Myogenic program dysregulation is contributory to disease pathogenesis in spinal muscular atrophy

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Mutations in the survival motor neuron (SMN) gene lead to the neuromuscular disease spinal muscular atrophy (SMA). Although SMA is primarily considered as a motor neuron disease, the importance of muscle defects in its pathogenesis has not been fully examined. We use both primary cell culture and two different SMA model mice to demonstrate that reduced levels of Smn lead to a profound disruption in the expression of myogenic genes. This disruption was associated with a decrease in myofiber size and an increase in immature myofibers, suggesting that Smn is crucial for myogenic gene regulation and early muscle development. Histone deacetylase inhibitor trichostatin A treatment of SMA model mice increased myofiber size, myofiber maturity and attenuated the disruption of the myogenic program in these mice. Taken together, our work highlights the important contribution of myogenic program dysregulation to the muscle weakness observed in SMA.

INTRODUCTION

Spinal muscular atrophy (SMA) is an autosomal recessive disorder characterized by the degeneration of α-motor neurons in the spinal cord and is a major leading genetic cause of infant deaths (1). The deletion, rearrangement or mutation of the disease causing gene, survival motor neuron 1 (SMN1), is the cause of SMA in over 95% of patients (2–4). There are two virtually identical copies of the SMN gene, a telomeric copy, SMN1, and a centromeric copy, SMN2 (5). Compared with the SMN1 gene, a single nucleotide substitution identified in SMN2 has a profound functional impact as only 10% of SMN2 translated products are full-length and stable (6). In contrast to humans, mice have a single Smn gene and the homozygous deletion of the gene leads to death early during preimplantation embryonic development (7). The addition of the human SMN2 transgene onto the Smn-null background rescues the embryonic lethality but leads to a severe phenotype in mice (8). These mice, designated Smn−/−;SMN2, live up to 6 days before succumbing to the disease. We have previously generated an intermediate mouse model of SMA (Smn−/−/−) that survives to 4 weeks of age due to slightly higher Smn protein levels than the severe model (9). The 2B mutation consists of a three-nucleotide substitution in the exon splicing enhancer of exon 7 of the endogenous mouse Smn gene (10).

Although SMA is primarily considered as a motor neuron disease, the involvement of muscle in its pathogenesis has not been fully investigated. C2C12 myoblasts with reduced Smn protein display abnormal proliferation, aberrant myoblast fusion and malformed myotubes (11). The maturation of muscle is coordinated by the sequential expression of myogenic regulatory factors, namely myoblast determination 1 (MyoD), myogenin and the muscle-specific regulatory factor 4 (MRF4; also known as Myf6). MyoD is an early marker of myogenesis while myogenin and MRF4 are expressed later and mark muscle differentiation. During postnatal muscle development, a high proportion of paired box protein 7 (Pax7) positive satellite cells undergoes proliferation and differentiation, and contributes to muscle growth (12). The idea of delayed muscle development in mouse models of SMA has been suggested by several groups, however this has, for the most part, been proposed on the basis that myofibers do not appear to increase in size shortly after birth in severe mouse models of SMA (13,14). Whether skeletal muscle defects contribute to the SMA phenotype has only recently begun to be investigated. Much remains to be uncovered in diseased skeletal muscles including why they are smaller in SMA.

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Mechanisms underlying muscle weakness in SMA can be targeted therapeutically to increase muscle strength, regardless of whether they are attributed to intrinsic defects, or the consequence of motor neuron pathology.

Here, we show abnormal expression of the myogenic program in primary myoblasts from Smn\textsuperscript{2B/−} mice and in vivo, where we demonstrate the presence of delayed skeletal muscle development independent of myofiber degeneration and muscle denervation in mouse models of SMA. The administration of the histone deacetylase (HDAC) inhibitor trichostatin A (TSA) ameliorated muscle maturity in SMA model mice. These data demonstrate that Smn is required for proper perinatal muscle development.

