Modeling Spinal Muscular Atrophy in Drosophila

The Harvard community has made this article openly available. Please share how this access benefits you. Your story matters

<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Published Version</td>
<td>doi://10.1371/journal.pone.0003209</td>
</tr>
<tr>
<td>Citable link</td>
<td><a href="http://nrs.harvard.edu/urn-3:HUL.InstRepos:10235312">http://nrs.harvard.edu/urn-3:HUL.InstRepos:10235312</a></td>
</tr>
<tr>
<td>Terms of Use</td>
<td>This article was downloaded from Harvard University’s DASH repository, and is made available under the terms and conditions applicable to Other Posted Material, as set forth at <a href="http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA">http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA</a></td>
</tr>
</tbody>
</table>
Modeling Spinal Muscular Atrophy in Drosophila

Howard Chia-Hao Chang1, Douglas N. Dimlich1, Takakazu Yokokura1, Ashim Mukherjee2, Mark W. Kankel2, Anindya Sen1, Vasanthi Sridhar1, Tudor A. Fulga1, Anne C. Hart3, David Van Vactor1, Spyros Artavanis-Tsakonas1,4*

1 Department of Cell Biology, Harvard Medical School, Boston, Massachusetts, United States of America, 2 Department of Molecular and Human Genetics, Banaras Hindu University, Varanasi, India, 3 Massachusetts General Hospital, Cancer Center and Department of Pathology, Harvard Medical School, Boston, Massachusetts, United States of America, 4 Collège de France, Paris, France

Abstract

Spinal Muscular Atrophy (SMA), a recessive hereditary neurodegenerative disease in humans, has been linked to mutations in the survival motor neuron (SMN) gene. SMA patients display early onset lethality coupled with motor neuron loss and skeletal muscle atrophy. We used Drosophila, which encodes a single SMN ortholog, survival motor neuron (Snm), to model SMA, since reduction of Smn function leads to defects that mimic the SMA pathology in humans. Here we show that a normal neuromuscular junction (NMJ) structure depends on SMN expression and that SMN concentrates in the postsynaptic NMJ regions. We conducted a screen for genetic modifiers of an smn phenotype using the Exelixis collection of transposon-induced mutations, which affects approximately 50% of the Drosophila genome. This screen resulted in the recovery of 27 modifiers, thereby expanding the genetic circuitry of Smn to include several genes not previously known to be associated with this locus. Among the identified modifiers was wishful thinking (wit), a type II BMP receptor, which was shown to alter the Smn NMJ phenotype. Further characterization of two additional members of the BMP signaling pathway, Mothers against dpp (Mad) and Daughters against dpp (Dad), also modify the Smn NMJ phenotype. The NMJ defects caused by loss of Smn function can be ameliorated by increasing BMP signals, suggesting that increased BMP activity in SMA patients may help to alleviate symptoms of the disease. These results confirm that our genetic approach is likely to identify bona fide modulators of SMN activity, especially regarding its role at the neuromuscular junction, and as a consequence, may identify putative SMA therapeutic targets.


Editor: Alfred Lewin, University of Florida, United States of America

Received June 11, 2008; Accepted August 18, 2008; Published September 15, 2008

Copyright: © 2008 Chang et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Funding: SMA foundation, NIH

Competing Interests: The authors have declared that no competing interests exist.

* E-mail: artavanis@hms.harvard.edu

† These authors contributed equally to this work.

Introduction

Spinal Muscular Atrophy (SMA) is the second most common autosomal recessive genetic disease in humans and is the leading cause of genetically linked infant mortality, with an incidence rate of approximately 1 in 6000 births [1,2,3]. Clinical manifestation of SMA shows degeneration of spinal cord motor neurons and muscle atrophy [4]. SMA has also been linked to two nearly identical genes located on chromosome 5, survival motor neuron 1 (SMN1) and survival motor neuron 2 (SMN2) [5]. SMN2 differs from SMN1 in that only 10% of SMN2 transcripts produce functional Smn protein (SMN) due to a mutation that results in its aberrant splicing [6,7,8]. Elegant biochemical studies established the importance of the SMN protein in a ubiquitous, multimeric complex involved in the assembly of spliceosomal small nuclear ribonucleoproteins (snRNPs) [9,10,11,12,13,14]. Despite its seemingly fundamental and indispensable role in cellular metabolism, reduction of SMN leads to a specific neurodegenerative profile associated with this disease [1,15,16,17,18]. Though several recent studies indicate that SMN influences motor neuron axonal morphology [19,20], it remains unclear whether SMN has a specific neuromuscular junction (NMJ) function, and whether the functional requirement for SMN activity is increased at the NMJ than elsewhere in the organism.

