



NO production results in suspension-induced muscle atrophy through dislocation of neuronal NOS

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Forkhead box O (Foxo) transcription factors induce muscle atrophy by upregulating the muscle-specific E3 ubiquitin ligases MuRF-1 and atrogin-1/MAFbx, but other than Akt, the upstream regulators of Foxos during muscle atrophy are largely unknown. To examine the involvement of the dystrophin glycoprotein complex (DGC) in regulation of Foxo activities and muscle atrophy, we analyzed the expression of DGC members during tail suspension, a model of unloading-induced muscle atrophy. Among several DGC members, only neuronal NOS (nNOS) quickly dislocated from the sarcolemma to the cytoplasm during tail suspension. Electron paramagnetic resonance spectrometry revealed production of NO in atrophying muscle. nNOS-null mice showed much milder muscle atrophy after tail suspension than did wild-type mice. Importantly, nuclear accumulation of dephosphorylated Foxo3a was not evident in nNOS-null muscle, and neither MuRF-1 nor atrogin-1/MAFbx were upregulated during tail suspension. Furthermore, an nNOS-specific inhibitor, 7-nitroindazole, significantly prevented suspension-induced muscle atrophy. The NF- κ B pathway was activated in both wild-type and nNOS-null muscle during tail suspension. We also show that nNOS was involved in the mechanism of denervation-induced atrophy. We conclude that nNOS/NO mediates muscle atrophy via regulation of Foxo transcription factors and is a new therapeutic target for disuse-induced muscle atrophy.

Introduction

Reduced muscle activity such as bed rest, limb immobilization, denervation, or unloading (e.g., tail suspension or space flight) leads to significant muscle atrophy (1, 2). In these conditions, the atrophying muscles show increased rates of protein degradation mainly through activation of the ubiquitin proteasome system (3, 4), and the muscle-specific E3 ubiquitin ligases muscle-specific RING finger protein 1 (MuRF-1) and atrogin-1/muscle atrophy F-box protein (atrogin-1/MAFbx) are commonly upregulated (3, 4). Recent studies further showed that muscle inactivity results in suppression of the IGF-1/PI3K/Akt pathway (5–8) and activation of transcription factors such as the forkhead box O (Foxo) family and NF- κ B (9–11).

Foxo family of forkhead transcription factors regulates a variety of biological process such as metabolism, cell proliferation and death, tumor growth, response to stress, and longevity (12–15). Mammals have 4 members, Foxo1a, Foxo3a, Foxo4, and Foxo6 (12). Among them, Foxo1a is activated in almost all forms of muscle atrophy (16). Importantly, several experiments indicate that forced expression of Foxo1a or Foxo3a upregulates the expression of a variety of atrophy-related genes including MuRF-1 and atrogin-1/MAFbx genes and induces muscle atrophy both in vitro and

in vivo (4, 10, 16, 17). These observations indicate that Foxo1a and Foxo3a are central players in atrophy signaling.

The activities of Foxo factors are thought to be regulated mainly at posttranslational levels by a serine/threonine kinase Akt. In the absence of muscle activities, Akt is inactivated, leading to dephosphorylation of Foxo transcription factors. As a result, dephosphorylated Foxos enter into the nucleus and activate atrophy-inducing genes (10, 18). Conversely, when Akt is activated, Foxos are phosphorylated and bound by 14-3-3 proteins and move from nucleus to cytoplasm (13, 19).

NF- κ B is another key signaling molecule in muscle atrophy. In particular, crucial roles for NF- κ B in both cachexia- and inactivity-induced muscle atrophy have been well investigated (9, 20, 21).

Several molecules are proposed as a mechanical sensor or a trigger of disuse atrophy. Recently it has been reported that muscles from tumor-bearing mice exhibited reduced levels of dystrophin, the protein that is mutated in Duchenne muscular dystrophy, together with reduced levels of dystrophin-associated glycoprotein (22, 23). Furthermore, forced expression of dystrophin in transgenic mice counteracted cachexia-induced muscle atrophy (22). The role of the dystrophin glycoprotein complex (DGC) in inactivity-induced muscle atrophy is not known yet, but these results raise the possibility that the DGC works as a regulator of muscle atrophy or serves as a scaffold for anti-atrophic signal transduction.

To clarify the roles for the DGC in muscle atrophy, we examined the expression and function of the members of DGC in skeletal muscle during tail suspension, a model of unloading. Here we demonstrate that neuronal NOS (nNOS), a peripheral member of the DGC, is activated in unloading conditions, regulates Foxo3a, and promotes muscle atrophy. We also show that a nNOS-specific

Nonstandard abbreviations used: DGC, dystrophin glycoprotein complex; EPR, electron paramagnetic resonance; Foxo, forkhead box O; IKK β , inhibitor of NF- κ B kinase β ; L-NAME, N-nitro-L-arginine methylester; MAFbx, muscle atrophy F-box protein; MGD, N-methyl-D-glucamine-dithiocarbamate; mTOR, mammalian target of rapamycin; MuRF-1, muscle-specific RING finger protein 1; 7NI, 7-nitroindazole; nNOS, neuronal NOS.

Conflict of interest: The authors have declared that no conflict of interest exists.

Citation for this article: *J. Clin. Invest.* 117:2468–2476 (2007). doi:10.1172/JCI30654.

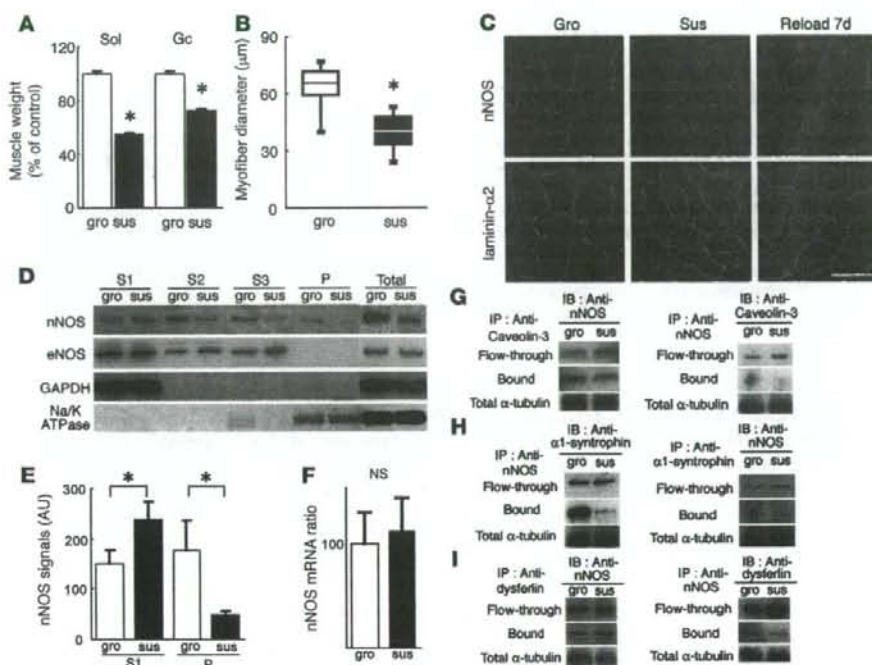


Figure 1

nNOS disappears from the sarcolemma during tail suspension. (A) Weights of soleus (Sol) and gastrocnemius (Gc) muscles from tail-suspended (sus) wild-type mice are normalized to body weight and are expressed as percentage of ground control (gro) ($n = 15/\text{group}$). * $P < 0.05$, Student's t test. (B) Box and whiskers plot of myofiber diameter size of soleus. Boxes represent the middle 50% of the data, lines represent the median, and whiskers represent the range. More than 200 fibers were measured on laminin- $\alpha 2$ chain-stained cross sections. (C) Immunofluorescent staining for nNOS and laminin- $\alpha 2$ chain. Transverse muscle sections from ground control mice, tail-suspended mice, and mice after reloading for 7 days (reload 7d) were stained with anti-nNOS (green) and anti-laminin- $\alpha 2$ chain antibodies (red). Scale bar: 50 μm . (D) Western blot using anti-nNOS antibody on subcellular fractions of muscle extracts. P indicates insoluble pellet after sequential extraction of skeletal muscle homogenates with 100 mM NaCl (S1), 500 mM NaCl (S2), and 0.5% Triton X-100 (S3). GAPDH signals in S1 and Na/K-ATPase signals in P confirmed that our fractionation was correctly done. Fractionation and western blotting were repeated 5 times, and representative data are presented. Note the slight increase of nNOS levels in S1 fraction and loss of nNOS signal in insoluble P fraction during tail suspension. (E) Quantification of nNOS signals in S1 and P fractions of muscle extracts shown in D ($n = 5/\text{group}$). The signals in S1 and P fractions were normalized to GAPDH or Na/K-ATPase, respectively. Mann-Whitney, * $P < 0.05$. (F) Levels of nNOS mRNA in muscles from ground control mice and tail-suspended mice for 2 weeks were evaluated by real-time PCR ($n = 5/\text{group}$). No significant difference was found by Mann-Whitney test. (G) Immunoprecipitation with caveolin-3 antibody and immunoblot with nNOS antibody, and vice versa, for ground control and tail suspension groups. (H) Immunoprecipitation with $\alpha 1$ -syntrophin Ab and immunoblot with nNOS antibody, and vice versa. (I) Immunoprecipitation of dysferlin antibody and immunoblot with nNOS Ab, and vice versa. In G-I, flow-through fraction was also examined by western blotting with anti- α -tubulin antibody.

inhibitor, 7-nitroindazole (7NI), significantly attenuates suspension-induced muscle atrophy. Furthermore, we show the involvement of nNOS in denervation-induced muscle atrophy process. Thus nNOS and NO are to our knowledge new therapeutic targets for disuse-induced muscle atrophy.

Results

nNOS disappears from the sarcolemma during tail suspension. To elucidate molecular mechanisms of unloading-induced muscle atrophy, we performed tail suspension (14 days) and reloading (7 days) experiments using wild-type C57BL/6 mice. The weights of the soleus and gastrocnemius (Figure 1A) muscles were decreased to 50%–70% of those of the control mice after tail suspension. The mice showed weakened grasping power and less endurance in running on the rotarod test after tail suspension (Supplemental

Figure 1; supplemental material available online with this article; doi:10.1172/JCI30654DS1). The diameter of myofiber was also drastically decreased (Figure 1B). The expression patterns of the components of DGC, dystrophin, β -dystroglycan, α -sarcoglycan, dystrobrevin, laminin- $\alpha 2$, $\alpha 1$ -syntrophin, and caveolin-3 were not changed during tail suspension (data not shown). The serum creatine kinase level was not elevated, and Evans blue dye uptake by myofibers was not evident in atrophied muscles (Supplemental Figure 2), indicating that the sarcolemmal integrity was maintained during tail suspension. nNOS mRNA levels were not significantly reduced (Figure 1F), and total nNOS protein was slightly decreased during tail suspension (Figure 1D). Importantly, immunohistochemistry revealed that nNOS was lost from the sarcolemma during tail suspension (Figure 1C). The sarcolemmal expression was gradually restored during the reloading process

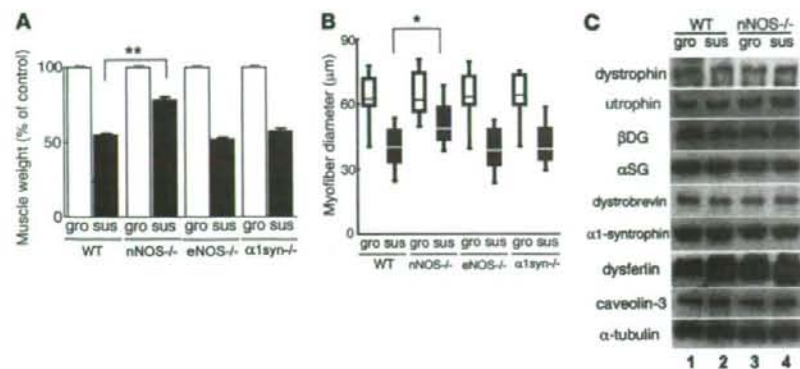


Figure 2

nNOS-null mice show partial tolerance to disuse-induced muscle atrophy. (A) Soleus muscle weight from ground control and tail-suspended wild-type ($n = 20$), nNOS-null ($n = 20$), eNOS-null ($n = 10$), and $\alpha 1$ -syntrophin-null ($n = 10$) mice after 2-week tail suspension is shown as percent of wild-type ground controls. $**P < 0.01$, Student's t test. (B) Box and whiskers plot of diameter of myofiber in soleus. Diameters were measured on H&E-stained cross sections of soleus muscles. $n = 200$ fibers in each experiment. $*P < 0.05$, Student's t test. (C) Immunoblots of mouse gastrocnemius muscle extracts for DGC components from wild-type ground control (lane 1), wild-type tail-suspended (lane 2), nNOS-null ground control (lane 3), and nNOS-null tail-suspended (lane 4) mice. All lanes contain 30 μ g of total protein. The experiments were performed 5 times, and representative pictures are presented.

(Figure 1C). eNOS expression was not changed (Figure 1D), and iNOS was not expressed (data not shown) during the course.

