A transgene carrying an A2G missense mutation in the SMN gene modulates phenotypic severity in mice with severe (type I) spinal muscular atrophy

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q spinal muscular atrophy (SMA) is a common autosomal recessive disorder in humans and the leading genetic cause of infantile death. Patients lack a functional survival of motor neurons (SMN1) gene, but carry one or more copies of the highly homologous SMN2 gene. A homozygous knockout of the single murine Smn gene is embryonic lethal. Here we report that in the absence of the SMN2 gene, a mutant SMN A2G transgene is unable to rescue the embryonic lethality. In its presence, the A2G transgene delays the onset of motor neuron loss, resulting in mice with mild SMA. We suggest that only in the presence of low levels of full-length SMN is the A2G transgene able to form partially functional higher order SMN complexes essential for its functions. Mild SMA mice exhibit motor neuron degeneration, muscle atrophy, and abnormal EMGs. Animals homozygous for the mutant transgene are less severely affected than heterozygotes. This demonstrates the importance of SMN levels in SMA even if the protein is expressed from a mutant allele. Our mild SMA mice will be useful in (a) determining the effect of missense mutations in vivo and in motor neurons and (b) testing potential therapies in SMA.

Introduction
Proximal spinal muscular atrophy (SMA)* is a common autosomal recessive neurodegenerative disease in humans characterized by loss of the spinal motor neurons and atrophy of the limb and trunk muscles (Crawford and Pardo, 1996; Melki, 1997). It occurs with a frequency of 1 in 10,000 individuals and is the most common genetic cause of infant mortality (Roberts et al., 1970). Based on the age at onset and severity of the disease phenotype, the proximal SMAs have been classified into type I (severe), type II (intermediate), and type III (mild) SMA (Munsat and Davies, 1992). All three forms of the disease are due to loss or mutation of the telomeric survival of motor neurons gene (SMN1) (Bussaglia et al., 1995; Lefebvre et al., 1995; Parsons et al., 1996; Hahnen et al., 1997; Talbot et al., 1997). Mutations in an almost identical copy gene, SMN2, do not cause disease. The critical difference between the two genes is a C to T transition in exon 7 of SMN2, which affects splicing of this exon (Lorson et al., 1999; Monani et al., 1999a). Thus, SMN1 produces a majority of the full-length SMN transcript, whereas SMN2 generates mostly an isoform lacking exon 7. The protein product of the Δ7 transcript is thought to be unstable and rapidly degraded (Lorson and Androphy, 2000). SMA patients who lack SMN1 but carry a varying number of copies of SMN2 presumably produce insufficient full-length SMN protein for motor neuron survival. The disease phenotype is...
modulated by SMN2 copy number, likely due to the low levels of full-length SMN produced by SMN2 (Campbell et al., 1997; McAndrew et al., 1997).

The 38-kD SMN protein is ubiquitously expressed (Coovert et al., 1997; Lefebvre et al., 1997), often localizing in dot-like structures termed gems. Gems overlap with, or are in close proximity to, coiled bodies (Liu and Dreyfuss, 1996; Young et al., 2000). SMN is thought to be important in snRNP biogenesis and mRNA splicing (Pellizzoni et al., 1998), but is most likely a multifunctional molecule (Fischer et al., 1997; Liu et al., 1997; Buhler et al., 1999; Strasswimmer et al., 1999; Charroux et al., 1999; Campbell et al., 2000; Gangwani et al., 2001; Jones et al., 2001; Pellizzoni et al., 2001a,b; Terns and Terns, 2001; Young et al., 2001). However, it is not clear which of SMN’s functions is critical specifically to motor neurons.

In keeping with its housekeeping functions, an Smn knockout in mice is embryonic lethal (Schrank et al., 1997). To create a viable animal model of SMA, the SMN2 gene was introduced into Smn−/− mice (Hsieh-Li et al., 2000; Monani et al., 2000). One to two–copy SMN2;Smn−/− mice exhibit a type I SMA phenotype. 8–16 copies of SMN2 completely ameliorate the disease phenotype. Inducing SMN2 to produce higher levels of SMN protein therefore seems an attractive option in treating SMA. A number of groups have reported molecules capable of inducing SMN2 to produce higher levels of SMN (Baron-Delage et al., 2000; Andreassi et al., 2001; Chang et al., 2001; Zhang et al., 2001). It is essential that these be tested in appropriate animal models before human clinical trials are undertaken. Although the existing animal models have been extremely important in furthering the understanding of the pathophysiology of the SMA disease process, it is clear that a more suitable animal model is needed to address the next generation of in vivo experiments. In this study, we show that an SMN2 missense mutation rescues the severe SMA phenotype in low copy SMN2;Smn−/− mice but is unable to rescue Smn−/− embryonic lethality in the absence of the SMN2 gene. Increased SMN protein in SMN2;SMN2;Smn−/− mice affects the timing of motor neuron loss and results in animals with a mild SMA phenotype. Mild SMA mice exhibit muscle atrophy, motor neuron degeneration, and abnormal electromyographs (EMGs). These characteristics, in particular the electromyographs, serve as easily assayed outcome measures in therapeutic strategies in SMA. Importantly, we also show that SMN2 is unable to efficiently self-assemble, a property required for the formation of “active” SMN complexes. We suggest that mutant oligomers are unstable and fail to bind components that are essential for one or more of SMN’s functions. This results in a rapid turnover of the protein, underlining the importance of some, albeit low levels of, full-length SMN in the SMN complex and provides insight into the mechanism involving functional complex formation.

