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Duchenne muscular dystrophy hiPSC-derived myoblast drug screen identifies compounds that ameliorate disease in mdx mice

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Introduction

Duchenne muscular dystrophy (DMD) is the most common muscular dystrophy. In the present study, when human induced pluripotent stem cells (hiPSCs) were differentiated into myoblasts, the myoblasts derived from DMD patient hiPSCs (DMD hiPSC-derived myoblasts) exhibited an identifiable DMD-relevant phenotype: myogenic fusion deficiency. Based on this model, we developed a DMD hiPSC-derived myoblast screening platform employing a high-content imaging (BD Pathway 855) approach to generate parameters describing morphological as well as myogenic marker protein expression. Following treatment of the cells with 1524 compounds from the Johns Hopkins Clinical Compound Library, compounds that enhanced myogenic fusion of DMD hiPSC-derived myoblasts were identified. The final hits were ginsenoside Rd and fenofibrate. Transcriptional profiling revealed that ginsenoside Rd is functionally related to FL T3 signaling, while fenofibrate is linked to TGF-β signaling. Preclinical tests in mdx mice showed that treatment with these 2 hit compounds can significantly ameliorate some of the skeletal muscle phenotypes caused by dystrophin deficiency, supporting their therapeutic potential. Further study revealed that fenofibrate could inhibit mitochondrion-induced apoptosis in DMD hiPSC-derived cardiomyocytes. We have developed a platform based on DMD hiPSC-derived myoblasts for drug screening and identified 2 promising small molecules with in vivo efficacy.
To date, for the most part drug preclinical screening and testing have been conducted in DMD animal models, with the mdx and the canine golden retriever muscular dystrophy models being the most commonly employed (10). These models are suitable for drug validation, but not amenable for large-scale screening due to the time-consuming drug development stage and high costs associated (11). As an alternative for large-scale drug screening, dystrophin-deficient Caenorhabditis elegans and zebrafish models have been used (12, 13); however, hit compounds found using these organisms have failed to successfully translate into effective DMD treatments (14). While the most promising DMD model for effective drug discovery has relied on use of DMD patient myoblasts, the major restrictions in their application are that myoblasts obtained from DMD patient biopsies are limited in number and phenotypically diverse. In this study, we circumvent the poor expandability of primary myoblasts by using human induced pluripotent stem cells (hiPSCs).

We recently developed a novel system to differentiate DMD hiPSCs into myoblasts using chemically defined conditions that are free of animal feeder cells, serum, or growth factors (15). This myogenic specification protocol involves plating single hiPSCs on defined extracellular matrix material and growing them for 25–30 days in serum-free medium with temporal activation of WNT and inhibition of Notch pathways. On day 25–30, myoblasts can be purified by NCAM+/HNK1− cell surface markers. One reproducible and distinguishable DMD disease phenotype of hiPSC-derived myoblasts is a deficiency in myoblast differentiation and fusion (15, 16). Therefore, we designed a high-content imaging–based screening platform to identify compounds that can correct DMD hiPSC–derived myoblast fusion defects. After performing tiered screening with small-molecule compounds from the Johns Hopkins Clinical Compound Library (JHCCL), 2 final hit compounds were selected and further studied to elucidate their mechanism of action, and subsequently tested preclinically in mdx mice and in hiPSC-derived cardiomyocytes (CMs), demonstrating their effectiveness and therapeutic potential. Overall, we performed a comprehensive drug screen using DMD hiPSC–derived myoblasts and demonstrated its feasibility as a platform to identify potential drugs that could be used to treat DMD.

Results
Primary screening of a small-molecule compound library using DMD patient hiPSC–derived myoblasts. We generated DMD patient hiPSC–derived myoblasts in a chemically defined system of Wnt activation and Notch inhibition from the D2325 hiPSC line of a DMD patient (referred to hereafter as “D2 myoblasts”). The DMD gene in these D2 myoblasts carried a nonsense mutation (c.457C>T) that completely abolished dystrophin protein expression (15) (Supplemental Figure 1, A and B; supplemental material available online with this article; https://doi.org/10.1172/jci.insight.134287DS1). Compared with healthy hiPSC–derived myoblasts, D2 myoblasts formed very few myotubes based on myosin heavy chain (MyHC) antibody staining (Supplemental Figure 1, C and D). This is consistent with our previous studies, in which myoblasts derived from multiple DMD hiPSC lines with various DMD gene mutations formed significantly fewer myotubes, based on MyHC staining (15–17), and similar observations made on primary myoblasts of DMD patients (17–19). Inefficient myotube formation was partially reversed by a known stop codon readthrough compound, gentamicin (Figure 1A) (20). Although not used in the clinical setting due to an unfavorable risk-benefit profile (21), gentamicin served as a positive control in our screen. To test the feasibility of the compound screening format, we imaged myoblasts treated with gentamicin or vehicle control (DMSO) and analyzed them with a high-content imaging analysis system (BD Pathway 855) that could detect and outline the cells on the plate (Figure 1A). We compared a variety of parameters after the treatment of gentamicin or vector DMSO on D2 myoblasts as a pilot experiment in differentiation conditions, and found that when the average length of cells was considered, positive and negative control values were statistically different (Z′ = 0.59) (Figure 1C). MyHC immunofluorescence intensity was also considered, as MyHC protein expression is a hallmark of myotube formation (22). To minimize plate-to-plate variation, we normalized the values obtained from each tested compound to positive and negative controls. Thus, we established algorithm 1 as the following equation: normalized cell average length + 0.3 × normalized MyHC intensity (Z′ = 0.58) (Figure 1B). Also, in order to include the compounds that can restore the myotube shape without increasing MyHC immunofluorescence intensity, we used absolute values of cell average length (without normalization) as algorithm 2, which also helped to eliminate the compounds that were autofluorescent.