Next we performed subcellular fractionation of muscle homogenates as described previously (24). In ground control mice, nNOS remained in the insoluble pellet (Figure 1D). In tail-suspended mice, nNOS was largely extracted with 100 mM NaCl and barely detected in the pellet fraction (Figure 1D). Quantification of nNOS bands clearly showed that nNOS dislocated from the sarcolemma to the cytoplasm during tail suspension (Figure 1E). These results indicate that nNOS exists mainly in the cytoplasm during tail suspension. Immunoprecipitation experiments also revealed that nNOS completely dissociated from $\alpha 1$ -syntrophin and caveolin-3 during tail suspension (Figure 1, G and H). In contrast, a considerable amount of dysferlin was immunoprecipitated with nNOS antibody during tail suspension (Figure 1I).

nNOS-null mice represent tolerance to disuse-induced muscle atrophy. To examine the roles of dislocated nNOS in muscle atrophy, we then performed tail suspension experiments using wild-type, nNOS-null, eNOS-null, and $\alpha 1$ -syntrophin-null mice. The body weight (Figure 2A), average muscle fiber diameter (Figure 2B), and total number of muscle fibers (data not shown) of nNOS-null mice in the ground condition were similar to those of wild-type mice. However, after tail suspension for 14 days, reduction of muscle weight (Figure 2A), muscle size (Figure 2B), and muscle power (Supplemental Figure 1) were significantly less severe in the nNOS-null mice. Except for nNOS, dystrophin and other components of DGC were expressed in nNOS-null muscle at the same level as in wild-type muscle in both ground and suspended conditions (Figure 2C). eNOS-null muscle revealed atrophy during tail suspension similar to that seen in wild-type muscle (Figure 2, A and B), indicating that eNOS is not essential for atrophy signaling. We previously reported that disruption of the $\alpha 1$ -syntrophin gene resulted in dislocation of nNOS from the sarcolemma to the cytoplasm without dystrophic phenotypes (25, 26). Suspension of $\alpha 1$ -syntrophin-null mice induced severe muscle

atrophy as it did in wild-type muscle (Figure 2, A and B).

Production of NO by nNOS in tail-suspended skeletal muscle. To directly measure the levels of NO in skeletal muscle during tail suspension, we employed electron paramagnetic resonance (EPR) spectrometry with *N*-methyl-D-glucamine-dithiocarbamate (MGD) and Fe^{2+} (27, 28). We injected MGD and Fe^{2+} into the wild-type and nNOS-null mice at the final stage of 2-week suspension, sacrificed the mice 30 minutes after the injection, and immediately measured the NO levels in muscle tissues. In EPR, the signal height, which is proportional to the amount of NO, was obtained by measuring the peak-to-peak height of the lower field side signal (arrow in Figure 3A) in the characteristic 3-line NO spectrum (29). NO levels in skeletal muscles increased during tail suspension, and the increase was inhibited by daily administration of 7NI to the

mice. We used 50 mg/kg of 7NI to selectively inhibit nNOS (30, 31). The increase of NO levels in skeletal muscle during tail suspension was also inhibited by daily administration of 10 mg/kg of *N*-nitro-L-arginine methyl ester (*L*-NAME; pan-NOS inhibitor) (30) to the same extent (data not shown). NO levels in the skeletal muscle of nNOS-null mice after tail suspension were not different from those of ground control mice (Figure 3B), indicating that nNOS is mainly responsible for elevated levels of NO in muscle during tail suspension. Assay of the catalytic activity of NOS showed a higher level in the soluble (cytoplasmic) fraction than in the particulate fraction of suspended wild-type mice (Figure 3C).

Production of NO by nNOS is upstream of Foxo3a pathway. Foxo transcription factors are reported to upregulate many atrophy-related genes and promote muscle atrophy (9, 10). We found that Foxo3a was dephosphorylated and accumulated in the myonuclei of wild-type mice but not nNOS-null mice in western blotting (Figure 4, A and B) and in immunohistochemistry (Supplemental Figure 3). Foxo1 and Foxo4 were not changed during tail suspension in both wild-type and nNOS-null mice (Figure 4B). Recently, several groups have pointed out that the ubiquitin proteasome pathway is largely involved in selective protein degradation during the muscle atrophy process (3, 4). Consistent with this, mRNA levels of 2 muscle-specific E3 ubiquitin ligases, MuRF-1 and atrogin-1/MAFbx, increased during tail suspension in wild-type mice (Figure 4C) (9, 10). Remarkably, the upregulation of these E3 ligases was modest in nNOS-null mice. These observations suggest that nNOS regulates Foxo3a via NO production and thereby upregulates MuRF-1 and atrogin-1/MAFbx. To further examine whether nNOS regulates Foxo3a, we overexpressed nNOS in myotubes by a retrovirus vector (Supplemental Figure 4). Overexpressed nNOS increased both total and nuclear Foxo3a protein levels and decreased phosphorylated Foxo3a in myotubes (Supplemental Figure 4).

NF- κ B pathway is activated during muscle atrophy in nNOS-null mice. NF- κ B has been shown to be a major regulator of tail suspension-induced

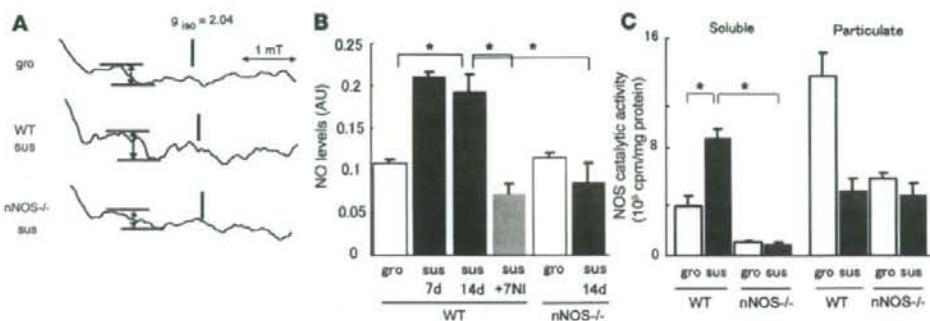


Figure 3

Measurement of NO in muscle and NOS activity during tail suspension. (A) EPR spectra of the NO adduct of Fe-MGD complex observed in skeletal muscle at room temperature. The NO-trapping agent was injected 30 minutes before measurements were taken. The EPR spectra of ground control and tail-suspended wild-type and nNOS-null mice were shown. Each spectrum represents the average of 5 accumulations. The signal height was obtained by measuring the peak-to-peak height of the lower field side signal (vertical arrows) in the 3-line spectrum. (B) NO levels of the skeletal muscle with and without tail suspension for 7 or 14 days were analyzed in EPR spectrometry ($n = 6$; $*P < 0.05$, Mann-Whitney). Note that NO level in muscle is elevated in wild-type tail-suspended mice at 14 days but not in nNOS-null tail-suspended mice. 7NI was used as a selective nNOS inhibitor. (C) NOS catalytic activity in soluble and particulate fractions ($n = 5$; Mann-Whitney). [^3H]-citrulline, converted from [^3H]-arginine in vitro by NOS, was quantified by liquid scintillation spectroscopy. Note higher NOS activities in the soluble fraction than in the particulate fraction for suspended wild-type mice.

muscle atrophy (20, 21). EMSA showed that binding activity of NF- κ B to its authentic binding sequence is increased by tail suspension in both wild-type and nNOS-null mice (Figure 4D). Importantly, there was no difference between tail-suspended wild-type and nNOS-null mice in the NF- κ B binding activity (Figure 4D). In addition, western blotting revealed that p50 is increased by tail suspension (data not shown). These results suggest that NF- κ B pathway was activated during tail suspension in the absence of nNOS. Whether the NF- κ B activities mediate the residual muscle atrophy that occurred in nNOS-null mice during tail suspension remains to be clarified in a future study.

Inhibitor of NF- κ B kinase β is nitrosylated during tail-suspension. Foxo3a is known to be phosphorylated by Akt in skeletal muscle (10, 18). In contrast to our expectation, there was no difference between wild-type and nNOS-null mice in the phosphorylation levels of Akt (Figure 5, A and B). There was no difference between the levels of S6k1 and mammalian target of rapamycin (mTOR), which are under regulation by PI3K/Akt signaling and positively regulate protein synthesis between wild-type and nNOS-null mice during tail suspension (5) (Figure 5A). A recent study reported that NO S-nitrosylates inhibitor of NF- κ B kinase β (IKK β) and thereby inhibits its activity (32). Other reports described inhibition of Foxo3a by IKK β (33). Intriguingly, we found that tyrosine residues of IKK β were nitrosylated during tail suspension in wild-type mice but not in nNOS-null mice (Figure 5C). However, whether S-nitrosylation of IKK β detected during tail suspension contributes to activation of Foxo3a remains to be determined.

7NI alleviates tail suspension-induced muscle atrophy. To further examine the effect of inhibition of nNOS activity on muscle atrophy, 7NI, a nNOS-selective inhibitor, was injected daily into the peritoneal space of the wild-type mice during the 2-week tail suspension (Figure 6). This treatment significantly prevented muscle atrophy during tail suspension but did not increase muscle mass of ground control mice (Figure 6A). 7NI considerably increased phosphorylated Foxo3a and inhibited the increase in dephosphorylated and nuclear Foxo3a during tail suspension (Figure 6C). We also found that upregulation in mRNA levels of MuRF-1 and atrogin-1/

MAFbx was abolished by 7NI during tail suspension (Figure 6B). These data imply that nNOS-specific inhibitor is a potential therapeutic strategy for disuse-induced muscle atrophy.

nNOS-null mice show milder muscle atrophy than wild-type mice after cutting of the sciatic nerve. We next examined the role of nNOS in denervation-induced muscle atrophy. Cutting the sciatic nerve on the denervated side resulted in greatly reduced muscle weight 14 days after operation (Figure 7A). Importantly, nNOS had already disappeared from the sarcolemma 3 days after denervation (Figure 7A). We observed much milder muscle atrophy in denervated muscle of nNOS-null mice than wild-type mice (Figure 7B), suggesting that nNOS is also involved in denervation-induced muscle atrophy. We then tested whether an nNOS inhibitor (7NI) or a pan-NOS inhibitor (L-NAME) counteracts denervation-induced muscle atrophy (Figure 7B). These 2 inhibitors limited the muscle atrophy (Figure 7B), indicating that NO is indeed a mediator and therefore a therapeutic target for denervation-induced muscle atrophy.

Discussion

Dislocation of nNOS is a major step in tail suspension-induced muscle atrophy. Involvement of the DGC in cachexia-induced muscle atrophy was recently reported (22). In our report, we demonstrate for what we believe to be the first time that nNOS is dislocated from the sarcolemma to the cytoplasm during tail suspension, whereas other members of the DGC are normally expressed at the sarcolemma. This observation implies that different mechanisms are involved in unloading-induced muscle atrophy and muscle atrophy seen in cachexia. Sarcolemmal nNOS is reported to be a versatile molecule that modulates satellite cell activation (34), formation of neuromuscular junction (35), glucose uptake (36), muscle contraction, and vasodilation (37). To clarify the mechanisms of nNOS translocation, we examined the effects of clenbuterol, streptomycin, and nifedipine on nNOS dislocation during tail suspension. After administration of these drugs, however, we still observed dislocation of nNOS during tail suspension (data not shown). These results suggest that sympathetic nerves, stretch-activated chan-

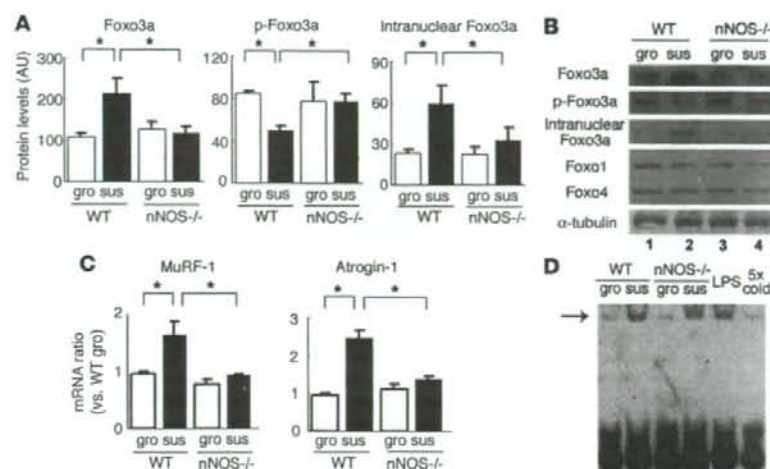


Figure 4

Participation of nNOS in regulation of Foxo3a and upregulation of MuRF-1 and atrogenin-1/MAFbx. (A) The amounts of total Foxo3a, phosphorylated Foxo3a (p-Foxo3a), and intranuclear Foxo3a in wild-type and nNOS-null muscle during tail suspension were quantified ($n = 5$). Note that Foxo3a was dephosphorylated and accumulated in the myonuclei of wild-type mice but not of nNOS-null mice. * $P < 0.05$, Mann-Whitney. (B) Representative immunoblot analysis for Foxo3a, phosphorylated Foxo3a, Foxo1, and Foxo4 in total muscle extract, and Foxo3a in nuclear extracts in wild-type ground control (lane 1), wild-type tail-suspended (lane 2), nNOS-null ground control (lane 3), and nNOS-null tail-suspended (lane 4) muscles. α -Tubulin was used as a loading control. (C) mRNA levels of ubiquitin ligases (MuRF-1 and atrogenin-1/MAFbx) ($n = 5$) were quantified by real-time RT-PCR. * $P < 0.05$, Mann-Whitney. (D) EMSA of NF- κ B. Biotin-labeled double-stranded oligonucleotides containing NF- κ B binding sites were incubated with nuclear extracts prepared from ground control and suspended muscles. An arrow indicates the DNA-protein complex. LPS was injected intraperitoneally into mice, and the muscle was used as a positive control for NF- κ B binding activity. 5x cold, 5-fold excess of nonlabeled competitors.

nels, and L-type calcium channels are not involved in the dissociation of nNOS from the DGC.

nNOS is anchored at the sarcolemma by interaction with α 1-syntrophin (25), a member of the DGC; interestingly, however, α 1-syntrophin remains at the sarcolemma during tail suspension (data not shown). To examine whether modification of α 1-syntrophin is involved in the dissociation of nNOS from α 1-syntrophin, we performed 2-dimensional PAGE and western blotting with anti- α 1-syntrophin antibody as previously described (38). The first dimensional isoelectric focusing reveals posttranslational modifications of α 1-syntrophin. The results showed slight changes in mobility pattern of α 1-syntrophin during tail suspension (data not shown), suggesting that some posttranslational modifications of α 1-syntrophin may cause dissociation of nNOS from α 1-syntrophin.

