RESEARCH ARTICLE

Muscle strength deficiency and mitochondrial dysfunction in a muscular dystrophy model of Caenorhabditis elegans and its functional response to drugs

Jennifer E. Hewitt1, Amelia K. Pollard2, Leila Lesanpezeshki1, Colleen S. Deane3, Christopher J. Gaffney3,4, Timothy Etheridge3, Nathaniel J. Szewczyk2,4 and Siva A. Vanapalli1,2,*

ABSTRACT

Muscle strength is a key clinical parameter used to monitor the progression of human muscular dystrophies, including Duchenne and Becker muscular dystrophies. Although Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) are muscular wasting disorders that affect both skeletal and cardiac muscle and result from mutations in the dystrophin gene (Le Rumeur, 2015). Dystrophin is a protein encoded by the longest human gene, which is over 2.3 million base pairs long and has complex interactions with muscle contraction and muscle cell membrane stability (Den Dunnen et al., 1989; Blake et al., 2002). DMD results from null mutations in the gene, while BMD, a less severe form of the disorder, is typically caused by a mutation resulting in a partially functional dystrophin protein (Le Rumeur, 2015). The prevalence of these diseases is more than 1 in 4000 male births, expressing as an X-linked disorder. Prognosis is poor (Moser, 1984), and the only standard approved treatment in the USA for symptoms of DMD is the corticosteroid prednisone, which typically has the effect of extending ambulation by a couple of years (DeSilva et al., 1987). Although the increase in ambulatory period is a favorable outcome of treatment, chronic prednisone use typically results in a cushingoid appearance and other unfavorable side effects (Mendell et al., 1989; Malik et al., 2012). Thus, the prognosis and options for DMD/BMD treatment are rather limited.

To monitor progression of the disease or to test for efficacy of treatments, various diagnostic tools have been studied to monitor the deterioration of muscle in DMD patients. One diagnostic tool used is an electronic strain gauge that measures isometric muscle strength; this tool can discern DMD patients from the control in all muscle groups tested, with the most drastic differences occurring in the knee extensors, where DMD patients have less than a tenth of the strength of the control group (Brussock et al., 1992). Quantitative muscle testing (QMT), a method that is more sensitive to small changes in muscle strength, is also being implemented in young patients with DMD to monitor muscle strength across age. QMT is able to detect isometric and isokinetic losses in strength before the end of the first decade of life (Lerario et al., 2012). These are just two examples of a larger research effort to obtain more reliable measures of muscle strength, as muscle strength is regarded as a key clinical parameter of interest in tracking DMD disease progression. Over the past half century, research efforts surrounding muscular dystrophy have grown significantly, but we still have much to learn about this debilitating disease.

Although there have been extensive research efforts to better understand the mechanisms of and treatments for muscular dystrophy in vertebrate model organisms such as rodents and canines, these systems are limited in their throughput, can be cost prohibitive and also have some ethical issues (McGreevy et al., 2018). This article has an associated First Person interview with the first author of the paper.

INTRODUCTION

Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) are muscular wasting disorders that affect both skeletal and cardiac muscle and result from mutations in the dystrophin gene (Le Rumeur, 2015). Dystrophin is a protein encoded by the longest human gene, which is over 2.3 million base pairs long and has complex interactions with muscle contraction and muscle cell membrane stability (Den Dunnen et al., 1989; Blake et al., 2002). DMD results from null mutations in the gene, while BMD, a less severe form of the disorder, is typically caused by a mutation resulting in a partially functional dystrophin protein (Le Rumeur, 2015). The prevalence of these diseases is more than 1 in 4000 male births, expressing as an X-linked disorder. Prognosis is poor (Moser, 1984), and the only standard approved treatment in the USA for symptoms of DMD is the corticosteroid prednisone, which typically has the effect of extending ambulation by a couple of years (DeSilva et al., 1987). Although the increase in ambulatory period is a favorable outcome of treatment, chronic prednisone use typically results in a cushingoid appearance and other unfavorable side effects (Mendell et al., 1989; Malik et al., 2012). Thus, the prognosis and options for DMD/BMD treatment are rather limited.

To monitor progression of the disease or to test for efficacy of treatments, various diagnostic tools have been studied to monitor the deterioration of muscle in DMD patients. One diagnostic tool used is an electronic strain gauge that measures isometric muscle strength; this tool can discern DMD patients from the control in all muscle groups tested, with the most drastic differences occurring in the knee extensors, where DMD patients have less than a tenth of the strength of the control group (Brussock et al., 1992). Quantitative muscle testing (QMT), a method that is more sensitive to small changes in muscle strength, is also being implemented in young patients with DMD to monitor muscle strength across age. QMT is able to detect isometric and isokinetic losses in strength before the end of the first decade of life (Lerario et al., 2012). These are just two examples of a larger research effort to obtain more reliable measures of muscle strength, as muscle strength is regarded as a key clinical parameter of interest in tracking DMD disease progression. Over the past half century, research efforts surrounding muscular dystrophy have grown significantly, but we still have much to learn about this debilitating disease.

Although there have been extensive research efforts to better understand the mechanisms of and treatments for muscular dystrophy in vertebrate model organisms such as rodents and canines, these systems are limited in their throughput, can be cost prohibitive and also have some ethical issues (McGreevy et al., 2018).

KEY WORDS: Muscular dystrophy, C. elegans, Muscle strength, Prednisone, Melatonin

Received 19 June 2018; Accepted 30 October 2018
This has led researchers to utilize Caenorhabditis elegans to study muscular dystrophy over the past couple of decades (Ségalat, 2006; Chamberlain and Benian, 2000). C. elegans is a premier model organism for studying a number of biological processes and human diseases, with an estimated 40% of human disease genes having an ortholog in C. elegans (Culettó and Sattelle, 2000). The ability to translate results from C. elegans to humans comes, in part, from conserved major biological pathways between the two organisms and a fully sequenced nematode genome (The C. elegans Sequencing Consortium, 1998). C. elegans also has musculature strikingly similar to that of humans, with the presence of dense bodies (analogous to z-disks) and m-lines (Gieseler et al., 2016). A number of muscle proteins in C. elegans resemble human proteins in their function, making C. elegans an excellent model for studying muscle ailments such as sarcopenia or muscular dystrophy (Ségalat, 2002). In addition to these factors, C. elegans also has a short lifespan of only 3 weeks, produces a new generation every 3.5 days and is low maintenance, with cultures grown on agar medium and an Escherichia coli diet.