Results

Generation of transgenic mice and genotype–phenotype analysis

We previously identified three unrelated SMA patients (two with type III SMA and one with type II SMA) carrying a single SMN2 allele and an SMN A2G missense mutation (Parsons et al., 1998). A cDNA carrying the A2G mutation under a 3.4-kb SMN promoter fragment (Monani et al., 1999b) (Fig. 1 A) was microinjected into fertilized mouse oocytes. Of the four founders obtained, the two transmitting lines, 2002 and 2023, were first analyzed for transgene copy number and then mated to low copy SMN2;Smn−/− mice (Monani et al., 2000). To assess the number of copies of the SMN2 allele in each of the lines, Southern blot analysis of tail DNA using probes that bound SMN2 and murine Smn, respectively, was performed. Relative to the single copy murine Smn gene, line 2002 was found to have 15 copies of the transgene whereas line 2023 carried 11 copies (Fig. 1 B). Double transgenic SMN A2G;SMN2;Smn−/− mice were interbred or crossed to SMN2;Smn−/− animals, resulting in mice carrying one or two copies of SMN2 and the mutant transgene but completely lacking mouse Smn (SMN2 A2G;SMN2;Smn−/−) (Fig. 1 C). Mice of this genotype from line 2002 were different from the severe type I SMA mice we have previously described. On Western blot analysis, this line was found not to express the A2G transgene (unpublished data), possibly due to a site-specific integration effect. However, SMN2;Smn−/− mice carrying the A2G transgene from line 2023 display all of the characteristics of type III SMA. Smn−/− animals with a single copy of SMN2 and heterozygous for the A2G transgene are 20–40% smaller (1.14 ± 0.06; n = 5) than their normal littermates (1.62 ± 0.18; n = 11) at birth and continue to remain so during development and into adulthood (Fig. 1, D and F). At 3 wk of age, these mice are less active than normal sibs. In addition, they begin to display signs of muscle weakness, as evidenced by a tendency to clasp the hind limbs when suspended by the tail (Fig. 1 E). SMN2;Smn−/− mice that are homozygous for the A2G transgene have a considerably milder phenotype and are indistinguishable from normal littermates often into adulthood. This is consistent with previous reports indicating a tight correlation between SMN2 copy number/protein levels and disease severity (Lefebvre et al., 1997; Coovert et al., 1997). Both heterozygous and homozygous A2G SMN2;Smn−/− mice breed, although the former are less efficient and live ≤1 yr. Mean survival of heterozygous A2G SMN2;Smn−/− mice is 227 d (n = 14) versus 5.16 d for type I SMA mice (n = 57) and 736 d for Smn−/− mice (n = 12) (see Fig. S1, available online at http://www.jcb.org/cgi/content/full/jcb.200208079/DC1). Toward the end of their lives, type III SMA mice heterozygous for the A2G transgene exhibit very little activity, short, shallow breathing, lose considerable weight, and fail to groom efficiently. In contrast, the oldest SMN2; Smn−/− mice homozygous for the A2G transgene are currently 15 mo of age, healthy, and the males continue to breed well.

To determine whether the A2G transgene is capable of rescuing Smn−/− embryonic lethality on its own, SMN A2G;Smn−/− intercrosses were set up. Out of 102 progeny mice genotyped, none were found to be Smn−/−. This suggests that the A2G mutant transgene is unable to rescue embryonic lethality. To determine when embryonic lethality occurs in SMN A2G;Smn−/− mice, E12 embryos (n = 60)
from SMN A2G;Smn+/− intercrosses were genotyped. None were found to be Smn−/−, indicating that death occurs before this stage in development. This is similar to Smn−/− and Smn+/− mice, which also die early in embryogenesis (Schrank et al., 1997; Hsieh-Li et al., 2000).