We seeded D2 myoblasts onto 96-well plates and screened 1524 small-molecule compounds from the compound library, which contained both FDA- and foreign agency–approved drugs (23). The compounds in the library are structurally diverse, and some are natural compounds. Therefore, they are suitable for
drug repurposing for rare diseases. Twenty-four compounds were selected based on their algorithm 1 and 2 values being near or above the average of the positive control. After retesting, 9 final hit compounds were selected (Supplemental Figure 2, A and B). These 9 compounds were also distinct from negative controls and aligned with the gentamicin-positive control group (Figure 1D).

To our knowledge, 2 of the 9 hit compounds (methazolamide and clomiphene) have previously been reported to ameliorate the disease phenotype of the \textit{mdx} mouse model. Methazolamide was identified in a drug screening of the \textit{C. elegans} model, and it was shown to increase the tetanic force in \textit{mdx} mice (12). Clomiphene is an analog of tamoxifen that was shown to increase force production and suppress fibrosis in \textit{mdx} mice (12, 24). The identification of methazolamide and clomiphene by our 2 algorithms supported the validity of our screening efforts and data analysis.

**Secondary and tertiary screening to obtain 2 final hit compounds.** To further evaluate the efficacy of the 9 hit compounds and determine their optimal concentrations, we performed an 8-point dose-response assay based on 3 parameters: anti-MyHC immunocytochemistry, anti–α-actinin immunocytochemistry, and average cell length (Supplemental Figure 3, A and B). We determined the final hit compounds by their ability to generate dose-dependent response curves with at least 2 of the 3 parameters. Based on the
dose-response curves, we selected 3 hit compounds: clomiphene, saponin Q (saponin from quillaja bark), and fenofibrate (Figure 2, A and B, and Supplemental Figure 3, A and B). As the analog of clomiphene, tamoxifen, is already in clinical trials for DMD treatment, we did not further pursue clomiphene (24). Saponin Q and fenofibrate were selected for further analysis. However, saponin Q has relatively high toxicity among all members of the saponin family (25), and thus we observed cell death after high-concentration treatment. Therefore, we tested 4 analogs of saponin (akebia, soya saponin, sarsasapogenin, and ginsenoside Rd) (Figure 2C and Supplemental Figure 3, C–E). Among these, ginsenoside Rd treatment not only had a dose-dependent effect on D2 myoblasts, but also increased the levels of MEF2C protein expression (26), whereas saponin Q did not (Figure 2, D–F, and Supplemental Figure 4A). Therefore, ginsenoside Rd holds advantages over saponin Q not only due to its lower toxicity, but also because it improved MEF2C expression, which is critical for myogenic differentiation. When fenofibrate and ginsenoside Rd were tested in other DMD hiPSC–derived myoblasts carrying different mutations (GM05127 05533G>C and GM05114 Ex45del), both hit compounds improved myotube formation, as indicated by increased average cell length and MyHC antibody signal intensity (Figure 3, A and B). As a result, our selected final lead compounds were fenofibrate and ginsenoside Rd (Supplemental Figure 4B).

