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REVIEW ARTICLE

Is the fundamental pathology in Duchenne's muscular dystrophy caused by a failure of glycogenolysis–glycolysis in costameres?

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Abstract. Duchenne muscular dystrophy (DMD) is the most common form of progressive childhood muscular dystrophy associated with weakness of limbs, loss of ambulation, heart weakness and early death. The mutations causing either loss-of-expression or function of the full-length protein dystrophin (Dp427) from the *DMD* gene are responsible for the disease pathology. Dp427 forms a part of the large dystroglycan complex, called DAPC, in the sarcolemma, and its absence derails muscle contraction. Muscle biopsies from DMD patients show an overactivation of excitation-contraction-coupling (ECC) activable calcium incursion, sarcolemmal ROS production, NHE1 activation, IL6 secretion, etc. The signalling pathways, like Akt/PBK, STAT3, p38MAPK, and ERK1/2, are also hyperactive in DMD. These pathways are responsible for post-mitotic trophic growth and metabolic adaptation, in response to exercise in healthy muscles, but cause atrophy and cell death in dystrophic muscles. We hypothesize that the metabolic background of repressed glycolysis in DMD, as opposed to excess glycolysis seen in cancers or healthy contracting muscles, changes the outcome of these 'growth pathways'. The reduced glycolysis has been considered a secondary outcome of the cytoskeletal disruptions seen in DMD. Given the cytoskeleton-crosslinking ability of the glycolytic enzymes, we hypothesize that the failure of glycogenolytic and glycolytic enzymes to congregate is the primary pathology, which then affects the subsarcolemmal cytoskeletal organization in costameres and initiates the pathophysiology associated with DMD, giving rise to the tissue-specific differences in disease progression between muscle, heart and brain. The lacunae in the regulation of the key components of the hypothesized metabolome, and the limitations of this theory are deliberated. The considerations for developing future therapies based on known pathological processes are also discussed.

Keywords. Duchenne muscular dystrophy; muscle; metabolism; glycolysis; therapeutic interventions.

The *DMD* locus, the protein complex of dystrophin and the disease aetiology

Duchenne muscular dystrophy (DMD) is a severe, childhood-onset, progressive muscle-degenerative disease. Clinical symptoms typically include progressive muscle weakness apparent by around 3–5 years of age, pseudo-hypertrophy of calf muscles, Growers' sign, joint contractures, and loss of ambulation by 10–12 years of age. Patients surviving beyond 20 years often develop heart weakness, kyphoscoliosis, and breathing difficulties due to the diminishing capacity of the respective muscles. Some patients suffer from nonprogressive cognitive delay or disability. Lung failure was the primary cause of death before ventilators became available; now, it is majorly attributed to heart

failure (Wittlieb-Weber *et al.* 2020). A whole range of severity and disease progression is seen in patients with several genetic aberrations in the causal gene *Dystrophin* (*DMD/DYS*) (Bladen *et al.* 2015; Juan-Mateu *et al.* 2015).

The human *DMD* locus on chromosome Xp2.1 forms one of the largest genes, with 79 exons spanning 2.4 Mbp, coding for a ~14-kb mRNA (Koenig *et al.* 1987), which produces the protein dystrophin (Hoffman *et al.* 1987). The *DMD* gene transcribes several minor isoforms of dystrophin, abbreviated as Dp40, Dp71, Dp116, and Dp260, from internal promoters, but the absence of only the functional full-length isoform Dp427 is associated with DMD. The full-length isoform is expressed in skeletal muscle, heart, and brain from three different promoters. The two separate promoters produce Dp427b and Dp427p in brain regions, while

the Dp427m isoform from the third promoter is expressed in skeletal and cardiac muscles (reviewed by Blake *et al.* 2002). Mutations generating partially functional Dp427m lead to milder and late-onset Becker's muscular dystrophy (BMD). This locus is also responsible for X-linked dilated cardiomyopathy (XLDCM) without skeletal muscle phenotype. There could be several plausible reasons for the lack of muscle pathology in XLDCM (reviewed by Nakamura 2015), but the most accepted view is that the skeletal muscles alone upregulate the brain-specific isoforms of Dp427, and are hence spared (Muntoni *et al.* 1995).

The Dp427m protein is associated with the large membrane-associated dystroglycan complex (DGC), forming a larger complex called dystrophin associated protein complex (DAPC). The DAPC consists of roughly 28–30 proteins, connecting the extracellular matrix (ECM) to the subsarcolemmal cytoskeleton called 'costameres' (Peter *et al.* 2011) for lateral force transmission during muscle contraction (Ramaswamy *et al.* 2011). The costameric cytoskeleton is composed of several intermediate filaments like desmin, vinculin, dystrophin, nonsarcomeric F-actin, actinins, and microtubules. The DAPC with integrins forms a major hub by binding the costameric structures from the interior and laminins (also called merosin) in the ECM to perform structural, scaffolding, enzymatic and signalling functions, several of which are disturbed in DMD (Ervasti 2007). The mechanical fragility during muscle contraction is still considered primary pathology, which consequently leads to membrane lesions and ion incursion, oxidative stress, aberrant signalling, apoptosis or necrosis, inflammation, fibrosis and ultimately loss of functional muscles.

The molecular details behind most of these pathological pathways have been discerned with the help of the *mdx*-mouse model of DMD. The therapeutic strategies that ameliorated the *mdx* pathology have consistently failed during clinical trials. Newer approaches, such as gene therapies, are starting to show promise in clinical trials, but are not applicable or accessible to all patients. In addition, the immune response towards vectors or transgene continues to be a cause of concern.

The disease escape by Jagged1 overexpression in a severe golden retriever model of DMD (GRMD) shows that dystrophin or upregulation of its embryonic paralogue utrophin need not be invoked to rescue this disease (Vieira *et al.* 2015). This demands a look at the pathological processes involved into more defined cause-effect relations, which could then direct the therapeutic approaches independent of dystrophin, hence useful for all DMD patients. This review discusses the more accepted hypotheses and their contribution to understanding disease pathology. Also, the possibility of a lack of glycogenolysis–glycolysis derived energy in costameres as the primary initiator of pathology and considerations for therapy development based on the collectivity of pathological processes described in DMD.

The mechanical fragility and membrane damage hypothesis

Classically, the DAPC and integrins bound to trimeric laminins in the ECM, and several cytoskeletal elements in the subsarcolemmal region, provide mechanical support or stability during muscle contraction. The absence of dystrophin causing increased membrane lesion, injury, and death has been proved beyond doubt by several early studies. Thus, the prevalent hypothesis is that the protein dystrophin provides a passive scaffold or shock absorber to the subsarcolemmal cytoskeleton during muscle contraction, which is compromised in DMD (Le *et al.* 2018). The direct mechanical stiffness measurements with the help of atomic force microscopy on *mdx* myotubes found contrasting results (Puttini *et al.* 2009; Canato *et al.* 2010). While recent human *in vitro* muscle culture studies showed early fatigue in dystrophic conditions (Uchimura *et al.* 2021). It is now known that in the subsarcolemmal regions, the actin and microtubule filaments are actively reformed to maintain force and structure during muscle contraction. This goes against the idea of maintaining passive tension by binding of dystrophin to the cytoskeleton.