**Decreased self-association of mutant A2G SMN molecules**

SMN self-associates using domains encoded by exons 2b and 6 (Lorson et al., 1998; Young et al., 2001). We investigated the effect of the missense A2G mutation on self-association. A GST–SMN A2G fusion protein was immobilized on glutathione-linked agarose beads and then incubated with 35S-labeled SMN A2G protein. Bound fractions were washed extensively and resolved by SDS-PAGE. As controls, similar self-association studies were performed with full-length SMN and Δ7 SMN. Our results show that SMN A2G molecules self-associate with an efficiency between that of full-length SMN and Δ7 SMN (Fig. 2 A) as do other mild SMA mutations (Lorson et al., 1998). This is consistent with the mild SMA phenotype we see in patients carrying this mutation and our SMN A2G;SMN2;Smn+/−/+ mice. To determine the effect of the A2G mutation on the ability of the mutant protein to bind native full-length (FL) SMN and Sm proteins, GST–SMN and GST–SmN fusion proteins immobilized on agarose beads were incubated with labeled SMN A2G. Bound fractions were washed as described above. As a comparison, the ability of Δ7 SMN and FL-SMN each to bind to SmN and native SMN was assessed. As expected, SMN A2G binds FL-SMN with a higher affinity than does Δ7 SMN but with a lower affinity than does native SMN (Fig. 2 B). Interestingly, the ability of SMN A2G to bind the Sm protein SmN was greatly decreased even though the mutation does not lie in the Sm binding domain (Fig. 2 C).
Expression of the mutant SMN A2G transgene

To assess the expression of the SMN A2G transgene, RT-PCR studies (Fig. 3 A) on A2G animals lacking SMN2 and Western blot analyses on mild SMA animals (Figs. 3, B and C) were performed. Our data show that the transgene is expressed in all of the tissues examined. This is similar to the expression of the endogenous gene, suggesting that the 3.4-kb promoter fragment used here contains the necessary elements for ubiquitous expression. Western blot analysis performed on SMN A2G;SMN2; Smmn−/− animals shows that mild SMA mice express significantly higher SMN levels than do age-matched type I SMA mice, but not as much as normal littermates (Fig. 3 B). Furthermore, type III SMA animals homozygous for the A2G transgene express higher levels of the SMN protein than do heterozygous animals (Fig. 3 C). This is consistent with previous data showing that a tight correlation exists between SMN levels and phenotypic severity in SMA.

Figure 2. In vitro binding studies on SMN A2G. (A) Self-association studies between 35S-labeled SMN proteins and bound GST–SMN fusion proteins. (B) The interaction of SMN A2G, FL-SMN, and Δ7 SMN each with FL-SMN. (C) Binding of FL-SMN, SMN A2G, or Δ7 SMN (as indicated) with the Sm protein SmN. In all three studies, binding values were calculated as a % of 35S-labeled SMN A2G, FL-SMN, or Δ7 SMN.

Figure 3. Expression analysis of the mutant SMN A2G transgene in transgenic mice. (A) RT-PCR on RNA from indicated tissues of an SMN A2G;Smn−/−/− animal was performed as described in the Materials and methods. The β-actin gene was simultaneously amplified as a control. (B) Western blot analysis on 5-d-old type I SMA, type III SMA, and an Smmn−/− mouse was performed using the anti-SMN monoclonal antibody, MANSMA2. The blot was subsequently stripped and probed with an anti-β-actin antibody to control for loading amounts. Type I SMA mice produce very little SMN, which is visible only after longer exposures. (C) Western blot analysis on 3.5-mo-old type III SMA mice (heterozygous for the A2G transgene, Het.), type III SMA mice (homozygous for the A2G transgene, Hom.), and normal mice (Smmn−/−) using the anti-SMN monoclonal antibody, MANSMA2. β-actin or β-tubulin serve as loading controls.
Type III SMA mice exhibit muscle atrophy and partial restoration of gems in the spinal motor neurons

One of the most striking features of spinal muscular atrophy is the loss of the anterior horn cells (α motor neurons) of the spinal cord and a greatly reduced amount of SMN in these cells. We have previously shown that there is little or no staining of SMN in the motor neurons of type I SMA mice (Monani et al., 2000). To ascertain whether type III SMA mice express SMN in their spinal motor neurons, spinal cord sections from the lumbar and thoracic regions of 1-mo-old type III SMA mice, with a single copy of SMN2 and heterozygous for the A2G transgene, and age-matched Smn−/− controls were immunocytochemically stained (Fig. 4, A and B). Based on the cytoplasmic staining and presence of gems in the spinal cord of diseased animals, it is clear that SMN is restored in motor neurons (Fig. 4 A). To quantitate the number of gems in the motor neurons of normal (n = 2) and type III SMA mice (n = 3), 10 different fields, under 600× magnification, from spinal cord sections of each mouse were selected and the gems counted. An average of 4.5 nuclear gems were counted per field (~60 nuclei) in type III SMA mice versus 9.8 nuclear gems in the age-matched controls. Thus it is clear that although SMN is easily detected in the spinal motor neurons of type III SMA mice, it is only a partial restoration.

A second characteristic feature of SMA is muscular atrophy due to denervation. We examined the gastrocnemius, quadriceps, and intercostal muscles of type III SMA mice from the above study to look for atrophy. Transverse sections of the gastrocnemius muscle showed numerous angulated and atrophic fibers (Fig. 4 C) compared with uniform-sized fibers in the age-matched controls (Fig. 4 D). This was less pronounced in the quadriceps and intercostal muscles of these animals (unpublished data), but is consistent with findings in some human type III SMA patients (Dubowitz, 1995).