Figure 2. Secondary and tertiary screening to narrow list of candidate compounds to final 2 hits. (A) Representative images of saponin Q–, fenofibrate–, clomiphene–, gentamicin–, and DMSO–treated D2 myoblasts, along with healthy hiPSC–derived myoblasts showing MyHC–positive myotubes. (B) Cell average length dose–response curves for saponin Q, fenofibrate, clomiphene, and gentamicin, n = 3. (C) Representative image of ginsenoside Rd–treated myoblasts labeled with MyHC, and cell average length dose–response curve of ginsenoside Rd; n = 3. Scale bars: 50 μm. (D and E) Western blot quantification of MEF2C protein level after saponin Q and ginsenoside Rd treatment alongside healthy hiPSC–derived myoblast controls and DMSO negative controls; n = 3 for all 3 groups; **P ≤ 0.01. (F) Quantification of MEF2C–expressing nuclei of saponin Q– and ginsenoside Rd–treated D2 myoblasts; n = 3 for all 4 groups; *P ≤ 0.05. Data are presented as mean ± SEM; E and F: each point represents an experimental repeat, 1-way ANOVA with Dunnett’s multiple-comparisons test with DMSO negative control.
Fenofibrate treatment is beneficial to DMD hiPSC–derived CMs. Next, we sought to determine whether the 2 hit compounds had any effects on cardiac cells. It was previously reported that CMs derived from DMD iPSCs are associated with increased mitochondrion-mediated cell apoptosis (27). Thus, we evaluated mitochondrial membrane potential in DMD hiPSC–derived CMs (DMD-CMs) treated with the hit compounds using MitoProbe JC-1 dye. JC-1 dye exhibits potential-dependent accumulation in mitochondria, indicated by a fluorescence emission shift from green to red. Consequently, mitochondrial depolarization is indicated by a decrease in the red/green fluorescence intensity ratio. Treatment of CMs with fenofibrate (5 μM) for 7 days significantly increased the red/green ratio compared with untreated CMs, indicating the membrane potential change. Data were generated from DMD-CMs treated with DMSO (control), ginsenoside Rd (5 μM), and fenofibrate (5 μM) performed in triplicate. (E–G) Western blot quantification of cytochrome c and cleaved caspase-3 in DMD-CMs treated with ginsenoside Rd (5 μM), fenofibrate (8 μM), or DMSO; n = 3 for all 3 groups. Data are presented as mean ± SEM; each point represents an experimental repeat; 1-way ANOVA with Dunnett’s multiple-comparisons test with DMSO control.
that fenofibrate reduces mitochondrial depolarization and apoptosis (Figure 3, C and D, and Supplemental Figure 5A). However, ginsenoside Rd (5 μM) treatment did not have any effect on DMD-CM mitochondrial membrane potential (Figure 3C). In healthy hiPSC–derived CMs we observed an effect similar to that in DMD-CMs when treated with fenofibrate (data not shown). Mitochondria dysfunction is also related to cytochrome c release and caspase-3 cleavage, which indicate mitochondrial damage and apoptosis (28). In concert with the reduced mitochondrial membrane potential, fenofibrate-treated DMD-CM had a trend toward reduced cytochrome c and slight reduction in cleaved caspase-3 (Figure 3, E–G). On the other hand, healthy hiPSC–derived CMs showed no change or trend toward reduced cytochrome c or cleaved caspase-3 (Supplemental Figure 5, B–D). In summary, fenofibrate but not ginsenoside Rd improved the mitochondrial membrane potential and inhibited apoptosis in DMD-CMs.

Fenofibrate and ginsenoside function through TGF-β and ERK1/2 signaling pathways in DMD patient hiPSC–derived myoblasts. In order to elucidate the mechanism by which the 2 final hit compounds ameliorated fusion defects of the D2 myoblasts, we performed unbiased global transcriptional profiling on D2 myoblasts treated with fenofibrate (8 μM) or ginsenoside Rd (5 μM). A heatmap showed distinctive gene expression profiles among groups (Supplemental Figure 6A), and the transcriptional analysis results were validated by quantitative (qPCR) (29) (Supplemental Figure 6, B and C). Ingenuity pathway analysis (IPA) showed that the most significantly positive correlation (Z score > 2) after ginsenoside Rd treatment was with the FLT3 signaling pathway (Table 1). It has been reported that FLT3 regulates myogenic differentiation by enhancing the expression of p21 (WAF1/CIP1), a cell cycle inhibitor, resulting in cells exiting the cell cycle (30). We detected increased levels of p21 in D2 myoblasts under FLT3 treatment, and this effect was also seen in ginsenoside Rd–treated D2 myoblasts (Figure 4, A and B). At the same time, ERK1/2, a known FLT3 pathway downstream effector (31), was activated both by FLT3 recombinant protein and ginsenoside Rd in D2 myoblasts (Figure 4, C and D) (32). Fenofibrate treatment suppressed TGF-β signaling in D2 myoblasts (Z score < –2), as determined by IPA (Table 1). Moreover, when D2 myoblasts were treated with a combination of fenofibrate and TGF-β1 recombinant protein, SMAD2/3 phosphorylation was reduced, indicating that fenofibrate suppressed TGF-β signaling (Figure 4, E and F) (33). As TGF-β signaling plays a suppressive role in muscle differentiation, it is likely that fenofibrate improves D2 myoblast differentiation/fusion efficiency by inhibiting TGF-β (34). At the same time, we observed an inhibitory effect of fenofibrate on primary human fibroblast growth, which could have been caused by suppressed TGF-β signaling (Supplemental Figure 6D).