Yet, the idea of DAPC, integrin-mediating mechanical forces, has some foundation. Sarcospan, a small protein of these complexes, increases binding between DAPC and integrin. Human and mouse sarcospan overexpression rescued pathology in *mdx* (Gibbs *et al.* 2016) and improved cardiac phenotype (Parvatiyar *et al.* 2019). The sarcospan-mediated utrophin-DGC-integrin α 7 β 1 amelioration of DMD requires Akt/PKB activation (Marshall *et al.* 2012); however, utrophin (Utr) can rescue *mdx* even in the absence of sarcospan (Gibbs *et al.* 2021) indicating that these mechanisms are much more complicated. However, the fact that the never-resting cardiac muscles, suspended in the chest cavity, develop the pathology about a decade after the skeletal muscles do not support this mechanical fragility hypothesis. Despite the downregulation of DAPC components in DMD (Ervasti *et al.* 1990), later studies found only a small fraction of DAPCs contain dystrophin or Utrophin, and complex formation is not affected in its absence (Johnson *et al.* 2013). While overexpression of dystroglycan or sarcoglycan did not rescue *mdx* pathology, double knockout increased the severity of disease in *mdx* (Zhu *et al.* 2001; Hoyte *et al.* 2004; Li *et al.* 2009), indicating that intersecting but distinct pathological mechanisms in DMD than other forms of MDs.

As a part of costameres, integrin can possibly compensate for many of the DAPC functions. The protective functions of integrins against overload exercise are well-known (reviewed by Boppart and Mahmassani 2019). The overexpression of β 1D alone or α 7 β 1 integrin (major isoforms of muscle integrins) is able to amend the pathology in *mdx* (Burkin *et al.* 2001; Liu *et al.* 2012). Compensatory integrin

upregulation is seen in animal models and patient biopsy samples (Hodges *et al.* 1997). The gold-standard therapy, treatment with steroids, has also been shown to work via integrin activation (Wuebbles *et al.* 2013) and has consistently delayed several aspects of the disease progression in patients, despite its side effects (Schram *et al.* 2013; Matthews *et al.* 2016; Marden *et al.* 2020).

Although the membrane damage hypothesis was based on patient biopsy findings (Mokri and Engel 1975), later studies could not support this (reviewed in detail by Hutter 1992), as the properties of lipids contribute toward the fluidity of membranes more than that of proteins. The mutations in several DAPC components have been associated with other muscular dystrophies; the absence of desmin, vinculin or merosin, which causes a more severe form of congenital muscular dystrophy (MDC1A), does not cause membrane damage (reviewed by Ervasti 2007). Many of these proteins are other members of costameres capable of regulating F-actin in subsarcolemmal regions where dystrophin functions.

In normal muscles, it is known that membrane lesions routinely appear during exercise but get repaired either in a Ca^{2+} and ATP-dependent manner (reviewed by Barthélemy *et al.* 2018) or mediated by dysferlin. In DMD, however, dysferlin-mediated membrane repair is upregulated (Vila *et al.* 2017; Capitanio *et al.* 2020). This suggests that, given the high levels of Ca^{2+} and dysferlin, it must perhaps be the shortage of ATP itself which is the limiting factor for membrane repair. Hence, low energy production during contraction is more likely to result in increased membrane lesions in DMD.

The dynamics of costameric cytoskeleton organization require energy

Microtubules (MT) and nonsarcomeric F-actin form an active cytoskeleton in the costameres. The extensive microtubule (MT) networks of muscles are in perpendicular orientation to sarcomeres; hence, are important for horizontal force transmission and synchronization of the Z-lines. Studies have demonstrated that when this microtubule network is disrupted, there is an increase in cellular ROS and calcium levels (Kerr *et al.* 2015; Coleman *et al.* 2021). Since dystrophin is an MT-binding protein, its absence is hypothesized to directly result in MT-mediated initiation of pathology (Rando *et al.* 2002) via increased ROS and calcium (Prosser *et al.* 2013; Kerr *et al.* 2015; Coleman *et al.* 2021). But this cause-effect correlation is confounded by the observation that increased ROS itself can mediate MT disruptions (Loehr *et al.* 2018).

During muscle contraction, MT dynamics increase. In contracting *mdx* muscles, the initial rate of MT polymerization is high but is not maintained, forming short and dense MT networks (Oddoux *et al.* 2019). This MT shortening cannot be linked to the lack of dystrophin, which

inhibits the polymerization of MT (Belanto *et al.* 2014). On the other hand, the high MT density in dystrophic muscles is attributed to low depolymerization due to the detyrosination of tubulin (Kerr *et al.* 2015). This detyrosination is considered to be the consequence of the stable (polymerized) state of microtubules rather than the cause (Sanyal *et al.* 2021). Interestingly, the detyrosinated tubulins cannot repolymerize, and retyrosination of tubulin by the tubulin tyrosine ligase (TTL) requires ATP and L-tyrosine. The repolymerization of monomeric actin and tubulins also requires the exchange of bound ADP and GDP for ATP and GTP, respectively. This phenomenon emphasizes that there must perhaps be an underlying ATP crisis in the case of DMD.

A couple of findings vindicate this argument. First, the fact that in *mdx*, utrophin or micro-dystrophin, both lacking the MT binding domains, rescued the pathology without restoring microtubule organization (Belanto *et al.* 2016).

Second, the phenomenon of increased free monomeric tubulin binding to voltage-dependent anion channel (VDAC) and reduced ADP stimulation of mitochondria does not hold true for the pathology in DMD (Ramos *et al.* 2020). Together, these point against the microtubule theory of pathology initiation. Hence, we hypothesize that low energy and amino acid levels affect the dynamics of the costameric cytoskeleton resulting in disorganization.

The glycolysis-derived energy for calcium reabsorption during ECC

Membrane depolarization, in response to neuronal stimulation, causes the ingress of extracellular Ca^{2+} , and the activation of ryanodine responsive (Ryr) calcium release channels, in the sarcoplasmic reticulum (SR), leading to the amplification of excitation contraction coupling (ECC). The sudden ingress of calcium allows myosin and actin to come in contact, thus, allowing contraction. These calcium spikes are crucial for muscle activity. Hence, several types of calcium channels and pumps function coordinately. In DMD, several types of calcium channels are aberrant, resulting in pathology mediated by persistent levels of calcium and calcium-dependent proteases (reviewed by Mareedu *et al.* 2021). Yet, therapeutic targeting of these has consistently failed, pointing to defects in calcium reabsorption (reviewed by Duan *et al.* 2021).