Electrophysiological studies and evidence of axonal sprouting in type III SMA mice

To further characterize the muscle weakness in our type III SMA mice, EMG recordings were made on 4–6-mo-old SMN2;Smn−/− animals heterozygous for the mutant SMN A2G transgene. Recordings were made on resting muscle as it is difficult to obtain controlled, voluntary muscle contraction in mice. Normal muscle is electrically silent at rest and no spontaneous activity is detected after cessation of movement of the recording needle. In both of the type III (15SMN A2G;SMN2;Smn−/−) animals we tested, we found abnormal spontaneous activity of single muscle fibers (fibrillation potentials) and of motor units (fasciculation potentials) accompanied occasionally by biphasic positive sharp waves (Fig. 5, A and B). These observations made on multiple pelvic (cranial tibial, vastus lateralis, and gastrocnemius; see Fig. S2, available online at http://www.jcb.org/cgi/content/full/jcb.200208079/DC1) and thoracic (suprascapular) muscles are a clear indication of denervation and provide a simple diagnosis of this process, as previously demonstrated in human patients (Dubowitz, 1995). We did not see abnormal electrical activity in age-matched type III SMA animals homozygous for the A2G transgene, indicating that increased levels of SMN from the A2G transgene correct this abnormality.
This is consistent with data from some very mildly affected type III SMA patients (Hausmanowa-Petrusewicz and Karwanska, 1986). To assess the nature of the muscle weakness in mild SMA mice, we analyzed evoked compound action potentials and motor nerve conduction velocities (MNCVs) of the tibial nerve (Fig. 5 C). Although nerve conduction velocity tests on type III SMA (30.1 ± 5.6; n = 4) mice did not significantly change, axonal sprouting in the (D) gastrocnemius and (E) triceps of type III SMA mice is a further sign of denervation. The former is an example of nodal sprouting whereas the latter depicts terminal sprouts (red arrows). Arrow in white indicates main axonal branch. Motor axons are silver stained in black while neuromuscular junctions stain blue. Normal gastrocnemius (F) shows at least three different motor axons, each innervating a separate muscle fiber (running diagonally from lower left to upper right; magnification 400×). Graphical representation (G) of the extent of sprouting (terminal and nodal) in type III SMA mice and unaffected littermates. Data are given as mean ± SD.

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To compensate for chronic denervation in motor neuron diseases, the surviving axons often sprout and reinnervate the denervated fibers. In rat soleus muscle, cross innervation by a foreign nerve at a site distant from the original end plate often preserves the old end plate. The original end plate may persist as long as 4 mo after the fiber has lost its nerve connection (Frank et al., 1976). We observed an increased number of neuromuscular junctions in the gastrocnemius of type III SMA mice (90; n = 3) compared with age-matched controls (51; n = 3). To investigate whether axonal sprouting might account for this, 50-μm sections of freshly frozen gastrocnemius, triceps, and intercostal muscle were dual stained for axons and acetylcholine-esterase activity. We show that sprouting does indeed occur both in type III SMA mice (n = 3) heterozygous for the A2G transgene as well as type III SMA mice homozygous for the A2G transgene (Fig. 5, D–G). Sprouts were nodal and were also seen to emerge from the neuromuscular junction (terminal sprouts). This was not observed in Smn−/− (n = 2) or eight-copy SMN2;Smn−/− mice (unpublished data) and is consistent with data from mild SMA patients (Vogt and Nix, 1997). To determine the extent of sprouting, synapses in the gastrocnemius and triceps muscles from mild SMA mice heterozygous for the A2G transgene (n = 3) and Smn−/− littermates (n = 2) were scored for the presence or absence of sprouts. Our data show that there is a significant increase in the number of sprouts in both gastrocnemius (SMA, 22 ± 4%; normal, 7 ± 2.5%) and triceps (SMA, 21 ± 3%; normal, 7.2 ± 3%) muscles of mild SMA mice (Fig. 5 G).
Spinal motor neurons 3,144 neurons in the former. In the lumbar spinal cord, SMA mice previously difference between the SMA mice and age-matched morphology and numbers of the cells determined. The most obvious difference between the SMA mice and age-matched controls is a significant decrease in the numbers of motor neurons in the former. In the lumbar spinal cord, SMA mice have 29% fewer motor neurons than age-matched Smn−/− controls, while in the facial nucleus there is a ~19% loss of motor neurons (Table I; Fig. 6, A and B). Previously, we showed a significant loss of motor neurons in the spinal cord and brain stem of 5-d-old severe SMA mice (Monani et al., 2000). To determine whether motor neuron loss occurs this early in type III SMA mice, 5-d-old SMN2;Smn−/− animals heterozygous for the A2G transgene were killed and motor neuron cell bodies in the facial nucleus counted. We found no evidence of motor neuron loss at this age in type III SMA mice (unpublished data). This is consistent with our previous finding that motor neuron loss is a late event in SMA.