Based on the results above, we conclude that the positive effects of ginsenoside Rd and fenofibrate are associated with the FLT3 and TGF-β pathways, respectively.

Table 1. Top pathways selected by IPA of microarray result from D2 myoblasts treated with ginsenoside Rd and fenofibrate for 24 hours

| Ingenuity canonical pathway | Z score |
|----------------------------|---------|
| **Ginsenoside Rd treatment** |         |
| FLT3 signaling             | 2.236   |
| Role of CHK proteins in cell cycle checkpoint control | 2   |
| Role of IL-17F in allergic inflammatory airway diseases | 2   |
| cAMP-mediated signaling    | 1.604   |
| PKA signaling              | 1.606   |
| ERK/MAPK signaling         | 1.508   |
| **Fenofibrate treatment**  |         |
| TGF-β signaling            | –2.449  |
| NO signaling in the cardiovascular system | 2.121 |
| AMPK signaling             | 1.414   |
| cAMP-mediated signaling    | 1.342   |

Absolute Z score values of at least 2 are highlighted in bold.

Ginsenoside Rd and fenofibrate ameliorate the disease phenotype of the mdx mouse model of DMD. Since ginsenoside Rd and fenofibrate were effective in correcting the in vitro DMD phenotype of DMD hiPSC–derived myoblasts, we sought to determine whether they also had a therapeutic effect in vivo. We tested
each of the 2 compounds in mdx<sup>sv</sup> mice (35). We treated the mice with ginsenoside Rd (10 mg/kg) through daily intraperitoneal injections and fenofibrate (0.1% wt/wt) through diet beginning postnatal day 21, for 8 weeks (36) (Figure 5A). Neither of the compounds affected the growth curve of the mdx mice (Figure 5B).

At the end of the treatment period, the pathology of different muscles was assessed. Skeletal muscle fibrosis is most prominent in the diaphragm of mdx mice (37), and the levels of fibrosis in diaphragm were reduced by treatment with ginsenoside Rd (29%) and fenofibrate (42.1%) (Figure 5, C and D, and Supplemental Figure 7A). Decreased levels of fibrosis were further confirmed by quantifying hydroxyproline, which is a modified amino acid found in fibrosis. Fenofibrate treatment reduced hydroxyproline in the diaphragm by 29% (Supplemental Figure 7B). Numbers of Evans blue dye–positive (EBD-positive) fibers (a marker of cell membrane damage) and centrally nucleated fibers (a marker of muscle degeneration and regeneration) were not significantly different in treated muscles (Supplemental Figure 7, C and D). Cross-sectional area (CSA) analysis of TA muscle showed that the number of very small fibers (0–1000 μm<sup>2</sup>) decreased and the medium-sized fibers (1000–2000 μm<sup>2</sup>) increased in both ginsenoside Rd– and fenofibrate-treated mdx when compared with sham-treated control mice (Figure 5E). Mean CSA was not significantly different across treatment groups (Supplemental Figure 7E). However, the standard deviations of the ginsenoside Rd–treated group, 1476, and fenofibrate-treated group, 1315, were lower than that of the sham-treated group, 1588, indicating that both compounds reduced the variability of the fiber sizes.

We performed a series of functional assessments, including grip strength and treadmill running endurance. Both fenofibrate and ginsenoside Rd significantly improved mdx mouse forelimb grip strength, by 16% and 19%, respectively (Figure 5F). Fenofibrate treatment improved endurance in treadmill running by 50% compared with control treatment in mdx mice, while ginsenoside Rd had no effect on treadmill performance.
running (Figure 5G and Supplemental Figure 7F). In situ physiology testing, there was no significant difference in maximal isometric force generated by tibialis anterior (TA) or quadriceps muscle with either treatment compared with the sham control (Supplemental Figure 7, G and H). However, repeated maximal isometric contractions showed that TA muscles of mice treated with fenofibrate or ginsenoside Rd were less susceptible to fatigue compared with untreated mdx TA muscles (Figure 5H). As in previous studies, mdx quadriceps muscles were highly susceptible to injury (78% ± 5.3% loss in muscle force after injury), but treatment with ginsenoside Rd or fenofibrate resulted in significantly less contraction-induced injury (56% ± 4.8% and 50% ± 3.5% loss in muscle force, respectively) (Figure 5I).

Overall, our results indicate that ginsenoside Rd and fenofibrate treatment ameliorated disease phenotypes in mdx mice.
Discussion

Drug discovery and repurposing for treatment of DMD has mostly employed 2 strategies: restoring dystrophin expression; and modifying downstream pathological pathways, including inflammation, fibrosis, and oxidative stress (38). A rapid and relevant method to identify disease-modifying treatments for DMD could enable a swift translational process, from drug screening to therapy. To improve drug discovery and repurposing of known or approved drugs for DMD, human dystrophic muscle cells that demonstrate a distinguishable phenotype are needed. Recently, the use of hiPSCs has gained interest as an emerging approach in drug discovery for genetic diseases (39). hiPSCs provide a scalable source of starting material that can be easily used in drug screens for DMD. Despite this advantage, to our knowledge there have been no reported applications of hiPSCs for DMD drug screens due to the lack of efficient and reproducible DMD hiPSC models.