SMA results from loss of SMN1 function [6,21], however, the clinical severity of the disease correlates with SMN2 copy number, which varies between individuals [22]. As the small amount of functional SMN2 protein produced by each copy is capable of partially compensating for the loss of the SMN1 gene function, higher copy numbers of SMN2 result in generally milder forms of SMA. Given that the severity of SMA depends on the levels of functional SMN, genetic modifiers capable of altering SMN cellular activity may define useful therapeutic targets. This reasoning prompted us to explore the genetic circuitry capable of affecting SMN activity in Drosophila, an experimental model amenable to sophisticated genetic manipulations, to investigate the role of SMN in this system.

The Drosophila genome harbors a single copy of the Smn gene, which encodes a highly conserved homologue of SMN. The Smn loss of function allele, Smn73Ao, results in recessive larval lethality and, importantly, neuromuscular junction abnormalities [15,18,23]. In this study, we characterized additional Smn alleles and demonstrate that they also display NMJ defects. To analyze tissue-specific requirements of SMN, we used RNA interference (RNAi) to create a series of loss of function Smn alleles, whose
phenotypes mimic the dosage dependent nature of SMA pathology. By using muscle (mesoderm) and neuronal drivers to direct expression of the Smn RNAi constructs, we determined that Smn function is required in both tissues, though there appears to be a higher sensitivity to the loss of Smn function in the muscle.

To identify enhancers and suppressors of Smn activity and the genetic circuitry of Smn, we carried out a genetic screen for modifiers of the Smn73Ao allele using the Exelixis collection of insertional mutations, which affects approximately 50% of the Drosophila genome [24,25,26]. Of the 17 enhancers and 10 suppressors uncovered by the screen, a significant subset was shown to be capable of affecting Smn-related NMJ phenotypes, validating our approach. Amongst these Smn modifiers was wishful thinking (wft), which encodes a type II BMP receptor [27,28]. Further experiments defined genetic interactions between Smn and other members of the BMP signaling pathway. We also demonstrated that modulation of BMP signaling rescues Smn-related NMJ phenotypes, further validating this genetic approach as a means to identify novel targets of Smn function. Moreover, it seems likely that some of the novel targets may provide potential therapeutic value.

Results
SMN concentrates in the post-synaptic regions at the NMJ
The dichotomy between the ubiquitous housekeeping function of Smn and the very specific neuromuscular SMA phenotype raises the question whether Smn functions differently at the neuromuscular junction (NMJ) than in other tissue types. Specifically, whether Smn has a differential expression pattern in neurons and muscle and whether Smn concentrates to any particular cellular compartments at the NMJ remain open questions.

To determine in which tissue(s) Smn is expressed in Drosophila, we raised antibodies against full-length Drosophila SMN (See Materials and Methods) and monitored its expression pattern particularly at the NMJ. In Western blots performed on lysates derived from S2 cells, 3rd instar larvae and wild-type adult heads the antibody recognizes a single ~28 kDa band [18], corresponding to the predicted molecular weight of Drosophila SMN (Figure S1 and data not shown). Moreover, when a FLAG-tagged Smn transgenic construct (UAS-FLAG-Smn) was expressed under the control of the vestigialGAL4 driver, SMN and FLAG staining overlapped at the dorsal-ventral (DV) boundary of 3rd instar larval wing discs. In addition, vestigialGAL4-directed expression of an inducible RNAi allele of Smn (see below) abolished the Smn staining pattern along the DV boundary of the larval wing disc (Figure S1). Together, these results indicate the specificity of the antibody we raised against SMN.

Using this antibody we probed SMN expression at the NMJ and found antigens to be clearly concentrated at the post-synaptic regions in the muscle, co-localizing with the post-synaptic marker Discs Large (DLG) (Figure 1A–D) [29]. Under these conditions, we did not detect antigens in the pre-synaptic region of the motor neuron terminal (as defined by horseradish peroxidase (HRP) staining) at the NMJ (Figure 1A–D). SMN staining was also observed within muscle fibers and at discrete foci in muscle nuclei (Figure 1C and E), which presumably reflect SMN localization in Cajal bodies (gems) as demonstrated for mammalian cells [9], and in Drosophila ovarian nurse cells and oocytes [30]. This post-synaptic NMJ expression pattern of SMN is abolished by muscle-specific Smn RNAi knockdown, again demonstrating the specificity of the anti-SMN antibodies (Figure S2). Consistent with its general role in snRNP assembly, SMN was detected in all tissues examined, including muscle (Figure 1A–D) and neurons (Figure 1F). However, at the Drosophila NMJ, SMN is concentrated at the post-synaptic regions in the muscle.