The Ca^{2+} -ATPases (SERCA) in the SR reabsorb Ca^{2+} by expending ATP. The SERCA-1 overexpression rescued the more severe DMD/Utr double knockout mice (Mázala *et al.* 2015). SERCA activity can be modulated in two ways. First, available ATP. In fact, creatine supplementation, by increasing the phosphocreatine energy stores, improved the Ca^{2+} handling via Ca^{2+} /ATPase activity, in *mdx* (Pulido *et al.* 1998). The creatine-phosphocreatine cycles ATP only for a few seconds, and thereafter, glycolysis-derived ATP is used for SERCA and other ion pumps during the early stage of contraction. Second, the

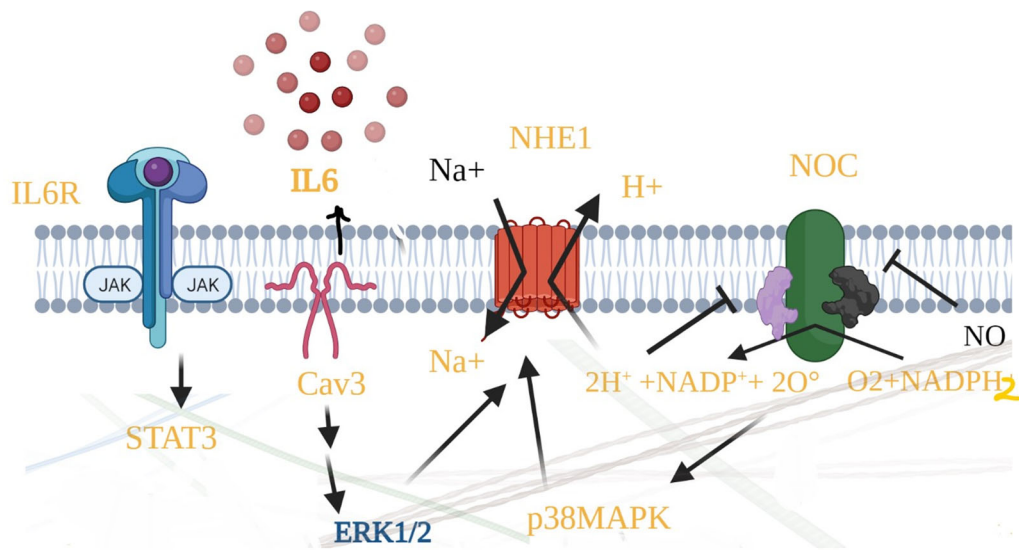


Figure 1. ECC or mechanical stretch activable processes involved in the pathology of DMD.

muscle-specific Acyl or acetyl phosphatase (ACYP2) can remove phosphate from SERCA to regulate calcium. Interestingly, ACYP2 can increase the glycolytic volume by removing product inhibition of enzymes of the pathway (Stefani *et al.* 1997), and the TCA volume by cleaving acetyl phosphate (Xu *et al.* 2018). However, in DMD, ACYP2 has been reported to have low activity (Landi *et al.* 1986), but its implications remain unstudied. This finding further corroborates the underlying energy deficiency in DMD.

The higher NADPH levels lead to elevated ROS burst and NHE1 activation

The primary sources of ROS in dystrophic muscles are considered to be mitochondria (Hughes *et al.* 2019), xanthine oxidase (XO) (Lindsay *et al.* 2018) and NADPH oxidase complex (NOC). First, calcium persistence is considered to cause mitochondrial ROS generation (Rybalka *et al.* 2014), which in turn is attributed to the low activity of SERCA in DMD (previous section). Second, the possible reasons for XO upregulation in DMD could be due to high purine breakdown. This can also increase uric acid, as seen in patients. However, clinical trials with XO inhibitors were discontinued due to a lack of benefits.

Third, there are five different *Nox* genes that encode the catalytic subunit of the NOC, of which Nox2 and Nox4 are active in muscles. Nox4 is constitutive and ER-associated, while Nox2, present in the cell membrane complex, is activated by mechanical stretch during exercise (Xia *et al.* 2003), and converts NADPH₂ and O₂ to NADP⁺, 2 \dot{O} , and

2H⁺. The ROS augments membrane depolarization during ECC and force production (reviewed by Roy *et al.* 2017), and is necessary for adaptation to exercise (reviewed by Powers *et al.* 2010). The NOC can auto-inactivate as local acidic pH from its own H⁺ generation can reduce its activity significantly (Brennan-Minnella *et al.* 2015). To continue its activity, contracting muscles expulse H⁺ ions in exchange for Na⁺ through a channel called NHE (NHE1 is predominant in the heart muscles). In fact, this Na⁺ in turn can further increase Ca²⁺ ingress by Na⁺/Ca²⁺ exchangers. This sequence of mechanical stretch- NOC-NHE1 activation should be reversed at the end of the ECC. The NHE1 inactivation would increase local pH and inactivate NOC.

The Nox2 containing NOC is responsible for the pathogenic levels of ROS generated in the muscles of *mdx* mice (Whitehead *et al.* 2010). In DMD, one of the reasons for the higher oxidative burst from NOC could be high NADPH levels (Gupte *et al.* 2006) generated by the increased pentose phosphate pathway (PPP) metabolism. Another possibility is the lack of an inactivating mechanism at the end of the contraction. NHE1 is hyperactive, contributing to DMD pathology in skeletal and cardiac muscles (Bkaily and Jacques 2017). Although NHE1 hyperactivity has been attributed to ATP receptor P2A in *mdx* (Iwata *et al.* 2007), its other regulators like p38 MAPK, ERK1/2, calcineurin, PTPN11, etc. are anomalous in DMD, as discussed in following sections. NHE1 inhibitors, as therapy for DMD, are under clinical trials (Previtali *et al.* 2020) as they potentially target skeletal muscle and heart pathology simultaneously. It is important to note that the calcium ingress, membrane ROS production, and NHE activation are all part of the normal ECC; hence therapies targeting these may affect normal muscle function and should be considered carefully.