During the past 4 years, protocols have emerged for myogenic differentiation of DMD hiPSCs. In 2016, 2 groups, including ours, independently reported protocols to directly differentiate hiPSC using a chemically defined system (15, 16). Applying Wnt activator and Notch inhibitor, Choi et al. depicted a distinct transcription profile and phenotype of DMD hiPSC–derived myoblasts from the healthy hiPSC–derived myoblasts. With Wnt activation and BMP inhibition, Chal et al. reported that myotubes formed from myoblasts derived from mdx mice presented abnormal branching. While both differentiation protocols showed myogenic commitment and ex vivo contraction of skeletal muscle myotubes, Hicks et al., using Chal’s protocol, did not report fusion defects in myoblasts derived from DMD hiPSCs following NCAM+/HNK1− purification (40). The discrepancy in reported phenotypes of NCAM+/HNK1− DMD hiPSC–derived myoblasts could be due to the fact that the IGF-1 and HGF growth factors, which were used in Chal’s protocol, can enhance myoblast fusion potential (41, 42). In comparison, our myoblasts culture system does not contain any growth factors, demonstrating the native myotube formation potential. Moreover, our transcriptional and translational profile data showed increased BMP and TGF-β signaling in DMD hiPSC–derived myoblasts. A similar phenomenon was found in myoblasts isolated from DMD patient biopsies, and these myoblasts also demonstrated limited growth capability (17). Using the hiPSC differentiation method described above, we developed an imaging-based screening system in which myotube formation was visualized by staining chemically induced DMD iPSC–derived myoblasts with antibodies. This straightforward, easily detectable phenotype via imaging can be used in future compound library screens.

The JHCCL used in this study contains around 1000 FDA-approved and 500 foreign agency–approved compounds. While designing and testing a new drug is costly and time consuming, screening approved drugs for previously unidentified activities could significantly speed the process of drug development. Using this compound library together with the imaging-based screen system described above, we selected 2 final compounds — ginsenoside Rd and fenofibrate. Ginsenosides are a group of active components found in Panax ginseng, a well-known herbal medicine touted to improve thinking, concentration, memory, work efficiency, physical stamina, and athletic endurance (43). Although the therapeutic potential of ginseng has been studied extensively, ginsenosides, which belong to the saponin family, have not yet been thoroughly investigated. Ginsenosides are reported to function primarily via antiinflammatory and antioxidant effects (44). Ginsenoside Rd was chosen among all the ginsenosides because of its function of inhibiting calcium influx (a hallmark of DMD pathology), inhibiting ROS, decreasing cellular apoptosis, and stabilizing mitochondrial membrane potential (45). In this study, we found that ginsenoside Rd helped restore fusion of DMD hiPSC–derived myoblasts. We performed gene ontology analyses using microarray results from DMD hiPSC–derived myoblasts treated with ginsenoside Rd to uncover this drug’s mechanism of action. When analyzing the pathways affected by ginsenoside Rd treatment, the FLT3 pathway was the top most significantly regulated pathway. FLT3 is a type III tyrosine kinase, and its mutation in leukemia results in aberrant cell growth (46). To date, there has been only one study to our knowledge reporting FLT3 as necessary for myogenic differentiation; overexpression of FLT3 appeared to promote cell cycle exit and myoblast fusion by inhibiting ERK activity through p120RasGAP (30). In our study, enhanced ERK phosphorylation was observed in D2 myoblasts by recombinant FLT3 (100 ng/mL) treatment as well as ginsenoside Rd (20 μM) treatment (Figure 4, C and D), which is in contrast to the result of Ge et al. (30). There are a couple of potential explanations. In leukemia, activated FLT3 receptor is known to induce RAS/ERK activation (47). Additionally, several reports have claimed that ERK phosphorylation is induced when myoblasts are terminally differentiated into myotubes (48, 49). Therefore, FLT3 is more likely to activate ERK and induce D2 myoblast differentiation upon recombinant FLT3 or ginsenoside Rd treatment. In this study, when ginsenoside Rd was given to mdx mice, we observed that ERK was activated, as suggested by
which were reported to recapitulate the DMD disease phenotype by exhibiting increased cytosolic Ca²⁺ and is followed by fibrosis of the heart (56). Therefore, we performed compound treatment of DMD-CMs, mortality. CMs that lack dystrophin protein are vulnerable to membrane fragility, resulting in cell death, which β signaling.

ment in vitro (Supplemental Figure 5D) (55), supporting the hypothesis that the mechanism underlying proliferation of fibroblasts was inhibited by fenofibrate treatment (Supplemental Figure 8, E and F), we observed decreased fibrosis and increased muscle function in fenofibrate-treated mdx mice. Moreover, proliferation of fibroblasts was inhibited by fenofibrate treatment in vitro (Supplemental Figure 5D) (55), supporting the hypothesis that the mechanism underlying fenofibrate’s effects is inhibition of TGF-β signaling.