Mutations in Smn compromise viability
Previous studies determined that loss of Smn function results in larval lethality [15,18]. We examined two additional Smn alleles found within the Exelixis collection, Smn73Ao and Smn73Ao/Df(3L)X73Ao [25,26]. Sequence analysis of both strains indicates each allele harbors a transposon insertion within the Smn coding region (at amino acids 193 for Smn73Ao/Df(3L)X73Ao and K136 for Smn73Ao, see Figure 2A) that is predicted to introduce a premature stop codon. (Figure 2A). Unlike the Smn73Ao allele [15,18], which is 100% lethal in homo- and hemizygous (Smn73Ao/Df(Smnn)) backgrounds (Figure 2B), the Smn73Ao allele produces a small percentage of escapers (3.3%) when mutant larvae are isolated and cultured at low density. On the other hand, Smn73Ao/Df(3L)Smnn alleles is semi-viable (67.7%) (Figure 2B), indicating that the Smn73Ao and Smn73Ao/Df(3L)Smnn alleles are not null mutations as previously suggested [18]. By examining the viability of various Smn allelic combinations (Figure 2B), we determined that Smn73Ao is weakly hypomorphic as it retains some degree of viability in all cases tested, while Smn73Ao/Df(3L)Smnn appears to act as a strong loss-of-function allele since it fails to complement both Smn73Ao and a small deficiency that uncovers Smn, Df(3L)Smnn (Figure 2B). Ubiquitous (tubulinGAL4, actinGAL4) expression of UAS-FLAG-Smn rescued Smn73Ao lethality, demonstrating the lethality was associated with a loss of Smn activity. This is consistent with earlier studies showing ectopic SMN expressed under the control of a ubiquitous driver (tubulinGAL4) rescued Smn73Ao lethality [15].

Constructing RNAi-based hypomorphic Smn alleles
Since the clinical severity of SMA correlates with the amount of SMN expression, we sought to better model the disease by generating a set of Smn alleles with varying degrees of SMN activity using RNAi. A GAL4-inducible vector was used to produce three different double-stranded RNAi transgenic constructs targeted against the full-length SMN protein (FL) as well as the amino-terminal (N) (the entire 5′ portion of the protein up to and including the Tudor domain) and carboxy-terminal (C) (the 3′ portion of the protein after, but not including, the Tudor domain) SMN regions (Fig 2A).

Ten independent transgenic strains for each type of construct (C, N and FL) were generated and examined for their effects on lethality when SMN activity was reduced or eliminated using either tubulinGAL4 or actinGAL4, two ubiquitous GAL4 drivers. It was difficult to differentiate between the lethal phases of many strains in the tubulinGAL4 background, presumably due to its higher levels of expression. Instead, we were able to use the timing of lethality in the presence of actinGAL4 to choose three lines ([UAS-Smn-RNAi]N73Ao (N4), [UAS-Smn-RNAi]C24 (C24) and [UAS-Smn-RNAi]FL26B (FL26B) that define a set of alleles representing the broadest range of detectable lethality for further analysis (Figure 3A).

Of all strains generated, N4 displayed the most severe phenotype, causing mortality at the early pupal stage. C24 was less severe and results in lethality at a later pupal stage than N4, while FL26B was semi-viable and was therefore the weakest allele of the three (Figure 3A). Under the control of the tubulinGAL4 driver, N4 caused a similar phenotype to those observed for the Smn73Ao and Smn73Ao/Df(3L)Smnn mutations, suggesting that N4 is a strong hypomorphic Smn allele (data not shown). The efficiency of RNAi in the N4 and C24 strains precluded us from testing whether ectopic SMN expression could rescue the RNAi-induced lethality.
However, we do note that the fully penetrant pupal lethality induced by the expression of tubulinGAL4-directed FL26B is completely rescued by the addition of the UAS-FLAG-Smn construct to this genetic background (data not shown). Consistent with these results, examination of protein derived from 3rd instar larvae from the above strains in the presence of the actinGAL4 driver revealed significant reductions in SMN expression levels (Figure 3D), further suggesting the observed lethality is the direct result of SMN protein attenuation. Though the three strains did not display apparent differences in the degree of reduction of SMN under these conditions, the genetic results with respect to viability and subsequent experiments investigating NMJ morphology (see below) strongly suggest these RNAi-induced Smn strains result in varying degrees of SMN activity and therefore, alleles of different strengths. Importantly, these reagents provide important genetic tools that will allow us to examine the requirement of SMN in muscle and neurons.