Several mutant strains of C. elegans have been generated for investigating the mechanistic details of and pharmacological treatments for dystrophin deficiency. About two decades ago, Bessou et al. reported a gene in C. elegans that they called dys-1 (Bessou et al., 1998). dys-1 encodes a protein resembling the human dystrophin protein not properly transcribed in DMD and BMD. These C. elegans dys-1 mutants are hyperactive, have exaggerated head bending, hypercontract their bodies during backwards movements and are hypersensitive to the acetylcholinesterase inhibitor aldicarb. However, the animals do not show visible defects in their musculature, which the authors attribute to the short timescale of the nematode’s life (Bessou et al., 1998). To address the need for a health measure related directly to the musculature in dys-1 mutants, Gieseler et al. generated a sensitized dys-1 mutant containing an additional mutation in the hlh-1 gene, which is a homolog for the mammalian MyoD (also known as Myod1) gene (Gieseler et al., 2000). The presence of the hlh-1 mutation in a dys-1 mutant background results in significant muscle cell degeneration that is not present in mutants with either the hlh-1 or dys-1 mutation alone (Gieseler et al., 2000). This type of double mutation was modeled after a similar MyoD mutation studied in conjunction with the mdx mouse model, which was generated, in part, to create a system that recapitulated the pathophysiology of DMD in humans (Megency et al., 1996). Using this dys-1; hlh-1 model of muscular dystrophy, pharmacological compounds like prednisone and serotonin have been shown to be effective in reducing muscle cell degeneration. These two treatments came as hits out of large-scale screens, from which hundreds of other compounds were deemed ineffective (Gaud et al., 2004; Carre-Piechart et al., 2006).

Although these studies have helped to establish C. elegans as a model organism for muscular dystrophy and pharmacological treatments for the disease, two main criticisms arise. First, it is unknown whether results from the dys-1; hlh-1 double mutant models can be translated to muscular dystrophy in humans, especially given that the mechanism of these enhanced muscular degeneration effects in C. elegans is not fully understood. Second, although several assays for assessing health of dys-1 mutants have been proposed, most fail to directly score animals for muscle function and instead look at indirect physiological parameters, such as locomotion speed, or subcellular markers, such as muscle cell damage. Beron et al. scored the percentage of worms that can travel a set distance in a certain amount of time when placed in a 3D burrowing environment (Beron et al., 2015). Animals were stimulated by chemotaxis to burrow down the length of a plastic pipette filled with agar, and dys-1(cx18) and dys-1(eg33) were both highly deficient in burrowing ability compared with the wild-type control. This work indicates that the dys-1 mutants might be unable to burrow correctly due to defects in muscular strength.

Although these assays are undoubtedly valuable, the ability to directly evaluate muscle function would offer a more meaningful dimension for assessing the health of dystrophin mutants under treatments, given that strength is a clinical measure used to assess progression of DMD in humans. Previously our group established a novel technique and workflow for reliably measuring the muscle strength of C. elegans, independent of their behavior. This platform, NemaFlex, consists of a microfluidic device containing deformable pillars that the worm deflects as it crawls in the chamber. Nematode strength is scored from the maximal pillar deflections via a sophisticated image-processing software (Rahman et al., 2018). To establish strength as a phenotype of interest for assessing health in dys-1 mutants, we used NemaFlex for studying two different dys-1 strains, dys-1(cx18) and dys-1(eg33), alongside the wild-type animal. We show that our platform can detect pharmacologically induced improvements by assessing the effects that melatonin and prednisone, compounds known to improve muscle health, have on the muscular strength of the same animals. We also evaluated whether the thrashing data and mitochondrial integrity for control and treatment groups agreed with the strength data. Finally, we show that mitochondrial network integrity and mitochondrial function are impaired in dys-1(eg33), and treatment with prednisone repairs these defects. This work addresses the current gap in the ability to obtain strength measures in DMD model mutants, which will ultimately lead to a better understanding of muscular dystrophy. Additionally, our results indicate that dys-1(eg33) has a more pronounced and clinically relevant phenotype than what has been reported previously for dys-1 mutants. We can detect our clinically relevant phenotype in the absence of the hlh-1 sensitizing mutation, which better establishes C. elegans dys-1 mutants as a useful model for studying muscular dystrophy.

RESULTS
dys-1(eg33), but not dys-1(cx18), worms are weaker than wild type

Although both dys-1 mutants have previously been shown to have declined locomotory capability and decreased lifespan compared with the wild-type animal (Oh and Kim, 2013), direct measures of muscle functionality in clinically relevant models do not exist. We addressed this limitation by utilizing our microfluidic platform called NemaFlex that enables measurement of the muscular strength of C. elegans (Rahman et al., 2018). Using two previously studied dystrophin-deficient mutants, dys-1(eg33) and dys-1(cx18), we investigated whether these animals were weaker than the wild-type animal (N2). The alleles eg33 and cx18 are nonsense mutations predicted to encode truncated forms of DYS-1 at amino acid (AA) 3287 and AA 2721, respectively (Oh and Kim, 2013). Animal strength of wild type, dys-1(cx18) and dys-1(eg33) was measured on Days 1, 3 and 5 of adulthood (Fig. 1A). Although neither mutant strength value was significantly different from that of wild type on the first day of adulthood, dys-1(eg33) animal strength essentially plateaued, whereas wild type and dys-1(cx18) continued to grow stronger at the later time points, which was potentially partially attributable to the increase in animal diameter in early adulthood. This led to dys-1(eg33) being significantly weaker than the wild-type control on Days 3 and 5, thus establishing the dys-1(eg33) strain as a model exhibiting muscular weakness with
age, which is similar to the phenotype displayed in muscular
dystrophy. It is important to note that animal diameter, but not
length, strongly affects the muscle strength of *C. elegans*, as we
previously reported that strength tends to increase with body
diameter (Rahman et al., 2018). Therefore, we checked whether
muscle strength deficiencies in *dys-1(eg33)* were attributable to
differences in their diameters compared with wild-type animals
(Fig. 1B). At no time point are *dys-1(eg33)* animals significantly
thinner than wild type, thus indicating that their strength defect is
not a size-based effect, and that we are truly measuring strength
deficiencies resulting from defects in muscle function.

**All treatments improve *dys-1(eg33)* strength, some
to wild-type levels**

Because NemaFlex can detect muscular weakness in *dys-1(eg33)*, a
meaningful next step is to test whether compounds known to
improve muscle health can also improve muscle strength in
muscular dystrophy models. Melatonin and prednisone were
selected for validation of NemaFlex as a platform for screening
compounds for treatment of dystrophin deficiency in *C. elegans*.
Melatonin is thought to be potentially useful in treating muscle
degradation with age (Coto-Montes et al., 2016) and has also been
used to treat muscular dystrophy patients (Chahbouni et al.,
2018). Prednisone is the standard treatment for muscular
dystrophy patients (Malik et al., 2012) and has also been
shown to decrease the number of abnormal muscle cells in the
*dys-1; hlh-1* double mutant strain of *C. elegans* (Gaud et al.,
2004). The mechanism behind prednisone’s improvement in
muscle function is still up for debate, but the efficacy of
prednisone previously shown in *C. elegans* provides evidence
that corticosteroids treat the muscle in ways other than reducing
inflammation, given that *C. elegans* does not have an
inflammatory pathway (Gaud et al., 2004).