RESULTS

Decreased levels of myogenic regulatory factors and fusion defects in Smn\textsuperscript{2B/−} primary myoblasts

To study myogenesis in a genetically relevant manner and in an intrinsic way by eliminating the negative contribution that motor neuron degeneration might have on muscle cells, we isolated primary myoblasts from Smn\textsuperscript{2B/−} mice. As expected, Smn protein levels were dramatically reduced in Smn\textsuperscript{2B/−} myoblasts (Fig. 1A). Surprisingly, myoblasts under normal growth conditions displayed a 4-fold decrease in Pax7, and a 28-fold decrease in MyoD protein levels (Fig. 1A). To assess whether the misregulation of Pax7 and MyoD might have an impact on myoblast differentiation, cells were seeded at equal densities, grown to confluence and induced to differentiate by serum deprivation for 5 days. We observed a significant decrease (2.6-fold) in the level of myogenin, an early marker of myogenic differentiation, and a similar decrease (1.6-fold) in myosin heavy chain (MHC), a late marker of myogenic differentiation (Fig. 1B). To assess whether the aberrant expression of the myogenic program had any biological consequences, we examined the fusion potential of Smn\textsuperscript{2B/−} myoblasts. Upon differentiation, we observed a general decrease in fusion in Smn\textsuperscript{2B/−} myotubes as evidenced by an increased number of mononucleated MHC positive cells and a corresponding decrease in myotubes with 8 or more nuclei in Smn\textsuperscript{2B/−} myotubes compared with control myotubes (Fig. 1C). These results are reminiscent of those we have previously obtained using the hypomorphic Smn knockdown C2C12 cells (11). Together, our results suggest that in culture, myoblasts from Smn\textsuperscript{2B/−} mice have differentiation and fusion defects.

The myogenic program is delayed in skeletal muscle from mouse models of SMA

Myogenic regulatory factors are normally highly expressed early during postnatal skeletal muscle development and their levels decrease significantly over time. By postnatal day (P) 21, these factors are difficult to detect relative to P2 (Supplementary Material, Fig. S1A). Interestingly, Smn protein expression from P2 to P21 follows a very similar trend suggesting a need for Smn early in muscle development (Supplementary Material, Fig. S1A). We assessed the expression of myogenic proteins at P0, P2 and P5 in hindlimb muscle from Smn\textsuperscript{−/−};SMN2 and control mice (Fig. 2A and quantified in Supplementary Material, Fig. S2A). The protein levels of Pax7 in Smn\textsuperscript{−/−};SMN2 mice were comparable to controls at P0 however, we observed a significant decrease at P2 and P5. Moreover, Pax7 transcripts were significantly decreased at P5 in Smn\textsuperscript{−/−};SMN2 animals compared with control (Supplementary Material, Fig. S1B). The decreased levels of Pax7 at P2 and P5 translated to fewer Pax7 positive cells in skeletal muscles from Smn\textsuperscript{−/−};SMN2 mice compared with controls (Supplementary Material, Fig. S3). At P0, no change in MyoD protein levels was detected and at P2 a trend towards decreased levels of MyoD was observed. Both protein and transcript levels of Myogenin were significantly decreased at P5 in Smn\textsuperscript{−/−};SMN2 mice compared with controls (Fig. 2A and Supplementary Material, Fig. S1C). Myogenin levels were unchanged at P0 and P2 in Smn\textsuperscript{−/−};SMN2 mice compared with controls (Fig. 2A and Supplementary Material, Fig. S1C).

Figure 1. Altered myogenic program and aberrant myotube formation in primary cells from Smn\textsuperscript{2B/−} mice. (A) Immunoblot analysis reveals decreased Smn, Pax7 and MyoD protein levels in proliferating primary myoblasts established from control and Smn\textsuperscript{2B/−} mice. Bar graph showing a significant decrease in Pax7 and MyoD protein levels. (B) Immunoblot analysis and quantification reveals significantly decreased levels of myogenic differentiation markers myogenin (MyoG) and myosin heavy chain (MHC) in cultured primary cells differentiated for 5 days. (C) Representative images of control and Smn\textsuperscript{2B/−} myoblasts differentiated into myotubes for 72 h and stained for MHC. Quantification of the number of nuclei per myotube revealed that there is a decrease in myoblast fusion in Smn\textsuperscript{2B/−} cells compared with controls. Scale bar = 50 μm. N = 3 for all experiments. *, P < 0.05; **, P < 0.01.
Furthermore, we observed increased Pax7 transcript levels and expression of myogenic proteins at different time points in muscle from Smn2B/− animals relative to controls (Fig. 2B). MyoD levels remained high up to P21 where significantly more MyoD mRNA and protein levels were observed in Smn2B/− mice compared with control mice (Fig. 2B and Supplementary Material, Fig. S1E). The protein levels of MRF4 were significantly decreased at P2 and were not different than controls until P21 where the levels were increased in Smn2B/− mice (Fig. 2B). MRF4 transcripts were increased at P21 in Smn2B/− mice in agreement with the protein data (Supplementary Material, Fig. S1E). The delay in expression of the myogenic regulatory factors becomes even more apparent when control and Smn2B/− samples from P2, P9 and P21 are processed together on the same blot (Fig. 2C). Normally, the levels of MyoD decline dramatically from P2 onwards, however this phenomenon is delayed in the Smn2B/− muscle.