Loss of Smn causes neuromuscular junction defects
SMA patients experience motor neuron degeneration and muscle atrophy [1,4]. Consistent with this, previous work has shown that a loss of Smn function results in defects at the Drosophila NMJ [15]. To confirm and extend these results, we examined the NMJ phenotype observed in various Smn genetic backgrounds by quantitatively assessing the morphology of the NMJ through examination of synaptic bouton numbers between muscles 6 and 7 of the 3rd instar larval NMJs. These boutons are visualized by using antibodies against the Synaptotagmin (SYT) (pre-synaptic) and DLG (post-synaptic) proteins, respectively (Figure 4A–G) (Materials and Methods [29,31,32]). The following Smn genotypes,

Figure 1. SMN localizes to the post-synaptic region of the Drosophila NMJ. (A–D) SMN expression at the NMJ between muscle fibers 6 and 7. (A) Pre-synaptic anti-HRP staining (red), (B) post-synaptic anti-DLG staining (blue), (C) anti-SMN staining (green) and (D) a merge of (A–C). SMN expression co-localizes with DLG at the post-synaptic region of the NMJ. (E) SMN staining is also observed in muscle fibers and discrete foci in nuclei (arrow). (F) Though no pre-synaptic SMN staining is observed, robust levels of SMN expression are seen in the larval brain. Scale bars in (D), (E), (F) represent 10 μm, 20 μm, and 50 μm.

doi:10.1371/journal.pone.0003209.g001

A

B

C

D

E

F

Anti-HRP

Anti-DLG

Anti-SMN

Merge

Anti-SMN
which were capable of reaching the 3rd instar larval stages (Smn
73Ao/Smn
f01109, Smn
f05960/Smn
f01109, and Smn
f01109/Smn
f01109) and therefore amenable to dissection, were examined.

The most severe reduction in NMJ bouton numbers was observed in a Smn
73Ao/Smn
f01109 genetic background (Figures 4A–D and F). The semi-viable Smn
f01109 mutation displayed a moderate reduction in NMJ bouton numbers, consistent with its weakly hypomorphic nature (Figure 4C). Surprisingly, the strong loss of function Smn
f05960 mutation, though homozygous lethal, failed to exhibit a detectable change in NMJ bouton numbers in an Smn
73Ao background. However, an increase in pre-synaptic ghost bouton numbers [33,34] (where pre-synaptic SYT was not accompanied with postsynaptic DLG) was observed in these individuals (Figure S3), indicating that the Smn
f05960 allele does, indeed, disrupt NMJ

---

**Figure 2. Smn mutations cause lethality.** (A) Schematic representation of the SMN protein and location of mutations corresponding to the Smn alleles used in this study. The conserved Tudor domain and YG box are indicated. Insertion sites of the transposon induced Smn
f05960 and Smn
f01109 alleles are denoted by triangles. Regions of the Smn transcript targeted by RNA interference (RNAi) are illustrated as lines under the SMN protein schematic. (B) Loss of Smn function elicits lethality. For individuals of given phenotypes, the percentages of surviving individuals are shown and are normalized to wild-type. Smn
73Ao and Smn
f05960 homozygotes die during late 2nd/early 3rd larval and pupal stages, though some Smn
f05960 escapers are detected. In contrast, 67% of the Smn
f01109 homozygotes survive to adulthood. Smn
f01109/Smn
73Ao and Smn
f05960/Smn
73Ao trans-heterozygous combinations are also viable. In addition, a small deficiency uncovering the entire Smn transcript was generated (Df(3L)Smn
X7). We crossed all three Smn alleles to Df(3L)Smn
X7 and found that both Smn
73Ao/Df(3L)Smn
X7 and Smn
f05960/Df(3L)Smn
X7 heterozygotes die between the 2nd and 3rd instar larval stages, while ~60% of Smn
f01109/Df(3L)Smn
X7 are viable. Therefore, using lethality as a criterion, all three alleles behave as loss-of-function mutations with Smn
f01109 displaying the weakest phenotype of the three. No obvious maternal or paternal effect is observed for the different alleles. m: maternal contribution, p: paternal contribution. WT is wild-type (Canton-S). At least 100 individuals were examined for each genotype.

doi:10.1371/journal.pone.0003209.g002
The NMJ phenotype associated with \( \text{Smn}^{73\text{Ao}/\text{Smn}^{f01109}} \) individuals was rescued partially by neuronal or muscle-directed expression of a \( \text{UAS-FLAG-Smn} \) transgene (Figure 4E–G), suggesting that SMN expression in either tissue is sufficient to restore, at least partially, NMJ morphology.