In general, we find that wild-type and *dys-1(cx18)* animals treated
during development and continuing through adulthood were not
significantly different from their control counterparts at all three
time points (Fig. 2A,B). In contrast, beginning on Day 3 of
adulthood, when *dys-1(eg33)* animals are significantly weaker than
wild type, all four treatments improve muscular strength compared
with the untreated *dys-1(eg33)* animals (Fig. 2C). Moreover, it is
important to note that worm diameters are minimally affected under
treatments for wild type (Fig. 2D), *dys-1(cx18)* (Fig. 2E) and
*dys-1(eg33)* (Fig. 2F). Of particular importance is that on Days 3
and 5, when *dys-1(eg33)* has significant improvements in muscle
strength, there are no changes in worm diameter under any treatment
condition. Thus, improvements in animal strength are not due to
changes in animal size, but rather due to improvements in muscle
function. Under some treatments, differences between the wild-type
control and treated *dys-1(eg33)* are indiscernible. Several treatments
improve animal strength by over 50% and get within 10% of the
wild-type control strength value. As anticipated, these treatments
improve muscle functionality in the muscular dystrophy model in a
manner that can be detected by NemaFlex. This establishes our
technology as a useful platform for future studies screening novel
compounds on *dys-1(eg33)* to select potential therapies for
muscular dystrophy. Because *dys-1(eg33)* is showing such a
distinct phenotype from *dys-1(cx18)*, which has been studied
more thoroughly, we were interested in investigating the difference
between these two strains and why *dys-1(eg33)* seems to have more
clinical relevancy.

**Functional defects are apparent in swimming-based
movement assays**

A standard assay for detecting locomotion defects is to record a
worm’s thrashing frequency when placed in a liquid environment,
and this assay has been used previously to look at dystrophin-
deficient worms, although not in both the *dys-1* strains we used in
this study (Hueston and Suprenant, 2009). We were curious to
compare the outputs of an indirect measure of muscle function,
thrashing, with our more direct measure, the strength measurement.
Interestingly, although the muscle strength of *dys-1(cx18)* was not
significantly less than that of the wild-type animal, its thrashing rate
was significantly less than that of wild type. *dys-1(eg33)* also
showed a thrashing rate lower than that of both wild type and
dys-1(cx18), consistent with its lower strength (Fig. 3A). When all strains were treated with life-long melatonin or prednisone, there were some noticeable changes in the thrashing rate, although not the same as the changes in muscle strength in all cases. Wild-type animals had varying responses to the drugs, with the drugs not having a consistent effect on the worms across the time points studied (Fig. 3B,C). However, both treatments give a minor improvement in dys-1(cx18) (Fig. 3C), and they both offer a significant improvement in thrashing rate at all time points in dys-1(eg33) (Fig. 3D). This result matches well with the strength data, where all drug treatments improve muscle strength in dys-1(eg33). The thrashing assay thus helps to further implement dys-1(eg33) as a more clinically relevant model, where measures from two unique modes of locomotion show improvement when animals are treated with compounds known to improve muscle health, particularly in patients with muscular dystrophy.
Dystrophin mutants display normal sarcomere structure

We visualized the sarcomere structure of dys-1(cx18) and dys-1(eg33) worms to determine whether defects in muscle structure account for the reduced strength and motility in the dys-1 worms. Similar to previous studies (Gieseler et al., 2000), we also detect no major differences in sarcomere structure in the dys-1(eg33) and dys-1(cx18) compared with wild-type worms, by either phalloidin staining (Fig. 5A) or visualization of myosin-tagged GFP (Fig. 5B). These findings suggest that the reductions in strength are not attributed to changes in muscle architecture in the dys-1 strains and are perhaps a result of different mechanism(s).

Mitochondrial fragmentation is a phenotype of dystrophin mutants

To determine the possible underlying mechanisms behind the loss of muscle strength in dystrophin mutants, we looked at the integrity of the mitochondrial network of dys-1(cx18) and dys-1(eg33) animals that had been crossed with the CB5600 strain, which expresses GFP in the mitochondria and nuclei of the body wall muscles. Recently, Scholtes et al. (2018) reported mitochondrial fragmentation as a phenotype of their sensitized muscular dystrophy

dys-1(eg33) mutants have a more severe phenotype than dys-1(cx18)

Given that strength and thrashing ability are not compromised to the same extent in dys-1(cx18) as in dys-1(eg33), we wanted to further investigate the differences between the two strains. Upon reviewing the published literature on dys-1(cx18), we found that Hueston and Suprenant (2009) had previously observed worse locomotion at 25°C than at 20°C, which would be consistent with cx18 being a temperature-sensitive allele. We confirmed that dys-1(cx18), but not dys-1(eg33), displays temperature sensitivity in the extent of thrashing ability (Fig. 4A). We next examined whether differences between dys-1(cx18) and dys-1(eg33) extended to differences in excitation-contraction coupling. Both dys-1(cx18) and dys-1(eg33) display resistance to levamisole-induced paralysis, indicative of defects in postsynaptic excitation-contraction coupling, with dys-1(eg33) displaying more pronounced levamisole resistance (Fig. 4B). Similar to the thrashing ability, dys-1(cx18) displayed temperature sensitivity to the effects of levamisole (Fig. 4C). These results confirm the past observation that dys-1(cx18) is a temperature-sensitive allele of dys-1 and confirm that muscle responsiveness to a depolarizing signal is more compromised in dys-1(eg33).
strain, dys-1; hlh-1. Here, we report that mitochondrial network integrity is also compromised in dys-1(cx18) and dys-1(eg33) compared with wild-type animals of the same age, with the defect in dys-1(eg33) being more severe (Fig. 5C-E). Both prednisone and melatonin improve the mitochondrial integrity of dys-1(eg33) animals. This offers a potential mechanistic explanation for why muscle function appears to be more severely affected in dys-1(eg33) than in dys-1(cx18), as well as further evidence that prednisone and melatonin are directly improving muscle health in dys-1(eg33).

**Mitochondrial function is affected in dys-1(eg33) mutants**

Having identified that mitochondrial network structure appears disrupted in dys-1 mutants and that this is improved with prednisone treatment, we were curious whether mitochondrial function was similarly affected. We first used mitochondrial dyes to assess mitochondrial membrane potential. JC-10 is a dye that collects in the mitochondria based on membrane potential and exits as the mitochondrial membrane potential changes over time, as previously shown in another *C. elegans* mutant (Gaffney et al., 2015). Compared with wild-type animals, dys-1(cx18) has a somewhat reduced mitochondrial membrane potential, while dys-1(eg33) is more severely affected (Fig. 6A). To confirm these defects in mitochondrial membrane potential, we used a second dye, MitoTracker Red, which collects in the mitochondria based upon membrane potential, but, unlike JC-10, does not exit the mitochondria once inside (Gaffney et al., 2014). The MitoTracker Red accumulation matched that of JC-10 (Fig. 6A), demonstrating that the impaired membrane potential in the JC-10-dyed worms was not an artifact of loss of membrane potential during the staining procedure. Interestingly, with both dyes, prednisone does not improve the defect in membrane potential in dys-1(eg33), indicating that improvements that we see in strength and thrashing rate in dys-1(eg33) under prednisone treatment can be attributed to a different mechanism.