Dislocated nNOS leads to production of NO and regulates Foxo/E3 ubiquitin ligases pathway. EPR spectrometry confirmed that cytoplasmic nNOS led to production of NO during tail suspension (Figure 3, A and B). Tail suspension-induced muscle atrophy was blunted in nNOS-null mice (Figure 2, A and B) and 7NI-treated mice (Figure 6A) but not in eNOS-null mice (Figure 2, A and B). iNOS protein was not detected by western blotting in skeletal muscle during tail suspension (data not shown). These data indicate that dislocated nNOS, but neither eNOS nor iNOS, is involved in tail suspension-induced muscle atrophy.

We clearly show that 2 atrophy-related E3 ubiquitin ligases, MuRF-1 and atrogenin-1/MAFbx, are not upregulated in nNOS-null muscle

during tail suspension (Figure 4C and Figure 6B). Therefore, the induction of these genes is a downstream event of dislocation of nNOS in tail suspension-induced muscle atrophy.

Foxo transcription factors are reported to induce skeletal muscle atrophy by upregulating MuRF-1 or atrogenin-1/MAFbx (4, 10, 16, 17). For example, transgenic mice overexpressing Foxo1 in skeletal muscle display a decrease in size of muscle fibers (17). Importantly, Foxo3a remained phosphorylated in nNOS-null mice during tail suspension, and total Foxo3a protein was not increased in tail-suspended nNOS null mice. Moreover, Foxo3a accumulated in the myonuclei of wild-type but not in nNOS-null mice during tail suspension (Figure 4B and Figure 6C).

When we overexpressed nNOS in muscle cells using a retrovirus vector, we found that Foxo3a was activated in nNOS-overexpressing myotubes (Supplemental Figure 4).

How does nNOS/NO regulate Foxo3a pathways? Our observations suggest that nNOS/NO is an upstream regulator of Foxo3a in the tail suspension-induced muscle atrophy process. There are at least 2 possible explanations for how Foxo3a regulates nNOS/NO. First, NO produced by nNOS might inhibit protein kinases, which phosphorylate Foxo3a, thereby protecting Foxo3a from degradation and promoting its translocation from the cytoplasm to the nucleus. There are several kinases that can phosphorylate Foxo, including Akt (10), IKK β (33), BCR (39), and CDK2 (40). In the present study, we show that Akt activities in nNOS-null muscle were not different from those in wild-type muscle during tail suspension. A fraction of IKK β was nitrosylated (inactivated) during tail suspension (Figure 5C), but NF- κ B was activated in both wild-type and nNOS-null muscle during suspension. This observation suggests that IKK β activity was not meaningfully disrupted (Figure 4D). Involvement of other kinases remains to be investigated in a future study.

Second, nNOS/NO signal might decrease nuclear export of Foxo3a, resulting in accumulation of Foxo3a in myonuclei and protecting it from phosphorylation by Akt. Foxo is exported from the nucleus in a 14-3-3 protein-dependent process (19), and these molecular interactions remain to be examined.

Dislocation of nNOS and production of NO have no obvious effects on the activity of NF- κ B. It has been reported that reduced muscle activity induces muscle atrophy via activation of both Foxo and NF- κ B transcription factors (9), at the same time suppressing the Akt pathway (5, 6), resulting in activation of the transcription of MuRF-1 and atrogenin-1/MAFbx genes. In this report we demonstrated that dephosphorylation and nuclear accumulation of Foxo3a were largely attenuated in nNOS-null muscle during tail suspension. In contrast, our EMSA assay suggested that the NF- κ B pathway was activated in nNOS-null

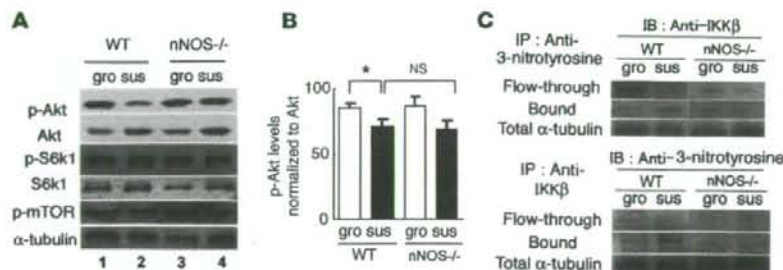


Figure 5

Phosphorylation of Akt and nitrosylation of IKK β during 2-week tail suspension. (A) Immunoblots for protein synthesis pathway components (p-Akt, Akt, p-S6k1, S6k1, and p-mTOR) in wild-type ground control (lane 1), wild-type tail-suspended (lane 2), nNOS-null ground control (lane 3), and nNOS-null tail-suspended (lane 4) muscles. Densities of the bands were normalized to α -tubulin. (B) The ratio of phosphorylated Akt to total Akt is shown ($n = 5$; * $P < 0.05$, Mann-Whitney). (C) Detection of nitrosylated IKK β . Muscle proteins were immunoprecipitated with anti-3-nitrotyrosine antibody (upper panel) or with anti-IKK β antibody (lower panel) and immunoblotted with anti-IKK β or anti-3-nitrotyrosine antibodies, respectively. α -Tubulin signals in flow-through fractions are also shown.

mice to a similar extent as in wild-type mice in tail suspension experiments. This observation raises the possibility that NF- κ B mediated the residual atrophy that occurred in nNOS-null mice, but further investigation is needed to correctly answer this question.

nNOS and other muscle atrophies. Many conditions induce muscle atrophy, including space flight, immobilization, denervation, cancer cachexia, motor neuron diseases, starvation, and aging (41). Recently it has been reported that muscles of tumor-bearing mice exhibited membrane abnormalities accompanied by reduced levels of dystrophin and increased glycosylation on DGC proteins (22, 23). It was also shown that the DGC could counteract atrophic signaling in cancer cachexia when overexpressed at the sarcolemma (22). In the tail suspension model, we observed dislocation of nNOS but no changes in the sarcolemmal expression of other members of the DGC (Figure 2C). Therefore it is possible that dystrophin deficiency in cancer cachexia induces nNOS dislocation, which results in activation of nNOS and its downstream effectors.

We also found nNOS dislocation in denervation-induced muscle atrophy (Figure 7A). Remarkably, denervation-induced muscle atrophy was modestly blunted in nNOS-null mice or selective nNOS inhibitor-treated mice (Figure 7B). Although iNOS was induced during denervation (data not shown), both 7NI and L-NAME showed a similar effect on muscle atrophy, suggesting that iNOS does not contribute to denervation-induced muscle atrophy.

In conclusion, we demonstrate that nNOS dislocated from the sarcolemma to the cytoplasm in 2 models of disuse-induced muscle atrophy, tail suspension and denervation. We also show that dislocated nNOS led to the production of NO and regulated Foxo3a, MuRF-1, and atrogen-1/MAFbx, key molecules in muscle atrophy. Our model is illustrated in Figure 8. The identification of nNOS as a regulator of unloading-induced muscle wasting suggests that pharmacological intervention targeting nNOS or its downstream or upstream pathways would prevent or diminish this debilitating process.

Methods

Animals and tail suspension model. Twelve-week-old female C57BL/6, nNOS-null and eNOS-null mice were purchased from the Jackson Laboratory. α 1-Syntrophin-null mice were produced in our previous study (25). These

mice were backcrossed to the C57BL/6 strain for more than 10 generations. The animals were allowed ad libitum access to food and drinking water. The Experimental Animal Care and Use Committee of the National Institute of Neuroscience approved all experimental protocols. The mice were randomly assigned to control or tail suspension groups. To induce muscle atrophy by disuse, mice were suspended so that their hind limbs were 1 mm off the cage floor for 14 days. After 14 days of tail suspension, some groups were allowed 7 days of reloading by normal weight bearing. Muscle weight was normalized to body weight and is presented as a percentage of control in each experiment.

Denervation model. The left sciatic nerve of mice was excised for nearly the full length of the thigh (approximately 10 mm) from a small incision (approximately 4 mm) made in the mid-lateral thigh under general anesthesia under a surgical microscope (Olympus) (42). The mice were sacrificed 3 or 14 days after denervation by cervical dislocation under general anesthesia, and soleus and gastrocnemius muscles were excised for analysis. The right gastrocnemius muscle served as a control.

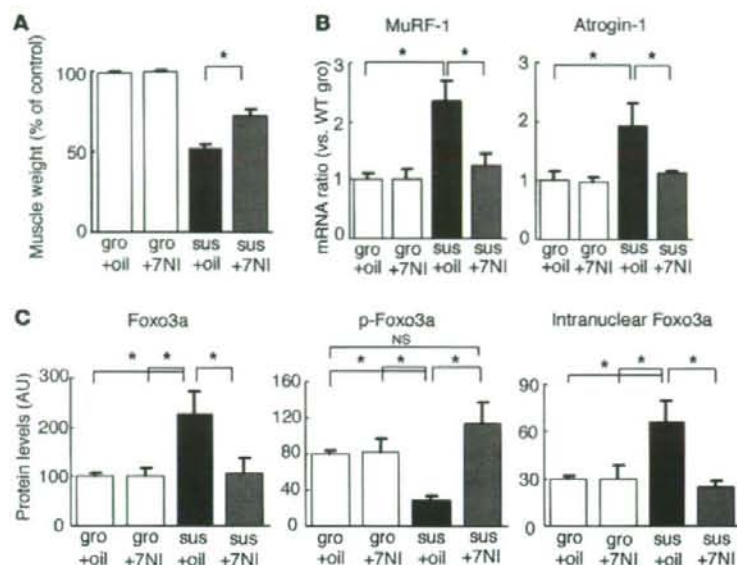
Reagents. Lipopolysaccharide from *E. coli* (0.1 ml, 3 mg/kg; *E. coli*, serotype 055:B5; Sigma-Aldrich) was administered via intraperitoneal injection. 7NI (Dojindo) was dissolved in peanut oil (50 mg/kg). L-NAME was injected daily into the intraperitoneal cavity of mice (10 mg/kg body weight). Clenbuterol (1 mg/kg; Sigma-Aldrich), streptomycin (300 mg/kg; Sigma-Aldrich) and nifedipine (5 mg/kg; Wako) were dissolved in PBS. PBS was injected into control mice.

Tissue preparation. Control and tail-suspended mice were sacrificed with cervical dislocation. Body and wet muscle were weighed. The gastrocnemius and soleus muscles were collected individually using standard dissection methods and cleaned of excess fat, connective tissue, and tendons. Several of the muscles were frozen in isopentane cooled by liquid nitrogen for histological and immunohistochemical analysis, and the other muscles were frozen directly in liquid nitrogen for RNA isolation or protein extraction and stored at -80°C .

Real time PCR. Total RNA was isolated using TRIzol (GIBCO). For RT-PCR, first-strand cDNA was synthesized using oligo-dT primers. Expression levels of selected genes (nNOS, MuRF-1, atrogen-1/MAFbx, and 18S-rRNA) were analyzed using Applied Biosystems SYBR Green gene expression assays on ABI7700 Sequence Detection System (Applied Biosystems) following the manufacturer's instructions.

H&E staining. Ten-micrometer cryosections were cut in the middle part of the muscle belly to obtain the largest myofiber diameter, placed on poly-L-lysine-coated slides, air dried, and stained with H&E. The sections were viewed and photographed using an HC-2500 digital camera system (Fuji Photo Film).