We have also extended our analysis to a third mouse model of SMA, the commonly used Smn−/−; Smn2D7 mouse. Using skeletal muscle lysate collected from phenotypic P13 Smn−/−; Smn2D7 and control mice, we show a decrease in the protein levels of Pax7, MyoD and myogenin, and to a lesser extent MRF4 (Supplementary Material, Fig. S5). Taken together, this data demonstrate that there is a significant disruption in the myogenic program across the three mouse models of SMA examined. In severe models (Smm−/−; Smn2 and Smn−/−; Smn2D7) this is evidenced by a dramatic decrease in factors regulating myogenesis. In our milder model (Smm−/−), this is evidenced by an early decrease in the levels of the factors followed by an increase at later stages of disease. We hypothesize that this difference is due to the more prolonged nature of the pathology in the milder models allowing myogenesis to ultimately proceed, albeit at a later time point.

The proper temporal expression of these myogenic transcription factors is essential for the subsequent expression of genes involved in muscle function. We investigated whether the aberrant expression of the myogenic program affected the expression of developmental MHC isoforms in muscles from SMA model mice. The expression of the embryonic and neonatal MHC transcripts was mis-regulated in a similar fashion as the myogenic regulatory factors in both mouse models of SMA (Supplementary Material, Fig. S6). That is, compared with control counterparts, a decrease in the mRNA expression of embryonic and neonatal MHC was detected in phenotype stage Smn−/−; Smn2D7 mice, while these transcripts were increased in Smn2B/− samples at P21. These data suggest that the pathological reduction of Smm leads to muscles with altered levels of developmentally important myogenic genes.
Increased immature myofibers in skeletal muscles of mouse models of SMA

Since our analysis of the myogenic program suggested a delay in skeletal muscle development in mouse models of SMA, we performed a histological analysis to assess the consequence of this molecular phenotype. The cross-sectional area of tibialis anterior (TA) myofibers from P5 Smn<sup>−/−</sup>;SMN2 and P21 Smn<sup>2B/−</sup> mice was significantly decreased compared with control (Fig. 3A). We also noted a higher proportion of myofibers with

![Figure 3](https://academic.oup.com/hmg/article-abstract/23/16/4249/626021)
centrally located nuclei in both Smn<sup>−/−</sup>;SMN2 and Smn<sup>2B/−</sup> mice at phenotypic (P5 and P21 respectively) stages. Importantly, this was also seen at prephenotypic stages, demonstrating that centrally located nuclei are an early feature of disease pathogenesis (Fig. 3B and C).

Central nucleation is observed during muscle development and can also be a histological hallmark of muscle fiber regeneration following a bout of degeneration. To investigate whether this central nucleation was due to regeneration following degeneration, we performed the Evan’s blue dye assay to assess whether skeletal muscles from mouse models of SMA have degenerating myofibers. We did not observe any degenerating fibers present in phenotype stage Smn<sup>−/−</sup>;SMN2 and Smn<sup>2B/−</sup> muscles (Fig. 3D). In contrast, muscle fibers from the mdx mouse model of muscular dystrophy display numerous examples of degeneration as evidenced by dye uptake (Fig. 3D). These data suggest that TA muscle fibers from mouse models of SMA are not undergoing degeneration, but rather that the increase in central nucleation observed is indicative of impairment in muscle development.