In order to quantify the defect in mitochondrial function in dys-1(eg33) mutants, we assessed oxygen consumption rates (OCRs). Although dys-1(cx18) have normal OCR compared with wild type, dys-1(eg33) have abnormally high baseline respiration (Fig. 6B). Treatment with the uncoupling agent carbonyl cyanide-4-(trifluoromethoxy)phenylhydrazone (FCCP) revealed that unlike dys-1(cx18), dys-1(eg33) have abnormally high baseline respiration (Fig. 6B). No statistically significant differences in non-mitochondrial respiration, as assessed by treatment with sodium azide, were found between the strains. Thus, the lack of spare respiratory capacity in dys-1(eg33) is likely a key driver of the increased severity of muscle defects in dys-1(eg33) versus dys-1(cx18).

Given that prednisone treatment improves muscle strength, thrashing rate and mitochondrial network integrity in dys-1(eg33), we were interested in determining whether prednisone could also normalize the aberrantly high basal OCR. Indeed, treating dys-1(eg33) with prednisone returned basal OCR to wild-type levels (Fig. 6C). These results, combined with the lack of major effect of prednisone on mitochondrial membrane potential (Fig. 6A), suggest that prednisone has a predominant effect on mitochondrial respiratory function rather than restoring membrane potential. This is interesting, as Brouilly et al. (2015) recently showed that prednisone improves muscle membrane structure, including the mitochondria, in dys-1; hlh-1.

**DISCUSSION**

**Strength as a novel phenotype for *C. elegans* DMD studies**

In the present study, we demonstrate the ability to measure the strength of *C. elegans* dys-1 mutants and detect functional improvements in...
muscle strength in *dys-1(eg33)* after treatment with compounds known to improve muscle health. Previously, there was not a means to directly measure the strength of *C. elegans*, but recently our group established a consistent and reliable strength measurement routine using our microfluidic NemaFlex device (Rahman et al., 2018). This has allowed us to demonstrate, for the first time, that strength deficiency is a phenotype of the *dys-1(eg33)* strain, which further represents *C. elegans* as a useful model for replicating some of the pathophysiologies of human diseases in nematodes.

For high-throughput drug screens with dystrophin-deficient *C. elegans*, it might not be feasible to measure a large quantity of parameters to quantify nematode health. We show here that the thrash assay detects deficiencies in both *dys-1* mutants and improvements under treatment with compounds. However, a decrease in thrashing rate does not necessarily correlate with a loss of muscle strength. For example, wild-type animals have lower thrashing rates on Days 3 and 5 than on Day 1, although there is not a strength decline at this same time point. Therefore, thrashing rate and muscle strength measures do not necessarily report on the same aspect of worm physiology. For the purpose of high-throughput drug screens, an automated version of the thrashing assay would be a quicker way of determining hits (Buckingham et al., 2014); we propose that our NemaFlex system would be useful in validating whether these drugs also improve the more clinically relevant measure of muscle strength. Further automation of our NemaFlex imaging and postimaging analysis protocol could help make NemaFlex more reasonable as a first-step screening assay; however, under the current protocol, throughput is somewhat limited and would thus be more appropriate as an assay to validate hits that come out of a thrashing-based drug screen or other high-throughput screening method.

Therefore, we propose that a direct measure of muscle function is perhaps the most valuable single measure to extract from drug screens. We recognize the value in assessing other physiological abilities, as *dys-1(eg33)* animals are also deficient in thrashing and burrowing. Advantages of our system over the previously reported burrowing assay (Beron et al., 2015) include the ability to culture the nematode over its whole life while maintaining individual worm identity and controlling the contents of the fluidic environment in a temporal manner. There is also no requirement of a stimulus for observation of the desired phenotype, which is easy to observe due to the transparency of the platform, which allows for clear imaging.

Previous studies with dystrophin-deficient *C. elegans* have also looked at non-physiological measures that aim to assess the integrity of the muscle rather than the function. If muscle strength is improved under a certain drug treatment, previously described assays looking at non-physiological measures should then be used to further assess the efficacy of the treatment. Our transgenic *dys-1* strains expressing GFP in mitochondria of the body wall muscle that we report here are perfectly suited for this purpose, although other methods have previously been reported as well. Beron et al. (2015) looked at muscle degeneration in burrowing animals by tagging muscle cell nuclei and mitochondria with GFP, and others have looked at body wall muscle integrity after staining (Gieseler et al., 2000; Mariol and Ségalat, 2001). Looking at muscle cell integrity under a certain drug treatment could thus entail using the *dys-1*;
**Differences in muscle strength and other phenotypes between dys-1(eg33) and dys-1(cx18)**

The inability of NemaFlex to detect muscular defects in dys-1(cx18) in a crawling environment is not surprising, given that adult worms similarly aged to the ones studied here have no abnormal muscle cells and are indiscernible from wild-type animals based on this parameter (Gieseler et al., 2002). Additionally, the mitochondrial fragmentation is not as severe in dys-1(cx18) as in dys-1(eg33). However, the question still remains on what the key differences are between dys-1(eg33) and dys-1(cx18) that lead to these drastic differences in muscle functionality, especially given that both animals are deficient in thrashing (our results here) and burrowing (Beron et al., 2015). Crawling, swimming and burrowing are kinematically distinct from one another and offer unique challenges for the worm; observing different phenotypes among these environments could result from this distinction. It is likely that the burrowing assay challenges the muscles in a way not done in NemaFlex. Burrowing relies on the head muscles, while the NemaFlex analysis selects for the maximum force exertion, typically coming from body wall muscles. Therefore, if head muscles were weaker, our system would not detect this under the current workflow. We also see that in the swimming worms, where both dys-1(cx18) and dys-1(eg33) are slower thrashers, dys-1(cx18) does not respond quite as strongly to the drug treatments.

Further assessment with these three unique functional readouts, along with future efforts targeting mechanistic questions, could help answer why dys-1(eg33) shows an impaired phenotype and dys-1(cx18) does not. Previous work with *C. elegans* has identified defects in calcium signaling and acetylcholine sensitivity as pathophysiologies associated with dystrophin deficiency, so it is possible that these defects are more severe in dys-1(eg33) than in dys-1(cx18) (Mariol and Ségalat, 2001; Zhan et al., 2014; Bessou et al., 1998; Giugia et al., 1999). However, both strains are also reported as having null mutations, indicating that neither strain should produce even a partially functional dystrophin product. It thus remains unclear why the worms exhibit some distinct phenotypes from one another, but our data reported in this paper support the notion that there are fundamental differences between dys-1(eg33) and dys-1(cx18). The more severe phenotype of dys-1(eg33) in its levamisole resistance and basal OCR, as well as the temperature-sensitive nature of dys-1(cx18), offer further perspective on why these strains differ from one another in their physiologies.