Apart from skeletal muscle, the heart is also significantly affected in DMD and is a major cause of mortality. CMs that lack dystrophin protein are vulnerable to membrane fragility, resulting in cell death, which is followed by fibrosis of the heart (56). Therefore, we performed compound treatment of DMD-CMs, which were reported to recapitulate the DMD disease phenotype by exhibiting increased cytosolic Ca²⁺ and mitochondria damage. We found that fenofibrate reduced mitochondrial depolarization, indicating that it may have therapeutic benefits for cardiac muscle in addition to skeletal muscle (27).

In summary, our study shows the application of hiPSC-derived myoblasts in a high-content imaging–based drug screening platform to discover 2 compounds, ginsenoside Rd and fenofibrate. These 2 compounds ameliorated the dystrophic phenotype in the mdx mouse model. In treadmill and grip strength assays, fenofibrate-treated mdx mice ran longer distances, and mice treated with either compound had enhanced forelimb grip strength (Figure 5, F and G). In physiology testing, TA muscle of mdx mice treated with either compound showed significantly less susceptibility to muscle fatigue (Figure 5H), a major symptom of DMD. Although specific force of TA and torque of quadriceps did not improve, mdx mice treated with either fenofibrate or ginsenoside Rd showed a significant reduction in susceptibility to contraction-induced injury (Figure 5I). The above evidence raises the possibility that these drugs could be tested in the context of DMD. The results of this study indicate the feasibility of using hiPSC-based medium-scale drug screening to identify FDA-approved drugs or natural products for orphan diseases.

**Methods**

*Animal and treatment.* mdx²cv (B6Ros.Cg-Dmdmdx-5Cv/J) mice were obtained from the Jackson Laboratory. Mice were maintained in a 12-hour/12-hour dark light cycle (7 am−7 pm) with ad libitum access to food and water. Male mdx mice at 3 weeks of age were randomly assigned to one of the 3 groups: sham, fenofibrate, or ginsenoside Rd. Mice received a standard chow diet (Global 18% Protein Rodent Diet-Control, Teklad) or a diet containing fenofibrate (0.1%, wt/wt, MilliporeSigma) (57) mixed into the standard chow. Ginsenoside Rd was suspended in saline containing 10% 1,3-propanediol as vector. Ginsenoside Rd (10 mg/kg) (58) was provided to mdx mice through intraperitoneal injection. The sham group received standard chow diet and intraperitoneal injection of vector at the same time.

*Generation of DMD patient iPSCs.* D2325 fibroblasts were obtained from a DMD patient at the Kennedy Krieger Institute. Genetic testing revealed that this patient had a stop codon mutation at c.457. Other fibroblasts were purchased from Coriell Institute for Medical Research (GM05127 and GM05114) with appropriate Material Transfer Agreement documents. Human cells were cultured in DMEM containing 10% FBS. Fibroblasts were plated onto 24-well plates and reprogrammed with a CytoTune-iPS Sendai Reprogramming Kit (Invitrogen) with the standard protocol. After 9 days, cells were seeded onto a mouse embryonic fibroblast (MEF) feeder layer.
iPSC differentiation and myoblast maintenance. The DMD hiPSC–derived myoblasts were differentiated using the CHIR-DAPT protocol (15). Briefly, hiPSCs were plated as single cells on Geltryx-treated (Gibco) dishes at a density of 1.5 × 10^4 cells per well in a 24-well plate, in the presence of MEF-conditioned N2 media containing 10 ng/mL FGF-2 (PeproTech) and 10 μM Y-27632 (Cayman). The cells were induced to differentiate into myoblasts by adding CHIR99021 (3 μM) in N2 medium for 4 days and DAPT (10 μM) for the following 8 days. Cells continued to differentiate and mature in N2 medium for the next 13 days. Myoblasts were collected by FACS with the selection marker NCAM+/HNK1– (NCAM: 5.1H11, Developmental Studies Hybridoma Bank [DSHB]; HNK1: C6680, MilliporeSigma).

The NCAM+/HNK1– myoblasts were maintained in a humidified incubator containing 5% CO₂ at 37°C and grown in N2 media supplemented with 10% FBS. To induce myotube formation, expanded NCAM+/HNK1– myoblasts were plated to confluence and switched to N2 media without serum.