The aberrant myogenic program correlates with muscle denervation but can occur independently of muscle denervation in mouse models of SMA

The mis-regulation of the myogenic program in SMA model mice could be due in part to the innervation status of the muscle. To address this question, we have assessed the innervation status of various muscle groups namely, cranial muscles, the rectus abdominis (RA) muscle, and the transversus abdominis (TVA) muscle. Upon quantification of the percentage of fully occupied endplates, we observed that the cranial muscles appear fully innervated while the RA and the TVA are both muscles with pronounced denervation in P21 Smn<sup>2B/−</sup> mice (Fig. 4A and B). Therefore, we took advantage of our Smn<sup>2B/−</sup> mouse model in which there is differential vulnerability to denervation in various muscles, and assessed the levels of Pax7, MyoD and myogenin in these muscles at P21 phenotype stage. Pax7 and MyoD protein levels were significantly increased in all three Smn<sup>2B/−</sup> muscle types tested compared with controls (Fig. 4C and D). However, the degree to which Pax7 and MyoD levels were altered is much greater in the more denervated TVA and RA muscles (Fig. 4C and D). Interestingly, the level of myogenin was not statistically different between control and Smn<sup>2B/−</sup> muscles from the three groups despite muscle denervation being significantly present in the TVA and RA muscles (Fig. 4D).

To investigate whether Pax7 and MyoD levels could change following muscle denervation, we experimentally denervated wild-type mice. Interestingly, denervation did not impact on Pax7 and MyoD levels 1 and 7 days postdenervation but rather, caused a pronounced increase in myogenin levels as early as 1 day postdenervation (Fig. 4C). Thus, our results show that the increase in Pax7 and MyoD correlates with the degree of denervation in Smn<sup>2B/−</sup> mice, severe denervation does not influence the levels of Pax7 and MyoD.

**Trichostatin A (TSA) rescues skeletal muscle defects in Smn<sup>2B/−</sup> mice**

Administration of the HDAC inhibitor TSA has previously been shown to extend survival in a severe mouse model of SMA. This improvement was associated with a modest increase in full-length SMN expression from the SMN2 gene (16). Furthermore, TSA decreased the expression of atrogenes in skeletal muscles of SMA model mice, which likely contributed to the motor behavior improvements observed following treatment (16,17). Interestingly, TSA treatment is also beneficial in the Smn<sup>2B/−</sup> mouse model that does not harbor the SMN2 transgene; however in this case there was no detectable increase in Smn. Furthermore, other studies have demonstrated that TSA treatment of C2C12 cells increased myoblast fusion, and that TSA can increase the expression of early myogenic regulatory factors (18,19). We therefore investigated whether TSA could increase myofiber size and ameliorate muscle maturity in Smn<sup>2B/−</sup> mice. We began by testing whether TSA could improve the fusion capacity of Smn<sup>2B/−</sup> primary myoblasts. To do so, we treated Smn<sup>2B/−</sup> myoblasts with TSA or vehicle [dimethyl sulfoxide (DMSO)] for 24 h and subsequently induced the cells to differentiate for 72 h. We observed a >3-fold increase in TSA treated cells with regards to the number of myotubes with 5 nuclei, and 6 nuclei or more (Fig. 5A and B). These results demonstrated that TSA can improve the fusion potential of Smn<sup>2B/−</sup> primary myotubes.

To test whether systemic administration of TSA could benefit the muscle defects in SMA model mice, we treated phenotypic Smn<sup>2B/−</sup> mice for 2 weeks with either vehicle or TSA via intraperitoneal injection from P12. Histological analyses of treated muscles revealed that TSA reduced the proportion of myofibers with centrally located nuclei (Fig. 5C and D). Moreover, Smn<sup>2B/−</sup> mice treated with TSA had significantly fewer small caliber myofibers and more large caliber myofibers compared with Smn<sup>2B/−</sup> mice given DMSO (Fig. 5C and D). TSA administration resulted in a significant decrease in the transcript levels of embryonic MHC and neonatal MHC isoforms suggesting that these muscles were further along the maturation process than those from Smn<sup>2B/−</sup> animals given DMSO (Fig. 5F). Finally, to assess whether TSA could increase early markers of myogenesis prior to any motor phenotype, we treated Smn<sup>2B/−</sup> animals with TSA from P3 to P6. Relative to DMSO controls, we observed a significant increase in Pax7 and MyoD protein levels following TSA administration (Fig. 5G). These results demonstrate that TSA can increase myogenic proteins early in SMA model mice prior to overt motor neuron pathology. Furthermore, the administration of TSA led to a further increase in the proportion of Pax7 positive cells in P21 Smn<sup>2B/−</sup> animals when compared with DMSO treated Smn<sup>2B/−</sup> mice (Fig. 5H).