Oh and Kim (2013) previously showed that dys-1(eg33) has higher levels of GST-4 reporter than dys-1(cx18). Increased gst-4 expression leads to increased resistance to oxidative stress (Leiers et al., 2003), and this is entirely consistent with our OCR data for dys-1(eg33). Additionally, we also showed that dys-1(cx18) display temperature sensitivity in their thrashing movement. Similar movement data for dys-1(cx18) were reported at 25°C (Hueston and Suprenant, 2009); thus, our data are consistent with published data. The nonsense mutation in dys-1(cx18) corresponds to termination at AA 2721, which is immediately before the start of spectrin repeat domain 5,
which starts at AA 2725. The temperature-sensitive nature of the movement decline in dys-1(cx18), but not dys-1(eg33), suggests that dys-1(cx18) probably produces a partially functional protein in a temperature-sensitive fashion. This idea of more unfolding occurring at 25°C is consistent for other metastable temperature-sensitive mutations in C. elegans (Ben-Zvi et al., 2009).

**Prednisone and melatonin improve strength in C. elegans**

The two pharmacological compounds that we test here, prednisone and melatonin, offer improvements in muscle strength and may also elucidate mechanisms behind muscle strength loss in muscular dystrophy. Previously, Gaud et al. (2004) reported that prednisone reduces the number of abnormal muscle cells in their dys-1: hlh-1 model. We demonstrate here that prednisone gives a functional improvement in the dys-1(eg33) animal as well. Although dys-1(eg33) does not exhibit major defects in the sarcomeres like in the sensitized models, we can still detect and treat strength declines. This is in contrast to our past work with integrin attachment complex mutants, where both sarcomere and mitochondrial defects were present in animals that were detectably weaker (Etheridge et al., 2015). Our results here indicate that NemaFlex can detect alterations in strength in the absence of major structural defects in muscle, which raises the question of whether mitochondrial deficits, rather than very minor sarcomere defects, underlie the detected loss of strength.

While we are able to detect functional improvements under both drug treatments, the exact mechanism by which prednisone helps to alleviate symptoms is not known, although efficacy is at least, in part, attributed to reduction of inflammation (Parrillo and Fauci, 1979; Mendell et al., 1989). Another proposed mechanism is protection against mechanically induced muscle damage (Jacobs et al., 1996). Also, little is known about the mechanism of melatonin in the treatment of dystrophin-deficient muscle, although it has been demonstrated to reduce oxidative stress markers in erythrocytes in blood samples from humans with DMD (Chahbouni et al., 2011). In DMD patients treated with melatonin, several measures scoring oxidation and inflammation were also improved over a 9-month treatment period (Chahbouni et al., 2010). Functional measures were not reported for this study, but mdx mice treated with melatonin show decreased creatine kinase levels and improved muscle function in another study (Hibaoui et al., 2011). These proposed mechanisms could be studied further using the C. elegans DMD model that we present here.

**dys-1(eg33) shows clinical relevancy**

Given that dys-1(eg33) is weaker than the wild type and responds well to prednisone treatment, the standard treatment for muscular dystrophy in humans, we are convinced that this particular strain could currently be the most clinically relevant model of C. elegans for muscular dystrophy, especially when considering that much of the muscular dystrophy work has been done with the genetically sensitized strain, dys-1(cx18): hlh-1. Null mutations of hlh-1, although not inhibitory to muscle development, do lead to muscle that contracts poorly and animals that are uncoordinated (Chen et al., 1994). The dys-1: hlh-1 mutant has been utilized as a way to strengthen the effects of the dys-1 mutation on muscle degeneration (Gieseler et al., 2000).

While this sensitized worm may be useful for studying certain aspects of muscular dystrophy, its relevance to the mechanisms of muscular dystrophy in humans could be confounded by the presence of the additional mutation. As a result, any technique that offers a way to detect muscular defects or decreased function in muscle in worms with a mutation only in the dys-1 gene arguably offers a large advantage over these previous assays. We propose that future work with C. elegans muscular dystrophy models should follow two main thrusts: screening novel compounds and probing mechanisms using dys-1(eg33). Our platform is capable of identifying novel drugs or already approved drugs used for other purposes that improve muscle function in dys-1(eg33). This could lead to clinical studies and may also help to unearth unknown mechanisms associated with dystrophin deficiency. Thus, answering mechanistic questions in future work is a huge priority.

**Conclusion**

NemaFlex is a promising platform for screening compounds that could potentially help to alleviate the loss in muscle strength associated with muscular dystrophy. This allows us to study muscular dystrophy mechanisms and treatments in the worm without having to use sensitizing mutations. Subcellular analyses looking at mitochondrial integrity also enable further assessment of the health of muscle in dys-1 mutants. The muscular weakness, thrashing deficiencies, mitochondrial fragmentation, impaired mitochondrial function and drug response of dys-1(eg33) indicate a clinically relevant model for future investigations in the worm. Determination of muscle strength, when paired with other previously established measures of worm physiology, muscle integrity and overall health, will offer a more robust method for determining novel compounds for treating dystrophin-deficient worms.

**MATERIALS AND METHODS**

**Nematode strains and culture**

C. elegans strains used in this study were wild-type N2, provided by the Driscoll Laboratory (Department of Molecular Biology and Biochemistry, Rutgers University, Piscataway, NJ, USA), and dys-1(cx18) (strain BZ3) and dys-1(eg33) (strain LS292), provided by the Caenorhabditis Genetics Center (CGC). Both mutants have nonsense mutations in the dys-1 gene (Oh and Kim, 2013). We also used four new strains – CC96 [dys-1(eg33) I; (jls01 (myo-3::GFP, rol-6 (su1006)); unc-54::lacZ V)], CC97 [dys-1(cx18) I; (jls01 (myo-3::GFP, rol-6 (su1006))); unc-54::lacZ V]), CC90 [dys-1(cx18) I; ccs4251 I; him-8(e1489) IV] and CC91 [dys-1(eg33) I; ccs4251 I; him-8(e1489) IV] – generated for this study to evaluate sarcomere and mitochondrial network integrity in dys-1(eg33) and dys-1(cx18), along with PJ727 [hsp:im3-GFP, rol-6 (su1006); unc-54::lacZ V] and CB5600 [ccs4251 (Pmyo-3::Ndp-lacZ; Pmyo-3::Ndpglp) I; him-8 (e1489) IV] also provided by the CGC. The PD55 strain was used for OCR experiments. Animals were maintained at 20°C (unless otherwise noted) on nematode growth medium (NGM) plates with E. coli OP50 using standard protocol. Animals for the study were age synchronized by transferring ∼30 gravid adult nematodes of each strain to the various agar plates (with or without pharmacological treatments) and then leaving them to lay eggs for ∼3 h. Adult animals were then removed, and the agar plates with eggs were left in the 20°C incubator for 3 days. Animal age is given as day of adulthood.