Drug screen. The JHCCL (v1.3) was provided by David Sullivan of the Johns Hopkins Bloomberg School of Public Health. The FACS-sorted DMD hiPSC–derived myoblasts were seeded at 25,000 cells per well in 96-well plates. Medium was changed to N2 without additional serum, and cells were treated with compounds from the JHCCL (1 μM), DMSO (0.1%, negative control), or gentamicin (500 μg/mL, MilliporeSigma) every 3 days for 9 days. The compound library consisted of 1524 small molecules. Cells were then fixed with 4% paraformaldehyde and stained with MyHC antibody (2235587, DSHB) (59, 60).

Automated image acquisition protocol with high-content imaging/analyzing system (BD Pathway 855, at ChemCore, Johns Hopkins School of Medicine), and automated analysis programming (BD AttoVision) were used to image and analyze myotube formation. Primary hits were validated in secondary replicate experiments (n = 3). Antibodies used for immunofluorescence in secondary as well as tertiary screen were MEF2C (1410781, MilliporeSigma) and α-actinin (A7811, MilliporeSigma).

Western blot. Whole-cell extracts were prepared by lysing cells on a plate with RIPA buffer (Cell Signaling Technology [CST]) supplemented by protease inhibitor and phosphatase inhibitor cocktail (CST). Western blotting was performed according to the standard protocol using precast NuPAGE (4%–12%) Bis-Tris gel (Invitrogen). Protein transfer was performed with the Bio-Rad Turbo or wet/tank blotting system. Nitrocellulose membranes were incubated with primary antibodies overnight at 4°C. Membranes were then incubated with a secondary IRDye 800–conjugated anti-rabbit IgG or Alexa Fluor 680–anti-mouse IgG, and proteins were visualized and quantified using the LI-COR Odyssey Infrared Imaging System. Primary antibodies used in Western blotting were p-ERK1/2 (9101, CST), ERK (9102, CST), p-SMAD2/3 (9102, CST, p-SMAD2/3 (8828, CST), SMAD2/3 (3102, CST), p21 (2947, CST), and MEF2C (1410781, MilliporeSigma).

Affymetrix microarray and qPCR. Triplicate samples were used in microarray analysis. D2 hiPSC–derived myoblasts were treated with ginsenoside (5 μM), fenofibrate (8 μM), or DMSO for 24 hours in the differentiation medium. RNA was isolated using TRIzol (Invitrogen Life Technologies), followed by purification and DNase digestion using RNeasy Mini Kits (QIAGEN) according to the manufacturer’s instructions. Quantification of total RNA was performed on a NanoDrop spectrophotometer (Thermo Fisher Scientific), and RNA quality was tested on an Agilent TapeStation with R6K ScreenTapes (RNA integrity number [RIN] 7.6–9.8). Generation of sense strand cDNA from purified total RNA was followed by second-strand synthesis, in vitro transcription cDNA synthesis, and single-stranded cDNA synthesis and RNA hydrolysis. Fragmentation and labeling were performed according to the manufacturer’s instructions (GeneChip WT PLUS Reagent Kit, Affymetrix). RNA extraction and qPCR were performed according to previous protocols (61), and primers are listed in Supplemental Table 1. The microarray data have been deposited in the NCBI’s Gene Expression Omnibus database (GEO GSE121023).

Hierarchical clustering was performed using Spotfire Genomics Suite with Functional Genomics v9.1.2 (TIBCO). Clustering of the 1042 mean-subtracted values used the unweighted average (unweighted pair group method with arithmetic mean [UPGMA]) method on correlation similarity with input rank ordering function. The heatmap (Supplemental Figure 6A) displays the hierarchical clustering of 1042 transcripts selected for having P values less than 0.05 for differentiating among the 3 biological classes: control, fenofibrate, and ginsenoside Rd. Raw microarray CEL files were extracted with Partek Genomics Suite 7.0 and the log, values quantile normalized with the RNA protocol, then mean-subtracted for each transcript before hierarchical clustering.