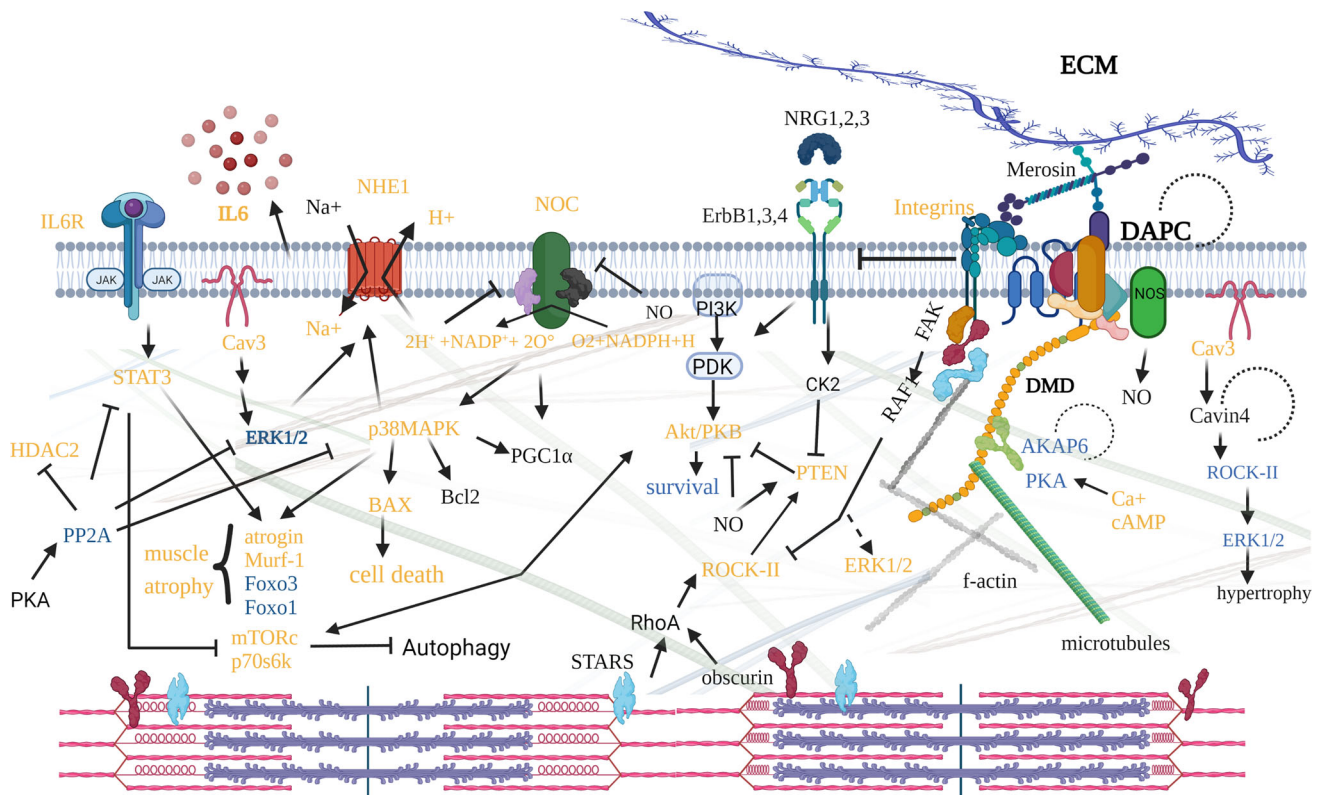


Figure 2. The pathology-associated pathways in detail. Yellow represents hyperactive pathways, and blue represents hypoactive pathways. Black represents either unaffected or undetermined activity. The dotted semicircle represents the mislocalization of proteins.

The hyperactive ‘growth pathways’ elicit pathology in DMD against the backdrop of altered metabolite fluxes

Muscle contraction and growth are intrinsically linked. The interesting feature of DMD is activity-induced muscle atrophy via hyperactivity of the very signalling pathways that stimulate growth in response to exercise in normal muscles (figure 2). Some of these pathways include p38 MAPK, ERK1/2, and AKT signalling. The activation of the p38MAPK pathway during exercise occurs via several mechanisms (Combes *et al.* 2015), as it is required for metabolic adaptation (reviewed by Bengal *et al.* 2020) by stabilizing and activating PGC1- α (Fan *et al.* 2004). In cardiac muscles, p38MAPK activity protects against stress-mediated telomere shortening (Ludlow *et al.* 2017). However, in DMD, the reasons behind why P38MAPK activates Bax-mediated apoptosis (Wissing *et al.* 2014), instead of PGC1- α remain unclear. The presence, in DMD patients, of other activators of PGC1- α , like ROS (Nalbandian *et al.* 2019), calcium-calmodulin (Handschin *et al.* 2003) suggests that PGC1- α activity might, in fact, be high, although it has not reported. Moreover, in DMD, PGC1- α could be behind upregulation of its target uncoupling protein 2 (UCP2) (Markham *et al.* 2017), which is thought to shunt the mitochondrial electron potential towards heat production instead of ATP.

The ERK1/2, via a broad range of effectors, stimulates Akt/PKB-independent muscle growth (Hodson *et al.* 2019) in response to exercise (reviewed by Long *et al.* 2004). The ERK1/2 activation occurs in two different microenvironments in skeletal muscles; (i) membrane-associated caveolin-3-cavin4-mediated (similar to heart, discussed in caveolae section), and (ii) sarcomere-associated proteins, like obscurin and STARS, which activate the ERK1/2 via ROCK in a Rho/Rac dependent manner (Ford-Speelman *et al.* 2009). Protein levels of obscurin are upregulated, while the STARS, RhoA and SRF are downregulated in DMD patients (Capitanio *et al.* 2020). Downstream of ERK1/2, lies in different effectors, such as Janus Kinase (JNK) (Long *et al.* 2004), the CREB binding protein (CBP), and Sphingosine kinase. However, the details of its contribution to dystrophic pathology remain elusive. On the other hand, the overexpression of CPB (a part of histone acetylase complex CBP/p300) rescued the *Sapje* zebrafish model of DMD (Bajanca and Vandel 2017). Sphingosine Kinase (S1PK) generates sphingosine-1-phosphate (S1P) (Pitson *et al.* 2003). Increasing S1P levels, improved regeneration (Ieronimakis *et al.* 2013), in a STAT3-dependent manner (Loh *et al.* 2012), to rescue the *mdx* pathology, when its degradation enzyme, SP lyase (SPL), was chemically inhibited. This suggests that in dystrophic muscles, ERK1/2 is unable to either activate its targets, such as S1PK or CBP, or, despite their activation, these effectors are nonfunctional.

Interestingly, it has been shown that nutritional and acetylation status can have an impact on PGC1- α and S1PK activity (Dominy *et al.* 2010; Yu *et al.* 2012), determining their pro-growth function. Thus, the lack of glycolysis-derived acetyl and other metabolites, in DMD, can subvert the expected outcomes of these growth and survival pathways.

Akt/PKB and PTEN regulating muscle mass in DMD-an indirect consequence of low glycolysis?

The Akt/PKB is a well-known pathway for cell survival and growth in various tissues, including skeletal muscles, by stimulating protein synthesis and inhibiting proteasomal degradation (reviewed by Schiaffino and Mammucari 2011). As an autophagy inhibitor, Akt/PKB is not activated in response to muscle contraction, but rather responds to nutritional cues, like insulin (Deldicque *et al.* 2008). One of its inactivating phosphatases, PTEN, gets activated by sarcomere-associated RhoA during normal muscle contraction. However, there is controversy because, despite the hyperactivity of PTEN (Feron *et al.* 2009), in DMD, the Akt/PKB remains highly active (Peter and Crosbie 2006). Other factors, such as regenerating fibres (Peter and Crosbie 2006), or upregulated integrin signalling (Boppart *et al.* 2011) could contribute to Akt/PKB hyperactivity in this case.

Besides stimulating protein synthesis, Akt/PKB-mTORC signalling promotes muscle growth by inhibiting autophagy. Although beneficial in normal muscles, this same pathway, in DMD, contributes to pathology, also by reducing the efficiency of autophagy (De Palma *et al.* 2012; Yazid and Hung-Chih 2021). While chemical inhibition of PTEN rescued the dystrophic phenotype in animal models (Alexander *et al.* 2014; Vieira *et al.* 2017; Yue *et al.* 2021), Akt/PKB activation by IGF1 treatment failed to improve muscle function during clinical trials despite improving muscle mass in DMD patients (Rutter *et al.* 2020). This reiterates that although nutritional cues or ECC-activable signalling are intact in DMD, their outcomes are altered, which could be due to the unique metabolic background of dystrophic muscles.

The muscle protein synthesis and autophagic renewal connected to energy starvation

Autophagy removes dysfunctional organelles and recycles material for the proper functioning of cells and tissues. The details of the autophagic pathway in skeletal muscles have been reviewed extensively (Xia *et al.* 2021), where AMPK and mTOR emerge as major positive and negative regulators, respectively. The trimeric AMPK, which has several subunit isoforms responding to different cues, acts as a major energy sensor in several tissues (KjØbsted *et al.* 2018) to mitigate energy scarcity by upshifting catabolism. When

activated by increasing AMP/ATP, and ADP/ATP ratios in contracting muscles, AMPK stimulates glucose uptake (Cokorinos *et al.* 2017), glycogenolysis, and proteolysis by removing the mTOR-mediated block on autophagy (reviewed by Garcia and Shaw 2017); inhibits FA synthesis and stimulates FAO (Wu *et al.* 2017).

