

## CHAPTER FIVE

# BIOLOGY OF THE STRIATED MUSCLE DYSTROPHIN–GLYCOPROTEIN COMPLEX

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### Contents

1. Introduction	192
2. Composition of the Core Dystrophin–Glycoprotein Complex	192
2.1. Dystroglycan complex	193
2.2. Sarcoglycan complex	193
2.3. Dystrobrevin/syntrophin complex	194
3. Function in Mammals	195
3.1. Mechanical stabilization and force transmission	195
3.2. Organization and stabilization of the neuromuscular junction	202
3.3. Cellular signaling	203
4. Function in Model Organisms	205
4.1. <i>Caenorhabditis elegans</i>	205
4.2. <i>Drosophila</i>	206
4.3. Zebrafish	207
5. Concluding Remarks	207
Acknowledgments	208
References	208

### Abstract

Since its first description in 1990, the dystrophin–glycoprotein complex has emerged as a critical nexus for human muscular dystrophies arising from defects in a variety of distinct genes. Studies in mammals widely support a primary role for the dystrophin–glycoprotein complex in mechanical stabilization of the plasma membrane in striated muscle and provide hints for secondary functions in organizing molecules involved in cellular signaling. Studies in model organisms confirm the importance of the dystrophin–glycoprotein complex for muscle cell viability and have provided new leads toward a full understanding of its secondary roles in muscle biology.

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## 1. INTRODUCTION

Dystrophin is the largest protein isoform expressed from the gene defective in Duchenne muscular dystrophy (Hoffman *et al.*, 1987; Koenig *et al.*, 1988), a lethal muscle-wasting disease that afflicts 1 in 3500 live-born males (Engel, 1986). Based on sequence homology, dystrophin is divided into four distinct domains (Koenig *et al.*, 1988). The amino-terminal 250 residues encode a pair of calponin homology (CH) modules common to several proteins that bind filamentous actin. Adjacent to the amino-terminal domain, more than 2800 amino acids encode 24 homologous triple helical repeats and four hinge domains (Koenig and Kunkel, 1990) that are thought to confer flexibility and elasticity. A third domain of  $\sim 400$  residues is more complex, encoding a WW module (Bork and Sudol, 1994), two EF hand modules (Koenig *et al.*, 1988), and two ZZ modules in series (Ponting *et al.*, 1996). Finally, the carboxy-terminal  $\sim 240$  amino acids are unique to dystrophin and its related proteins (Tinsley *et al.*, 1992; Wagner *et al.*, 1993). In total, the four domains of dystrophin are encoded by 3685 amino acids with a molecular weight of 427 kDa.

In skeletal muscle, dystrophin was isolated as part of a large, tightly associated oligomeric complex of proteins synonymously referred to as the dystrophin–glycoprotein complex or dystrophin-associated protein complex (Ervasti *et al.*, 1990; Yoshida and Ozawa, 1990; Ervasti and Campbell, 1991). Investigations into the biological function of the dystrophin–glycoprotein complex suggest it plays an important mechanical function in stabilizing the plasma membrane (the sarcolemma) against stresses imposed during muscle contraction or stretch. The dystrophin–glycoprotein complex has also garnered attention as a putative cellular signaling complex. Here, we review the data supporting current views on the biological function(s) of the dystrophin–glycoprotein complex in striated muscle.

## 2. COMPOSITION OF THE CORE DYSTROPHIN–GLYCOPROTEIN COMPLEX

In addition to dystrophin, the core dystrophin–glycoprotein complex contains nine protein subunits encoded by eight different genes. Other proteins include dystroglycans, sarcoglycans, sarcospan, dystrobrevins, and syntrophins. The constituents of the core dystrophin–glycoprotein complex

remain associated in stoichiometric amounts even after multiple purification steps under moderately stringent buffer conditions (Ervasti *et al.*, 1990; Yoshida and Ozawa, 1990; Ervasti and Campbell, 1991). However, several biochemical perturbations further resolve the dystrophin–glycoprotein complex into three subcomplexes (Ervasti and Campbell, 1991; Ervasti *et al.*, 1991; Butler *et al.*, 1992; Yoshida *et al.*, 1994; Kramarcy *et al.*, 1994), each of which will be discussed in greater detail in the following.

## 2.1. Dystroglycan complex

The dystroglycan subcomplex consists of  $\alpha$ - and  $\beta$ -dystroglycan, which are encoded as a single polypeptide from one highly conserved gene (Ibraghimov-Beskrovnaya *et al.*, 1992) that undergoes posttranslational proteolytic cleavage to yield the two tightly (but noncovalently) associated subunits (Ibraghimov-Beskrovnaya *et al.*, 1992; Gee *et al.*, 1993; Smalheiser and Kim, 1995; Deyst *et al.*, 1995; Holt *et al.*, 2000; Esapa *et al.*, 2003; Jayasinha *et al.*, 2003).  $\alpha$ -Dystroglycan is an extensively glycosylated extracellular protein (Ervasti and Campbell, 1991, 1993; Gee *et al.*, 1993; Smalheiser and Kim, 1995; Ervasti *et al.*, 1997) consisting of two globular domains connected by an extensible stalk such that  $\alpha$ -dystroglycan appears dumbbell shaped when viewed by electron microscopy (Brancaccio *et al.*, 1995, 1997; Bozic *et al.*, 2004; Kunz *et al.*, 2004). Although the chemical makeup of the sugar moieties remains poorly understood, the glycoepitopes on  $\alpha$ -dystroglycan mediate binding to components of the extracellular matrix and proper glycosylation is essential to dystroglycan function (Ervasti and Campbell, 1993; Grewal *et al.*, 2001; Michele *et al.*, 2002; Kanagawa *et al.*, 2004; Barresi *et al.*, 2004).  $\beta$ -Dystroglycan is a single-pass transmembrane protein with a largely unstructured amino-terminal extracellular domain that binds to the carboxy-terminal globular domain of  $\alpha$ -dystroglycan (Di *et al.*, 1999; Boffi *et al.*, 2001) and a 121-residue carboxy-terminal cytoplasmic domain that binds directly to the WW, EF, and ZZ modules in dystrophin (Suzuki *et al.*, 1992; Jung *et al.*, 1995; Rosa *et al.*, 1996; Rentschler *et al.*, 1999; Chung and Campanelli, 1999; Huang *et al.*, 2000; Ishikawa-Sakurai *et al.*, 2004).