Immunohistochemistry. Cryostat sections of muscle tissue (10 μm thick), were postfixed in acetone or 4% paraformaldehyde at -20°C and preincubated in PBS containing 5% goat serum and 1% bovine serum albumin for 30 minutes at room temperature. Polyclonal anti-nNOS (Zymed), anti-Foxo3a (Sigma-Aldrich), and anti-laminin- α 2 (Alexis) were applied overnight at 4°C . Following incubations with appropriate secondary antibodies, mounted sections were observed by using a Leica confocal microscope. Muscle fiber diameters were determined on cross sections of soleus muscle using the greatest distance between the oppo-

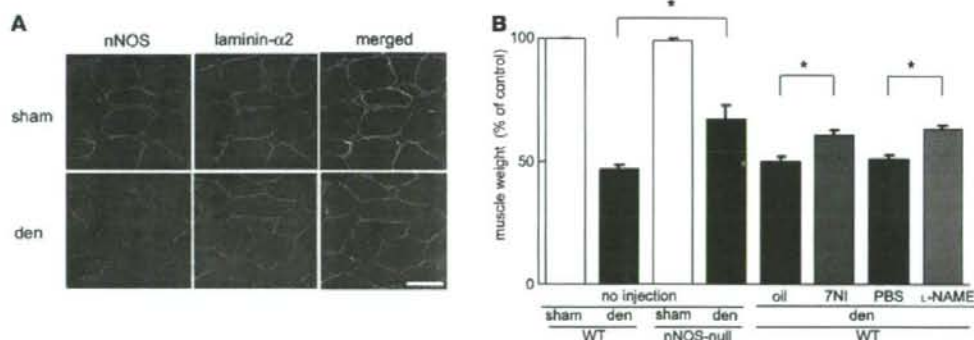
**Figure 6**

7NI alleviates muscle atrophy during tail suspension. (A) Soleus muscle weight of wild-type ground control and wild-type tail-suspended mice with (+7NI) or without 7NI (+oil). Oil or 7NI (50 mg/kg/d) was injected daily into the abdominal cavity of the mice during 2-week tail suspension ($n = 5-10$ per group; $*P < 0.05$, Mann-Whitney). (B) mRNA levels of MuRF-1 and atrogin-1/MAFbx ($n = 4$) in muscle from wild-type ground control and wild-type tail-suspended mice with or without 7NI were quantified by real-time RT-PCR ($*P < 0.05$, Mann-Whitney). (C) The amount of total Foxo3a, dephosphorylated Foxo3a, and intracellular Foxo3a ($n = 4$) were analyzed by western blotting, and band densities were normalized to α -tubulin ($*P < 0.05$, Mann-Whitney).

site sides of the narrowest aspect of the fiber. Total number of muscle fibers was also counted on cross sections.

Western blotting. Total skeletal muscle protein was extracted from mouse hindlimb muscle for western blot analysis. We used the Bradford method and Coomassie Brilliant Blue G-250 (Bio-Rad) to determine the protein concentrations. Then protein fractions were extracted with a reducing sample buffer containing 10% SDS, 70 mM Tris-HCl, 5% β -mercaptoethanol, and Complete inhibitor cocktail (Roche). Protein (15 or 30 μ g per lane) was separated on an SDS-polyacrylamide gel. The resulting gel was subsequently transferred to a polyvinylidene difluoride membrane (Millipore) using 242 mA for 1 hour. The blot was later incubated with primary antibodies. The signals were detected using the enhanced chemiluminescence

method (GE Amersham). Relative quantities of proteins in western blots were determined by scanning densitometry (Alpha Innotech) and expressed in arbitrary units. The following antibodies were used for immunoblotting: anti- α 1-syntrophin (Biogenesis), anti-laminin- α 2 (Alexis), anti-dystrophin (dys2), anti-utrophin, anti- β -dystroglycan, anti-dystrobrevin, anti-dysferlin, anti-caveolin-3 (Novocastra), anti-hsp90 (Stressgen), anti-nNOS, anti-IKK β , anti-Akt, anti-p-Akt, anti-p-mTOR, anti-p50 (Transduction Laboratories), anti-Foxo3a, anti-p-Foxo3a, anti-Foxo1/4, anti-Na/K-ATPase (Upstate Biotechnology), anti-Hsp70, and anti-iNOS antibody (Santa Cruz Biotechnology Inc.). Anti- α -sarcoglycan antibody was kindly provided by Michihiro Imamura (National Institute of Neuroscience, National Center of Neurology and Psychiatry).

**Figure 7**

Inhibition of nNOS activities counteracts denervation-induced muscle atrophy. (A) Sarcolemmal expression of nNOS in control and denervated muscles. Transverse muscle sections from denervated (den) and sham-operated mice were stained with anti-nNOS (green) and anti-laminin- α 2 chain (red) antibodies 3 days after sciatic nerve excision. Scale bar: 50 μ m. (B) Reduction in soleus muscle weight of wild-type and nNOS-null mice 2 weeks after sham operation or denervation. Weight of wild-type denervated muscle was also measured after 2-week administration of oil, 7NI, PBS, or L-NAME. Values (muscle weight/body weight) were expressed as percentage of the values of sham-operated wild-type muscles ($n = 5-10$ per group). $*P < 0.05$, Mann-Whitney.

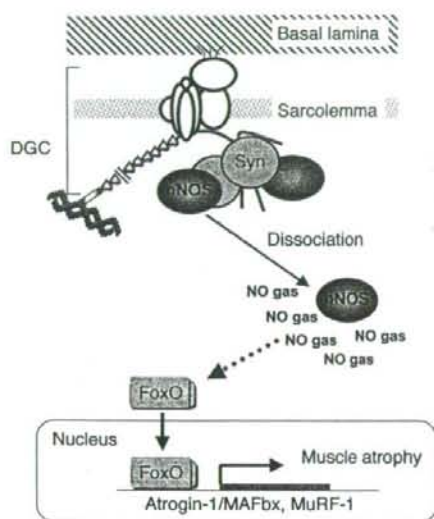


Figure 8

A model of nNOS involvement in tail suspension-induced muscle atrophy. Under normal conditions nNOS is located at the sarcolemma as a peripheral member of the DGC. During tail suspension, nNOS dissociates from $\alpha 1$ -syntrophin (syn) and dislocates into the cytoplasm, generating NO, which ultimately regulates Foxo transcription factors, and muscle-specific E3 ubiquitin ligases, MuRF-1, and atrogin-1/MAFbx, which promote muscle protein degradation by the ubiquitin-proteasome system.

Nuclear and cytosolic protein extraction. Nuclear extracts were prepared from mouse skeletal muscle according to the method of Hunter et al. (20). Briefly, the cytosolic extract was obtained from the first supernatant of the nuclear extract preparation. The supernatant was placed in Millipore Ultrafree-4 centrifugal columns that had been pre-wetted with 0.5 ml of dilution buffer (20 mM HEPES, 40 mM KCl, 10% glycerol, 0.2 mM EDTA, 1 mM DTT), and centrifuged (7,500 g) at 4°C for 30 minutes. Dilution buffer (0.8 ml) was added to the column, and the 30-minute spin was repeated. Protein concentrations were determined using the Bradford protein assay (Bio-Rad).

Immunoprecipitation. Skeletal muscle samples were homogenized in 0.15 M NaCl, 10 mM HEPES (pH 7.5) and Complete inhibitor cocktail (Roche), with or without 1% digitonin (Wako). nNOS and caveolin-3 immunoprecipitation was performed with anti-nNOS goat polyclonal antibody (Santa Cruz Biotechnology Inc.) and anti-caveolin-3 antibody (Transduction Laboratories). The samples were incubated with protein G gel (GE Amersham) overnight at 4°C. After the gel was washed with the equilibrating buffer, the bound fraction was eluted with 1% SDS, 1 mM tris-(2-carboxyethyl) phosphine, and 14 mM Tris-HCl (pH 6.7) and concentrated. Coimmunoprecipitates were resolved by SDS-PAGE and analyzed by western blotting. α -Tubulin was used as internal control for total protein inputted.

Two-dimensional PAGE. Muscle extracts from ground control and tail suspension mice were resolved on 2-dimensional PAGE and analyzed by western blotting as described in ref. 38.

EMSA. EMSA was performed according to the manufacturer's instructions (Panomics). Briefly, probes were end-labeled with biotin. Binding reactions were performed for 30 minutes in a volume of 10 ml. Specificity of DNA binding was determined by addition of a 5-fold molar excess of unlabeled competitor DNA to the binding reactions. The binding reactions were loaded onto 6% non-denaturing polyacrylamide gels and electrophoretically resolved in 0.5 \times tris-borate EDTA (TBE) buffer.

NOS catalytic assays. NOS catalytic assays were carried out according to the method described by Brennan et al. (24). Muscles from wild-type and nNOS-null mice with or without tail suspension were homogenized in 10 volumes of buffer containing 25 mM Tris-HCl, pH 7.4, 1 mM EDTA, 1 mM EGTA, and 0.1 mM NaCl. The homogenate was centrifuged at 20,000 g to separate the soluble fraction. The pellet was extracted in the same buffer containing 0.5 M NaCl and centrifuged at 20,000 g to create a particulate

fraction. Aliquots from these fractions were assayed in 125- μ l reactions containing 1.8×10^4 cpm of [3 H]-arginine (53.0 Ci/mmol; GE Amersham), 1 mM NADPH, 640 μ M CaCl₂, 1 μ M calmodulin, and 3 μ M each of tetrahydrobiopterin, FAD, and FMN. After incubation for 20 minutes at 37°C, the assays were terminated with 2 ml of 20 mM HEPES, pH 5.5, and 2 mM EDTA. The samples were then applied to AG50WX-8 columns (Na⁺ form; Dowex), which were centrifuged, and the supernatant was collected. [3 H]-citrulline was quantified by liquid scintillation spectroscopy.

Subcellular fractionation. The subcellular fractionation was performed according to the method described by Brennan et al. (24). The gastrocnemius muscle was homogenized in 10 volumes (w/v) of buffer A (25 mM Tris-HCl, pH 7.4, 100 mM NaCl, 1 mM EDTA, 1 mM EGTA). The nuclei of the muscle were pelleted by centrifugation at 1,000 g. The supernatant was then centrifuged at 20,000 g to yield the supernatant S1. The resulting heavy microsomal pellet was resuspended in buffer B (500 mM NaCl added to buffer A), incubated for 30 minutes at 4°C with agitation, and centrifuged at 15,000 g, yielding supernatant S2. The pellet from this last centrifugation was resuspended in buffer B containing 0.5% Triton X-100, incubated for 30 minutes at 4°C with agitation, and centrifuged at 15,000 g to create supernatant S3 and the final pellet. The fractions were resolved using the sample buffer and analyzed by SDS-polyacrylamide gel electrophoresis. The proteins were transferred to a polyvinylidene difluoride membrane (Millipore), which was later incubated with anti-nNOS antibody. The bands were quantified in densitometry.

Direct measurement of NO by EPR spectroscopy. Concentrations of NO in the skeletal muscle of mice were measured using the NO-trapping technique combined with EPR spectroscopy (29). Spin traps react with unstable free radicals such as NO to form a relatively stable radical adduct. This long-lived adduct formation results in accumulation of a steady-state formation of these free radicals, and thus the resultant radical adduct can be detected readily by EPR spectroscopy. We used a Fe-MGD complex as the trapping agent to quantify NO levels in the skeletal muscle tissues of the mice. Solutions of FeSO₄ (62 mg/kg; Wako) and MGD (348 mg/kg; Dojindo) were injected subcutaneously. The Fe-MGD complex formed had a high specificity for NO (27, 29), and the NO-Fe-MGD complex was detected by EPR spectroscopy. The amplitude of the signal measured from the peak-to-peak height of the lower field side signal in the 3-line spectrum is known to be proportional to the amount of NO (29). The level of NO-Fe-MGD complex was estimated by comparing it with the signal height of a standard solution of a chemically synthesized NO complex. The concentration in tissues was determined 30 minutes after injection of the NO-trapping reagent. Thirty minutes after administration of the reagent, the gastrocnemius and soleus muscle were removed and weighed (approximately 100–120 mg). The tissue was minced and subjected to immediate measurement of NO by EPR spectroscopy. X-band EPR spectra were measured at room temperature with a TE-200 EPR spectrometer (JEOL). The homogenates were drawn into a capillary tube (75 mm in length, 46 μ l in internal volume) that had been inserted first into an EPR quartz tube (outside diameter, 5 mm), then introduced into the cavity. The instrument settings were as follows: center field, 331 mT; field scan, 4 mT; sweep time, 2 min; time



constant, 0.3 s; modulation amplitude, 0.32 mT; modulation frequency, 9.44 GHz; microwave power, 60 mW.

Statistics. Statistical differences were determined by either 2-tailed unpaired Student's *t* test or the Mann-Whitney test. All data are expressed as mean \pm SEM. Statistical significance is defined as $P < 0.05$.

Acknowledgments

We thank S. Masuda, A. Fukase, and T. Harano for technical support; K. Asanuma and J. Yoshitake for EPR spectrometry; Y. Onodera and M. Tateyama for immunohistochemistry; and all members of the Department of Molecular Therapy, National Institute of Neuroscience, for technical assistance and useful discussion, especially M. Yoshida, M. Ikemoto, and Y. Mochizuki. We also thank K. Ono for correcting our English. This work was supported by Research on Nervous and Mental Disorders (grant 16B-2); Health Science Research Grants for research on the human

genome and gene therapy (H16-genome-003) and for research on brain science (H15-kokoro-021 and H18-kokoro-019) from the Japanese Ministry of Health, Labor and Welfare; Grants-in-Aid for Scientific Research (14657158, 15390281, 16590333, 17590857, and 18590392) from the Japanese Ministry of Education, Culture, Sports, Science and Technology; and the Ground-based Research Program for Space Utilization, promoted by Japan Space Forum.

Received for publication October 16, 2006, and accepted in revised form May 29, 2007.