**Pharmacological treatments**

There were five different groups in this experiment for each of the three strains studied: no pharmacological intervention (control), melatonin or prednisone received during development only, and melatonin or prednisone received during both development and adulthood (Fig. 7A). NGM plates were prepared normally for the control groups. For the treatments, melatonin (Sigma-Aldrich) and prednisone (Sigma-Aldrich) were added to the NGM plates prepared normally for the control groups. For the treatments, melatonin (Sigma-Aldrich) and prednisone (Sigma-Aldrich) were added to the NGM immediately after autoclaving to final concentrations of 1 mM and 0.37 mM, respectively. The prednisone concentration was chosen as 0.37 mM, as this is a concentration falling within the range of concentrations previously reported by Gaud et al. (2004) to reduce the number of damaged muscle cells in the dys-1: hlh-1 model. Similarly, a concentration of 1 mM of melatonin is within the range of concentrations previously reported to affect physiology, specifically the...
number of body bends, in wild-type C. elegans (Tanaka et al., 2007). Thus, drug concentrations that were selected are values known to fall within the range of concentrations that affect animal physiology and/or muscle health. Animals that continued to receive treatment after development, corresponding to introduction to the microfluidic device on Day 1 of adulthood, received treatments at concentrations of 0.1 mM and 0.037 mM for melatonin and prednisone, respectively. Lower concentrations were used due to the more direct contact with the drug in the microfluidic device compared with the agar plates.

Animal culture and imaging in microfluidic devices
When animals were ∼72 h posthatching, they were loaded into the microfluidic devices along with a solution of 100 mg of E. coli ml⁻¹ of liquid NGM (NGM without the agar). For animals continuing to receive the pharmacological treatment after development, the compound was introduced into the E. coli solution at the appropriate concentration before the concentrated bacteria solution was added to the device (Fig. 7B). On each day for the remainder of the experiment, the devices were washed using liquid NGM to remove progeny and debris, and a fresh solution of bacteria was added to the device (Fig. 7C,D). The arena of pillars and barriers in the outlet ports allow for the retention of adult animals and the filtering out of unwanted progeny, as has been previously demonstrated for C. elegans maintenance in microfluidic devices (Hulme et al., 2010; Wen et al., 2012; Xian et al., 2013; Wen et al., 2014).

After clearing the devices of progeny and debris, and before adding fresh E. coli, animals were imaged in the microfluidic chambers (Fig. 7C,D) for 45-s episodes at a rate of five frames per second. A Nikon Eclipse TI-E microscope with Andor Zyla sCMOS 5.5 camera was used. Any animals that remained stationary during the first image sequence, although few in number, were re-imaged until a movie including sufficient worm locomotion was obtained.

Strength measurements using NemaFlex
Deflections and strength measurements were obtained using standard NemaFlex processing protocol, which involves automated tracking of the deflectable pillars (Fig. 7E) (Ghanbari et al., 2012; Johari et al., 2013; Khare et al., 2015; Qiu et al., 2015). Pillar deflection values extracted during image processing were converted to forces using Timoshenko beam deflection
theory (Etheridge et al., 2015; Rahman et al., 2018). We then obtained animal strength from these forces by selecting for the maximal force exerted in each frame of the acquired image sequence and selecting for the 95th percentile value (defined as f_{95}) among these maximal forces. The f_{95} value for an individual worm is analogous to the maximum voluntary force in humans, and thus defines a measure of animal muscular strength. Further details on the methodology and data analysis can be found in Rahman et al. (2018), and the custom-built software can be obtained by directly contacting our laboratory. Animal strengths were compared using a two-sample t-test (MATLAB, R2015b), with each individual animal strength value being treated as an independent sample. The only animals excluded from the analysis were those for which the custom-built MATLAB software failed to process the movie, which can result from too many air bubbles inside the microfluidic devices or non-uniform illumination. Animal diameters were measured using ImageJ (https://imagej.nih.gov/ij/).

Thrashing assay
To crosscheck whether worms lacking in strength also exhibit functional deficiencies in swimming, we used a simple thrashing assay (Gaffney et al., 2014). There were three different groups for each of the three strains studied [wild type, dys-1(eg33) and dys-1(cx18)]: no pharmacological intervention (control) and melatonin (1 mM) or prednisone (0.37 mM) treatment through the last day of assessment. Animals were age synchronized as described in the strength assay and maintained on NGM agar plates throughout the experiment. Animals were manually picked to new plates every other day during the egg-laying period.

On Days 1, 3 and 5 of adulthood, movement rates of the worms were recorded using a thrashing assay (also referred to as swim test). Thrashing assays were carried out by picking a worm into 20 µl M9 buffer on a microscope slide. The number of bends in 10 s was counted and repeated five times for each worm for three independent biological replicates. One body bend was recorded as one rightward body bend and leftward body bend. For each treatment, movement rates for ten worms were measured. The differences in movement rates between treatment groups were analyzed using a two-sample t-test in MATLAB. The same method was utilized for temperature sensitivity experiments, with the exception that animals were cultured at 25°C instead of 20°C and significance was assessed using a two-way ANOVA with Tukey’s multiple comparison test.

Levamisole sensitivity assay
To check for differences in levamisole sensitivity among wild type, dys-1(cx18) and dys-1(eg33), the groups were exposed to levamisole hydrochloride (Sigma-Aldrich, 31742) at 100 µM in M9 buffer. Animals were placed in 2.5 ml levamisole in 30 mm Petri dishes. Starting from t=0 min, the numbers of paralyzed animals were scored every 10 min until all wild-type worms were paralyzed. Experiments were performed for populations of Day 1 adult worms cultured at 20°C or 25°C. For worms cultured at 20°C, two independent biological replicates were performed, where n=50 for each experiment (total n=100 per strain). For 25°C, a single experiment was performed where n=50 per strain.

Sarcomere structure
To determine whether dys-1(cx18) and dys-1(eg33) worms showed defects in sarcomere structure, the worms were stained with Rhodamine Phalloidin Stain (Invitrogen, R415). The phalloidin staining procedure was carried out as described by Gieseler et al. (2000).

In addition to actin staining using phalloidin, crosses were made using PJ727 [jls01 (myo-3::GFP, rol-6 (su1006)); unc-54::lacz V], which has GFP fusion proteins localized to the contractile apparatus, with dys-1(eg33) and dys-1(cx18). The resulting crosses were referred to as CC96 [dys-1(eg33) I; jls01 (myo-3::GFP, rol-6 (su1006)); unc-54::lacz V] and CC97 [dys-1(cx18) I; jls01 (myo-3::GFP, rol-6 (su1006)); unc-54::lacz V]. Images were taken on Days 0, 1, 2 and 3 of adulthood. All images were taken at 40× magnification using a Nikon Eclipse 50i microscope.

Mitochondrial strains and imaging
The CB5600 [ccls4251 (Pmyo-3::Npgf-lacZ; Pmyo-3::Mpgf) I; him-8 (e1489) IV] strain, which has GFP fusion proteins localized to muscle mitochondria and nuclei, was used for this study. Crosses were made between the CB5600 strain and dys-1(cx18) (LS292 strain) and dys-1(eg33) (BZ33 strain). The resulting strains were CC90 [dys-1(cx18) I; ccls4251; him-8(e1489) IV] and CC91 [dys-1(eg33) I; ccls4251; him-8(e1489) IV]. CB5600 was used for the wild-type imaging. On Days 1, 3 and 5 of adulthood, animals were imaged in 20 µl M9 buffer on a microscope slide with a cover slip. All images were taken at 40× magnification using a Nikon Eclipse 50i microscope.