## 2.2. Sarcoglycan complex

The sarcoglycan/sarcospan subcomplex is composed of  $\alpha$ -,  $\beta$ -,  $\gamma$ -, and  $\delta$ -sarcoglycan isoforms, each encoded by a separate gene (Roberds *et al.*, 1993; Lim *et al.*, 1995; Noguchi *et al.*, 1995; Nigro *et al.*, 1996), and sarcospan (Crosbie *et al.*, 1999). All sarcoglycans are single-pass transmembrane glycoproteins with long extracellular domains and relatively short cytoplasmic domains (Roberds *et al.*, 1993; Lim *et al.*, 1995; Noguchi *et al.*, 1995; Nigro *et al.*, 1996).  $\alpha$ -Sarcoglycan differs from  $\beta$ -,  $\gamma$ -, and  $\delta$ -sarcoglycan

in that its amino terminus is oriented extracellularly (Roberds *et al.*, 1993). Sarcospan encodes four transmembrane-spanning segments homologous to the tetraspanin family of proteins (Crosbie *et al.*, 1997), which are thought to mediate interactions between transmembrane proteins. Beyond the four sarcoglycan isoforms initially characterized as a subcomplex of the dystrophin–glycoprotein complex in striated muscle, two additional sarcoglycan genes have been identified.  $\epsilon$ -Sarcoglycan is most similar in sequence homology and membrane topology to  $\alpha$ -sarcoglycan (Ettinger *et al.*, 1997; McNally *et al.*, 1998); it can compensate for the absence of  $\alpha$ -sarcoglycan in skeletal muscle (Imamura *et al.*, 2005), but also forms part of a high-molecular-weight complex in muscle that is distinct from the dystrophin–glycoprotein complex (Durbeej *et al.*, 2000).  $\zeta$ -Sarcoglycan is most homologous to  $\delta$ - and  $\gamma$ -sarcoglycan (Wheeler *et al.*, 2002), and, accordingly, expression studies in heterologous cells suggest that  $\zeta$ -sarcoglycan can substitute for  $\gamma$ -sarcoglycan in the sarcoglycan complex (Shiga *et al.*, 2006).

### 2.3. Dystrobrevin/syntrophin complex

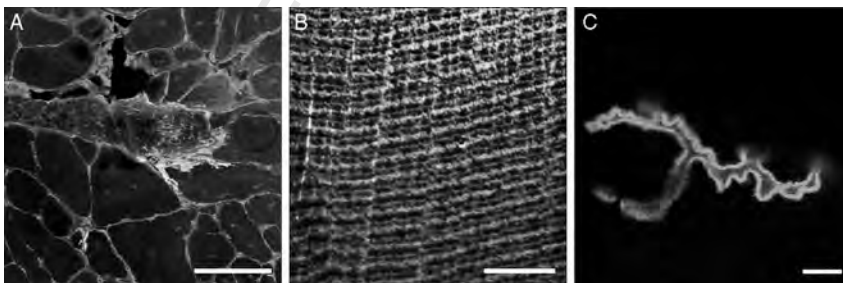
Several studies indicate that dystrophin directly interacts with syntrophins (Butler *et al.*, 1992; Kramarcy *et al.*, 1994; Dwyer and Froehner, 1995; Ahn and Kunkel, 1995; Suzuki *et al.*, 1994, 1995; Yang *et al.*, 1995b; Peters *et al.*, 1997a) and dystrobrevins (Butler *et al.*, 1992; Suzuki *et al.*, 1994; Dwyer and Froehner, 1995; Sadoulet-Puccio *et al.*, 1997; Nawrotzki *et al.*, 1998; Peters *et al.*, 1998), two families of cytoplasmic proteins encoded by multiple genes expressed in a tissue-specific manner (Yang *et al.*, 1994; Ahn *et al.*, 1994, 1996; Adams *et al.*, 1995; Piluso *et al.*, 2000). All syntrophins share a common modular structure consisting of one domain unique to syntrophins, one PDZ domain, and two pleckstrin homology domains that suggest syntrophins function as adaptor proteins involved in anchoring cell signaling molecules to the plasma membrane (Adams *et al.*, 1995; Piluso *et al.*, 2000). The syntrophin unique domain and carboxy-terminal pleckstrin homology domain interact with the extreme carboxy terminus of dystrophin (Ahn and Kunkel, 1995; Suzuki *et al.*, 1995). Of the five known syntrophins, all except  $\gamma 1$  are expressed in skeletal muscle (Peters *et al.*, 1997a; Piluso *et al.*, 2000), but  $\beta 1$  and  $\beta 2$  syntrophins show differences in fiber-type distribution or cellular location that argue for distinct functions (Peters *et al.*, 1997a). Dystrobrevins are so named because they share significant sequence homology with the carboxy-terminal domains of dystrophin (Wagner *et al.*, 1993; Sadoulet-Puccio *et al.*, 1996). Two dystrobrevin genes encode multiple isoforms expressed in a wide array of tissues with  $\alpha$ -dystrobrevins expressed predominantly in skeletal muscle (Wagner *et al.*, 1993; Yoshida *et al.*, 1995; Sadoulet-Puccio *et al.*, 1996; Peters *et al.*, 1997b; Blake *et al.*, 1996, 1998; Puca *et al.*, 1998; Holzfeind

*et al.*, 1999).  $\alpha$ -Dystrobrevin-1 localizes to the neuromuscular junction while  $\alpha$ -dystrobrevin-2 is distributed uniformly throughout the sarcolemma (Peters *et al.*, 1998; Nawrotzki *et al.*, 1998). Pairs of coiled-coil motifs present in  $\alpha$ -dystrobrevin and the dystrophin carboxy terminus are responsible for their binding interaction (Sadoulet-Puccio *et al.*, 1997; Peters *et al.*, 1998). In addition to their independent interactions with dystrophin, syntrophins and dystrobrevins directly bind one another (Butler *et al.*, 1992; Dwyer and Froehner, 1995), suggesting that two syntrophin molecules associate with each dystrophin–glycoprotein complex through independent interactions with dystrophin and dystrobrevin. Finally,  $\alpha$ -dystrobrevins interact with the sarcoglycan complex (Yoshida *et al.*, 2000), suggesting a role in coupling dystrophin to the glycoprotein complex.