To further examine motor neuron degeneration, we also conducted ventral root counts on our type III SMA mice. Mice perfused with 4% paraformaldehyde, 1% glutaraldehyde were used to isolate the ventral roots from the L1–L5 lumbar spinal cord region. Semi-thin sections were cut, stained with toluidene blue (Fig. 6, C and D), and at least four different fields examined to quantitatively determine the number of motor axons in the roots of diseased mice and an age-matched control. Two striking differences were observed. First, type III SMA mice have fewer myelinated axons (Table II). The loss in motor axons correlates with the loss of motor neuron cell bodies in the spinal cord. Second, many of the remaining axons in the diseased mice are shriveled and exhibit signs of Wallerian degeneration (Fig. 6 D).

Discussion

Mice lacking murine Smn but carrying one to two copies of human SMN2 provide a suitable animal model of type I spinal muscular atrophy (Hsieh-Li et al., 2000; Monani et al., 2000). In this study, we have introduced a transgene carrying a missense mutation in exon 1 of the SMN gene into the severe SMA genetic background. SMN2;Smn−/− mice that are heterozygous for the mutant transgene exhibit many of the clinical and pathological characteristics of type III (mild) SMA. These mice suffer from motor neuron degeneration and its associated effects. They include evidence of motor axon degeneration, loss and sprouting, muscle atrophy, and abnormal EMG patterns. Other obvious clinical features of SMA in our mice include muscle weakness, reduced activity, and a decreased life span. In keeping with numerous previous studies showing a tight correlation between levels of SMN2 copy number/SMN protein and disease severity, SMN2;Smn−/− mice homoygous for the mutant transgene exhibit a very mild disease phenotype. Indeed, there are few overt signs of muscle weakness in 6-mo-old animals and a relatively prolonged lifespan (~15 mo) compared with heterozygous SMN2 A2G transgenic mice. We have previously shown that type I SMA mice lose 35–40% of their motor neurons by the time they die, while Jablonka et al. (2000) showed up to 50% spinal motor neuron loss in 12-mo-old Smn−/− animals. Yet type I SMA mice rarely live beyond 6 d of age, whereas Smn−/− animals live completely normal lives and exhibit no clinical signs of SMA. The implications are, first, that a 50% motor neuron loss is completely compatible with life and, second, that the surviving motor neurons in type I SMA mice are too sick to function normally thus resulting in early death. Motor neuron loss in type III SMA mice occurs significantly earlier than in Smn−/− heterozygotes but not as early as in type I SMA mice. The widely varying phenotypes but similar numbers of motor neurons lost in severe, mild, and Smn−/− mice imply that the timing of cell loss, rather than the actual numbers lost, is important. Disease symptoms in type III SMA mice, as evidenced by muscle weakness, occur as early as 1 mo of age. If, as we suspect, onset of the disease correlates with motor neuron dysfunction, we would expect to see electrophysiological abnormalities at this age. Interestingly, recent similar studies involving motor unit number estimation (MUNE) in pre- and post-symptomatic human patients revealed that a large number of motor neurons are present before the onset of the phenotype and that there is a rapid decline in the numbers of motor units with disease progression (Bromberg and Swoboda, 2002). This is similar to studies involving morphometric counts in severe SMA mice, which show a correlation between motor neuron loss and onset of disease symptoms. As EMG studies can be performed on mild SMA mice, it will be possible to correlate motor neuron counts with MUNE/EMG studies in order to determine if neuronal loss in SMA occurs as a dying back process, as has been found in another mouse model of motor neuron disease (Holtmann et al., 1999).

It is intriguing to consider how the A2G mutation on an SMN2;Smn−/− background results in a mild SMA phenotype. The mutation is the most 5′ one reported so far. It is neither in the oligomerization domain in exon 6 nor in exon

Table I. Number of facial and spinal motor neurons in the brain stem and lumbar (L1–L6) spinal cord, respectively, of 3.5-mo-old SMN2; Smn−/− type III SMA mice heterozygous for the A2G transgene and age-matched controls

<table>
<thead>
<tr>
<th>Type of motor neurons</th>
<th>Type III SMA</th>
<th>Normal</th>
<th>Reduction</th>
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<tr>
<td>Facial nucleus</td>
<td>2,994 ± 94 (n = 4)</td>
<td>3,695 ± 171 (n = 2)</td>
<td>−19% (P &lt; 0.05)</td>
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<tr>
<td>Spinal motor neurons</td>
<td>3,144 ± 201 (n = 4)</td>
<td>4,421 ± 76 (n = 2)</td>
<td>−29% (P &lt; 0.05)</td>
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Table II. Number of motor axons in the lumbar ventral roots of type III SMA mice and normals