It seems, however, that in dystrophic muscles, AMPK-based energy-sensing mechanisms fail despite high levels of its stimulators, like ADP, liver kinase B1 (LKB1), and calcium/calmodulin-dependent protein kinase kinase (CaMKK). As discussed in the previous section, the reduced efficiency of autophagy has largely been attributed to Akt/PKB-mTOR in DMD. Independent of Akt/PKB, phospholipase D (PLD) can also activate mTOR via its product phosphatidic acid (O'Neil *et al.* 2009). Because PLD is mechanically stimulated by contraction (Vandenburgh *et al.* 1993), its higher activity in DMD (Touboul *et al.* 2005; Dabaj *et al.* 2021) could contribute to the pathology.

Stimulation of autophagy by Simvastatin (Verhaart *et al.* 2021; Mucha *et al.* 2021) or knocking out its negative regulator TRAF6 (Hindi *et al.* 2014) failed to ameliorate the *mdx* pathology. Treatment with aminoimidazole-4-carboxamide ribonucleotide (AICAR), a known activator of AMPK, ameliorated pathology in *mdx* (Ljubicic *et al.* 2014; Bueno Júnior *et al.* 2012; Pauly *et al.* 2012) in a utrophin-dependent manner (Al-Rewashdy *et al.* 2015), although utrophin upregulation alone, as therapy, has not been successful yet (Wilkinson *et al.* 2020). It seems that the AMPK-based catabolic shift is only transiently required during contraction as long-term AMPK activation attenuated the adaptive metabolic response (Ljubicic *et al.* 2012). However, AICAR treatment stimulates IL6 expression from human myotubes (Weigert *et al.* 2007), which is considered pathological in DMD, and hence, it may not serve as a promising drug candidate for human patients. Another activator of AMPK, Metformin, has shown nonstatistical, but clinically relevant improvement in patients, when supplemented with L-citrulline amino acid (Hafner *et al.* 2019). Thus, when viewed in the context of energy starvation, stimulation of autophagy allows proteins to be used for energy production, but results in loss of muscle mass, and its inhibition preserves muscle structure, but reduces the energy needed for muscle function; this is the tight-rope toed by DMD.

The mystery of dysfunctional phosphatases in DMD

As discussed previously, muscle contraction results in activation of the calcium cascade and CaM Kinases, ERK1/2, p38MAPKs, etc. To counterbalance the activities of these kinases, several phosphatases also get activated. Although PP2A impinges on and inhibits several of the hyperactive signalling pathways described in DMD pathology (review by Eichhorn *et al.* 2009), it has not yet been considered a target for treating DMD. For example, compound FTY720,

an activator of PP2A (Saddoughi *et al.* 2013), has not been evaluated in DMD models. FTY720 has ameliorated LGMD2C in mouse models (Heydemann 2017), though the rescue is attributed to S1PK receptor (S1PKR) activation and not that of PP2A. PP2A can oppose cardiac hypertrophy via HDAC2 inhibition (Yoon *et al.* 2018), making it a promising therapeutic candidate.

The calcium–calmodulin-dependent phosphatase (calcineurin) PP2B activity is low despite high calcium in DMD. Its overexpression or activation rescued the *mdx* phenotype (Stupka *et al.* 2006; Delacroix *et al.* 2018). The calcineurin rescue is considered to be via activation of a transcription programme required for the transition of fast to slow oxidative type muscles, which are preserved longer in DMD. But, in DMD, the antagonist of calcineurin-mediated muscle-type transition, myospryn/AKAP6, is already low, as it depends on dystrophin for its localization and activity (Kielbasa *et al.* 2011). AKAP6 mislocalization also deregulates PKA activity (Reynolds *et al.* 2008) in the subsarcolemmal compartment, which, among its many targets, also regulates PP2A and PP1.

During exercise, PKA is also activated by cAMP generated by adenylyl cyclases. The cAMP and cGMP act as second messengers to nitric oxide signalling, which is considered to be low in DMD. Hence, increasing cAMP/cGMP by inhibiting cAMP/cGMP degrading phosphodiesterase (PDE) seemed like a promising two-fold therapy. However, two such PDE inhibitors, sildenafil and tadalafil, failed in clinical trials, exacerbating patient conditions (Timpani *et al.* 2020).

Protein phosphatase-1 (PP1) localizes in different compartments in skeletal muscle. The glycogen-bound PP1 regulates intermediary metabolism via PKG, where its activity depends on insulin and adrenalin signalling (reviewed by Aggen *et al.* 2000). PP1 is upregulated in a GSK3 β -dependent manner in *mdx* (Villa-Moruzzi *et al.* 1996), despite the low intermediary metabolism in dystrophic muscles (discussed in later sections). The GSK3 β (and GSK3 α), identified for regulating glycogen synthase (GS) activity, does not respond to muscle contraction (Wojtaszewski *et al.* 2001), and can inhibit PGC1- α , and calcineurin signalling. GSK3 β has a reciprocal inhibitory relation with insulin/IGF1-stimulated Akt/PKB (reviewed by Mirzoev *et al.* 2021). Thus, inhibiting GSK3 β can improve several aspects of pathological processes, including reducing glucose levels by glycogen synthesis, but cannot stimulate glycogenolysis–glycolysis in response to exercise.

The caveolae, caveolin-3 and IL6-STAT3 dysbalance in DMD

There is an increase in membrane caveolae and associated protein caveolin-3 (Cav3) in DMD patient muscles (Repetto *et al.* 1999; van Westering *et al.* 2020). The Cav3 upregulation could either be an adaptative response to differentiation and mechanical defects seen in dystrophic muscles

(Pradhan and Prószyński 2020) or a direct consequence of p38MAPK hyperactivity (Galbiati *et al.* 1999). The Cav3 and its associated cavins 1, 2, 3, and 4 localize to membranes of various cells, while Cav4 is enriched in heart and skeletal muscles. Cav4/MRUC activates Rho/ROCK pathway during cardiac dysfunction and activates the ERK1/2 pathway in caveolae to drive cardiac hypertrophy (Ogata *et al.* 2008, 2014). Recent findings suggest that the association of Cav4 with the membrane is disrupted in the *mdx* heart, which cannot be rescued with mini dystrophin (Wang *et al.* 2021).

IL6 released from exercising muscles (Pedersen and Febbraio 2008) activates STAT3 transiently, as opposed to constitutively, in DMD. IL6 is considered pathological as its inhibition rescued DMD/Utrn DKO mice (Wada *et al.* 2017). IL6 also upregulates neuregulin (NRG/HRG) cleavage-mediated ligand activation (Juretić *et al.* 2017), which correlates with exercise-induced activation of its ErbB (1,2,3,4) receptors (Lebrasseur *et al.* 2003). The study also found that IL6-NRG-ErbB stimulates utrophin transcription in *mdx* via the ERK pathway (Juretić *et al.* 2017). IL6 is also considered an energy sensor (Kistner *et al.* 2022) and can stimulate glucose and fatty acid oxidation in contracting muscles (Al-Khalili *et al.* 2006; Trinh *et al.* 2021), possibly via AMPK (Carey *et al.* 2006). Thus, the underlying metabolic deficiency could be driving the IL6 secretion in DMD.