### 3. FUNCTION IN MAMMALS

#### 3.1. Mechanical stabilization and force transmission

While detectable beneath the entire sarcolemma of normal skeletal muscle, dystrophin is particularly concentrated in three subcellular structures implicated in the transmission of contractile force from myofibrils to extracellular elements of muscle tissue. Dystrophin immunostaining is enriched at myotendinous junctions (Fig. 5.1A; Samitt and Bonilla, 1990), and intrafascicular fiber terminations (Paul *et al.*, 2002), which are also referred to as myomuscular junctions (Bassett *et al.*, 2003). Myotendinous and myomuscular junctions are the sites of attachment between the ends of muscle fibers and tendons or serially arranged muscle fibers, respectively, and which

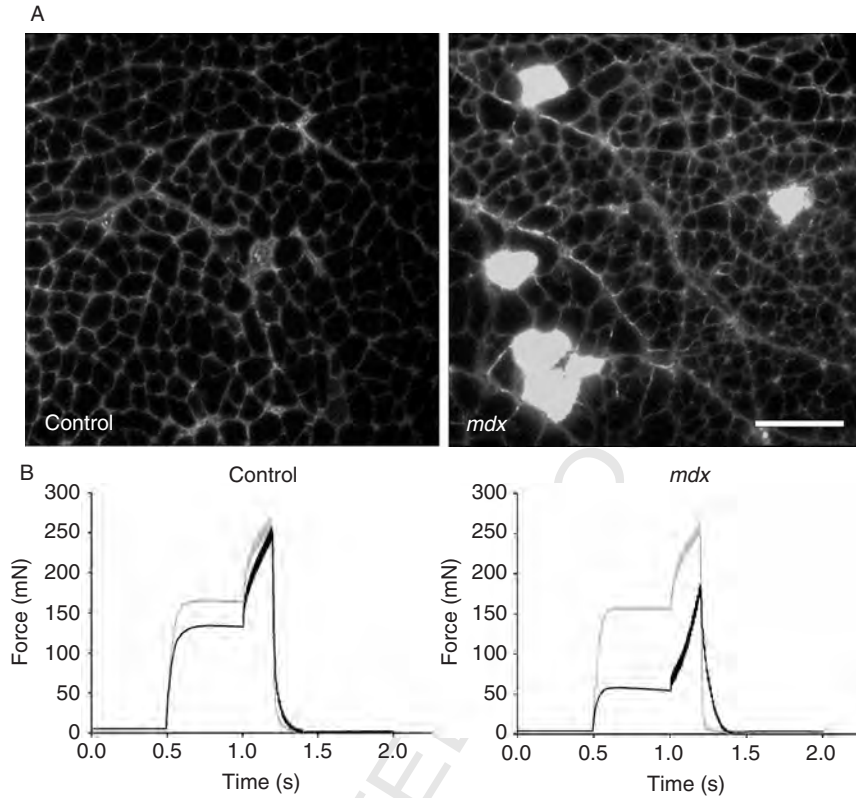


**Figure 5.1** Sites of dystrophin–glycoprotein complex enrichment in skeletal muscle. (A) The myotendinous junction identified by immunostaining for tenascin C (green) with individual muscle fibers delineated by immunostaining for laminin (red) and myonuclei (blue) labeled with TO-PRO-3 iodide. Scale bar = 50  $\mu\text{m}$ . (B) Dystrophin immunoreactivity detected at costameres. Scale bar = 10  $\mu\text{m}$ . (C) Neuromuscular junction detected with  $\alpha$ -bungarotoxin. Scale bar = 10  $\mu\text{m}$ . (See color insert.)

ultimately transmit the force of muscle fiber contraction to bone. The sarcolemma is highly folded at the myotendinous junction, presumably to increase the surface area contact between muscle fiber ends and tendons. The myotendinous junctions of dystrophin-deficient *mdx* mice are less folded than in wild-type muscle, but also show defective lateral association of terminating sarcomeric thin filaments with the sarcolemma (Tidball and Law, 1991; Law and Tidball, 1993). The dystrophin homologue utrophin is also enriched at myotendinous junctions (Khurana *et al.*, 1991) and mice deficient in both dystrophin and utrophin exhibit more marked reduction in sarcolemmal folding at the myotendinous junction compared to dystrophin-deficient *mdx* mice (Deconinck *et al.*, 1997b).

At nonjunctional regions of the sarcolemma, dystrophin immunostaining displays a rectilinear pattern (Fig. 5.1B) with a major transverse element aligning to myofibrillar Z disks and finer strands aligning with M lines or the long axis of the myofiber (Porter *et al.*, 1992; Straub *et al.*, 1992). The rectilinear lattice is commonly called a costamere, coined from the rib-like appearance of its major Z disk element (Pardo *et al.*, 1983). Clever experiments on carefully dissected bundles of frog myofibers and isolated cardiac myocytes adhered to flexible substrata suggested that costameres physically transmit myofibrillar force across the sarcolemma to the extracellular matrix and adjacent muscle cells (Street, 1983; Danowski *et al.*, 1992). Electron microscopy studies suggested that costameres may also coordinate folding of the sarcolemma during muscle contraction (Street, 1983; Shear and Bloch, 1985). The costameric lattice is disorganized in dystrophin-deficient muscle (Minetti *et al.*, 1992, 1994; Porter *et al.*, 1992; Ehmer *et al.*, 1997; Williams and Bloch, 1999). Costameric disruption is accompanied by greatly increased sarcolemmal fragility/permeability (Mokri and Engel, 1975; Menke and Jockusch, 1991, 1995) resulting in dramatically increased movement of membrane-impermeant molecules across the sarcolemma (Fig. 5.2A; Engel, 1986; Weller *et al.*, 1990; Cox *et al.*, 1993; Clarke *et al.*, 1993; Menke and Jockusch, 1991, 1995; Matsuda *et al.*, 1995; Tinsley *et al.*, 1996; Straub *et al.*, 1997; Vilquin *et al.*, 1998; Harper *et al.*, 2002; Barton *et al.*, 2002; Bansal *et al.*, 2003). Both sarcolemmal permeability and necrosis of dystrophin-deficient muscle are exacerbated by physical exercise and improved by muscle immobilization (Karpati and Carpenter, 1986; Weller *et al.*, 1990; Mizuno, 1992; Clarke *et al.*, 1993; Vilquin *et al.*, 1998; Mokhtarian *et al.*, 1999; Bansal *et al.*, 2003). Thus, enrichments of dystrophin in three structural elements of muscle are important for muscle function, as these structures are perturbed when dystrophin is absent.