Treadmill and grip strength. Forelimb grip strength was measured as maximal tensile force using a computerized force transducer (Grip Strength Meter, Bioseb). Five measurements were performed for each animal, and the maximum value was used for the analysis. Treadmill testing was performed using a motor-driven treadmill (Columbus Instruments). Before the test day, acclimatization was performed.
were plated as single cells on Geltrex-treated dishes, at a density of 0.5 × 10^5 to 2 × 10^5 cells per well in a
Hz and expressed as a percentage of initial tension. Muscle tension was measured after 5 minutes of tetanic stimulation (200-ms train duration) repeated at 1 g/g was therefore normalized to TA mass to calculate as specific force (\( \text{specific force} \)). To provide an index of fatigue, it is assumed to be a constant, physiological CSA of the TA was solely a function of muscle mass. Force the TAs were harvested and weighed. As muscle length was fixed in all experiments, and muscle density (PolyVIEW 16, Grass Instruments). After contractile function experiments, animals were euthanized, and ular nerve, and the resulting force generated was sampled at 1 kHz and analyzed with acquisition software (FT03, Grass Instruments). The load cell was adjusted via a micromanipulator to stretch the muscle to resting length (optimal length). TA contraction was then triggered via subcutaneous stimulation of the fib-tibia was stabilized, and the distal tendon of the TA was surgically released and attached to the load cell onto a lever arm. The knee was aligned with the axis of the stepper motor (model T8904, NMB Technologies) and a torque sensor (QWFK-8M, Sensotec), and the femoral nerve was stimulated via subcutaneous needle electrodes. A custom program based on commercial software (LabView version 8.5, National Instruments) was used to synchronize contractile activation and the onset of forced knee flexion. The position of the leg that results in optimal muscle length has been previously described, and maximum isometric torque was measured in Newton-millimeters (Nmm). Injury was induced by 15 forced lengthenings (knee flexion) superimposed onto maximal quadriceps contractions through a 40- to 100-degree arc of motion (with full knee extension considered 0 degrees) spaced 1 minute apart. Loss in maximal isometric torque was measured 5 minutes after the last lengthening contraction. Since the knee position, lever arm, and moment arm of the muscle are unchanged between tests, maximal isometric torque reflects maximal isometric muscle force.

TA muscle strength (maximal isometric force) and rate of fatigue were measured as described previously (64). Briefly, animals were anesthetized with 3%-5% isoflurane and placed in a supine position. The thigh was stabilized and the ankle was secured onto a lever arm. The knee was aligned with the axis of the stepper motor (model T8904, NMB Technologies) and a torque sensor (QWFK-8M, Sensotec), and the femoral nerve was stimulated via subcutaneous needle electrodes. A custom program based on commercial software (LabView version 8.5, National Instruments) was used to synchronize contractile activation and the onset of forced knee flexion. The position of the leg that results in optimal muscle length has been previously described, and maximum isometric torque was measured in Newton-millimeters (Nmm). Injury was induced by 15 forced lengthenings (knee flexion) superimposed onto maximal quadriceps contractions through a 40- to 100-degree arc of motion (with full knee extension considered 0 degrees) spaced 1 minute apart. Loss in maximal isometric torque was measured 5 minutes after the last lengthening contraction. Since the knee position, lever arm, and moment arm of the muscle are unchanged between tests, maximal isometric torque reflects maximal isometric muscle force.

hiPSC-CM differentiation and JC-1 assay. DMD hiPSC–derived cardiomyocytes (GM05114 Ex45del) were plated as single cells on Geltrex-treated dishes, at a density of 0.5 × 10^4 to 2 × 10^5 cells per well in a 6-well plate. Cells were cultured in E8 medium (Gibco) for 2 days before induction to CMs. When cells became 70%-90% confluent, cardiomyocyte differentiation was carried out in RPMI (Gibco) media supplemented with B27 without insulin. Differentiation was induced by addition of 6 \( \mu \)M CHIR99021 (Selleck Chemicals) to a confluent monolayer of cells for 2 days, followed by addition of 10 \( \mu \)M IWR-1 (Enzo Life Sciences) from day 3 to 5. CMs were metabolically enriched from day 8 to 10 in glucose-free DMEM supplemented with lactate (4 mM) as previously described (65). CMs (14 days old) were treated with ginsenoside Rd (5 \( \mu \)M) and fenofibrate (5 \( \mu \)M) for 7 days in RPMI media supplemented with B27 and 50 \( \mu \)M isoproterenol. Media was changed every 48 hours. JC-1 dye (Mitochondrial Membrane Potential Probe) assay was performed according to the manufacturer’s protocol (Invitrogen).

Statistics. All data are shown as mean ± SEM and were subjected to statistical analysis. Significance was analyzed by 1-way ANOVA using Dunnett’s or Tukey’s multiple-comparisons test or were analyzed by 2-tailed unpaired Student’s t test. \( P \leq 0.05 \) was considered significant. The \( n \) values indicate the number of independent biological samples. Data were analyzed and represented with GraphPad Prism. Investigators were blinded to allocation during animal experiments and outcome assessment.
Study approval. All human sample–related experiments were approved by the Institutional Stem Cell Research Oversight Committee (ISCR0: RN00000264 For ISCR000000017) and the Johns Hopkins Medicine Institutional Review Boards (JHM IRBs, NA_0019985), Johns Hopkins University School of Medicine. All animal experiments were approved by the IACUC of the Johns Hopkins University School of Medicine. Written informed consent was received from the patient who provided the D2 sample at the Kennedy Krieger Institute (IRB NA_0019985).

Author contributions
CS designed and conducted the experiments, analyzed the data, and wrote the manuscript. IYC conducted the cell differentiation. YIRG conducted the experiments. CCT analyzed the microarray data. SRI and RML conducted the mdx physiology experiments and data analysis. PA conducted the iPSC-CM experiments. GL and KRW designed the study. All authors reviewed the manuscript.

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