Chronic activation of STAT3 can lead to muscle atrophy via Murf-1 and atrogen1 (Zhang *et al.* 2013). However, in dystrophic conditions, Murf-1, atrogen-1, CHIP or NEDD4 are not responsible for the observed pathological proteasomal degradation (Assereto *et al.* 2016). Studies on DMD/Utrn DKO mice have shown that STAT3 is required for the repair and regeneration via the muscle stem cells (Zhu *et al.* 2001), and thus it may not be a promising therapy candidate. The mitochondrial localization of STAT3 depends on p300-mediated acetylation (Xu *et al.* 2016), which is considered as an important modulator of energy metabolism in various tissues, including the heart (Meier *et al.* 2017). Although muscle-specific knockout of STAT3 does not hamper energy production and exercise capacity (Dent *et al.* 2019) in nondystrophic mice, it could be a contributing factor in DMD, because of the disturbed metabolic landscape, which needs further investigation.

The histone deacetylases inhibition mitigates low acetyl levels to improve patient histopathology

The emerging details of all classes of HDACs on skeletal muscles and exercise have been reviewed (Tian *et al.* 2020). Many of the HDACs are involved in myogenesis, as expected. The activity of only HDAC2, out of HDAC1, 2, 3, and 8, in DMD patient samples, was found to be high (Colussi *et al.* 2008). Though reduced NO levels could contribute to higher HDAC2 activity in DMD (Colussi *et al.* 2008), increasing NO signalling as a strategy for BMD and

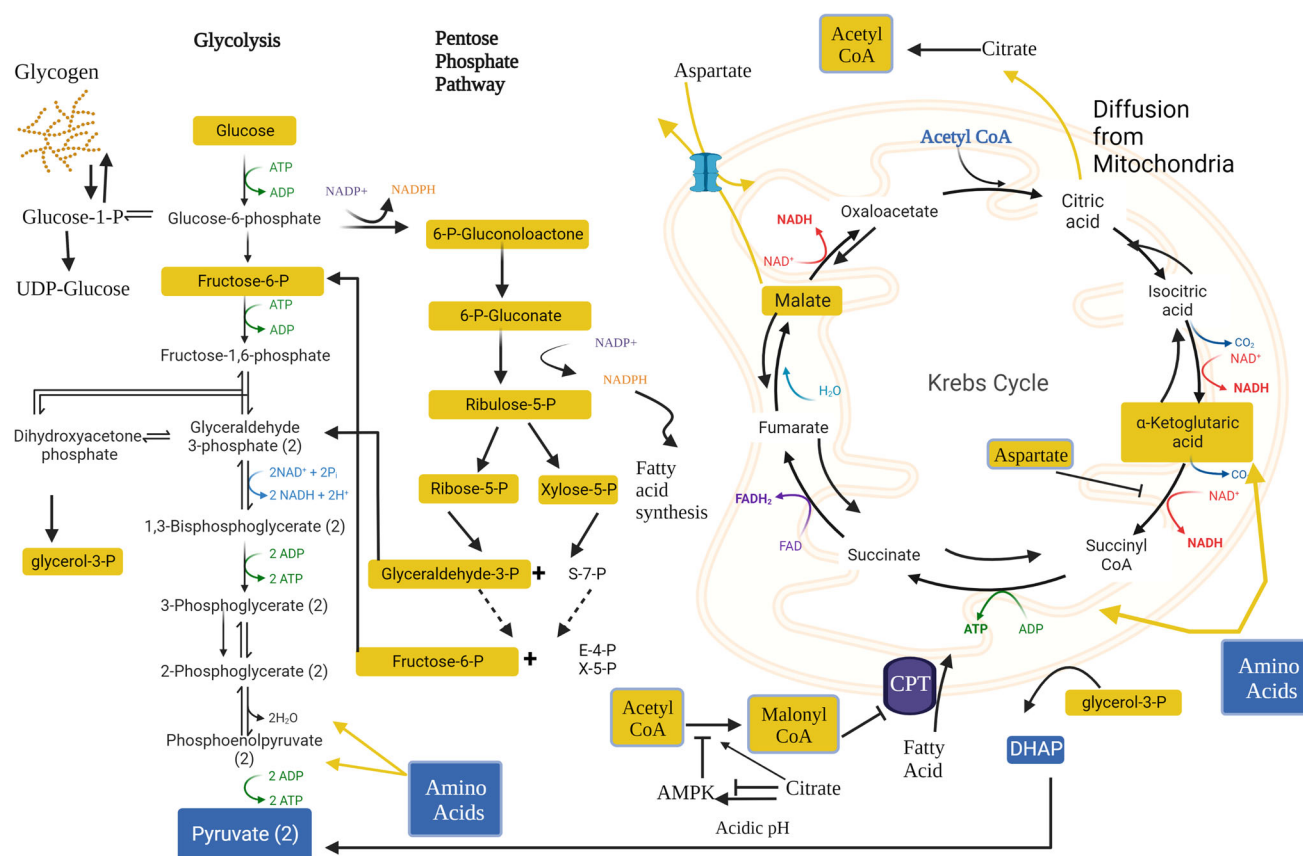


Figure 3. Glucose metabolism pathways. Yellow represents higher metabolite levels; blue represents lower metabolite levels.

DMD therapy failed. The knockout of HDAC1-2 in nondystrophic mice resulted in a blockage of autophagy in muscles, whereas a high-fat diet removed the block, improving muscle function (Moresi *et al.* 2012). In a recent study (Li *et al.* 2021), HDAC2 overexpression protected muscles against cigarette smoke-induced atrophy and senescence. Further, the HDAC class1 and class2 inhibitors reduced SERCA activity in zebrafish muscles (Simmonds and Seebacher 2017). The SERCA activity is required for calcium reabsorption in muscles, and its lower activity contributes to higher calcium-mediated pathology in DMD (Schneider *et al.* 2013; Voit *et al.* 2017; Mareedu *et al.* 2021). Thus, HDAC2 inhibitors as a therapy for DMD should be considered carefully.

The exercise-mediated nuclear export of HDAC4 and HDAC5 in an AMPK and CaMKII-dependent manner has been reported in healthy individuals (McGee *et al.* 2009) but has not been described in dystrophic conditions yet. Whether the activities of HDAC 4, 5, 7, and 9 are altered in DMD patients is not known. The pan HDAC inhibitor ‘Givinostat’ improved muscle pathology in DMD patients, for which clinical evaluation for functional aspects is ongoing (Bettica *et al.* 2016). HDAC inhibition may mitigate the low acetyl levels, by influencing the acetylation span of proteins, despite

limiting acetyl availability. This could be the reason behind the positive outcomes of the HDAC inhibitor treatment on patient muscle biopsies (NCT02851797) though functional improvements are yet to be seen.

The stimulation of another class of deacetylases, NAD⁺ dependent sirtuins or SIRT is also being developed as DMD therapy. Most of the evidence of SIRT involvement has been indirect, via rescue in the *mdx* model by resveratrol (reviewed by Kuno and Horio 2016). Though SIRT1, in DMD patients, was shown to be upregulated at transcript levels, its protein level in plasma remained unchanged (Rossi *et al.* 2021). The activity of sirtuins has not yet been reported in DMD patient muscles. Unlike the metabolic enzymes, sirtuins convert NAD⁺ to NAM with their activity; thus, activating sirtuins could lead to a reduction of NAD levels, which are already low in DMD. However, efforts to enrich NAD⁺ in muscles by supplementation with precursors or inhibition of ADP-ribosyl cyclases (that use NAD⁺) did not improve the *mdx* pathology (Frederick *et al.* 2020). During glycolysis or mitochondrial TCA, only the redox state of NAD is interchanged without changing the total concentrations; thus, NAD concentration, by itself, cannot improve energy levels if glycolysis is repressed.