Studies using noninvasive assays that measure the pulling force or grip strength of intact alert animals have demonstrated that dystrophin-deficient *mdx* mice are weak (Carlson and Makiejus, 1990; Tinsley *et al.*, 1998; Connolly *et al.*, 2001; Sonnemann *et al.*, 2006). Because muscle-specific expression of the dystrophin homologue utrophin in *mdx* mice restored



**Figure 5.2** Dystrophin-deficient muscle exhibits increased sarcolemmal permeability and contraction-induced injury. (A) Infiltration of membrane-impermeant Evans blue dye (red) into muscle fibers of dystrophin-deficient *mdx* muscle but not wild-type control muscle. Scale bar = 100  $\mu\text{m}$ . (B) Tetanic force is significantly depressed from the first (red) to the fifth (black) eccentric contraction in extensor digitorum longus muscles from dystrophin-deficient *mdx* mice compared to control. (See color insert.)

muscle strength to normal values (Tinsley *et al.*, 1998), it is likely that the primary cause of weakness is due to the absence of dystrophin from skeletal muscle and not from a nervous tissue defect. Numerous *ex vivo* studies confirm that dystrophin-deficient muscle is weak, particularly when force output is normalized against muscle cross-sectional area (Coulton *et al.*, 1988; Kometani *et al.*, 1990; Stedman *et al.*, 1991; Sacco *et al.*, 1992; Quinlan *et al.*, 1992; Cox *et al.*, 1993; Pastoret and Sebillé, 1993; Tinsley *et al.*, 1998; Deconinck *et al.*, 1997c, 1998; Bobet *et al.*, 1998; Stevens and Faulkner, 2000; Lynch *et al.*, 2001; DelloRusso *et al.*, 2001; Harper *et al.*, 2002; Barton *et al.*, 2002). Although the molecular basis for muscle weakness associated with dystrophin deficiency has been elusive, it seems not to involve a defect in sarcomeric force production (Lynch *et al.*, 2000; Lowe

*et al.*, 2006) but may be due in part to defective force transmission at the myotendinous junction (Deconinck *et al.*, 1997b). While excitation–contraction coupling is not altered, calcium release from the sarcoplasmic reticulum is significantly decreased in *mdx* myofibers, which also likely contributes to the observed force deficit (Woods *et al.*, 2004, 2005).

In addition to decreased normalized force production, dystrophin-deficient muscle is hypersensitive to lengthening (eccentric) contractions (Fig. 5.2B). When *mdx* muscle is forcibly lengthened during tetanic stimulation, force production is immediately and dramatically reduced (Petrof *et al.*, 1993; Moens *et al.*, 1993; Brooks, 1998; DelloRusso *et al.*, 2001). Consistent with a role in sarcolemmal stability, the drop in force generated by intact dystrophin-deficient muscle after experiencing eccentric contraction is well correlated with increased sarcolemmal permeability (Petrof *et al.*, 1993; Moens *et al.*, 1993; Deconinck *et al.*, 1996, 1997c, 1998; Brooks, 1998; Tinsley *et al.*, 1998; DelloRusso *et al.*, 2001; Harper *et al.*, 2002; Barton *et al.*, 2002). In contrast, permeabilized dystrophin-deficient myofibers are neither weaker nor more sensitive to eccentric contraction compared to controls (Lynch *et al.*, 2000).

Knockout of the dystroglycan or sarcoglycan subcomplexes also causes muscular dystrophy that is accompanied by defects in sarcolemmal integrity (Duclos *et al.*, 1998; Araishi *et al.*, 1999; Coral-Vazquez *et al.*, 1999; Cote *et al.*, 1999; Hack *et al.*, 1998, 2000; Durbeej *et al.*, 2000; Straub *et al.*, 2000; Cohn *et al.*, 2002; Sasaoka *et al.*, 2003). Genetic ablation of individual sarcoglycan genes results in a progressive muscular dystrophy phenotype associated with loss of expression of the other three sarcoglycan proteins and sarcospan (Duclos *et al.*, 1998; Araishi *et al.*, 1999; Durbeej *et al.*, 2000; Coral-Vazquez *et al.*, 1999; Hack *et al.*, 1998, 2000; Sasaoka *et al.*, 2003) while knockout of sarcospan caused no apparent muscle phenotype or effect on sarcoglycan complex expression (Lebakken *et al.*, 2000). Because the biochemical stability of the dystrophin–glycoprotein complex is greatly impaired in sarcoglycan-deficient muscle (Duclos *et al.*, 1998; Araishi *et al.*, 1999; Durbeej *et al.*, 2000), the sarcoglycan complex is thought to play a role in stabilizing the linkages formed by  $\beta$ -dystroglycan with  $\alpha$ -dystroglycan and dystrophin.

Dystrophin is also enriched in costameres and intercalated disks of cardiac muscle (Kaprielian *et al.*, 2000). Like skeletal muscle, dystrophin-deficient cardiac myocytes are abnormally vulnerable to mechanical stress-induced injury and contractile failure (Danialou *et al.*, 2001; Kamogawa *et al.*, 2001; Yasuda *et al.*, 2005). Interestingly, treatment with chemical-based membrane sealants was shown to correct the cardiac defects associated with dystrophin deficiency in mice (Yasuda *et al.*, 2005). Finally, coxsackie B virus infection results in dilated cardiomyopathy and a virally expressed protease specifically cleaves dystrophin (Badorff *et al.*, 1999, 2000) and is sufficient to induce dilated cardiomyopathy (Xiong *et al.*, 2007).



When taken together, the previous studies indicate that one primary function of the dystrophin–glycoprotein complex is to stabilize muscle cells, and particularly the sarcolemma, against mechanical forces transduced through costameres during muscle contraction or stretch.

While the impressive biochemical stability of the dystrophin–glycoprotein complex combined with the loss of sarcolemmal integrity when it is absent or defective strongly supports a role in mechanical stabilization, the complex does not function in isolation but instead through collaboration with several other cellular constituents. *In vitro* studies demonstrated that spectrin repeat 2 of the large dystrophin rod domain binds strongly to phospholipids, which may modify the physical properties of the sarcolemmal lipid bilayer and/or associated proteins (DeWolf *et al.*, 1997; Le *et al.*, 2003). In support of a role for phospholipid binding *in vivo*, truncated dystrophin transgenes lacking spectrin repeats 2 and 3 were less effective in rescuing the phenotype of dystrophin-deficient *mdx* mice compared to constructs containing these repeats, although substitution of hinge 2 with hinge 3 also complicated the interpretation (Harper *et al.*, 2002).

Several studies have demonstrated that dystrophin purified from a variety of tissues can bind actin filaments *in vitro* with submicromolar affinity (Ervasti and Campbell, 1993; Fabbrizio *et al.*, 1993; Senter *et al.*, 1993; Lebart *et al.*, 1995; Rybakova *et al.*, 1996). *In vivo*, dystrophin interacts with actin filaments composed of the nonmuscle  $\gamma$ -actin isoform (Rybakova *et al.*, 2000; Ursitti *et al.*, 2004), which concentrates primarily at the sarcolemma and particularly within costameres (Craig and Pardo, 1983; Rybakova *et al.*, 2000; Hanft *et al.*, 2006; Sonnemann *et al.*, 2006). Studies aimed at identifying the actin-binding sites within dystrophin have confirmed an important contribution by the amino-terminal, tandem calponin homology domain (Hemmings *et al.*, 1992; Way *et al.*, 1992; Fabbrizio *et al.*, 1993; Corrado *et al.*, 1994; Jarrett and Foster, 1995; Rybakova *et al.*, 1996), but also identified a second actin-binding domain encoded by a cluster of basic spectrin repeats located in the middle rod domain of dystrophin (Rybakova *et al.*, 1996; Rybakova and Ervasti, 1997; Amann *et al.*, 1998, 1999). Although either actin-binding domain is sufficient to physically anchor costameric actin filaments to the sarcolemma (Warner *et al.*, 2002; Hanft *et al.*, 2006), the amino-terminal actin-binding domain appears to be more important from a functional perspective (Warner *et al.*, 2002; Harper *et al.*, 2002).  $\alpha$ -Syntrophin also binds actin filaments *in vitro* (Iwata *et al.*, 1998, 2004), which suggests it may contribute to the actin-binding activity of the dystrophin–glycoprotein complex (Rybakova *et al.*, 1996). However, more recent quantitative comparisons of the actin-binding properties of full-length recombinant dystrophin with those measured for the dystrophin–glycoprotein complex indicate that dystrophin alone can account for all actin-binding activity of the complex (Rybakova