Loss of \( \text{Smn} \) function in muscles causes lethality

Though it is clear that global reduction of SMN function elicits a larval lethal phenotype (Figure 2B), the relative requirement of SMN in muscle versus neuron remains unresolved. We sought to address this question directly through use of our inducible \( \text{Smn} \) RNAi strains (N4, C24 and FL26B), which can be expressed using tissue-specific GAL4 drivers. Therefore, we chose to reduce SMN expression in neuronal and muscle lineages using the pan-neuronal \( \text{elavGAL4} \) and pan-muscle \( \text{how24BGAL4} \) drivers, respectively (\( \text{how24BGAL4} \) is a mesodermal driver that expresses in all muscles, and in the remainder of the text we refer to it as a muscle driver) [36,37].
Figure 4. *Drosophila* Smn mutations elicit neuromuscular junction (NMJ) defects. (A–F) The morphology of the NMJ, as judged by bouton numbers, between muscles 6 and 7 in the A2 segment was observed in different genetic backgrounds using the pre-synaptic (Synaptotagmin) and post-synaptic (Discs large) markers, shown in green and red, respectively. The following genotypes were examined: (A) wild-type (Canton-S), (B) Smn^{f05960}/Smn^{f01109} (C) Smn^{f01109}/Smn^{f01109}, (D) Smn^{73Ao}/Smn^{f01109}. Of these combinations, Smn^{73Ao}/Smn^{f01109} displayed the most robust NMJ defect. These defects are partially rescued by either (E) neuron-specific expression (elavGAL4) or (F) muscle-specific expression (how24BGAL4) of a UAS-FLAG-Smn transgene. (G) More complete rescue was achieved when this transgene was expressed using both drivers simultaneously. Bouton numbers were normalized to the ratio of the muscle area. Scale bars represent 20 μm. (H) Diagram of bouton numbers for genotypes from (A–F), normalized for muscle area. * P<0.05 was determined by the ANOVA multiple comparisons test. For each genotype at least 15 animals were examined. doi:10.1371/journal.pone.0003209.g004
Reduction of SMN in either tissue causes lethality, however, loss of SMN expression in the muscle results in an earlier onset of lethality, which we consider to be a more severe phenotype (Figure 3B–C). In the strongest Smn RNAi allele, N4, muscle-specific SMN reduction results in 70% mortality (Figure 3B), while neuronal specific reduction results in 7% mortality (Figure 3C). As RNAi is less efficient in neurons, we added a GAL4-driven *dicer* construct to increase the efficacy of SMN reduction under these conditions [39]; this resulted in no obvious enhancement of lethality in all Smn RNAi and *elavGAL4* backgrounds (data not shown). The GAL4 repressor GAL80 was expressed in neurons using the pan neuronal *n-syb* driver [39] to overcome the potential leakiness of the *howl24BGAL4* driver. Since the lethality observed for muscle specific reduction of SMN more closely resembles ubiquitous SMN reduction (compare Figure 3A and B), these indicate the requirement of SMN in the muscle (using *howl24BGAL4*) is more important for viability than its requirement in the neurons.

**Muscle and neuronal expression is required for normal NMJ morphology**

Similar to the tissue-dependent lethality experiments above, we sought to assess the impact SMN activity has on NMJ morphology using our *UAS-Smn-RNAi* strains, which can be expressed using tissue-specific GAL4 drivers.

We selectively reduced SMN expression in neuron and muscle tissues by crossing the *UAS-Smn-RNAi* alleles to the *elavGAL4* and *howl24BGAL4* drivers as they provide the earliest tissue specific expression and most robust lethal effect (Figure 3 and data not shown). Visualized by SYT (pre-synaptic) and DLG (post-synaptic) staining, NMJs of Smn RNAi animals containing either a muscle- or neuron-specific GAL4 driver revealed a reduction in the number of synaptic boutons compared to vector alone controls (Figure 5A–M). In the N4 strain, both neuron and muscle specific attenuation of SMN cause approximately 50% reduction in bouton numbers (Figure 5B, C, K–M), a reduction comparable to what is observed in Smn*73Ao/*Smn*101109* larvae (Figure 4D, H). Therefore, we conclude that the NMJ morphology is dependent upon both pre- and post-synaptic SMN activity.