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Autologous Transplantation of SM/C-2.6⁺ Satellite Cells Transduced with Micro-dystrophin CS1 cDNA by Lentiviral Vector into *mdx* Mice

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Duchenne muscular dystrophy (DMD) is a lethal muscle disorder caused by mutations in the dystrophin gene. Transplantation of autologous myogenic cells genetically corrected *ex vivo* is a possible treatment for this disorder. In order to test the regenerative efficiency of freshly isolated satellite cells, we purified quiescent satellite cells from limb muscles of 8–12-week-old green fluorescent protein-transgenic (GFP-Tg) mice using SM/C-2.6 (a recently developed monoclonal antibody) and flow cytometry. Freshly isolated satellite cells were shown to participate in muscle regeneration more efficiently than satellite cell-derived myoblasts passaged *in vitro* do, when transplanted into tibialis anterior (TA) muscles of 8–12-week-old cardiotoxin-injected C57BL/6 mice and 5-week-old dystrophin-deficient *mdx* mice, and analyzed at 4 weeks after injection. Importantly, expansion of freshly isolated satellite cells *in vitro* without passaging had no detrimental effects on their regenerative capacity. Therefore we directly isolated satellite cells from 5-week-old *mdx* mice using SM/C-2.6 antibody and cultured them with lentiviral vectors expressing micro-dystrophin CS1. The transduced cells were injected into TA muscles of 5-week-old *mdx* mice. At 4 weeks after transplantation, the grafted cells efficiently contributed to regeneration of *mdx* dystrophic muscles and expressed micro-dystrophin at the sarcolemma. These results suggest that there is potential for lentiviral vector-mediated *ex vivo* gene therapy for DMD.

Received 22 February 2007; accepted 28 July 2007; published online 28 August 2007. doi:10.1038/sj.mt.6300295

INTRODUCTION

Duchenne muscular dystrophy (DMD) is an X-linked, lethal disorder of skeletal muscle caused by mutations in the dystrophin gene.¹ Dystrophin is a 427 kd large sub-sarcolemmal protein that forms the dystrophin/glycoprotein complex at the sarcolemma with α - and β -dystroglycans, α -, β -, γ -, and δ -sarcoglycans, and

other molecules, and links the cytoskeleton with the basal lamina.^{2,3} The lack of dystrophin in the sarcolemma causes instability of the muscle membrane, leading to muscle degeneration and myofiber loss. Although there is no effective treatment for the disease at present, cell therapy could be a promising approach. Satellite cells are quiescent mononucleated cells located external to the muscle membrane but internal to the basal lamina in adult skeletal muscle.⁴ On muscle damage, they activate, proliferate, and then exit the cell cycle either to differentiate into mature myofibers or to renew the quiescent satellite cell pool. Because satellite cells have robust regenerative capacity,^{5,6} they are expected to be a feasible source for cell therapy in DMD. Indeed, transplantation of myoblasts successfully restored dystrophin expression in dystrophin-deficient muscle under immunosuppression.^{7,8} Nevertheless, in the early 90s, transplantation of satellite cell-derived myoblasts failed to improve muscle force in DMD patients.^{9–11} The failure has been ascribed to poor survival^{12–14} and limited distribution of the transplanted cells after injection.¹⁵ The latter problem could possibly be partly overcome by using high-density injections of myoblasts.^{16,17} On the other hand, the mechanisms by which grafted myoblasts are rapidly lost after injection have not been fully addressed.^{12–14}

Many studies have employed crude cell preparations containing both satellite cells and non-myogenic cells^{18,19} or satellite cell-derived myoblasts extensively amplified *in vitro*.^{15,20–22} In a recent study, Montarras *et al.* directly isolated (Pax3)green fluorescent protein (GFP)-expressing satellite cells from the diaphragm of adult Pax3^{GFP/+} mice by flow cytometry.²³ These cells constituted a homogeneous population and the majority were quiescent. When grafted into irradiated muscles of immunodeficient *nu/nu* dystrophin-deficient *mdx* mice, the freshly isolated satellite cells efficiently contributed to both fiber repair and the muscle satellite cell compartment,²³ thereby suggesting that fresh satellite cells are a potential source for cell therapy in DMD.

For transplanting autologous cells, which are expected to evade the host immune response to grafted cells, the lentiviral vector is a potential tool for introducing the therapeutic gene

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because it integrates into the host genome in a variety of dividing and non-dividing cells. Because the dystrophin complementary DNA is too large to be incorporated into a lentiviral vector, a truncated but fully functional version of the dystrophin complementary DNA²⁴⁻²⁷ has to be used instead of the full-length one. When compared with conventional transfection of myogenic cells with large dystrophin-coding plasmids²⁸ or nucleofection in combination with ϕ C31 integrase,²⁹ transfection by lentiviral vectors led to much more efficient expression of mini- or micro-dystrophin in *mdx* mice,³⁰ in non-human primate cells, and in human myogenic cells.³¹ Lentiviral vectors were also used for introducing the therapeutic genes into other types of stem cells. Bachrach *et al.* reported expression of human micro-dystrophin in *mdx*^{scv} muscles after systemic delivery of autologous side population cells modified with lentiviral vectors expressing micro-dystrophin.³² Sampaioles *et al.* reported intra-arterial delivery of autologous mesoangioblasts corrected by lentiviral vectors expressing α -sarcoglycan (α -SG), resulting in many α -SG-positive fibers, and morphological and functional recovery in downstream muscles of α -SG-null dystrophic mice.³³ A more recent study reported the autologous transplantation into skeletal muscle, of monkey muscle precursor cells transduced with micro-dystrophin by lentiviral vectors.³¹ However, whether *ex vivo* gene therapy using lentiviral vectors expressing micro-dystrophin is indeed beneficial in large animal models such as dystrophic dogs, is still subject to controversy.³⁴

Previously, Fukada *et al.* established a method of direct purification of quiescent satellite cells from adult mouse skeletal muscles, using fluorescence activated cell sorting (FACS) and a novel monoclonal antibody named SM/C-2.6.³⁵ The method is simple, and is expected to be applicable to the isolation of satellite cells from dystrophic (autologous) muscles for cell therapy.

In this study, we first directly isolated satellite cells from *mdx* mice using the SM/C-2.6 antibody and FACS. We showed that *mdx*-SM/C-2.6⁺ cells transduced with lentiviral vectors expressing micro-dystrophin efficiently contributed to regeneration of *mdx* muscles and expressed micro-dystrophin at the sarcolemma when grafted. Our results indicate that the autologous satellite cell isolated by the SM/C-2.6 antibody and genetically corrected by a lentiviral vector is a feasible tool for cell therapy of DMD or of localized forms of muscular dystrophy.

RESULTS

Passaged SM/C-2.6⁺ satellite cells show reduced regenerative capacity

We isolated satellite cells from the limb muscles of 8–12-week-old C57BL/6 mice using FACS and a novel monoclonal antibody, SM/C-2.6.³⁵ A previous study has shown that satellite cells are highly enriched in the SM/C-2.6⁺ fraction.³⁵ Immediately after isolation by FACS, SM/C-2.6⁺ cells expressed Pax7, but not MyoD, myogenin, or Ki67 (Table 1). After 4 days of culture, more than 95% of the cells expressed MyoD and Ki67 (data not shown). Pax7 marks quiescent, activated satellite cells and their progeny, myoblasts,³⁶ whereas MyoD marks activated satellite cells and myoblasts.^{37,38} Ki67 is a marker of proliferating cells. It follows, therefore, that SM/C-2.6⁺ cells are highly purified satellite cells in the G₀ phase immediately after isolation from muscle tissues.

Table 1 Expression of myogenic and proliferative markers of freshly isolated SM/C-2.6⁺ cells from limb muscles of C57BL/6 or *mdx* mice

Marker	B6-SM/C-2.6 ⁺ cells (%)	<i>mdx</i> -SM/C-2.6 ⁺ cells (%)
Pax7	95 ± 1.4	94 ± 2.1
MyoD	0 ± 0	19 ± 2.8
Myogenin	0 ± 0	7 ± 1.3
Ki67	0.6 ± 1.0	34 ± 1.8

The expression level of each marker is shown as the percentage of positive cells in total cells stained with 4',6-diamidino-2-phenylindole in three randomly selected fields. Data are represented as mean values ± SD.

To investigate the regenerative efficiency of SM/C-2.6⁺ satellite cells when grafted into mouse skeletal muscles, three kinds of cells were prepared from limb muscles of 8–12-week-old GFP-Tg mice: (i) quiescent SM/C-2.6⁺ cells freshly isolated by FACS (Figure 1a), (ii) expanded SM/C-2.6⁺ cells *in vitro* with or without passaging (Figure 1a), and (iii) cultured primary myoblasts isolated by a conventional pre-plating method.³⁹ These cells were injected at 2 × 10⁴ cells per muscle into the tibialis anterior (TA) muscle of 8–12-week-old C57BL/6 and 5-week-old dystrophin-deficient *mdx* mice. Twenty four hours before cell transplantation the recipient C57BL/6 muscles were injected with cardiotoxin (CTX) so as to induce regeneration. Four weeks after the injection, we investigated the contribution of each cell population to muscle regeneration by immunodetection of GFP-positive fibers. Freshly isolated SM/C-2.6⁺ cells (Figure 1b) produced many more GFP-positive fibers than those produced by the same number of cultured SM/C-2.6⁺ cells passaged once *in vitro* (Figure 1c, passage 1). We next examined the effects of expansion, without passaging and with repeated passaging, on the regenerative capacity of the cells. The number of GFP-positive myofibers derived from GFP-Tg SM/C-2.6⁺ cells dropped considerably after first passage *in vitro* and then gradually decreased with subsequent passages in both CTX-injected C57BL/6 mice (Figure 1d) and in *mdx* mice (Figure 1e). Primary myoblasts prepared by the pre-plating method³⁹ also showed low regenerative capacity (Figure 1d). Surprisingly, the regenerative efficiency of cells expanded *in vitro* without passaging was comparable to that of freshly isolated cells (Figure 1d and e). These results suggested to us that it is possible to genetically correct dystrophin-deficient satellite cells *ex vivo* before transplantation without causing a reduction in their regenerative capacity.

In order to know why fresh or "expansion" cells gave rise to more myofibers when compared with cells passaged *in vitro*, we compared the colony formation ability of fresh satellite cells with that of passaged myoblasts (passage 1). The results showed that fresh satellite cells formed larger colonies than passage 1 cells, when plated at a density of 1 cell/well on 96-well plates, although the rate of colony formation was not significantly different between these two cells (fresh, 26% versus passage 1, 23%) (Supplementary Figure S1). In contrast, there was no difference in fusion index between fresh satellite cells and passaged myoblasts (data not shown). Collectively, a reduction in the proliferative ability of passaged myoblasts *in vitro* might partly explain their lower regenerative capacity *in vivo*.

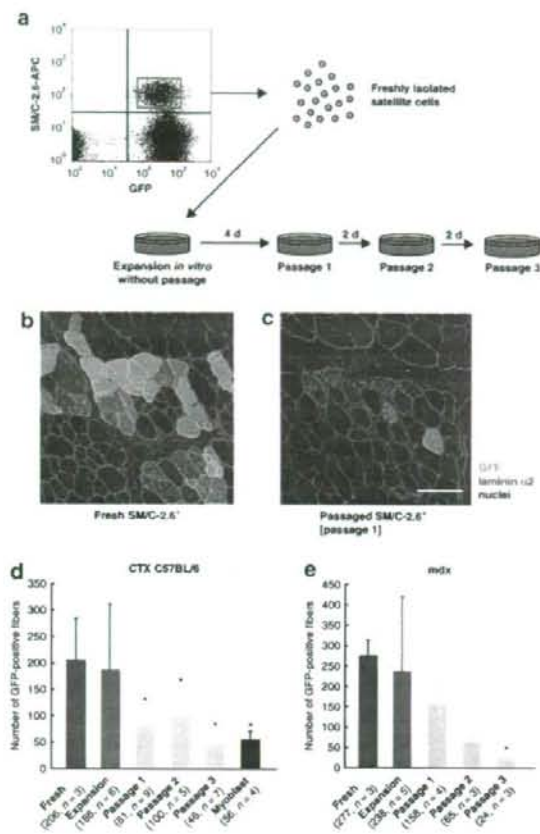


Figure 1 The regenerative capacity of SM/C-2.6⁺ satellite cells isolated from adult mouse skeletal muscles by fluorescence activated cell sorting (FACS). **(a)** Flow cytometry of mononucleated cells derived from limb muscles of green fluorescent protein-transgenic (GFP-Tg) mice after staining with SM/C-2.6 antibody and culture conditions of sorted cells. SM/C-2.6⁺ GFP⁺ cells (red square) were sorted as the satellite cell fraction. These cells were cultured in proliferation medium for 4 days (expansion *in vitro* without passage) and then passaged up to three times at 2-day intervals. **(b)** Freshly isolated and **(c)** passaged SM/C-2.6⁺ cells (passage 1) from GFP-Tg mice were injected into C57BL/6 tibialis anterior (TA) muscles. The muscles were treated with cardiotoxin (CTX) 24 hours before cell transplantation and then injected with 2×10^4 cells per TA muscle. Four weeks after the injection, cross-sections were stained with anti-GFP (green) and laminin $\alpha 2$ (red) antibodies. Nuclei were stained with TOTO3 (blue). Bar: 80 μ m. **(d, e)** Comparison of muscle regenerative efficiencies of three kinds of cells prepared from GFP-Tg mice: (i) quiescent SM/C-2.6⁺ cells freshly isolated by FACS (red bars), (ii) expanded SM/C-2.6⁺ cells *in vitro* without passaging (orange bars) or passaged SM/C-2.6⁺ cells (yellow bars with passage numbers), and (iii) primary myoblasts isolated by the pre-plating method (blue bar in **d**). The same numbers of cells (2×10^4 cells) were grafted into TA muscles of CTX-treated C57BL/6 (**d**) and *mdx* mice (**e**). The number of GFP-positive fibers per cross-section was counted after staining with anti-GFP antibody. Error bars represent SD. * $P < 0.05$ compared with freshly isolated SM/C-2.6⁺ cells.