*et al.*, 2006). Through direct interaction with the sarcoglycan complex (Thompson *et al.*, 2000), filaminC forms yet another linkage between the dystrophin–glycoprotein complex and the actin cytoskeleton. Like dystrophin, filamins contain an amino-terminal tandem calponin homology actin-binding domain but encode 24 immunoglobulin G (IgG) motifs rather than spectrin-type repeats (Stossel *et al.*, 2001). The phenotype of mice ablated for filaminC expression indicates that filaminC plays a crucial role in maintaining muscle structure (Dalkilic *et al.*, 2006).

In addition to interactions with the actin cytoskeleton, multiple studies have demonstrated an association of the dystrophin–glycoprotein complex with the intermediate filament cytoskeleton through several distinct pathways. First, two-hybrid screens and subsequent experiments identified desmuslin/synemin (Mizuno *et al.*, 2001) and syncollin (Newey *et al.*, 2001; Poon *et al.*, 2002) as two proteins that couple  $\alpha$ -dystrobrevin of the dystrophin–glycoprotein complex with the intermediate filament desmin. More recent biochemical studies have demonstrated the ability of desmuslin/synemin to directly bind sequences within the middle rod and WW/EF/ZZ domains of dystrophin (Bhosle *et al.*, 2006). Dystrophin also associates with cytokeratins 8 and 19 at costameres through a direct interaction of keratin 19 with the amino-terminal, tandem calponin homology domain of dystrophin (O'Neill *et al.*, 2002; Ursitti *et al.*, 2004; Stone *et al.*, 2005). Most recently, an isoform of the giant cytolinker plectin has been localized to the sarcolemma and costameres of skeletal muscle and was demonstrated to directly bind dystrophin and  $\beta$ -dystroglycan (Rezniczek *et al.*, 2007), which provides yet another mechanical linkage between the dystrophin–glycoprotein complex, the actin cytoskeleton, and the intermediate filament lattice. In conclusion, dystrophin,  $\beta$ -dystroglycan,  $\alpha$ -dystrobrevin, and sarcoglycans all appear to couple the dystrophin–glycoprotein complex to other structural elements, which provides additional support for an essential structural/mechanical role in striated muscle.

On the external surface of the sarcolemma, components of the dystrophin–glycoprotein complex have been shown to interact with several constituents of the extracellular matrix. Through its incompletely characterized carbohydrate epitopes (Section 2.1),  $\alpha$ -dystroglycan has been shown to interact with laminins (Ibraghimov-Beskrovnaya *et al.*, 1992; Ervasti and Campbell, 1993), agrins (Bowe *et al.*, 1994; Campanelli *et al.*, 1994; Gee *et al.*, 1994; Sugiyama *et al.*, 1994), and perlecan (Talts *et al.*, 1999; Peng *et al.*, 1999; Kanagawa *et al.*, 2005), which all bind  $\alpha$ -dystroglycan through a conserved G-domain motif (Gee *et al.*, 1993; Hohenester *et al.*, 1999). Laminin-2 is the predominant laminin isoform expressed in striated muscle (Patton *et al.*, 1997) and mutations leading to laminin-2 deficiency cause forms of congenital muscular dystrophy (Xu *et al.*, 1994; Sunada *et al.*, 1994; Helbling-Leclerc *et al.*, 1995). Unlike dystrophies caused by defects in the dystrophin–glycoprotein complex, laminin-2-deficient muscular dystrophy

is not associated with compromised sarcolemmal integrity (Straub *et al.*, 1997), but instead involves muscle cell apoptosis in its pathomechanism (Girgenrath *et al.*, 2004; Dominov *et al.*, 2005). While dystroglycan binding to agrin and perlecan has been most extensively studied at the neuromuscular junction (Section 3.2), it bears noting that transgenic expression of agrin minigenes (Moll *et al.*, 2001) or agrin/perlecan chimeras (Meinen *et al.*, 2007) can rescue the dystrophic phenotype of laminin-2-deficient muscle. These results suggest that dystroglycan plays an important role in anchoring muscle cells to the extracellular matrix. While strong, the mechanical linkages between the basement membrane, the dystrophin–glycoprotein complex, and the costameric cytoskeleton are not static and unchanging as denervation causes rapid reorientation of costameres and the laminin-2 matrix from a transverse to a longitudinal pattern (Bezakov and Lomo, 2001). Moreover, it appears that agrin isoforms secreted by muscle cells are important for the maintenance of costamere organization because the transverse to a longitudinal reorientation after denervation was prevented by exogenous application of muscle agrin (Bezakova and Lomo, 2001). More recently, experiments demonstrated that biglycan, a small proteoglycan, binds to  $\alpha$ -dystroglycan (Bowe *et al.*, 2000) and  $\alpha$ - and  $\gamma$ -sarcoglycans (Rafii *et al.*, 2006). Biglycan null mice display a mild dystrophic phenotype and a subpopulation of muscle fibers shows evidence of impaired sarcolemmal integrity (Mercado *et al.*, 2006), suggesting it may stabilize links between the dystroglycan and sarcoglycan complexes and between the sarcoglycan complex and the extracellular matrix. However, the loss of  $\alpha$ -dystrobrevin isoforms in biglycan null muscle may have also contributed to the dystrophic phenotype (Mercado *et al.*, 2006).

