead to non-viable embryos. These muta-431 tions most often lead to changes in the open probability of 432 the channel, leading to Ca<sup>2+</sup> leak. This hypersensitive acti-433 vation can come from mutations on either the luminal or 434 the cytosolic side of the receptor (Tong et al. 1997; Jiang 435 et al. 2004). One potential explanation is that defects at 436 the interface between the central and N-terminal regions 437 would weaken the interactions stabilizing the receptor 438 in the closed state, leading to increased susceptibility to 439 stimuli (Tateishi et al. 2009; Suetomi et al. 2011). Albeit 440 many disease-associated RyR1 mutations do increase the 441 open probability of the channel, this is far from certain for 442 all RyR1 mutations, in particular with regards to recessive 443 RyR1-related myopathies associated with reduction of the 444 RyR1 protein. Therefore, compounds enhancing the closed 445 probability of the channel would have limited application 446 in conditions where the RyR1 mutations result in reduced 447 rather than enhanced Ca<sup>2+</sup> conductance, or where the pre-448 cise functional consequences of the specific RyR1 muta-449 tions are not known. 450

Adjacent RyRs are known to signal cooperatively as 451 paracrystalline arrays in checkerboard patterns, allow-452 ing for simultaneous opening of multiple channels (cou-453 pled gating) in response to a stimulus (Marx et al. 1998; 454 Cabra et al. 2016). This provides a mechanism by which 455 RyR channels can effect the rapid and coordinated SR Ca<sup>2+</sup> 456 release (via mechanically triggering neighboring channels) 457 that is required for EC coupling. Thus, RyRs act as both 458

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signal amplifiers and integrators by triggering neighboring channels both physically and chemically with  $Ca^{2+}$  (Endo et al. 1970; Fabiato 1983).

Acknowledgements The studies described in this review were
supported by NIH grants (R01AR060037 and R01HL061503)
and the Fondation Leducq to A.R.M. G.S. is supported by the NIH
(K99DK107895). ARM is a consultant and member of the board
of ARMGO Pharma that is targeting RyR channels for therapeutic
purposes.

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