SM/C-2.6⁺ satellite cells transduced with lentiviral vectors efficiently contribute to muscle regeneration

Successful gene and cell therapy for DMD requires sustained expression of the therapeutic gene in striated muscle. The

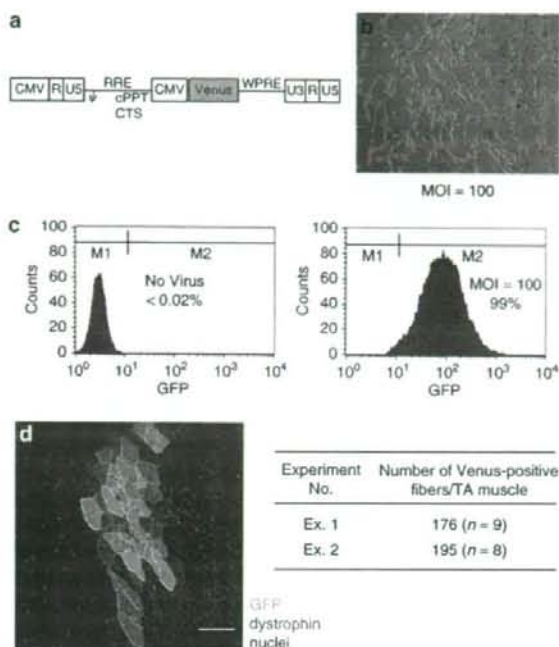


Figure 2 Lentiviral vector-mediated gene transfer into SM/C-2.6⁺ satellite cells and transplantation of transduced cells into *mdx* mouse muscles. **(a)** Structure of the lentiviral vector expressing Venus under the control of a cytomegalovirus (CMV) promoter. **(b)** Fluorescence image of Venus-expressing satellite cell-derived myoblasts. Freshly isolated SM/C-2.6⁺ cells from C57BL/10 limb muscles were transduced with lentiviral vectors expressing Venus at a multiplicity of infection (MOI) of 100 for 16 hours, and cultured in proliferation medium for 3 days. **(c)** Flow cytometric analysis of non-transduced (left panel) and transduced (right panel) SM/C-2.6⁺ cells 3 days after the transduction. M2 denotes the area of Venus-expressing cells. At a MOI of 100, 99% of the cells expressed Venus. **(d)** Venus- and dystrophin-positive fibers formed by SM/C-2.6⁺ cells transduced with lentiviral vectors *in vitro*. Transduced cells (2×10^4) were injected into tibialis anterior (TA) muscles of *mdx* mice. Four weeks after the injection, cross-sections were stained with anti-GFP (green) and dystrophin (red) antibodies. Nuclei were stained with TOTO3 (blue). The number of Venus-positive fibers per cross-section was counted. Bar: 80 μ m. cPPT, central polyuracil tract; CTS, central termination sequence; GFP, green fluorescent protein; RRE, rev responsive element; WPRE, woodchuck hepatitis virus post-transcriptional regulatory element.

lentiviral vector can carry a relatively large transgene and integrate it into the genome of non-dividing cells such as quiescent satellite cells. We therefore attempted lentiviral vector-mediated gene transfer into satellite cells. For this purpose, we used a human immunodeficiency virus-1-based lentiviral vector pseudotyped with vesicular stomatitis virus-G glycoprotein.⁴⁰ To start with, we used a vector that expresses Venus, a variant of yellow fluorescent protein⁴¹ under the control of a cytomegalovirus (CMV) promoter (Figure 2a). Freshly isolated satellite cells from limb muscles of 8–12-week-old C57BL/10 mice, which are syngenic to *mdx*, were transduced with the lentiviral vectors at a multiplicity of infection (MOI) of 100 for 16 hours. After removal of free viral vectors and *in vitro* expansion of the cells for 3 days, numerous Venus-positive cells were detected (Figure 2b). Flow

cytometric analyses revealed that 99% of the SM/C-2.6⁺ satellite cell-derived myoblasts expressed Venus when transduced at a MOI of 100 (Figure 2c, right panel). These transduced cells were injected into TA muscles of 5-week-old *mdx* mice at 2×10^4 per muscle. Four weeks after the injection, the muscle regeneration capacity of cells transduced with lentiviral vectors was investigated by immunodetection of Venus- or dystrophin-positive fibers. As in the case of the non-transduced cells (Figure 1d and e), grafting of transduced cells too led to many Venus- and dystrophin-positive fibers (Figure 2d). This serves to show that SM/C-2.6⁺ satellite cell-derived myoblasts transduced with lentiviral vectors contribute efficiently to muscle regeneration.

Direct isolation of SM/C-2.6⁺ satellite cells from dystrophic muscles of *mdx* mice

In order to test whether autologous myogenic precursor cells genetically corrected to express a dystrophin gene represent a possible tool in DMD therapy, we next attempted to directly isolate SM/C-2.6⁺ cells from limb muscles of 5-week-old *mdx* mice. Numerous inflammatory and fibroblastic cells reflecting the active cycles of the degeneration-regeneration process are found in dystrophic muscles. SM/C-2.6 antibody reacts with activated fibroblastic cells (Fukada *et al.*, unpublished data). Because satellite cells are negative for both Sca-1 and CD31,³⁵ we stained *mdx* muscle-derived mononuclear cells with a cocktail of CD45, CD31, Sca-1, and SM/C-2.6 antibodies and collected SM/C-2.6⁺ CD45⁻ CD31⁻ Sca-1⁻ cells as the satellite cell fraction (Figure 3a). When these cells were cultured in proliferation

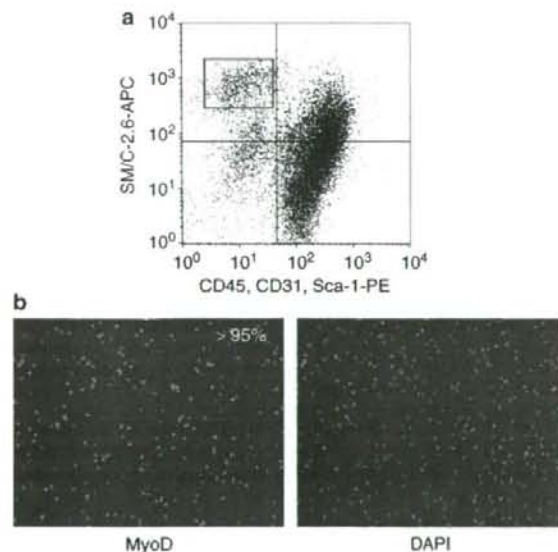


Figure 3 Direct isolation of SM/C-2.6⁺ satellite cells from dystrophic muscles of *mdx* mice. **(a)** Flow cytometry of mononucleated cells derived from *mdx* mice, and stained with a cocktail of CD45, CD31, Sca-1, and SM/C-2.6 antibodies. SM/C-2.6⁺ CD45⁻ CD31⁻ Sca-1⁻ cells (red square) were sorted as the satellite cell fraction. **(b)** Sorted *mdx*-satellite cells were cultured in proliferation medium for 4 days and stained with anti-MyoD antibody (green) and 4',6-diamidino-2-phenylindole (DAPI) (nuclei, blue). More than 95% of them expressed MyoD.

medium for 4 days, more than 95% of them expressed MyoD (Figure 3b). These results indicate that, using the SM/C-2.6 antibody, a pure population of satellite cells can be isolated, not only from wild-type muscle but also from dystrophic muscle of *mdx* mice. Immediately after isolation, the majority of satellite cells from C57BL/6 mice were negative for MyoD, myogenin, and Ki67. On the other hand, 19% of *mdx*-satellite cells were positive for MyoD and 34% of the cells were positive for Ki67 (Table 1). There was no difference between *mdx*- and B6-SM/C-2.6⁺ cells with respect to expression of Pax7 (Table 1). This proves that a considerable fraction of satellite cells are in an activated, proliferative state in skeletal muscles of *mdx* mice.

Successful micro-dystrophin gene transfer into *mdx*-SM/C-2.6⁺ satellite cells

The full-length dystrophin complementary DNA, at 14 kilobase (kb), is too large to be incorporated into a lentiviral vector. In previous studies, we constructed a rod-truncated micro-dystrophin CS1 and demonstrated that it effectively rescued

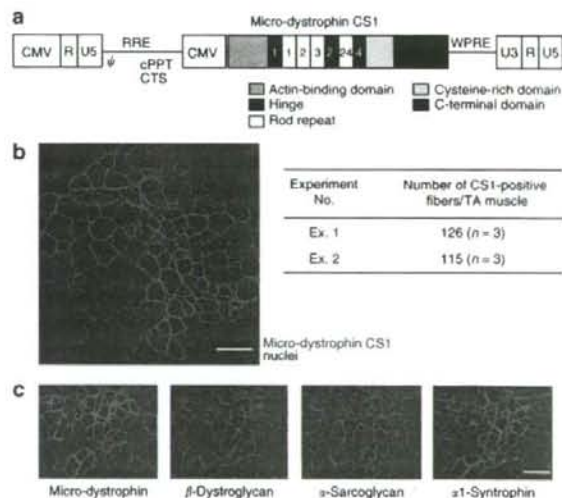


Figure 4 Lentiviral vector-mediated micro-dystrophin CS1 gene transfer into *mdx*-SM/C-2.6⁺ cells and transplantation of transduced cells into *mdx* muscles. **(a)** Structure of the lentiviral vector expressing micro-dystrophin CS1. CS1 complementary DNA was inserted downstream of the cytomegalovirus (CMV) promoter. CS1 has the N-terminal domain, a shortened version of the central rod domain with four rod repeats and three hinges, the cysteine-rich domain, and the C-terminal domain. The numbers of rod repeats and hinges are also shown. **(b)** Freshly isolated SM/C-2.6⁺ cells from *mdx* dystrophic muscles were transduced with lentiviral vectors expressing micro-dystrophin CS1 at a multiplicity of infection of 200 for 16 hours and cultured in proliferation medium for 2 days. Transduced cells (2×10^4) were injected into *mdx* tibialis anterior (TA) muscles. Four weeks after the injection, cross-sections were stained with anti-dystrophin antibody (red) and TOTO3 (nuclei, blue). The number of micro-dystrophin CS1-positive fibers per cross-section was counted. Bar: 80 μ m. **(c)** Restoration of dystrophin-associated proteins at the sarcolemma of micro-dystrophin-positive fibers. Serial cross-sections were stained with anti-dystrophin, β -dystroglycan, α -sarcoglycan, and α 1-syntrophin antibodies (red), and TOTO3 (nuclei, blue). Bar: 80 μ m. cPPT, central polypurine tract; CTS, central termination sequence; RRE, rev responsive element; WPRE, woodchuck hepatitis virus post-transcriptional regulatory element.

the dystrophic phenotypes of *mdx* mice when introduced as a transgene²⁴ or by adeno-associated viral vectors.²⁵ We therefore inserted a 4.9 kb micro-dystrophin *CS1* into the lentiviral vector as a therapeutic gene. Freshly isolated *mdx*-SM/C-2.6⁺ cells were transduced with lentiviral vectors expressing micro-dystrophin *CS1* under the control of a CMV promoter (Figure 4a) at a MOI of 200 for 16 hours. In this condition, 97% of the cells expressed micro-dystrophin *CS1* (data not shown). These transduced cells were injected into TA muscles of 5-week-old *mdx* mice at 2×10^4 cells per muscle. Four weeks after the injection, the muscle regeneration capacity of the cells was investigated by immunodetection of micro-dystrophin-positive fibers. Many myofibers expressed micro-dystrophin *CS1* on the sarcolemma at an average of 120 fibers per muscle (Figure 4b). Further, we examined the restoration of the dystrophin-associated protein complex in micro-dystrophin-positive fibers by immunodetection of α -SG, β -dystroglycan, and α 1-syntrophin. As shown in Figure 4c, all these proteins were expressed at the sarcolemma of micro-dystrophin *CS1*-positive myofibers, thereby suggesting the recovery of dystrophin-associated protein complex by the introduction of micro-dystrophin. These results indicate that *mdx*-SM/C-2.6⁺ cells transduced with lentiviral vectors expressing micro-dystrophin *CS1* efficiently contribute to regeneration of dystrophic muscles of *mdx* mice and restore the expression of the dystrophin/dystrophin-associated protein complex. It therefore follows that transplantation of autologous myogenic precursor cells prepared using the SM/C-2.6 antibody and genetically corrected by a lentiviral vector, is a possible approach for cell therapy in DMD or in localized forms of muscular dystrophy.

DISCUSSION

In vitro passaging reduced the regenerative capacity of satellite cells: In the present study, we directly isolated satellite cells from skeletal muscles of wild-type and *mdx* mice using SM/C-2.6, a novel monoclonal antibody,³⁵ and flow cytometry. Almost all satellite cells prepared from normal muscle are negative for MyoD, myogenin, and Ki67 immediately after isolation, thereby indicating that they are in a quiescent state. In contrast, approximately 20% of *mdx*-satellite cells are positive for MyoD and 35% are positive for Ki67 (Table 1). This result indicates that a fraction of *mdx*-satellite cells are already in an activated state.