Finally, a structural/mechanical role for the dystrophin–glycoprotein complex is supported by examining how muscle responds to the loss of dystrophin. Several structural proteins of costameres, myotendinous and/or myomuscular junctions are upregulated in *mdx* muscle including talin and vinculin (Law *et al.*, 1994),  $\alpha_7\beta_1$  integrin (Vachon *et al.*, 1997; Hodges *et al.*, 1997), plectin (Schroder *et al.*, 1997; Rezniczek *et al.*, 2007), filaminC (Thompson *et al.*, 2000), biglycan (Bowe *et al.*, 2000), dysbindin (Benson *et al.*, 2001), syncoilin (Newey *et al.*, 2001), and cytoplasmic  $\gamma$ -actin (Hanft *et al.*, 2006). While targeted to the neuromuscular and myotendinous junctions in adult muscle (Khurana *et al.*, 1991; Ohlendieck *et al.*, 1991), utrophin expression is increased in dystrophin-deficient muscle (Matsumura *et al.*, 1992; Porter *et al.*, 1998) and is redirected to costameres (Williams and Bloch, 1999; Rybakova *et al.*, 2000, 2002). These data suggest that dystrophin-deficient muscle responds to mechanical instability through compensatory remodeling of the cytoskeleton. Moreover, transgenic overexpression of  $\alpha_7$  integrin (Burkin *et al.*, 2001) or utrophin (Tinsley *et al.*, 1998) results in partial to complete rescue of the dystrophic phenotype. In summary, the proteins upregulated in response to dystrophin deficiency

are capable of compensating for the missing physical linkage between the sarcolemma and myofibrillar apparatus and thus support a mechanical function for the dystrophin–glycoprotein complex.

### 3.2. Organization and stabilization of the neuromuscular junction

The dystrophin–glycoprotein complex is also enriched at the motor end plate of the neuromuscular junction (Fig. 5.1C). However, differences in molecular composition and subcellular distribution suggest its function at this important site of nerve/muscle communication may vary as well. A dystrophin–glycoprotein complex with molecular composition very similar to that expressed throughout the extrasynaptic sarcolemma and costameres is localized to the deep troughs of the junctional folds (Byers *et al.*, 1991; Sealock *et al.*, 1991; Peters *et al.*, 1998). At the crests of junctional folds, dystrophin is replaced by its close homologue utrophin and the longer  $\alpha$ -dystrobrevin-1 isoform replaces the shorter  $\alpha$ -dystrobrevin-2 isoform that predominates in the extrasynaptic dystrophin–glycoprotein complex (Peters *et al.*, 1998). As noted earlier,  $\beta_2$ -syntrophin is exclusively localized to the neuromuscular junction (Peters *et al.*, 1997a).

Interest in the role of the dystrophin/utrophin–glycoprotein complex in neuromuscular synaptogenesis was piqued by reports from several laboratories that  $\alpha$ -dystroglycan bound with high affinity to agrin (Bowe *et al.*, 1994; Campanelli *et al.*, 1994; Gee *et al.*, 1994; Sugiyama *et al.*, 1994), an interaction that induces high-density clustering of acetylcholine receptors at the motor end plate (Gautam *et al.*, 1996). Furthermore,  $\beta$ -dystroglycan was shown to directly bind rapsyn (Cartaud *et al.*, 1998; Bartoli *et al.*, 2001), a cytoplasmic protein that is required for acetylcholine receptor clustering in muscle (Apel *et al.*, 1997). However, agrin can induce acetylcholine receptor clustering in dystroglycan null myotubes (Grady *et al.*, 2000), leaving the physiological relevance of agrin binding to  $\alpha$ -dystroglycan at the neuromuscular junction unclear. Perlecan binding to  $\alpha$ -dystroglycan, on the other hand, has been implicated in anchoring acetylcholinesterase to the neuromuscular junction (Peng *et al.*, 1999; Arikawa-Hirasawa *et al.*, 2002). Genetic ablation of dystrophin (Lyons and Slater, 1991; Grady *et al.*, 1997b), utrophin (Grady *et al.*, 1997a; Deconinck *et al.*, 1997a),  $\alpha$ -syntrophin (Adams *et al.*, 2000) or  $\beta_1$ -syntrophin (Adams *et al.*, 2004),  $\alpha$ -dystrobrevin (Grady *et al.*, 2000), or dystroglycan (Cote *et al.*, 1999) all caused morphological abnormalities in the neuromuscular junction. Similarly, the density of acetylcholine receptors at the neuromuscular junction is significantly decreased in mice lacking  $\alpha$ -dystrobrevin (Grady *et al.*, 2000; Akaaboune *et al.*, 2002) or  $\alpha$ -syntrophin (Adams *et al.*, 2000), suggesting that the dystrophin/utrophin–glycoprotein complex contributes to the long-term stability of functionally important elements in the motor end plate.

While  $\alpha$ -dystrobrevin and dystroglycan null animals present with muscular dystrophy (Grady *et al.*, 1999; Cote *et al.*, 1999; Cohn *et al.*, 2002), utrophin and syntrophin null animals are phenotypically normal (Grady *et al.*, 1997a; Deconinck *et al.*, 1997a), and dystrophic  $\alpha$ -dystrobrevin null mice can be rescued by transgenic expression of  $\alpha$ -dystrobrevin-2 without restoring neuromuscular junction morphology (Grady *et al.*, 2003). These data suggest that morphological defects in the neuromuscular junction do not contribute significantly to pathologies associated with absence or abnormality in the dystrophin–glycoprotein complex.

### 3.3. Cellular signaling

Through syntrophins, the dystrophin–glycoprotein complex is thought to anchor a variety of signaling molecules near their sites of action. Neuronal nitric oxide synthase (nNOS) was first shown to copurify with the dystrophin–glycoprotein complex (Brenman *et al.*, 1995) through a direct interaction with  $\alpha$ -syntrophin (Adams *et al.*, 2001). Syntrophins have since been found to bind a variety of channels (Gee *et al.*, 1998; Adams *et al.*, 2001; Vandebrouck *et al.*, 2007), kinases (Lumeng *et al.*, 1999; Abramovici *et al.*, 2003), and kinase substrates (Luo *et al.*, 2005). Because nNOS localization to the sarcolemma and enzymatic activity were disrupted in dystrophin-deficient *mdx* mice (Brenman *et al.*, 1995), it was hypothesized that aberrant nNOS regulation may importantly contribute to the muscle degeneration accompanying dystrophinopathy. However, genetic ablation of nNOS did not induce a muscular phenotype in mice (Huang *et al.*, 1993). Furthermore, transgenic expression of a truncated dystrophin (Harper *et al.*, 2002) or full-length utrophin (Tinsley *et al.*, 1998) fully reversed muscular dystrophy in *mdx* mice without restoring sarcolemmal nNOS (Judge *et al.*, 2006; Yokota *et al.*, 2006). Finally, mice knocked out for  $\alpha$ -syntrophin (Kameya *et al.*, 1999; Adams *et al.*, 2000),  $\beta_2$ -syntrophin (Adams *et al.*, 2004), or both genes (Adams *et al.*, 2004) exhibited no evidence of muscle disease. Thus, it appears that the loss of signal-molecule anchoring function plays no primary role in causing dystrophin-deficient muscular dystrophy, although it may contribute to secondary disease features such as impaired vascular perfusion during muscle contraction (Sander *et al.*, 2000; Thomas *et al.*, 1998, 2003), altered muscle regeneration (Anderson, 2000; Hosaka *et al.*, 2002), inflammation (Wehling *et al.*, 2001), or oxidative stress (Dudley *et al.*, 2006).