OCR
To investigate DMD-mediated changes in mitochondrial function, OCR measurements were performed using the Seahorse XF24 analyzer (Agilent), in line with previously described methods (Koopman et al., 2016). On Day 0 of adulthood, wild-type, dys-1(cx18) (LS292 strain) and dys-1(eg33) (BZ33 strain) animals were washed twice in M9 buffer and transferred into M9-filled wells (20 worms/well) in replicates of five per condition (i.e. five wells per strain). To generate stable OCR measurements, five measurement cycles were performed for basal OCR, five cycles for maximal OCR following the addition of FCCP (10 µM final well concentration) and five cycles for non-mitochondrial OCR, following the addition of sodium azide (40 nM final well concentration). A follow-up experiment was conducted to investigate whether prednisone treatment could rescue DMD-mediated changes in basal OCR. To do this, basal OCR was measured, as described, in adult (Day 1) wild-type (N2) and dys-1(eg33) animals both with and without prednisone treatment (20 worms/well, five replicates). Prednisone-treated worms were cultured, as previously described, on prednisone-treated (0.37 mM) agar. OCR measurements were normalized to the number of worms per well. To avoid unstable OCR measurements, the final three, seven and two measurement cycles were used for the statistical analysis of basal, maximal and non-mitochondrial OCR, respectively. Differences in OCR were detected with a one-way ANOVA with Tukey’s multiple comparison test using GraphPad Prism 6. The α-level of significance was set at P<0.05.

JC-10 and MitoTracker Red staining
To assess mitochondrial membrane potential, two in vivo dyes, JC-10 (Enzo Life Sciences, 52305) and MitoTracker Red CMXRos (Invitrogen, M7512), were used. Strains used for measuring mitochondrial membrane potential were wild type (N2), dys-1(cx18) (LS292 strain) and dys-1(eg33) (BZ33 strain). For prednisone-treated worms, animals were cultured as previously described on agar containing prednisone at a concentration of 0.37 mM. On the first day of adulthood, 40 worms were picked into 83 µM JC-10 in freeze-dried OP50 solution (LabTIE) for 4 h before imaging. The worms stained with MitoTracker Red were imaged on the first day of adulthood and the protocol by Gaffney et al. (2014) was followed. Representative images are shown for each strain stained with JC-10 and MitoTracker Red.

Acknowledgements
Some strains were provided by the CGC, which is funded by the NIH Office of Research Infrastructure Programs (P40 OD010440).

Competing interests
The authors declare no competing or financial interests.

Author contributions
Conceptualization: J.E.H., N.J.S., S.A.V.; Methodology: J.E.H., A.K.P., C.S.D., C.J.G., T.E., N.J.S., S.A.V.; Validation: J.E.H., A.K.P., T.E., N.J.S., S.A.V.; Formal analysis: J.E.H., A.K.P., C.S.D., C.J.G., T.E., N.J.S., S.A.V.; Investigation: J.E.H., A.K.P., T.E., N.J.S., S.A.V.; Resources: C.S.D., C.J.G.; Data curation: C.S.D., C.J.G., T.E.; Writing - original draft: J.E.H.; Writing - review & editing: J.E.H., A.K.P., T.E., N.J.S., S.A.V.; Visualization: J.E.H., A.K.P., N.J.S., S.A.V.; Supervision: N.J.S., S.A.V.; Project administration: N.J.S., S.A.V.; Funding acquisition: N.J.S., S.A.V.

Funding
This work was supported by the National Aeronautics and Space Administration [NNX15AL16G to S.A.V.], the National Institutes of Health [R21AG050503-01 to S.A.V.], Cancer Prevention and Research Institute of Texas [RP160806 to S.A.V.] and the Biotechnology and Biological Sciences Research Council [BB/N015894/1 to N.J.S.].
References

Ben-Zvi, A., Miller, E. A. and Morimoto, R. I. (2009). Collapse of proteostasis represents an early molecular event in Caenorhabditis elegans aging. Proc Natl Acad Sci USA 106, 14914-14919.

Brenn, C., Vidal-González, A. G., Cohn, J., Parikh, A., Hwang, G. and Pierce-Shimomura, J. T. (2015). The burrowing behavior of the nematode Caenorhabditis elegans: a new assay for the study of neuromuscular disorders. Genes Brain Behav. 14, 357-368.

Bessou, C., Giuglia, J.-B., Franks, C. J., Holden-Dye, L. and Ségalat, L. (1998). Mutations in the Caenorhabditis elegans dystrophin-like gene dys-1 lead to hyperactivity and suggest a link with cholinergic transmission. Neuronetgenics 2, 61-72.

Blake, D. J., Weir, A., Newey, S. E. and Davies, K. E. (2002). Function and genetics of dystrophin and dystrophin-related proteins in muscle. Physiol. Rev. 82, 291-328.

Brouilly, N., Lecroisey, C., Martin, E., Pierson, L., Mariol, M.-C., Qadota, H., Bessou, C., Giugia, J.-B., Franks, C. J., Holden-Dye, L. and Sehon, C., Vidal-Gadea, A. G., Cohn, J., Parikh, A., Hwang, G. and Pierce-Culetto, E. and Sattelle, D. B. (2002). Melatonin treatment normalizes plasma pro-inflammatory cytokines and nitrosative/oxidative stress in patients suffering from Duchenne muscular dystrophy. FEBS Lett. 463, 270-272.

Bilou, Y., Reutenauer-Patte, J., Pattehy-Vuadens, O., Ruegg, U. T. and Dorchies, O. (2001). Melatonin improves muscle function of the dystrophic mdx5cv mouse, a model for Duchenne muscular dystrophy. J Pineal Res. 31, 163-171.

Hueston, J. L. and Suprenant, K. A. (2009). Loss of dystrophin and the microtubule-binding protein ELP-1 causes progressive paralysis and death of adult C. elegans. Dev. Dyn. 238, 1878-1886.

Hulme, S. E., Shevokas, S. I., Labouesse, M., Streichenberger, N., Mounier, N. and Fire, A. (2007). Loss of dystrobrevin delays locomotion defects and muscle degeneration in a dystrophin-deficient Caenorhabditis elegans. Neuronmuscul. Disord. 12, 371-377.

Gieseler, K., Qadota, H. and Benian, G. M. (2016). Development, structure, and maintenance of C. elegans body wall muscle. In WormBook: the online review of Caenorhabditis elegans biology [Internet; updated 2016 Dec 2; released 2006 Apr 28]. doi: 10.1895/wormbook.1.57.1.

Glugia, J.-B., Gieseler, K., Arpagaus, M. and Ségalat, L. (1999). Mutations in the dystrophin-like dys-1 gene of Caenorhabditis elegans result in reduced acetycholinesterase activity. FEBS Lett. 463, 270-272.