**DISCUSSION**

Previous studies have focused on uncovering the reasons for the motor neuron vulnerability in SMA and developing therapeutic approaches aimed at increasing SMN levels in motor neurons. In this study, we demonstrate that Smn deficiency leads to delayed postnatal skeletal muscle development in primary myoblasts from Smn<sup>2B/−</sup> mice and in multiple mouse models of SMA with varying phenotypes. Furthermore, we show that the administration of TSA on SMA model mice can ameliorate the defects in muscle development observed.

A delay in muscle development had previously been suggested based on morphological studies in mice (13,14).
This led us to investigate whether the myogenic program was altered in muscles from mouse models of SMA. We show that the levels of Pax7, MyoD, myogenin and MRF4 were altered in both primary Smn2B/2 myoblasts and in SMA model mice. The expression of these myogenic genes rapidly decreases over time during postnatal development as the myofibers mature. Interestingly, the expression of Smn in muscle follows a similar profile, as levels drop dramatically in P21 wild-type mice. This observation suggests that Smn is more likely to play an important role in muscle development rather than in muscle structure maintenance.

In Smn2B/2 hindlimb muscles, levels of all myogenic proteins assessed were low at an early presymptomatic (P2) stage and increased at the phenotype stage (P21) when compared with controls. Immunoblot analyses performed on late presymptomatic muscle revealed a shift in levels of Pax7 and MyoD, as they were increased in P9 Smn2B/2 mice while myogenin and MRF4, which are markers of differentiation, remained low. In

Figure 4. The myogenic program is altered even in muscles not subject to denervation in Smn2B/2 mice. (A) Representative images showing fully intact NMJs from cranial, TVA and RA muscles of control and P21 Smn2B/2 mice. Postsynaptic acetylcholine receptors were labeled with alpha-bungarotoxin (BTX, red) while the presynaptic terminal was labeled with antineurofilament (NF, green) and antisyaptic vesicle protein 2 (SV2, green). (B) Quantification of fully occupied endplates revealed differences between control and the TVA and RA muscles from Smn2B/2 mice but not for cranial muscles, suggesting that the latter are not subject to denervation. (C) Representative immunoblots showing altered protein levels of Pax7 and MyoD in innervated (cranial) and denervated (RA and TVA) muscles of Smn2B/2 mice. Interestingly, Pax7 and MyoD levels are unaffected in muscles following experimental denervation, at 1 or 7 days postsurgery. By comparison, a robust increase in myogenin levels can be detected as early as 1 day postdenervation and persists to 7 days following denervation. (D) Quantification analyses revealed differences in Pax7 and MyoD protein levels in all three muscle groups examined. The levels of myogenin however, were similar between control and Smn2B/2 mice for innervated and denervated muscles. (MyoG = myogenin, DEN = denervated). Scale bar = 20 μm. N = 3 for all experiments. *, P < 0.05; **, P < 0.01, ****, P < 0.001.
our study, Pax7 and MyoD appear to be most affected and their mis-regulation is likely the reason for the aberrant expression of myogenin and MRF4. Our time-course analysis reveals that indeed the protein levels of MyoD peak at P9 and that the impaired muscle maturation is likely the result of this delay in expression. Decreased expression of Pax7 could be indicative of muscle differentiation initiation (20). However, our histological findings demonstrating the increased presence of immature myofibers in SMA model mice, and the results from our primary myoblast cultures also suggest otherwise.