The dystrophin–glycoprotein complex is also hypothesized to directly regulate the mitogen-activated protein (MAP) kinase and AKT signaling pathways in skeletal muscle (Rando, 2001; Batchelor and Winder, 2006). Early studies in support of this hypothesis documented *in vitro* binding of  $\beta$ -dystroglycan (Yang *et al.*, 1995a) and syntrophin (Oak *et al.*, 2001) to Grb2, an adaptor protein containing Src homology 2 and 3 domains that

couples receptor tyrosine kinases to MAP kinase cascades via small GTPase family members. More recent *in vitro* experiments have led one group to propose that laminin binding to  $\alpha$ -dystroglycan induces assembly of a syntrophin–Grb2–Sos1–Rac1–Pak1–JNK complex initiated by tyrosine phosphorylation of syntrophin and resulting in JNK activation (Oak *et al.*, 2003; Zhou *et al.*, 2006). Another group has reported that  $\beta$ -dystroglycan can directly bind either MEK or ERK alone *in vitro*, leading the authors to hypothesize that it serves a scaffold function important for MAP kinase signaling (Spence *et al.*, 2004). The relevance of both stories (Zhou *et al.*, 2006; Spence *et al.*, 2004) to the *in vivo* function of the dystrophin–glycoprotein complex remains to be demonstrated. In neither case have the signaling molecules actually been shown to interact with the fully assembled dystrophin–glycoprotein complex expressed in striated muscle. As noted previously, mice null for  $\alpha$ -syntrophin (Kameya *et al.*, 1999; Adams *et al.*, 2000),  $\beta$ -syntrophin (Adams *et al.*, 2004), or both genes (Adams *et al.*, 2004) exhibited no muscular dystrophy. Furthermore, the dystrophic phenotype of *mdx* mice was not improved by transgenic overexpression of dystroglycan (Hoyte *et al.*, 2004), Dp71 (Cox *et al.*, 1994; Greenberg *et al.*, 1994), or Dp116 (Judge *et al.*, 2006) even though the dystrophin–glycoprotein complex constituents necessary for signaling were restored to the sarcolemma.

To investigate a potential role for the dystrophin–glycoprotein complex in MAP kinase signaling *in vivo*, a number of groups have compared MAP kinase activity in muscle from wild-type and dystrophic mice lacking either dystrophin or  $\gamma$ -sarcoglycan (Kolodziejczyk *et al.*, 2001; Kumar *et al.*, 2004; Lang *et al.*, 2004; Nakamura *et al.*, 2001, 2002, 2005; Griffin *et al.*, 2005; Barton, 2006). Results have differed dramatically across studies even when the same MAP kinase was evaluated in the same animal model. Three studies found no difference in activated ERK1/2 of resting *mdx* muscle (Kolodziejczyk *et al.*, 2001; Nakamura *et al.*, 2005; Kumar *et al.*, 2004) while three others reported increased ERK1/2 activation in *mdx* muscle (Nakamura *et al.*, 2001, 2002; Barton, 2006). The activity of p38 in *mdx* muscle was not altered in four studies (Kolodziejczyk *et al.*, 2001; Kumar *et al.*, 2004; Nakamura *et al.*, 2005; Lang *et al.*, 2004), but was elevated in two others (Nakamura *et al.*, 2001, 2002). JNK1 was elevated in *mdx* in one study (Kolodziejczyk *et al.*, 2001) but was not found to be different from control in four others (Nakamura *et al.*, 2001, 2002, 2005; Kumar *et al.*, 2004). Even after taking into account the variation in animal ages and muscles analyzed, it is difficult to draw any firm conclusions over how defects in the dystrophin–glycoprotein complex may affect MAP kinase signaling. The results of several studies further suggest that a mechanotransduction pathway impinging on MAP kinase activation may be perturbed in muscle expressing a defective dystrophin–glycoprotein complex (Nakamura *et al.*, 2005; Kumar *et al.*, 2004; Griffin *et al.*, 2005; Barton, 2006), yet even

some of these data appear contradictory. ERK1/2 became more activated in stretched/exercised *mdx* muscle in two studies (Kumar *et al.*, 2004; Nakamura *et al.*, 2005), but activity was reduced by eccentric contraction in a third (Barton, 2006). Stretch had opposite effects on ERK1/2 activity when compared across two studies of  $\gamma$ -sarcoglycan null muscle (Griffin *et al.*, 2005; Barton, 2006). Finally, the activity of p38 was significantly enhanced in exercised *mdx* muscle (Nakamura *et al.*, 2005) but not in *mdx* muscle that was acutely stretched (Kumar *et al.*, 2004).

Toward a role for the dystrophin–glycoprotein complex in regulating Akt signaling in skeletal muscle, one group reported that disruption of laminin binding to  $\alpha$ -dystroglycan induced apoptosis in cultured myotubes accompanied by decreased Akt activity (Langenbach and Rando, 2002). It was suggested that loss of dystrophin–glycoprotein complex function may impair cell survival signaling through the Akt pathway with enhanced apoptosis contributing to dystrophic pathogenesis. However, two new studies have paradoxically reported elevated Akt activity in dystrophin-deficient *mdx* muscle (Dogra *et al.*, 2006; Peter and Crosbie, 2006). Moreover, transgenic overexpression of the antiapoptosis proteins ARC (Abmayr *et al.*, 2004) and BCL2 (Dominov *et al.*, 2005) failed to alleviate dystrophy in *mdx* muscle. Thus, it remains to be demonstrated that the dystrophin–glycoprotein complex directly regulates a signal transduction pathway or that its disruption directly alters muscle cell signaling in a manner that contributes substantively to the pathologies observed in dystrophic mammalian muscle. Alternatively, aberrant signaling may be an adaptive response by dystrophin-deficient muscle attempting to maintain homeostasis, or more interestingly, may be an adverse consequence of cytoskeletal remodeling (Rezniczek *et al.*, 2007).