<table>
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<th>Age (mo)</th>
<th>Type III SMA</th>
<th>Normal</th>
<th>Reduction</th>
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<tr>
<td>5</td>
<td>599 ± 61 (n = 4)</td>
<td>801 ± 90 (n = 5)</td>
<td>−25% (P &lt; 0.05)</td>
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2b. It is not in the Sm protein binding domain nor does it affect SIP-1 binding (unpublished data). Yet, we have shown that the A2G mutation does disrupt self-association and affects SmN binding presumably by disrupting the formation of SMN oligomers. A to G mutations have been shown to profoundly affect α-helices (Lyu et al., 1990; Chakrabartty et al., 1991). It is not unlikely that the mutation disrupts the three-dimensional structure of the protein enough to affect

Figure 6. **Motor neuron cell bodies and ventral roots in mild SMA mice.** Motor neuron degeneration in the (A) facial nucleus and (C) lumbar spinal cord of a 3.5-mo-old type III SMA mouse showing fewer cells with intact nuclei compared with the normal Smn+/− control in B and D, respectively. An examination of the motor axons in the ventral roots of (E) type III SMA mice by toluidine blue staining shows a myelin ovoid and numerous axons undergoing Wallerian degeneration (arrows). F represents an age-matched normal control (magnification 600×).
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The oligomerization domains in exon 2b and/or exon 6 as well as the Sm binding domain. Although the A2G protein retains some level of self-association activity, it is possible this deficiency results in that mutant’s inability to form higher order complexes necessary for SMN function and interactions with protein partners. This could explain why SMN A2G does not rescue \(Smn^{-/-}\) embryonic lethality. If, however, full-length SMN serves as a scaffold, then low levels of the protein might promote the formation of higher order FL-SMN:SMN A2G oligomers with an enhanced ability to bind other interacting proteins such as SmN. Our data show that SMN A2G binds with a higher affinity to FL-SMN than does \(\Delta 7\) SMN. FL-SMN:SMN A2G complexes would therefore be more stable than FL-SMN:\(\Delta 7\) SMN ones. Furthermore, it has been shown that protein levels in patients with missense mutations correlate with the disease phenotype (Lefebvre et al., 1997). These data and our observations lead us to a plausible molecular model of SMA (Fig. 7) in which SMN forms a number of complexes with different partners. These partners compete for the same sites on SMN, binding being determined by their relative affinities for SMN. In the presence of low levels of full-length SMN, low affinity binding partners are out-competed by high affinity proteins. It is possible that the low affinity binding partners are selectively found in motor neurons and are unable to form functional complexes in SMA patients due to the low SMN levels. Loss or disruption of the low affinity complex in motor neurons would result in the degeneration of these, but not other, tissues. Our model is consistent with the observation of increased SMN levels and a mild phenotype in mice carrying the A2G missense mutation on a severe SMA genetic background.

Despite recent advances in elucidating the functions of SMN, including studies implicating SMN to be important in neural growth cones and in RNA editing/transport in motor axons (Fan and Simard, 2002; Rossol et al., 2002), the selective loss of \(\alpha\) motor neurons in SMA remains far from clear. The functions attributed to SMN would seem to be important in all cells, yet it is the motor neuron that is most profoundly affected. The presence of a low affinity SMN interacting partner in these but not other cells may explain the specificity of the disease. A majority of the mutations in SMA affect either oligomerization, binding of one of SMN’s interacting partners, or both. This has been assessed either in vitro or in cell culture but not in motor neurons. It is unclear whether the same function(s) is disrupted in these cells in a diseased animal. Our type III SMA mice may allow us to address this by providing us with the ability to create motor neuron cell lines and study the effect of the A2G missense mutation on the SMN macromolecular complex. What is clear is that the A2G missense mutation is unable to rescue embryonic lethality in \(Smn^{-/-}\) mice. Because this is a mild mutation, we would expect severe missense mutations to have the same effect. This is in contrast to a study by Wang and Dreyfuss (2001) in which they report the ability of a number of missense mutations to rescue lethality in a chicken cell line. Two ways of explaining our discordant results are, first, leaky expression of very low levels of full-

![A molecular model of SMA that may explain the motor neuron specificity of the disease.](http://rupress.org/jcb/article-pdf/160/1/41/1307097/jcb160141.pdf)
length SMN in the chicken cell line, and, second, a critical requirement for intact SMN during development in a whole animal, but not in a cell line, which is disrupted in its absence, leading to embryonic lethality. A number of groups have reported compounds capable of increasing SMN from SMN/2. It will be important to assess these in an appropriate animal model of SMA. The mild SMA mouse we have generated here has certain distinct advantages over previously reported animal models. It has a clear and consistent SMA phenotype but is more robust than severe SMA mice and therefore amenable to drug administration protocols. We have shown that denervation in mild SMA mice may be measured electrophysiologically. Additionally, the abnormal EMGs indicative of denervation correlate with SMN protein levels. Standard EMG analysis could be complemented with MUNE studies, which would serve to further refine ways of measuring the outcome of any drug treatment studies. It is therefore clear that our mice are an important tool in (a) ensuring the safety and efficacy of drugs/molecules that we and others are currently isolating in high-throughput screens and (2) the evaluation of gene therapy procedures for SMA.