The theory of glycolysis as secondary pathology in DMD

Since the first description of the disease, its aspects of metabolic and energy deficiency have been studied in detail (reviewed by Timpani *et al.* 2015). The main features of dystrophic muscles are low glycogenolysis, glycolysis, fatty acid oxidation (FAO), excess amino acid catabolism, fatty acid synthesis, and PPP (figure 3). The TCA cycle is blocked at the α -ketoglutarate stage, lowering ETC-OXPHOS and ATP synthesis. The levels of metabolites are correspondingly high glucose, fructose-6-P, α -ketoglutarate, phosphatidic acid, sphingolipids and ADP, and low acetyl, pyruvate, branched amino acids, glutamine/glutamate and ATP (Sharma *et al.* 2003; Srivastava *et al.* 2018, 2020; Dabaj *et al.* 2021). Despite the pervasive glycolytic deficiency observed, because octanoate (whose catabolism is independent of glycolysis) failed to rescue the mitochondrial defects (Chinet *et al.* 1994), the mitochondrial deficiency was considered as an independent and primary defect. This does not correlate with the fact that primary mitochondrial deficiency invariably upregulates glycolysis, as seen in mitochondrial dystrophies (Arnold *et al.* 1985). The common mitochondrial pathology should also affect more oxidative tissues (brain and heart) earlier than less oxidative, glycolytic-type muscle, which contrasts with what is seen in DMD.

The early study compared glycogen and glucose metabolism between neurogenic muscle diseases and progressive muscular dystrophies, like DMD, LGMD, myotonic dystrophy, FSHD, and found that early-stage repression of these processes is common to all muscular dystrophies, and, hence, should be considered as a secondary pathology instead (Di Mauro *et al.* 1967). However, there are several key differences in terms of disease onset, abnormalities of ECC, slow versus fast muscle type affected, or defects of muscle formation, that set these diseases apart from DMD, where repression of glucose metabolism could be a secondary pathology or an adaptive response. For example, in the case of myotonic dystrophy, there is prolonged contraction (inability to return to resting state), where repression of glycogenolysis–glycolysis could be adaptive.

The detailed discussion about several types of muscular dystrophies with respect to glucose metabolism is beyond the scope of this review. The distinguishing aspects of DMD are normal resting ATP/ADP ratio and normal ECC (Mancinelli *et al.* 1989), which makes the failure of glycogenolysis–glycolysis more pertinent to the pathological mechanism. If dystrophic muscles are mechanically inefficient at contraction, there should be compensatory metabolic upregulation even during rest, which is not seen in DMD. The increased proteolysis and amino acid catabolism for energy production also oppose the notion that glycolysis is actively or adaptively repressed in DMD. The high α -ketoglutarate level inhibits ATP synthase (Chin *et al.* 2014), and increases fibrosis (Ge *et al.* 2018). Yet, an α -

ketoglutarate supplement was able to rescue the *mdx* pathology (Cai *et al.* 2018). This suggests that blocking the TCA cycle at α -ketoglutarate, is a mitochondrial adaptive response in the face of the limited availability of glucose-derived pyruvate, so as to limit protein degradation. As discussed in the previous sections, the mechanical force stabilization theory does not explain the small percentage of dystrophin-containing DGC or the slower disease manifestation in the heart.

The reduced glycogenolysis–glycolysis converges on shift to PPP and altered fat and amino acid metabolism from myoblast stages

An elegant radiolabelling study (Ellis 1980) showed that, in DMD, the glucose from glycolysis is shunted to glycerol-3-phosphate (G3P), rather than to pyruvate, and PPP-derived pyruvate is used for mitochondrial oxidation, which increases NADPH generation. The G3P and NADPH contribute to high FA synthesis and fat accumulation. The calcium and thyroid-responsive GPD2 enzyme usually reconverts G3P to DHAP, and, ultimately, to pyruvate. The G3P accumulation in DMD suggests that GPD2 activity is reduced (Liu *et al.* 2018).

The calcium spike during ECC also stimulates the activity of mitochondrial pyruvate dehydrogenase activity to increase pyruvate oxidation. Both the resting-induced (Liang 1986; Chinet *et al.* 1994; Kuznetsov *et al.* 1998; Rybalka *et al.* 2014) and the exercise-induced (Faist *et al.* 2001) mitochondrial O₂ consumption has been reported to be low in DMD. This may be either due to the reduced efficiency of OXPHOS or the lower content of ETC proteins in the mitochondria. ADP-phosphorylation per molecule of O₂ consumed, represented as the P/O ratio, remains similar between the control, *mdx* and in patients, indicating that the efficiency of OXPHOS is unchanged among these contexts (Olson *et al.* 1968). On the other hand, the low mitochondrial ETC content in both *mdx* and patient biopsy (Kuznetsov *et al.* 1998), and lower Co-enzyme A (CoA) levels in *mdx* (Jato-Rodriguez *et al.* 1975) could explain the reduced capacity of the dystrophic mitochondria to utilize not just pyruvate but fatty acids too.

The mechanisms of protein transport into mitochondria are only now emerging. For example, one such protein, Mortalin/mtHsp70 (also known as glucose response protein (GRP75), is low in *mdx* but high in patients (Thakur *et al.* 2018; Capitano *et al.* 2020). GRP75 gets activated by low glucose levels; hence, increased levels of GRP75 could be a compensatory response to its lower activity. However, further investigation is needed to establish the role of GRP75 and other proteins in the mechanisms of protein transport into dystrophic mitochondria.

The FAO is regulated at FA transport into mitochondria via carnitine palmitoyl transferase (CPT). A blockage of the α -ketoglutarate in the TCA cycle causes citrate diffusion

Alternate arm of glycolysis that additionally stimulates glycogenolysis

Glycogen is utilized in various ways in different tissues. It is very important for the proper functioning of skeletal muscles, supports extra work in the heart (reviewed by Depre *et al.* 1999), has shown to be localized in the area of higher neuronal activity in the brain (Vaishnavi *et al.* 2010), and to promote myoblast survival under stress (Lytridou *et al.* 2020). The glycogen synthesis mostly depends on nutritional cues and responds less to a contraction in skeletal muscles (Wojtaszewski *et al.* 2001; reviewed by Mirzoev *et al.* 2021). But glycogenolysis needs to be tightly linked with muscle contraction factors other than AMP, ADP, Pi and Ca^{2+} (reviewed by Katz 2022). The glucose-1-phosphate generated by glycogenolysis can inhibit muscle glycogen phosphorylase, which is less sensitive to inhibition by glucose-6-phosphate. The enzyme phosphoglucomutase (PGM) interconverts glucose-1-phosphate and glucose-6-phosphate depending on their ratios, and, hence, the glycogenolysis rate depends on G6P channelling into glycolysis. The PFK2 product fructose-2,6-bisphosphate can only activate the glycolytic enzymes already assembled onto stable sarcomeric A and Z bands but not the free cytoplasmic enzymes. The subsarcolemmal cytoskeleton during muscle contraction is unstable and dynamically reconstructed, requiring free cytoplasmic enzymes of glycolysis to get activated and assemble into congregates by crosslinking cytoskeletal filaments. The glucose-1,6-bisphosphate activates several free cytoplasmic enzymes, like PGM, GAPDH, PEP, PFK1 and pyruvate kinase, to meet the energy needs of costameric dynamics and ion channels (reviewed by Beitner 1984, 1993). The dependence on glycogenolysis, the contribution of tissue-specific PFK2 isozyme to glycolytic regulation, and the manifold increase in glycolytic flux between the resting and the active state decides the vulnerability to G1, 6BP deficiency, which fits the disease progression seen in muscles, heart and brain for DMD.