## 4. FUNCTION IN MODEL ORGANISMS

### 4.1. *Caenorhabditis elegans*

Of three popular model organisms interrogated, the function of the dystrophin–glycoprotein complex is best understood in the nematode worm, *Caenorhabditis elegans*. The *C. elegans* genome encodes genes for dystrophin/utrophin (*dys-1*), dystroglycan (*dgn-1*), sarcoglycans, dystrobrevins (*dys-1*), and syntrophins (*stn-1*) (Bessou *et al.*, 1998; Gieseler *et al.*, 1999, 2001; Grisoni *et al.*, 2002, 2003). Mutations or RNAi that target each gene similarly cause a mild phenotype characterized by exaggerated head bending, hyperactivity, and hypercontractility (Bessou *et al.*, 1998; Gieseler *et al.*, 1999, 2001; Grisoni *et al.*, 2002, 2003). Mutations in *dys-1*, *dys-1*, and *stn-1* also show increased sensitivity to acetylcholine and the acetylcholinesterase inhibitor aldicarb, which suggested that the motility phenotypes

were due to altered cholinergic signaling (Bessou *et al.*, 1998; Gieseler *et al.*, 1999, 2001; Grisoni *et al.*, 2003). In support of this hypothesis, the *snf-6* gene encodes a novel acetylcholine transporter localized to the motor end plate of the *C. elegans* neuromuscular junction, *snf-6* binds to *stn-1*, and *snf-6* mutations phenocopy *dys-1*, *dyb-1*, and *stn-1* mutants (Kim *et al.*, 2004). Ablation of *dys-1* (Gieseler *et al.*, 2000), *dyb-1* (Gieseler *et al.*, 2001), or *snf-6* (Kim *et al.*, 2004) combined with a mildly affected mutant of *MyoD* (*hllh-1*) causes a more severe, muscle degeneration phenotype consistent with the more severely affected *mdx/MyoD<sup>-/-</sup>* double knockout mice (Megency *et al.*, 1999). Furthermore, microarray comparisons between wild-type and *dys-1* mutants revealed altered transcript profiles (Towers *et al.*, 2006) comparable to the differences reported for patients with Duchenne muscular dystrophy (Chen *et al.*, 2000). Interestingly, mutations that slightly impair contractility at several steps downstream of nerve–muscle communication can suppress muscle degeneration in *dys-1/hllh-1* double mutants (Mariol *et al.*, 2007). Thus, it appears that the dystrophin–glycoprotein complex in *C. elegans* primarily functions to localize a protein (*snf-6*) important for termination of neuromuscular transmission and when disrupted, hypercontractility can initiate muscle degeneration on a sensitized background. Finally, the phenotype of *dyc-1* mutants resembles that of *dys-1* mutants and *dyc-1* overexpression partially suppresses the *dys-1* phenotype (Gieseler *et al.*, 2000). *dyc-1* is homologous with mammalian CAPON, which interacts with neuronal nitric oxide synthase through its PDZ domain (Gieseler *et al.*, 2000) and is upregulated in dystrophin-deficient *mdx* muscle (Segalat *et al.*, 2005). Thus, studies in *C. elegans* may help explain why defects in the dystrophin–glycoprotein complex cause perturbations in the neuromuscular junction without apparent functional consequence in mammals (Section 3.2).

## 4.2. *Drosophila*

As in *C. elegans*, the *Drosophila* genome encodes homologues for dystrophin, dystroglycan, dystrobrevin, sarcoglycans, and syntrophin (Roberts and Bobrow, 1998; Neuman *et al.*, 2001; Greener and Roberts, 2000). Consistent with studies in mammals (Section 3) and worms (Section 4.1), genetic and RNAi-mediated knockdown of dystrophin or dystroglycan in *Drosophila* causes decreased mobility and age-dependent muscle degeneration (Shcherbata *et al.*, 2007). Also like *C. elegans*, *Drosophila* mutants lacking a large dystrophin isoform localized to the neuromuscular junction show enhanced neuromuscular transmission, but through elevated release of neurotransmitter from presynaptic sites (van der Plas *et al.*, 2006) rather than impaired postsynaptic uptake as found in the worm (Kim *et al.*, 2004). Interestingly, a hypercontraction-induced myopathy has been described in



*Drosophila* with mutations in the myosin heavy chain (*mhc*) locus (Montana and Littleton, 2004). While not directly relevant to dystrophin–glycoprotein complex function, comparison of transcript expression profiles of *Drosophila mhc* mutants with those from mammalian dystrophies suggested that compensatory cytoskeletal remodeling may be a common response to muscle disease that is conserved across species (Montana and Littleton, 2006).

### 4.3. Zebrafish

The small vertebrate zebrafish (*Danio rerio*) has emerged as a model system to study the function of the dystrophin–glycoprotein complex. Orthologs for dystrophin, dystroglycan, dystrobrevin, and sarcoglycans have been identified in zebrafish through a variety of approaches (Parsons *et al.*, 2002; Guyon *et al.*, 2003; Bassett *et al.*, 2003; Jin *et al.*, 2007; Steffen *et al.*, 2007). Ablation of dystrophin or dystroglycan results in loss of stable muscle attachments analogous to the myotendinous or myomuscular junction in mammals, impaired muscle integrity, and necrosis (Parsons *et al.*, 2002; Bassett *et al.*, 2003). A more recent study further identified an important role for dystroglycan in the formation of distributed neuromuscular synapses as opposed to the focal neuromuscular junctions almost exclusively studied in mammals (Lefebvre *et al.*, 2007). Most interestingly, a zebrafish mutant in the nicotinic acetylcholine receptor (*sofa potato*) was shown to suppress myopathy associated with dystrophin deficiency but did not suppress the myopathy caused by dystroglycan ablation (Etard *et al.*, 2005), similar to conclusions that emerged from a study of the zebrafish *candyfloss* mutant, a model of laminin-2-deficient muscular dystrophy (Hall *et al.*, 2007). These studies suggest that decreased contractility can reduce mechanically induced injury in dystrophin-deficient muscle, but they also suggest that the absence of dystrophin and dystroglycan induces different mechanisms of pathogenesis. In summary, the zebrafish is emerging as the model organism that may best recapitulate the functional deficits associated with dystrophin–glycoprotein complex abnormalities in mammals (Section 3), and that may also provide the most insight into poorly understood functions of the complex.

## 5. CONCLUDING REMARKS

In comparing the studies in mammals (Section 3) with model organisms (Section 4), we notice two distinct but interrelated pathways to muscle degeneration associated with defects in the dystrophin–glycoprotein complex. First, the cytoskeletal framework of muscle may be compromised to the point that it cannot protect muscle cells against the normal forces generated within. In the second pathway, defects lead to excessive force

production that appears to overwhelm an otherwise normal cytoskeletal support structure. In both cases, there are indications that dystrophic muscle attempts to compensate through cytoskeletal remodeling. It also seems likely that the dystrophin–glycoprotein complex plays multiple roles in mammalian muscle but that some model organisms may employ the complex for fewer, and perhaps only one function. In conclusion, comparing and contrasting results of dystrophin–glycoprotein complex studies across a wide range of organisms promises not only to shed light on its versatility, but also on secondary functions that are difficult to address solely in mammals.

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