We had hypothesized that muscle denervation was influencing the expression of the myogenic program, however given our results in which the myogenic program was mis-regulated in the cranial muscles, it is likely that this defect is an intrinsic phenomenon. Further supporting this notion is the fact that the myogenic defects can be observed well before motor neuron loss and denervation which occurs after P2 and P9 in Smn<sup>-/-</sup>;SMN2 and Smn<sup>2B/-</sup> mice, respectively (21). However, it also remains equally possible that predegenerative changes in motor neurons or at the neuromuscular junction (NMJ) in SMA model mice could contribute to the changes observed in the muscle prior to those time points. We have also demonstrated that treatment with TSA can ameliorate muscle maturation in Smn<sup>2B/-</sup> mice. The effects of TSA on Smn<sup>2B/-</sup> primary myoblasts as well as on presymptomatic Smn<sup>2B/-</sup> animals demonstrate that this compound can have intrinsic benefits in skeletal muscle. Our data suggest that alterations of the myogenic program may be a reason for muscle vulnerability and that this defect can be targeted therapeutically. Regardless of whether the mis-regulation of the myogenic program is intrinsic or not, muscle defects are present in mouse models of SMA and can be targeted therapeutically to increase muscle function. Indeed, Martinez et al. (22) have demonstrated that using the Cre drivers MyoD<sup>cre</sup> or Myf5<sup>cre</sup> to restore the expression of SMN in skeletal muscle or in motor neurons using the ChAT<sup>cre</sup> mouse led to comparable benefits in a mouse model of SMA. These results contrast previous findings in which the HSA promoter was used to drive expression of SMN in the skeletal muscle of SMA model mice (23). These latter mice did not show any significant benefit. However, it is likely that the HSA promoter is active only in myotubes and would not have imparted SMN expression in satellite cells or myoblasts. Thus, we believe that the skeletal muscle expression in the HSA-SMN mice would be too late during myogenesis to yield any significant phenotypic improvements in the SMA mice.

During the initial embryonic muscle formation, the first muscle fibers are generated and these serve as templates for a second wave of muscle formation in the perinatal phase (24). This second wave is characterized by the significant contributions of myogenic progenitors, which proliferate, differentiate and increase muscle size. In Smn<sup>-/-</sup>;SMN2 skeletal muscle, it would appear that the level of Smn is too low at the required time point to fulfill its function(s) during the perinatal phase. In turn, this leads to a robust decrease in the myogenic program and to immature myofibers and muscle weakness. In Smn<sup>2B/-</sup> muscle however, our time-course analysis suggests that the myogenic program peaks at P9 instead of P0–P2 like in control mice. This ultimate lastly has a profound impact on muscle morphology of Smn<sup>2B/-</sup> mice as we observed decreased cross-sectional myofiber area and increased immature myofibers. Therefore, in Smn<sup>2B/-</sup> mice the level of full-length Smn protein appears to be sufficient to allow the progression of skeletal muscle development albeit in a delayed manner.

In summary, the present study demonstrates early and persistent delayed muscle development in mouse models of SMA. The depletion of Smn hinders the normal maturation of skeletal muscle at the molecular and morphological levels, and likely contributes to the SMA phenotype. Future studies should focus on elucidating the functions of Smn during perinatal and early postnatal life, in particular addressing how Smn depletion leads to the mis-regulation of the myogenic program. The study of muscle in SMA research allows for a better understanding of the contributions of this tissue in the pathophysiology of the disease and highlights the importance of including muscle as a target tissue in therapeutic development.

**MATERIALS AND METHODS**

**Mice and tissue dissections**

In the present study, we took advantage of three different SMA mouse models, the Smn<sup>-/-</sup>;SMN2 mice (Jackson Laboratories) that die around P6, the Smn<sup>-/-</sup>;SMN2Δ7 mice (Jackson Laboratories) that die at P13–P15, and the less severe Smn<sup>2B/-</sup> mice that die ~4 weeks of age (8,25). The Smn<sup>2B/-</sup> mice were established in our laboratory and maintained in our animal facility on a C57BL/6 × CD-1 hybrid background. The Smn<sup>-/-</sup> mice (26) obtained from Jackson Laboratories were crossed with Smn<sup>2B/-</sup> mice to produce Smn<sup>2B/-</sup> affected mice and Smn<sup>2B/+</sup> control littermates (9). The mice were housed and cared for according to the Canadian Council on Animal Care (CCAC) guidelines and the University of Ottawa Animal Care Committee protocols. Presymptomatic tissues were collected at P0 and P2 for severe Smn<sup>-/-</sup>;SMN2 mice, and P2, P6 (early presymptomatic) and P9 (late presymptomatic) for the Smn<sup>2B/-</sup> mice. Tissues were collected from phenotypic stages at P5 in Smn<sup>-/-</sup>;SMN2 mice, P13 in Smn<sup>-/-</sup>;SMN2Δ7 mice, and at P15 and P21 in Smn<sup>2B/-</sup> mice. Muscles used for RNA or protein extractions were flash frozen in liquid nitrogen, while muscles used for immunofluorescence and histology were embedded in optimum cutting temperature medium (Fisher) and frozen in cryomolds (Tissue-Tek). All tissues were stored at −80°C.