Previous studies demonstrated that mutations in *Smn* cause a decrease in staining for the post-synaptic neurotransmitter receptor subunit, GluRIIA [15]. To corroborate these results and to extend our characterization of the tissue-specific requirement of SMN at the NMJ, we examined the GluRIIA [40,41,42] expression pattern (See Materials and Methods) in the *UAS-Smn-RNAi* backgrounds. We found a consistent and significant quantitative reduction in synaptic GluRIIA levels when Smn expression was decreased using either neuron- (elavGAL4) or muscle-specific (nheGAL4) drivers. GAL4-only controls had no significant effect on GluRIIA staining intensity. Consistent with the trend observed for the severity of the lethal phenotype, the strongest Smn RNAi alleles caused the greatest reduction in GluRIIA expression levels, suggesting that GluRIIA levels are sensitive to the dose of functional SMN protein and thus, would be a useful phenotypic metric in which to validate potential modifiers of the *Smn* NMJ phenotype.

Our analysis indicates that normal NMJ morphology requires SMN activity in both muscle and neurons. However, it appears that loss of SMN activity in the muscle causes a more severe lethal phenotype (Figure 3B), a conclusion that is consistent with the finding that the SMN protein is concentrated in the post-synaptic regions in muscle (Figure 1A–D).

**Identification of genetic modifiers of Smn**

To gain insights into the genetic circuitry capable of modulating SMN activity *in vivo*, we employed a genetic approach to screen for genes that affect *Smn*-dependent processes using the Exelixis collection of transposon-induced mutations [25,26]. The benefits of using the collection in a genetic screen have been previously described [24]. Notably, the collection covers approximately 50% of the genome and harbors both gain- as well as loss-of-function mutations when exposed to GAL4 due to the presence of UAS sequences within the insertional transposons [25,26]. While the molecular coordinates of each insertion site is known, gene assignments are sometimes ambiguous, as the modifying transposon may have inserted between two genes.

The screen was carried out in two stages to identify both enhancers and suppressors of *Smn*-associated lethality (Figure 6). The strong correlation observed between the degree of lethality and NMJ phenotypes using the Smn RNAi lines suggested the use of lethality as a screening parameter would be successful in identifying components of the SMN genetic network that might also affect the NMJ. Both phases of the screen utilized the Smn*73Ao* allele, which gives a robust NMJ defect, and importantly, contains a point mutation in the YG box (Figure 2A), which is the location of a documented human SMN1 mutation [3].

The first stage was an F1 screen designed to identify insertions that produced synthetic lethality or semi-lethality (Materials and Methods) in an *Smn* heterozygous background, which will hereafter be referred to as enhancers. Using this criterion, we screened the entire Exelixis collection and identified 17 insertions that result in Smn*73Ao/+* lethality (Figure 7).

In the second stage of the screen we tested for the ability of mutations to suppress *Smn*-dependent larval lethality. This was accomplished using offspring from the F1 screen that failed to generate synthetic lethality. In this phase, we screened 7170 strains (as Smn*73Ao* is located on the third chromosome, we excluded third chromosome insertions) and identified ten suppressors of homozygous Smn*73Ao* lethality (Figure 7).

**NMJ analysis of Smn modifiers**

To correlate modifier activity with the NMJ, we investigated whether all of the Smn modifiers (10 suppressors and 17 enhancers) could disrupt *Smn* RNAi-dependent NMJ defects, using synaptic GluRIIA staining as an assay to quantify the degree to which the *Smn* phenotype was modified by the interacting mutation. For this assay, we employed the C24 Smn RNAi line because it displays intermediate phenotypic strength. In all but two cases, the combination of the modifier insertion mutation induced a statistically significant change in the C24 GluRIIA phenotype (Figure 7 and Figure S5 and S6). Amongst the validated modifier insertions, the degree of enhancement or suppression varied depending on the locus; control crosses demonstrated that there were no significant *Smn*-independent changes in GluRIIA localization for the tested insertion lines. Three lines (f04448, d09801 & d00698) failed to modify C24 GluRIIA staining and were retested using a weaker *Smn* RNAi strain, N13 (Strain f04448 and d09801 enhanced, whereas d00698 showed no interaction (data not shown), highlighting the importance of the NMJ phenotype as a secondary screening tool (Figure 7)). Thus, the majority modifiers of the Smn*73Ao* lethal phenotype were confirmed by a second, independent assay. All but one of these insertions modified the Smn NMJ phenotype, validating the efficacy of the screen and suggesting that the screen may prove to be an effective tool in the identification of candidate genes that may be relevant to the SMA disease state.