**Materials and methods**

**Generation of transgenic mice and breeding strategy**

A forward primer, 5'-CGGACTCATGGATTGAGCCGGG-3', in SMN exon 1 containing an engineered BamHI site and the C to G transition, which results in the A2G mutation, and a reverse primer in exon 8, 5'-CCGATTACATGCCAGACTTGCACATCCAC-3', containing an EcoRI site were used to amplify SMN by RT-PCR. The ~1.3-kb product was digested with BamHI and EcoRI and cloned into the pCDNA3 (Invitrogen) vector. Separately, a ~1.5-kb product of the SMN promoter fragment was cloned into the pEGFP (CLONTECH Laboratories, Inc.) vector and then excised out using KpnI and BamHI. This fragment was directionally ligated to the SMN exon containing an engineered BamHI site and the C to G transition. The 4.9-kb promoter–SMN transgene was then excised out with KpnI and BamHI and injected into fertilized FVB mouse oocytes. Potential founders were screened by Southern analysis using an SMN probe. Samples were then digested with KpnI and BamHI and injected into fertilized FVB mouse oocytes. Potency founders were screened by Southern analysis using an exon 6–8 SMN cDNA probe or by PCR using the following primers: 4.5F, 5'-ACTGGGACCGAAGGCACTG-3', and 6R, 5'-GCCAATGATGAGCAGCATCATG-3'. Founders were bred to SMN+/− mice we have previously generated. SMN A2G;SMN+/− animals were then intercrossed or backcrossed with SMN2;SMN+/− mice, resulting in SMN A2G;SMN2;SMN+/− animals.

**In vitro binding assays**

SMN A2G, FL-SMN, and Δ7 SMN cDNAs were subcloned into the vector pGEX-3X (Amersham Biosciences). GST fusion proteins were prepared and purified using glutathione-agarose beads as previously described (Lorson et al., 1998). To prepare 35S-labeled SMN proteins, the T7 transcription/translation kit (Promega) was used. The protocol was essentially the same as that described by Lorson et al. (1998) except that densitometry was performed using a Phosphorimage (Molecular Dynamics, Inc.).

**RT-PCR, Southern, and Western analysis**

To determine the expression of the mutant A2G transgene, SMN A2G;SMN+/− carrying the transgene but no SMN2 were killed by cervical dislocation and polyA+ RNA was isolated using the QuickPrep Micro mRNA purification kit (Amersham Biosciences) according to the manufacturer’s recommendations. After treating the RNA with DNase I to get rid of contaminating genomic DNA, ~100 ng was reverse transcribed and amplified using the following human SMN-specific primers in exons 1 and 4, respectively: Ex1F, 5'-GGGGCGATGAGTGGCCGGC-3', and Ex4R, 5'-TCAGAGATTCTGTCATGATGG-3'. Native murine Smn and the knockout allele were followed by Southern blot analysis after BamHI digestion of tail DNA using a probe in Smn intron 1. The probe was radioactively labeled and hybridized to the filter containing the DNA according to standard methods. The filter was washed at high stringency and then exposed to Hyperfilm MP (Amersham Biosciences) with an intensifying screen. Copy number of the SMN A2G transgene was determined by Southern blot analysis of DNA from SMN A2G;SMN A2G;SMN+/− animals. An SMN exon 6–8 cDNA fragment and a murine Smn intron 1 probe of approximately equal length and GC content were radioactively labeled and simultaneously hybridized to the blot. The blot was washed and exposed to film as described above. Intensities of bands corresponding to the transgene were then determined using a Shimadzu 9000 CS scanner. Copy number was determined by comparing the intensities of these bands to those of the single-copy murine Smn gene in each animal. For Western blot analysis, 100 μg of tissue from 5-d-old mice was dissolved in blending buffer (10% SDS, 62.5 mM Tris, pH 6.8, 5 mM EDTA). 25–50 μg of protein was mixed with an equal volume of sample buffer (62.5 mM Tris, pH 6.8, 10% glycerol, 10% 2 ME, 0.4 mg bromophenol blue) and electrophoresed on a 12.5% polyacrylamide gel. Samples were transferred to Immobilon P (Millipore) as previously described (Cockett et al., 1997). The blot was blocked in 5% milk powder, 0.5% BSA in TBS-Tween for 2 h, and then incubated for 1 h with anti-SMN primary antibody (MANSMA2). Bound primary antibody was detected by HRP-conjugated secondary antibody followed by chemiluminescence (Amersham Biosciences). The blots were then stripped and reprobed with a β-actin antibody to control for loading amounts.