The plausible involvement of dystrophin and lacunae in glycolytic congregation theory

There exists an inverse relationship between glucose and fatty acids. The excess glucose/glycogen can stimulate fatty acid synthesis. The excess FA, in turn, stimulates cGMP synthesis, which can inhibit G1,6BP synthesis, repressing glycogenolysis–glycolysis (Bassols *et al.* 1991). The dystrophic myoblasts synthesize FA at a higher rate than the control, even under low serum conditions, which can give rise to defects of glucose metabolism (Bonsett *et al.* 1979). This can also partly explain the disease exacerbation caused by the PDE inhibitors, which increase cGMP levels.

In myoblast and differentiated dystrophic muscles, excess fatty acid levels could be due to higher import or higher

production. However, elevated FA import has not been reported in DMD, and the normal resting ATP/ADP ratio suggests basal FAO is unaffected. Hence, it is more likely that the glycogenolysis defects are stimulating excess fatty acid synthesis in DMD. The proteomics profiling of DMD and BMD patients also support our hypothesis, as the differentially regulated pathways between BMD and DMD strongly correlate with their respective severity of glucose metabolism defects (Capitanio *et al.* 2020).

The study also found reduced hexosamine synthesis and related metabolites in the differential proteomes, which depend on glucose-1-phosphate generated by either glycogen phosphorylase or PGM, both of which are known to be low in DMD. The defects in hexosamine and other glycosyl moiety synthesis or transfer to proteins of DGC also give rise to specific MDs, which vary in their nature from congenital to late onset. However, the disease onset and progression in such diseases are markedly different from those in the DMD case, suggesting that the hexosamine pathway is affected secondarily in DMD.

The major caveat with our hypothesis is the lack of direct evidence of the active congregation of glycogenolytic and glycolytic enzymes in stimulated muscles. There is no direct interaction between dystrophin and the key regulatory glycolytic enzymes, except for the catalytically deficient PGM5/aciculin (Wakayama *et al.* 2000), which can interact with other PGM enzymes. The dependence of ACYP2 activation on dystrophin-mediated processes during muscle contraction could contribute to reduced glycolytic volume in sarcomeric regions, primarily stimulated by the PFK2 product. But the regulation of ACYP2 during muscle contraction remains understudied to refute or support such a hypothesis. The relationship between free glycolytic enzymes binding to monomeric versus polymerized cytoskeleton is complex. The binding to the cytoskeleton also affects binding to other glycolytic enzymes, further adding to the intricacy of the congregate formation model (Menard *et al.* 2014). Yet, it remains a fact that during ECC, the volume of glycogenolysis–glycolysis increases a thousand folds despite high ROS and calcium, and continually reforming subsarcolemmal cytoskeleton. This is because other energy stores (like PCr and adenylate kinase) are too short-lived, and the activation of oxygen-dependent mitochondria is 100 times slower than the rate of glycolysis.

We hypothesize that dystrophin acts as a modulator of glycogenolytic–glycolytic stimulation during ECC in differentiated muscles, in addition to its canonical DGC-related functions. Its similar function could also exist during the asymmetric division of satellite cells (Dumont *et al.* 2015; Chang *et al.* 2016), which might predispose the resulting myoblast to higher PPP and lower glycolysis. Further studies are needed to unveil the regulation of key enzymes to generate a well-informed model, details of which could also be useful in heart and neuronal diseases with glycogenolytic defects.

It is possible that dystrophin lies under both positive and negative regulation, to control the glycolytic switch. Given that in cancers, glycolysis is classically upregulated, suggesting that the dystrophin could be targeted in tumorigenesis. Dystrophin-mediated positive and negative regulation of glycometabolism is possibly associated with its dual (oncogenic and tumour suppressor) role in various cancers (reviewed by Jones *et al.* 2021).

The summary considerations for future DMD therapies

Muscles, irrespective of many complexities, work on a simple paradigm—one ATP for single myosin head flex; hence, energy and function are inseparable. The glycolysis needs a quick upshift during contraction, and the accumulated metabolites are shunted to protein synthesis and repair. The failure of IGF-1 treatment to improve muscle function, despite the consequently increased muscle mass, points to the same. The hyperactivity of pathways like p38MAPK, ERK1/2, Akt/PKB etc. are similar to the scenario in cancer, yet the lack of excess glycolysis-derived metabolites changes the outcome from tumour growth in cancer to atrophy in DMD. Despite these ‘growth pathways’ driving pathology in differentiated dystrophic muscles, their inhibition could affect not just muscle regeneration but nontarget tissues as well, considering that DMD patients are in the ‘growth phase’ of their life. Similarly, sarcolemma-associated ROS production, NHE1 activation, and calcium ingress are all part of excitation–contraction coupling; hence, their inhibition can affect muscle function, even if there is a preservation of the structure. Thus, there is a need to understand further how metabolites modulate the ‘dystrophic pathways’ for therapies to restore muscle function.

Many adaptive responses, like integrin, dysferlin, filamin C (Capitanio *et al.* 2020; Han *et al.* 2021), α -ketoglutarate, etc., are already active in DMD, and further activated by steroid therapy (Sanson *et al.* 2020; Herbelet *et al.* 2020). Hence, creating therapies to override steroid use will require metabolic rescue (Timpani *et al.* 2020).

While chemical approaches have been struggling to increase slow oxidative type muscles that persevere longer in DMD, certain nutritional approaches have ameliorated the *Sgca*^{-/-} model of dystrophy, with a transition to slow type muscles and additional mitigation of several of the pathological processes which are observed in DMD as well (Saclier *et al.* 2020). Thus, it might be worthwhile to adopt similar approaches for DMD.

Since its first description, DMD has been considered a metabolic disease, yet therapies targeting metabolism are very few (NCT04184882). Improving mitochondrial energy production significantly increased exon skipping efficiency (Ran *et al.* 2021), suggesting that metabolic targeting can, in fact, aid or complement advanced gene therapies. It should

be considered that stimulating mitochondrial OXPHOS without stimulating glycolysis/FAO can only burden amino acid catabolism for fuel supply. Moreover, mitochondrial protein transport also remains an unexplored area for DMD.

Trifluoperazine, an FDA-approved drug for schizophrenia, is shown to increase glucose-1,6-bisphosphate availability by inhibiting its breakdown in rat skeletal muscles (Frucht *et al.* 1984). Improving glycogenolysis–glycolysis in the myoblast stage might improve autologous cell transplantation efforts. The molecular mechanisms of cytoskeleton-based glycometabolic regulation need further investigation as it can be productive for some muscular dystrophies, with secondary loss of glycogenolysis–glycolysis capacity. The improvement of resting metabolism can reduce energy deficit, thus delaying disease progression, but the cure will need contraction-activable glycolysis. It will be a challenging yet worthwhile attempt to develop a therapy for DMD.

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Authors' contribution

VN, SB and UN conceived the idea, and VN wrote the initial draft with inputs from UN. All authors have read and agreed to the manuscript submitted.

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