Transplantation experiments showed that freshly isolated SM/C-2.6⁺ satellite cells possess a higher capacity for muscle reconstitution when compared with SM/C-2.6⁺ myoblasts passaged *in vitro* prior to transplantation. This result indicates that passaging and subsequent proliferation of satellite cells in culture reduce their intrinsic capacity for muscle reconstitution. In order to clarify the mechanisms of low myogenicity of passaged cells, we performed a colony-forming assay of freshly isolated satellite cells and passaged satellite cell-derived myoblasts (passage 1). When the cells were seeded at a density of 1 cell/well on 96-well plates, fresh satellite cells formed larger colonies than "passage 1" myoblasts (Supplementary Figure S1). In contrast, there was no difference in fusion index between these two cell populations (data not shown). Collectively, reduced efficiency

of muscle fiber regeneration by passaged myoblasts can be partly explained by gradual loss of proliferative ability during passaging.

Importantly, we also found that satellite cells that were expanded *in vitro* without passaging showed regenerative capacity comparable to freshly isolated satellite cells. We therefore hypothesized that it might be possible to introduce therapeutic genes into satellite cells *in vitro* by a lentiviral vector before transplantation without causing any reduction in their regenerative capacity.

Comparison of regenerative capacity of SM/C-2.6⁺ satellite cells with other reports: Previously, Montarras *et al.* directly isolated (Pax3) GFP-expressing satellite cells, which constitute a homogeneous population of small, non-granular, CD34⁺ CD45⁻ Sca-1⁻ cells, from diaphragms of adult Pax3^{GFP/+} mice by flow cytometry, and examined their regenerative capacity.²³ The researchers concluded that *in vitro* expansion of freshly isolated satellite cells for a few days prior to transplantation is a disadvantageous approach, because such satellite cell-derived myoblasts displayed considerably lower muscle regenerative efficiency than fresh satellite cells. In contrast, we observed no reduction in regenerative capacity as a result of *in vitro* expansion of freshly isolated satellite cells without passaging, although their capacity was remarkably reduced after passaging (Figure 1d and e). The discrepancy between the results of Montarras *et al.* and our results may be due to differences in the culture conditions employed. One possible explanation could be that our culture medium contained basic fibroblast growth factor. It has been reported that addition of basic fibroblast growth factor to culture medium improves transplantation efficiency.^{42,43} The modification of culture conditions may enable maintenance of the intrinsic muscle regenerative capacity of satellite cells.

Previous muscle transplantation experiments utilized the progeny of satellite cells enzymatically dissociated from myofibers and extensively cultured to increase their numbers.^{15,20-22} When 5×10^5 to 1×10^6 myoblasts taken from normal mice and prepared by the pre-plating method were transplanted into non-irradiated muscles of *mdx* mice, it resulted in fewer than 100 dystrophin-positive myofibers per muscle.²¹ On the other hand, when 5×10^5 cells were injected into muscles of immunodeficient *mdx nu/nu* mice that had been pre-irradiated to ablate endogenous satellite cell function, they formed an average of 328 dystrophin-positive fibers.¹⁸ Furthermore, grafting of 2×10^4 satellite cells freshly isolated from Pax3^{GFP/+} mice into pre-irradiated TA muscles of *mdx nu/nu* mice led to dystrophin expression in an average of 587 fibers.²³ In our experiment, the same number (2×10^4) of satellite cells freshly isolated from adult normal mice gave rise to an average of only 277 myofibers in non-irradiated *mdx* muscles (Figure 1d and e). This shows that grafted muscle precursor cells form a far greater number of dystrophin-positive fibers in irradiated muscle than in non-irradiated muscle. The use of immunosuppressants such as FK506 also greatly improves the efficiency of transplantation.⁷ In the present study, we injected myogenic cells into non-irradiated TA muscles of immunocompetent mice without any immunosuppressant. Therefore, in our experimental

conditions, the intrinsic function of SM/C-2.6⁺ satellite cells may be underestimated.

The use of the Lentiviral vector is feasible for ex vivo gene transfer. In this study we showed that, at a MOI of 200, lentiviral vectors can introduce the rod-truncated micro-dystrophin gene *CSI* into more than 97% of *mdx*-satellite cells without detrimental effects on cell viability and regenerative capacity. But at a MOI of 300 we observed cell toxicity, whereas at a MOI of 100, the transduction efficiency was below 80% (data not shown). When we injected the transduced autologous myoblasts into *mdx* muscle, the cells contributed to regeneration of myofibers and expressed micro-dystrophin and dystrophin-associated proteins at the sarcolemma. Our results therefore suggest that *ex vivo* gene transfer into autologous myogenic cells by a lentiviral vector is feasible. On the other hand, direct intramuscular injection of vesicular stomatitis virus-G glycoprotein-pseudotyped lentiviral vectors led to relatively low expression of the transgene in mouse skeletal muscles.^{30,44} Because the lentiviral vector genome is inserted into the host genome, the transduction of cells other than the target cell could introduce the risk of mutagenesis. Further, *in vivo* administration could induce undesirable immune responses to exogenous viral proteins. In effect, direct *in vivo* administration of lentiviral vectors poses a safety problem for clinical application. In contrast, *ex vivo* gene transfer has the merit of minimizing the risks of introducing free lentiviral vectors into the host. Transduced cells can efficiently proliferate and differentiate *in vitro* (data not shown).

Limitations of ex vivo gene therapy in DMD, using satellite cells: One of the demerits of our procedure, as compared to *in vivo* gene transfer, is that only a part of the genetically modified myogenic precursor cells contributes to regeneration of the host muscle, given the poor survival rate of these cells. In fact, by using real-time polymerase chain reaction on transcripts from the transgenic enhanced GFP gene, we found that more than 90% of the injected cells were lost within the first 24 hours after injection (data not shown). In addition, migration of the surviving cells is limited in the host muscle after injection. Furthermore, because *in vitro* passaging greatly reduces their myogenicity, it is difficult to obtain a sufficient number of satellite cells or their progeny from a small muscle biopsy of a DMD patient. Therefore current myoblast transfer might be more realistic for localized forms of muscular dystrophy, such as oculo-pharyngeal muscular dystrophy or facio-scapulo-humeral muscular dystrophy.⁴⁵ Surprisingly, however, Collins *et al.* transplanted a single intact myofiber into irradiation-ablated muscles and demonstrated that as few as seven satellite cells associated with one transplanted myofiber can generate over 100 new myofibers containing thousands of myonuclei.⁵ Their observations suggest that proper isolation and handling of satellite cells might greatly improve their myogenic potential.

In this study we have demonstrated transplantation of autologous satellite cells genetically corrected by a lentiviral vector *ex vivo* into *mdx* muscle. For treating DMD patients, however, it is necessary to find the optimum *in vitro* culture condition that will enable human muscle precursor cells to maintain their intrinsic myogenic potential. It would also be useful to identify the factors

that support survival and/or proliferation of transplanted cells in the host muscle.

MATERIALS AND METHODS

Animals. All procedures used on the experimental animals were approved by the Experimental Animal Care and Use Committee at the National Institute of Neuroscience. Eight-to-twelve-week-old C57BL/6 mice were purchased from Nihon CLEA (Tokyo, Japan). C57BL/6-GFP Tg mice were kindly provided by Dr. Okabe (Osaka University, Japan). C57BL/10 mice and C57BL/10-*mdx* mice were maintained in our animal facility and propagated by allowing mating.

In order to induce muscle regeneration, 50 μ l of CTX (10 μ mol/l in saline; Wako Pure Chemical Industries, Tokyo, Japan) was injected into the TA muscle 24 hours before cell transplantation.

Cell preparation and FACS analysis. Freshly isolated muscle-derived cells were prepared from 8-12-week-old GFP-Tg mice, C57BL/6 mice, C57BL/10 mice, or 5-week-old *mdx* mice as previously described.³⁵ Hind-limb and fore-limb muscles were isolated and digested with 0.2% type II collagenase (Worthington Biochemical, Lakewood, NJ) for 90 minutes at 37°C. The muscle slurries were filtered through 100 μ m nitex mesh (BD Biosciences, Franklin Lakes, NJ) and subsequently through 40 μ m nitex mesh (BD Biosciences, Franklin Lakes, NJ). Erythrocytes were eliminated by treatment with 0.8% NH₄Cl in Tris-buffer. Mononucleated cells were stained with biotinylated SM/C-2.6 monoclonal antibody,³⁵ and labeled by allophycocyanin-conjugated streptavidin (BD Pharmingen, San Diego, CA). Mononucleated cells derived from *mdx* muscles were stained with antibodies to additional surface markers, phycoerythrin-conjugated anti-CD45 antibody (clone 30-F11; BD Pharmingen, San Diego, CA), phycoerythrin-conjugated anti-CD31 antibody (clone 390; BD Pharmingen, San Diego, CA), and phycoerythrin-conjugated anti-Sca-1 antibody (clone D7; BD Pharmingen, San Diego, CA). After being washed, stained cells were re-suspended in phosphate-buffered saline (PBS) containing 2% fetal bovine serum (Trace Biosciences, New South Wales, Australia) and 2 μ g/ml propidium iodide (BD Pharmingen, San Diego, CA). Cell sorting was performed on a FACS VantageSE flow cytometer (BD Biosciences, Franklin Lakes, NJ). Debris and dead cells were excluded by forward scatter, side scatter, and propidium iodide gating. We used only propidium iodide-negative fractions for further experiments. We usually obtained approximately 1.5×10^5 sorted cells from 1 g of muscle of 8-12-week-old female C57BL/6 mice.

Cell culture and intramuscular transplantation. Freshly isolated SM/C-2.6⁺ cells from GFP-Tg mice were seeded at a density of 1×10^4 cells per 35-mm dish coated with Matrigel (BD Biosciences, Franklin Lakes, NJ) in a growth medium, Dulbecco's modified Eagle's medium (Invitrogen, Carlsbad, CA) containing 20% fetal bovine serum and 2.5 ng/ml basic fibroblast growth factor (Invitrogen, Carlsbad, CA), and expanded for 4 days. Further, these cells were passaged up to three times at 2-day intervals. Primary myoblasts isolated by the pre-plating method³⁸ from GFP-Tg mice were also cultured in growth medium. Freshly sorted cells, expanded and passaged cells, or cultured primary myoblasts were injected into TA muscles of 8-12-week-old CTX-treated C57BL/6 mice or 5-week-old *mdx* mice that show active cycles of the degeneration-regeneration process. The number of injected cells was 2×10^4 per TA muscle. Four weeks later, the injected muscles were isolated and fixed in 4% paraformaldehyde for 30 minutes, immersed sequentially in 10% sucrose/PBS and 20% sucrose/PBS, and frozen in isopentane cooled with liquid nitrogen.

Immunohistochemistry. Frozen muscle tissues were sectioned (6 μ m) using a cryostat. The sections were blocked with 5% goat serum (Cedarlane, Hornby, Canada) in PBS and then reacted with anti-GFP antibody (1:100; Chemicon International, Temecula, CA) and/or anti-laminin α 2 antibody (1:100; Alexis, San Diego, CA), or anti- α 1-syntrophin antibody

(1:500)* at 4°C overnight. Dystrophin (1:20; NCL-DYSB or DYS2; Novocastra, Newcastle, UK), α -SG (1:50; NCL- α -SARC; Novocastra, Newcastle, UK), and β -dystroglycan (1:50; NCL- β -DG; Novocastra, Newcastle, UK) were detected using monoclonal antibodies after blocking with a MOM kit (Vector Laboratories, Burlingame, CA). The sections were incubated with appropriate combinations of Alexa 488-, Alexa 568-, and Alexa 594-labeled secondary antibodies (Molecular Probes, Eugene, OR) for 30 minutes. The nuclei were counterstained with TOTO-3 (1:5,000; Molecular Probes, Eugene, OR). The stained sections were observed under the confocal laser scanning microscope system TCSSP (Leica, Heidelberg, Germany).

Immunocytochemistry. Cells sorted using FACS were collected by Cytospin3 (Thermo Fisher Scientific, Waltham, MA). After being fixed with 4% paraformaldehyde for 10 minutes, the cells were blocked with 5% goat serum in PBS and then reacted with anti-Pax7 antibody (1:2; Developmental Studies Hybridoma Bank, Iowa, IA), anti-MyoD antibody (1:200; Dako, Glostrup, Denmark), anti-myogenin antibody (1:200; Developmental Studies Hybridoma Bank, Iowa, IA), and anti-Ki67 antibody (1:2; Ylem, Rome, Italy) at 4°C overnight. Primary antibodies were detected by Alexa 488- or Alexa 568-labeled secondary antibodies (Molecular Probes, Eugene, OR) for 30 minutes. Stained cells were mounted in Vectashield with 4',6-diamidino-2-phenylindole (Vector Laboratories, Burlingame, CA) and observed with fluorescence microscopy IX70 (Olympus, Tokyo, Japan).