Hibault, Y., Reutenauer-Patte, J., Patthehy-Vuadens, O., Ruegg, U. T. and Dorchies, O. (2001). Melatonin improves muscle function of the dystrophic mdx5cv mouse, a model for Duchenne muscular dystrophy. J Pineal Res. 31, 163-171.

Khaire, S. M., Awasthi, A., Venkataraman, A. and Kousshia, S. P. (2015). Colored polyethyleneimine micropillars for high throughput measurements of forces applied by genetic model organisms. Biomicrofluidics 9, 014111.

Koopman, M., Michels, H., Dancy, B. M., Kamble, R., Mouchlioud, L., Auwerx, J., Nollen, E. A. A. and Houtkooper, R. H. (2016). A screening-based platform for high throughput assessment of cellular respiration in Caenorhabditis elegans. Nat. Protoc. 11, 1798.

Le Rumeur, E. (2015). Dystrophin and the two related genetic diseases, Duchenne and Becker muscular dystrophies. B. J. Basic Med. Sci. 15, 14.

Leiers, B., Kapkoätter, A., Greveling, C. G., Link, D. C., Johnson, T. E. and Henkle-Dührsen, K. (2003). A stress-responsive glutathione S-transferase confers resistance to oxidative stress in Caenorhabditis elegans. Free Radiol. Biol. Med. 34, 1405-1415.

Lerario, A., Bonfiglio, S., Sormani, M. P., Tettamanti, A., Marktel, S., Napolitano, S., Previtali, S., Scarlato, M., Natale-Sora, M. G. and Mercuri, E. (2012). Quantitative muscle strength assessment in duchenne muscular dystrophy: longitudinal study and correlation with functional measures. BMC Neurol. 12, 91.

Malik, V., Rodinio-Klapac, L. R. and Mendell, J. R. (2012). Emerging drugs for Duchenne muscular dystrophy. Expert Opin Emerg. Drugs 17, 281-277.

Marian, M.-C. and Ségalat, L. (2001). Muscular degeneration in the absence of dystrophin: a calcium-dependent process. Curr. Biol. 11, 1891-1894.

McGregor, J. W., Hakim, C. H., McIntosh, M. A. and Duan, D. (2015). Animal models of Duchenne muscular dystrophy: beyond basic mechanisms to gene therapy. Dis. Model. Mech. 8, 195-213.

McGeeney, L. A., Kablar, B., Garrett, K., Anderson, J. E. and Rudnicki, M. A. (1999). MyoD is required for myogenic stem cell function in adult skeletal muscle. Dev. Genet. 25, 1173-1183.

Megersen, D. E., Milne, T., Blawzdziewicz, J., Constantin-Teodosiu, D. et al. (2018). DRP-1-mediated apoptosis induces muscle degeneration in dystrophin mutants. Sci. Rep. 8, 14162.

Moser, H. (1984). Duchenne muscular dystrophy: pathogenetic aspects and genetic prevention. Hum. Genet. 66, 17-40.

Oh, K. H. and Kim, H. (2013). Reduced IGF signaling prevents muscle cell death in a Caenorhabditis elegans model of muscular dystrophy. Proc. Natl Acad. Sci. USA 110, 19624-19629.

Parrillo, E. J. and Fauci, A. S. (1979). Mechanisms of glucocorticoid action on immune processes. Annu. Rev. Pharmacol. Toxicol. 19, 179-201.

Qi, Z., Tu, L., Huang, L., Zhu, T., Nock, V., Yu, E., Liu, X. and Wang, W. (2015). An integrated platform enabling optogenetic illumination of Caenorhabditis elegans neurons and muscles to assess cell movement in microstructured environments. Biomicrofluidics 9, 014123.

Rahman, M., Hewitt, J. E., Van-Bussel, F., Edwards, H., Blawzdziewicz, J., Qiu, Z., Tu, L., Huang, L., Zhu, T., Nock, V., Yu, E., Liu, X. and Wang, W. (2015). An integrated platform enabling optogenetic illumination of Caenorhabditis elegans neurons and muscles to assess cell movement in microstructured environments. Biomicrofluidics 9, 014123.

Rahman, M., Hewitt, J. E., Van-Bussel, F., Edwards, H., Blawzdziewicz, J., Qiu, Z., Tu, L., Huang, L., Zhu, T., Nock, V., Yu, E., Liu, X. and Wang, W. (2015). An integrated platform enabling optogenetic illumination of Caenorhabditis elegans neurons and muscles to assess cell movement in microstructured environments. Biomicrofluidics 9, 014123.

Rahman, M., Hewitt, J. E., Van-Bussel, F., Edwards, H., Blawzdziewicz, J., Qiu, Z., Tu, L., Huang, L., Zhu, T., Nock, V., Yu, E., Liu, X. and Wang, W. (2015). An integrated platform enabling optogenetic illumination of Caenorhabditis elegans neurons and muscles to assess cell movement in microstructured environments. Biomicrofluidics 9, 014123.

Rahman, M., Hewitt, J. E., Van-Bussel, F., Edwards, H., Blawzdziewicz, J., Qiu, Z., Tu, L., Huang, L., Zhu, T., Nock, V., Yu, E., Liu, X. and Wang, W. (2015). An integrated platform enabling optogenetic illumination of Caenorhabditis elegans neurons and muscles to assess cell movement in microstructured environments. Biomicrofluidics 9, 014123.

Rahman, M., Hewitt, J. E., Van-Bussel, F., Edwards, H., Blawzdziewicz, J., Qiu, Z., Tu, L., Huang, L., Zhu, T., Nock, V., Yu, E., Liu, X. and Wang, W. (2015). An integrated platform enabling optogenetic illumination of Caenorhabditis elegans neurons and muscles to assess cell movement in microstructured environments. Biomicrofluidics 9, 014123.
The C. elegans Sequencing Consortium. (1998). Genome sequence of the nematode C. elegans: a platform for investigating biology. *Science* **282**, 2012-2018.

Wen, H., Shi, W. and Qin, J. (2012). Multiparameter evaluation of the longevity in C. elegans under stress using an integrated microfluidic device. *Biomed. Microdevices* **14**, 721-728.

Wen, H., Gao, X. and Qin, J. (2014). Probing the anti-aging role of polydatin in Caenorhabditis elegans on a chip. *Integr. Biol.* **6**, 35-43.

Xian, B., Shen, J., Chen, W., Sun, N., Qiao, N., Jiang, D., Yu, T., Men, Y., Han, Z., Pang, Y. et al. (2013). WormFarm: a quantitative control and measurement device toward automated Caenorhabditis elegans aging analysis. *Aging Cell* **12**, 398-409.

Zhan, H., Stanciauskas, R., Stigloher, C., Dizon, K. K., Jospin, M., Bessereau, J.-L. and Pinaud, F. (2014). In vivo single-molecule imaging identifies altered dynamics of calcium channels in dystrophin-mutant C. elegans. *Nat. Commun.* **5**, 4974.