**TSA administration**

Smn<sup>2B/-</sup> mice were treated with either TSA (10 mg/kg) or vehicle (DMSO) via intraperitoneal injections for 2 weeks starting at P12 following the appearance of the motor phenotype as previously described (16) for 2 weeks. To determine if TSA could increase myogenic protein expression in SMA model mice, Smn<sup>2B/-</sup> animals were treated from P3–P6 and skeletal muscles were collected and flash frozen for immunoblot analysis. In both experiments, samples were collected 2 h following the last injection.

**Hindlimb denervation**

Denervation surgeries were performed in accordance with the guidelines set by the CCAC and the Laurentian University Animal Care Committee. Young adult mice were anesthetized
by inhalation of isofluorane. The hindlimb muscles were bilaterally denervated by surgically exposing the sciatic nerve and removing a 2–3 mm segment of the nerve. This ensured that nerve transmission to hindlimb muscles was blocked and nerve regeneration was prevented. A sham procedure was performed as a control and consisted of exposing the mice to the same surgical procedures except for the sciatic nerve sectioning. Gastrocnemius muscles were collected and flash frozen from denervated and sham operated mice 1 and 7 days following surgery.

Primary cell isolation and culture

Smm2B/− primary myoblasts were isolated from hindlimb muscles of 3-week-old mice as originally described (27). Cells were cultured on collagen-coated plates (Gibco) and maintained under growth conditions using Ham’s F10 (Wisent) media supplemented with 20% fetal bovine serum, 2.5 mg/ml human recombinant basic fibroblast factor (Invitrogen), and 2% penicillin/streptomycin (Gibco). Primary myoblasts seeded at equal density were induced to differentiate with Dulbecco’s Modified Eagle Medium (Wisent) supplemented with 5% horse serum (Gibco) and 1% penicillin/streptomycin. To assess the impact of TSA on fusion, Smm2B/− myoblasts were treated with 100 nM of TSA for 24 h and then induced to differentiate for 72 h as previously described (19). In all experiments, cells were maintained at 37°C with 5% CO2 and were provided fresh media every other day.

Immunofluorescence

Cross-sections (10–12 μm) were collected using a cryostat (Leica) and fixed with 4% paraformaldehyde and then stained as previously described (28). A mouse-on-mouse kit (Vector Labs), and the primary antibodies targeting Pax7 (Developmental Studies Hybridoma Bank, DSHB) and M-cadherin (Santa Cruz) were used to highlight satellite cells while a laminin fluorescence microscope or a Zeiss Confocal microscope (LSM 510) were provided fresh media every other day. Immunofluorescence images were captured using a Zeiss Axioplan fluorescence microscope and the centrally located nuclei data are presented relative to total number of myofibers present as assessed by laminin staining. The fusion capacity of primary myoblasts was determined by counting the number of nuclei per myotube using the ImageJ counting tool. For each sample, the data were averaged from five different fields of view taken at 10×. Immunomicrographs from Smm2B/− myotubes treated with DMSO or TSA were randomly scrambled and the results were blinded to the person counting.

Evans’s blue dye injection

Phenotype stage Smm−/−;SMN2 and Smm−/− mice were injected with Evans’s blue dye (1%) diluted in phosphate buffered saline. The dye was administered by an intraperitoneal injection and at a concentration of 100 μl per 10 g of body weight for Smm−/− mice, and 50 μl per 10 g of body weight for Smm−/−;SMN2 mice. Tissues from Smm−/− mice were harvested 24 h postinjection and 6 h postinjection for Smm−/−;SMN2 mice. Skeletal muscles were sectioned using a cryostat, fixed with ice-cold acetone at −20°C for 10 min, and stained with laminin to visualize the myofibers. Degenerating fibers could be detected by the presence of a red signal using a fluorescence microscope. mdx mice, a model of Duchenne Muscular Dystrophy, were injected at phenotype stage with Evans’s blue dye in parallel and served as a positive control for the presence of degenerating myofibers.