Generation of lentiviral vectors and in vitro transduction. The third-generation self-inactivated human immunodeficiency virus-1-based lentiviral vector, pCII-CMV-IRES2-Venus, has been described previously.⁴⁷ The vector contains a CMV promoter; an internal ribosomal entry site (IRES) followed by Venus, which is a variant of yellow fluorescent protein⁴⁸; and a woodchuck hepatitis virus post-transcriptional regulatory element. A rod-truncated micro-dystrophin CS1 complementary DNA (four rod repeats, 4.9kb) was excised from pCAG-CS1⁴⁹ and cloned into pCII-CMV-IRES2-Venus, generating pCII-CMV-CS1-IRES2-Venus. The lentiviral vectors expressing Venus only, or micro-dystrophin CS1 followed by Venus, were generated by transient cotransfection of the pCII-CMV-IRES2-Venus or pCII-CMV-CS1-IRES2-Venus, respectively, with the packaging construct (pCAG-HIVgp), vesicular stomatitis virus-G protein, and Rev-expressing construct (pCMV-VSV-G-RSV-Rev) into 293T cells, using the calcium phosphate transfection method.⁴⁷⁻⁴⁹ Two days after transfection, the vector-containing supernatant was collected, filtered through a 0.45- μ m-pore-size filter (Thermo Fisher Scientific, Waltham, MA), and concentrated by centrifugation twice at 50,000g for 2 hours at 20°C. The virus pellet was re-suspended in Hank's Balanced Salt Solution (Invitrogen, Carlsbad, CA) and stored at -80°C until use. The titer of the concentrated virus was 5×10^8 to 1×10^9 infectious units/ml when assayed on 293T cells, and infectivity was determined by Venus expression as analyzed on a FACS VantageSE (BD Biosciences, Franklin Lakes, NJ).

Sixty thousand freshly isolated SM/C-2.6⁺ cells in 300 μ l growth medium were seeded in each well of 24-well plates and cultured for 16 hours with viral vectors expressing Venus or micro-dystrophin CS1 at MOI of 100 or 200, respectively. After removal of free viral vectors by changing the medium, the transduced cells were cultured for 2 or 3 days and trypsinized. A cell suspension containing 2×10^4 cells in 20 μ l of PBS was injected into the TA muscles of mdx mice. The infection efficiency of the injected cells was evaluated using a FACS VantageSE (BD Biosciences, Franklin Lakes, NJ).

ACKNOWLEDGMENTS

This work was supported by Research on Nervous and Mental Disorders (16B-2), and Health Science Research Grants for Research on the Human Genome and Gene Therapy (H16-genome-003), for Research on Brain Science (H15-kokoro-021, H18-kokoro-019) from the Japanese Ministry of Health, Labor and Welfare, Grants-in-Aids for Scientific Research

(14657158, 15390281, 16590333, and 18590392) from the Japanese Ministry of Education, Culture, Sports, Science and Technology, and the "Ground-based Research Program for Space Utilization" promoted by the Japan Space Forum.

SUPPLEMENTARY MATERIAL

Figure S1. Freshly isolated satellite cells give rise to larger colonies than passaged myoblasts *in vitro*.

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Gene therapy for Duchenne muscular dystrophy

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Gene therapy has great potential to treat Duchenne muscular dystrophy. Among many proposed strategies to deliver a therapeutic gene to muscle, recombinant adeno-associated virus-mediated gene transfer is the most promising. The recent isolation of new adeno-associated virus serotypes from human and nonhuman primates provides the opportunity to develop vectors that can achieve the long-term expression of a therapeutic gene in muscles of the entire body without detrimental effects. To translate the results from small animal models to clinical trials in humans, further work using larger animal models, such as dystrophic dogs or nonhuman primates, is required. This review also discusses recent progress in other gene transfer-related therapeutic approaches, including targeted exon skipping and gene correction.

Duchenne muscular dystrophy (DMD), which affects one in 3300 males, is a devastating, progressive, muscle-wasting disease caused by mutations in the dystrophin gene [1,2]. Skeletal muscles in DMD are characterized by myofiber degeneration and progressive fibrous and fatty changes. There is, currently, no way to prevent muscle fiber necrosis and patients suffer severely from respiratory and cardiac complications in the second decade of life. The *DMD* gene is among the largest genes known, spanning 2.4 Mb at Xp21 and encoding a 427-kDa subsarcolemmal cytoskeletal protein, dystrophin, and several shorter isoforms (Dp260, Dp140, Dp116 and Dp71). The full-length dystrophin protein is composed of four domains: an N-terminal actin-binding domain, a central rod domain consisting of 24 spectrin-like repeats, a cysteine-rich domain and a C-terminal domain. Dystrophin binds actin at the N-terminal domain, β -dystroglycan at the cysteine-rich domain and dystrobrevin and syntrophins at the C-terminal domain, forming the dystrophin-glycoprotein complex (DGC) at the sarcolemma (Figure 1) [3]. A lack of dystrophin at the sarcolemma causes secondary loss of the DGC and other functional molecules, such as neuronal nitric oxide synthase (nNOS) [4] and aquaporin-4 [5]. Importantly, mutations in the genes encoding other members of the DGC cause several different types of muscular dystrophy. The mechanism of the degeneration and death of dystrophin-deficient myofibers is not yet fully understood, but it is believed that myofibers lacking dystrophin and the DGC at the cytoplasmic membrane are mechanically weak and highly susceptible to contraction-induced injury. As a

result, the affected muscle experiences continuous cycles of myofiber death and regeneration, resulting in the gradual loss of myofibers and contractile force. In addition to mechanical weakness, abnormalities in calcium handling and changes in mitogen-activated protein (MAP) kinase and GTPase signaling in dystrophin-deficient muscle have been reported and proposed as underlying processes of muscular dystrophy [6,7].

At present, only corticosteroids are reported to effectively attenuate the progress of the disease [8], and current treatment options focus on respiratory and cardiac assistance and improvement of quality of life. Many research groups are still attempting to develop an effective therapy for DMD. In this review, we describe recent progress in gene and related therapies for DMD.

Recombinant adeno-associated virus vector: a promising tool for delivery of dystrophin gene to skeletal muscles

Among several gene transfer vectors and methods developed to date, the adeno-associated virus (AAV) vector is the most suitable to introduce the exogenous gene into postmitotic, nondividing myofibers. An AAV is a tiny, nonpathological, replication-defective virus, with a 4.7-kb single-stranded DNA genome, belonging to the parvovirus family. AAV vectors induce fewer immunological and inflammatory responses *in vivo* than adenovirus vectors [9]. Although the virus genome persists predominantly in episomal form, expression of the transferred gene lasts months to years in adult skeletal muscle. To date, more than 100 AAVs with distinct virus genome sequences have been isolated from humans, nonhuman primates and other species [10]. They display varying

Keywords: adeno-associated virus vector, Duchenne muscular dystrophy, dystrophin, exon skipping, gene therapy

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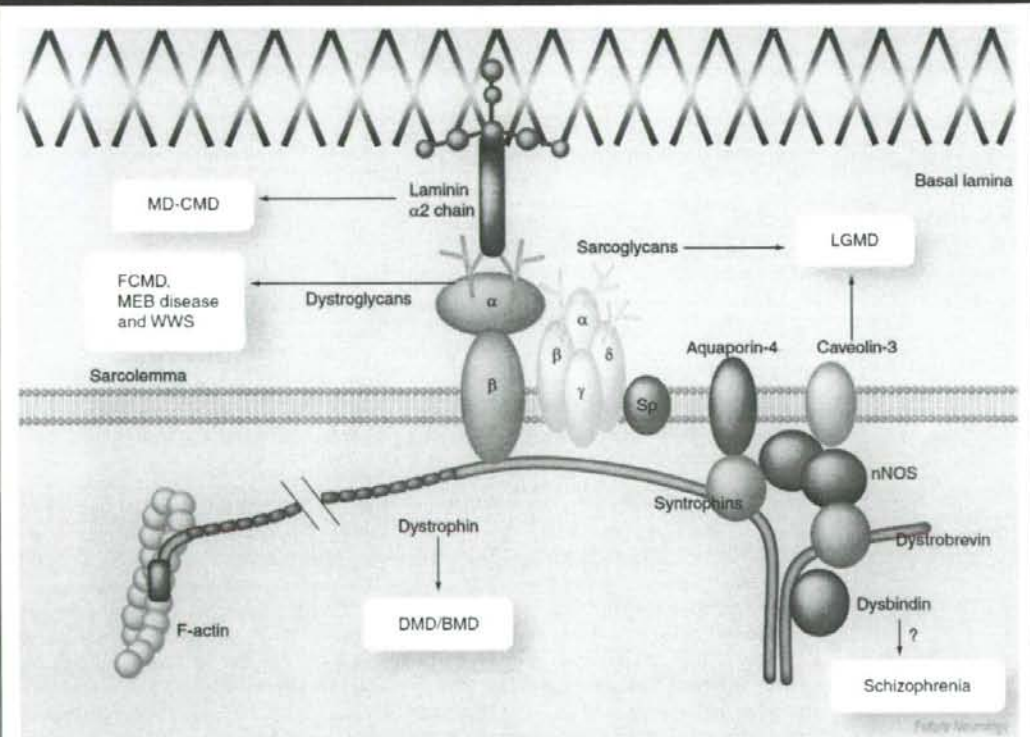
degrees of similarity in their capsid proteins and show diverse tissue tropisms. More than nine AAV vectors have already been developed and evaluated in animal models as a tool for gene transfer *in vivo* (Table 1) [10]. Although the molecular mechanisms of tissue and cell tropisms of AAV vectors are not fully explained, they are likely to use different cellular receptors for entry into and binding to the host cells. The expression of the therapeutic genes is not permanent, mainly because recombinant (r)AAV does not replicate in the host and is barely incorporated into the genome of satellite cells. They are diluted out with the turnover of myofibers and, therefore, repeated

administrations are required. New AAV serotypes would provide good options for follow-up treatments because they have the potential to evade pre-existing neutralizing antibodies against the previously used AAV serotype. However, to avoid the risks of *in vivo* vector delivery, it is important to better understand the vectors and the natural infection with the corresponding virus.

Generation of microdystrophin suitable for use in rAAV vectors

The rAAV vector is a promising tool for gene transfer to DMD muscle, but the limitation of the insertion size to 4.9 kb excludes incorporation of

Figure 1. Dystrophin forms the large dystrophin–glycoprotein complex at the sarcolemma, linking the basal lamina to the cytoskeletal actin.



Mutations in the dystrophin gene end in the secondary loss of dystrophin–glycoprotein complex and other functional molecules, such as nNOS and aquaporin-4. Mutation in the laminin α2 chain gene causes congenital MD. Abnormal glycosylation of α-dystroglycan is commonly observed in FCMD, MEB disease and WWS. Abnormal glycosylation of α-dystroglycan also causes abnormalities in the eye and the CNS. Mutations in any of four sarcoglycan genes (α, β, γ and δ) result in LGMD. These observations emphasize the importance of dystrophin and associated molecules for muscle integrity. The dysbindin (*DTNBP1*) gene is one of the several putative susceptibility genes for schizophrenia.

BMD: Becker MD; DMD: Duchenne MD; FCMD: Fukuyama-type congenital MD; LGMD: Limb girdle MD; MD: Muscular dystrophy; MD-CMD: Merosin-deficient congenital MD; MEB: Muscle-eye-brain; nNOS: Neuronal nitric oxide synthase; WWS: Walker-Warburg syndrome.

Table 1. Characterization of nine serotypes of AAV vectors.

Serotype	Amino acid homology to AAV2 (%)	Isolated from	Tissue tropism				Delivery system
			Skeletal muscle	Heart	Liver	CNS	
1	84	NHP	+++	++	+	+	Local
2	100	Human	+	+	+	+	Local
3	88	Human		+	±	+	Local
4	64	NHP		+	±	+	Local
5	61	Human	+	+	++	++	Local
6	84	Human	++	++	+	+	Local, systemic
7	83	NHP	+++	+++	++	++	Local, systemic
8	84	NHP	+++	+++	+++	++	Local, systemic
9	83	Human	+++	+++	+++	++	Local, systemic

AAV: Adeno-associated virus; NHP: Nonhuman primate.

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a full-length dystrophin gene (14-kb mRNA, 11-kb open reading frame). To overcome this drawback, several groups have designed small dystrophins in which the long, central rod domains are largely deleted, and tested their functions in dystrophin-deficient *mdx* mice [11]. The functions of three types of microdystrophins (CS1, AX11 and M3; Figure 2) have been tested on microdystrophin-transgenic, dystrophin-deficient *mdx* mice, and it was observed that over-expressed CS1 with four repeats and three hinges almost completely ameliorated dystrophic phenotypes [12]. Therefore, a rAAV2 vector was constructed expressing CS1, driven by a skeletal muscle-specific muscle creatine kinase promoter [13], and was injected it into the

anterior tibialis muscles of immunocompetent adult *mdx* mice. A total of 24 weeks after injection, 50% of myofibers, on average, expressed microdystrophin and the treated muscles demonstrated improved contractile force [14].

Systemic delivery of rAAV-serotype 6, 8 & 9 vectors

Systemic delivery systems for the treatment of DMD require improvement to enable transfer of the therapeutic genes to the complete musculature of the body, especially to the heart and diaphragm. Gregorevic and colleagues reported that intravenous injection of rAAV6 vectors efficiently delivered a microdystrophin gene to the

Figure 2. Structure of full-length dystrophin and constructs of mini- and microdystrophin (CS1, AX11 and M3).