**Neuronal overexpression of wishful thinking (wit) enhances Smn NMJ defects**

To validate further our approach, we sought to examine the relationship between *wishful thinking (wit)* and Smn in greater detail.
wit was of particular interest because it has been previously implicated in NMJ function [27,28] and thus could serve as a paradigm for validating the ability of the screen to identify bona fide Smn genetic modifiers.

wit encodes a type II BMP receptor that functions as a retrograde signaling component in neurons [27,28]. wit loss-of-function mutations cause NMJ defects, whereas wit gain-of-function causes no obvious NMJ morphological changes. As the wit allele identified as an Smn enhancer, wit<sup>d02492</sup>, is associated with a GAL4-responsive transposon, it seemed likely that it represented a gain-of-function mutation. Consistent with this notion, an independent UAS-wit transgene [27,28] behaved in a similar

---

**Figure 5. Muscle and neuron specific Smn RNAi knockdown causes NMJ defects.** (A–L) Reduced SMN expression in the N4, C24 and FL268 UAS-Smn-RNAi transgenic constructs elicits graded effects on NMJ morphology using the ubiquitous actinGAL4 (A, D, G) as well as the tissue-specific how24BGAL4 (muscle) (B, E, H) and elavGAL4 (neuron) (C, F, I) drivers. Vector only (pWIZ) controls are shown (J, K, L). In these images the pre- and postsynaptic tissues are labeled with antibodies against Synaptotagmin (green) and Discs large (red), respectively. (M) Bouton counts for the NMJs from the genotypes shown in (A–L) were normalized for muscle area and subtracted from vector only controls. For each genotype at least 15 animals were examined. * P<0.01 and **P<0.05 was determined by the ANOVA multiple comparisons test. Scale bars represent 15 μm. doi:10.1371/journal.pone.0003209.g005
Figure 6. Schematic representation of the Smn modifier screen. Depicted are the crosses performed to identify enhancers and suppressors of Smn-associated lethality. In the first stage of the screen, designed to identify Smn enhancers, Smn<sup>273Ao</sup> tubulinGAL4, e/+; TM6B/TM6B virgin females were mated to males from Exelixis collection strains. In this stage, the entire Exelixis collection, which affects approximately 50% of the Drosophila genome, was tested. In the F1 generation, mutations that resulted in synthetic lethality or reduced viability in trans with the Smn<sup>273Ao</sup> tubulinGAL4, e chromosome were defined as enhancers. In the second stage of the screen, males from F1 crosses that failed to show enhancement (p[Exelixis]/+; Smn<sup>273Ao</sup> tubulinGAL4, e/+; TM6B) were mated to Smn<sup>273Ao</sup> e/Me, Me virgin females to identify mutations that suppressed the Smn<sup>273Ao</sup> tubulinGAL4, e/+; Smn<sup>273Ao</sup>, e lethal phenotype. We performed the F2 suppressor screen with Exelixis mutations on first and second chromosomes as testing third chromosome mutations would require placing these mutations in cis with Smn. Additional assays were employed to eliminate false positives (See Materials and Methods). Seventeen enhancers and ten suppressors met these criteria. All 27 modifiers were subsequently examined for their ability to modify the Smn NMJ phenotype by Gluria staining (Figures S5 and S6). doi:10.1371/journal.pone.0003209.g006

A Mad mutation enhances the Smn NMJ phenotype

Given the involvement of wt in the NMJ and its interaction with Smn, we hypothesized that an Smn heterozygous background leads to an increase in sensitivity to the dosage of BMP during NMJ development. Thus, under conditions of elevated levels of WTI in wt<sup>p020392</sup> animals containing tissue-specific GAL4 drivers (data not shown).

Over-expression of WIT in neurons using the neuron-specific elavGAL4 driver in either an Smn<sup>273Ao</sup> or an Smn<sup>p01109</sup> heterozygous background resulted in reduced NMJ bouton numbers relative to elavGAL4 Smn<sup>273Ao</sup>+/+; elavGAL4 Smn<sup>p01109</sup>+/+ and UAS-wt; elavGAL4 controls (Figure 8). This result suggests that the Smn-dependent NMJ phenotype is sensitive to elevated WTI levels.