Reverse-transcription

Flash frozen hindlimb muscle samples were homogenized and RNA was isolated using a column-based technique with the RNaseq kit (Qiagen) as previously described (28). RNA concentrations were obtained for each sample using a Nanophotometer spectrophotometer (MBI Lab Equipment). Samples were treated with DNase (gDNA wipeout buffer, Qiagen) to eliminate any potential DNA contamination. RNA was reverse transcribed using the Quantitect reverse transcription kit (Qiagen) as per the manufacturer’s protocol.

Histological analyses

Histological analyses were performed on hematoxylin and eosin stained cross-sections (10 μm) from frozen TA muscles of P2 and P5 Smm−/−;SMN2, and P2, P9 and P21 Smm−/− mice. The TA muscle was selected as it is spared from histological denervation in mouse models of SMA and therefore it would likely not be influenced by muscle denervation induced atrophy (29,30). Sections were stained with hematoxylin and eosin using a standard protocol, images taken with a Zeiss Axioplan2 microscope, and the centrally located nuclei were counted using ImageJ software (NIH). The centrally located nuclei data are presented...
relative to the total number of myofibers present in a given field of view. Images to assess central nucleation were taken at 20× for P5, P9, P21 and the TSA data, and at 40× for P2 data. The cross-sectional area of the TA muscle from Smn2B−/− mice treated with either DMSO or TSA was calculated by tracing the contour of myofibers using the tracing tool in ImageJ. A minimum of 200 myofibers were traced. Cross-sections from control and SMA model mice were collected from the same area of the TA muscle.

Quantitative polymerase chain reaction (QPCR)

QPCR was performed to assess the mRNA levels of myogenic transcription factors such as paired box protein 7 (Pax7), myoblast determination 1 (MyoD), myogenin and the muscle-specific regulatory factor 4 (MRF4; also known as Myf6) in skeletal muscles from control and mutant mice. Each QPCR was performed in technical triplicate using primers described in Supplementary Material, Table S1. Each QPCR reaction contained 50 ng of cDNA, 2× SyBR Green JumpStart Taq Ready-Mix for QPCR (Sigma-Aldrich), RNase/DNase-free water and appropriate primers (200 nm) in a final volume of 25 µl. Each reaction was heated at 94°C for 3 min followed by 40 cycles of denaturing at 94°C for 30 s, annealing (Supplementary Material, Table S1) for 30 s and elongation at 72°C for 30 s. To confirm amplicon specificity and size, a melting curve analysis was performed and the final QPCR products were migrated on a 2% agarose gel for each primer set. Two negative controls were included in every QPCR plate and consisted of water in lieu of cDNA and RNA free cDNA. QPCR results from each plate were generated from a standard curve with known amounts of cDNA. Quantified results were normalized to glyceraldehyde 3-phosphate dehydrogenase (GAPDH) transcript levels to control for loading.

PROTEIN ANALYSIS

Protein analysis

Protein concentrations were determined using the Bradford method. Immunoblot analysis was performed as previously described (31). Primary antibodies used were: GAPDH (Abcam), MHC (MF20), MRF4 (Santa Cruz), MyoD (BD Transduction Laboratories), myogenin (BD Transduction Laboratories), Pax7, Smn (BD Transduction Laboratories), myogenin (BD Transduction Laboratories), MHC (MF20), MRF4 (Santa Cruz), MyoD (BD Transduction Laboratories), and tubulin (for the differentiated myotube data) as a loading factor. Immunoblot data are expressed as ratios using GAPDH as a loading control.

STATISTICAL ANALYSES

Data are presented as the mean ± standard error of the mean. A Student’s t test was performed using Excel to compare the means. Significance was set at P < 0.05.

SUPPLEMENTARY MATERIAL

Supplementary Material is available at HMG online.

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CONFLICT OF INTEREST STATEMENT

None declared.

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REFERENCES