**Histology and immunocytochemistry**

For hematoxylin-eosin stains and spinal cord immunocytochemistry, adult type III SMA mice and normal controls were killed by CO2 gas, transcardially perfused briefly with cold 1X PBS, and the muscle and spinal cord tissue dissected out, mounted on Kodak cryostat blocks, and flash frozen in liquid nitrogen-cooled isopentane. 12–15 μm thick coronal sections were cut, mounted on Superfrost (Fisher Scientific) slides, and then air dried before processing. Sections were fixed in 100% alcohol (30 s), rinsed in tap water, and stained in hematoxylin (Sigma-Aldrich) for 30 s followed by a second rinse in tap water. They were then stained in eosin (Sigma-Aldrich) for 20 s, rinsed in tap water, dehydrated in alcohol, and cleared in xylene before mounting in Permount (Sigma-Aldrich) for light microscopy. Immunocytochemistry on spinal cord sections was essentially performed as described previously (Monani et al., 2000). For motor neuron studies and ventral root counts, mice were transcardially perfused with 1X PBS followed by 4% paraformaldehyde, 1% glutaraldehyde. Ventral roots, lumbar spinal cord, and the brain stem were post-fixed for 24 h in the same solution. The brain stem and spinal cord were then embedded in paraffin according to conventional procedures. Serial sections (6 μm) were prepared with a rotary microtome (American Optical Instruments) were mounted on glass slides and Nissl’s stained as previously described (Sendtner et al., 1990). Ventral roots were post-fixed in 1% osmium tetroxide (1 h), rinsed in 0.1 M phosphate buffer (pH 7.3), and then dehydrated. They were then embedded in 2% osmium tetroxide and 0.5% uranyl acetate. The 500-μm sections were cut on a Reichert Ultracut E microtome. Sections were stained with toluidine blue and visualized by light microscopy. To look for axonal sprouting in type III SMA mice, animals were killed by cervical dislocation and the intercostals, gastrocnemius, and triceps muscles were dissected out. Muscle tissue was immersed in 3% sodium EDTA for 20 s, mounted on wooden blocks, and flash frozen in liquid nitrogen-cooled isopentane. 50-μm thick longitudinal sections were cut in a cryostat and placed on Superfrost (Fisher Scientific) slides. A drop of 3% sodium EDTA was immediately placed on the sections to prevent muscle contracture and the sections were placed to allow dry. Cholinesterase and axonal staining were performed as described previously (Pestronk and Drachman, 1978), except that sections were stained in a 10% rather than 20% silver nitrate solution for 10 min. We found this reduces the extent of muscle fiber shrinkage and separation and better preserves the integrity of intramuscular nerves. To determine the extent of sprouting, synapses in ten 50-μm thick sections from the gastrocnemius (medial and lateral parts) and triceps were examined. The 500-μm portion included the middle of the muscle and sections on either side. Synapses were systematically scored for those with or without sprouts. Terminal and nodal sprouts were combined and expressed as a percentage of the total readable synapses. Approximately 400 synapses in each muscle were scored.

**Electrophysiological studies**

4–6-mo-old mice were anesthetized with ketamine (60 mg/kg) and xylazine (3.5 mg/kg). They were main-
cles, cervical epaxial muscles, and remaining epaxial muscles. The minimum criteria used to define the presence of spontaneous activity was the persistence of an abnormal waveform (>3 s) after complete cessation of needle movement that was reproducible with redirection of the EMG needle. MNCV recordings of the tibial nerve were performed with an Evoked Potential Measuring System. Subdermal stimulating electrodes (10-mm platinum-safelaid steel insulated electrodes) were placed at the sciatic notch (proximal stimulation site) and the head of the fibula (distal stimulation site) for the sciatic nerve (upper tibial) evaluation. The distal portion of the tibial nerve was evaluated by placing subdermal stimulating electrodes at the head of the fibula (proximal stimulation site) and the ankle (distal stimulation site). Percutaneous intramuscular recording and reference electrodes (26 gauge, 40 × 0.45-mm monopolar needles; Dantec Neurosupplies) were placed on the extensor digitorum brevis muscle of the lateral toe. A ground subcutaneous electrode was placed over the ankle. Stimulation was performed with a single square wave pulse of 0.2-ns duration at 1 Hz with a current of 10–15 mA. Reading parameters for the M wave are an analysis time of 10 ms, sensitivity of 10 mV, and band filter of 50–3,000 Hz. Motor nerve conduction was determined by the formula Velocity (m/s) = Distance/time. Distance was measured using a flexible tape between the cathodes of each stimulation site.

Online supplemental material
The supplemental material (Figs. S1 and S2) is available online at http://www.jcb.org/cgi/content/full/jcb.200208079/D1C. Fig. S1 shows survival curves for mild SMA mice, and Fig. S2 shows EMG results in the muscles indicated.

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References
of the human centromeric and telomeric survival motor neuron genes (SMN2 and SMN1).