A Dad loss of function allele is capable of rescuing Smn NMJ defects

We extended these observations by probing the relationship between the BMP pathway antagonist, Daughters against dpp (Dad), and Smn. Dad encodes the Drosophila homolog of mammalian anti-Smad and acts as a Mad antagonist [44,49,50]. Since Dad mutants exhibit presynaptic overgrowth [49], we tested whether the Dad<sup>271-68</sup> loss of function allele could rescue the Smn<sup>271-68</sup> NMJ phenotype. Consistent with previous reports [49], <sup>9</sup>th instar larval homoyogous for Dad<sup>271-68</sup> display more dispersed SYT expression at the NMJ than control larvae (Figure 11C). However, in contrast to previous studies, we found the total bouton number, as determined by DLG post-synaptic staining, was only slightly reduced. Importantly, the Smn<sup>271-68</sup> NMJ phenotype was suppressed by the introduction of Dad<sup>271-68</sup> (Figure 11B, D, E), providing genetic evidence that a third element of the BMP pathway interacts with Smn. It appears that elevating BMP activity through a complete loss of Dad function suppresses the effects of Smn mutations on the NMJ (Figure 11D, E). A prediction of this model is that pharmacological reagents that increase BMP signaling may ameliorate Smn-associated NMJ defects, thereby identifying a set of targets of potential therapeutic value.

Discussion

SMN is the determining gene for Spinal Muscular Atrophy (SMA) [5], a devastating neurodegenerative disease in humans with no currently available FDA-approved drug treatment. Though the general biochemical function of SMN in snRNP assembly has been well documented [51,52,53], much remains to be learned about its action at the NMJ and the genetic circuitry that is capable of affecting SMN activity. Specifically, it remains unclear whether the NMJ pathology in SMA is due to the ubiquitous loss of SMN function or whether SMN has a unique role at the NMJ. Here, we have utilized Drosophila to investigate the tissue specificity of Smn and to identify genes that interact with Smn.
## Modifiers of Smn

<table>
<thead>
<tr>
<th>Enhancer insertion</th>
<th>NMU Phenotype</th>
<th>Corresponding Gene</th>
<th>Gene Name (Symbol)</th>
<th>Human Homolog (% of identities)</th>
<th>Annotated Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>d00712</td>
<td>+</td>
<td>CG4376</td>
<td>a-atcin (Adn)</td>
<td>Adn(76.8%)</td>
<td>F-actin binding protein</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG4380</td>
<td>ultraspiracle (ups)</td>
<td>RXRA(52%)</td>
<td>nuclear hormone receptor</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG4352</td>
<td>N/A</td>
<td>RNF49 (31%)</td>
<td>contains a ring domain</td>
</tr>
<tr>
<td>d03336</td>
<td>++</td>
<td>CG10706</td>
<td>small conductance calcium-activated potassium channel (SK)</td>
<td>KCNN3 (63.8%)</td>
<td>Calcium dependent K+ channel</td>
</tr>
<tr>
<td>d04197</td>
<td>+++</td>
<td>CG32796</td>
<td>brother of irig (bii)</td>
<td>BIOC (25%)/ICOD (27%)</td>
<td>binds and mediates response to Hedgehog</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG33590</td>
<td>terribly reduced optic lobes (tor)</td>
<td>HSPO2 (28%)</td>
<td>neuroblast proliferation</td>
</tr>
<tr>
<td>d05295</td>
<td>+++</td>
<td>CG34414</td>
<td>sprout (spr)</td>
<td>RIN1 (30%)</td>
<td>Ras GTPase binding</td>
</tr>
<tr>
<td>f01329</td>
<td>+++</td>
<td>CG8414</td>
<td>N/A</td>
<td>N/A</td>
<td>contains Esterase_Instance domain</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG33172</td>
<td>N/A</td>
<td>WDR86 (19%)</td>
<td>contains WD repeats</td>
</tr>
<tr>
<td>f05849</td>
<td>+++</td>
<td>CG1835</td>
<td>N/A</td>
<td>AZI1 (26%)</td>
<td>localized to the prearcosome region of spermatids</td>
</tr>
<tr>
<td>d08696</td>
<td>N.E.</td>
<td>CG17323</td>
<td>N/A</td>
<td>UGT1A9 (24%)</td>
<td>glucuronosyltransferase</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG17322</td>
<td>N/A</td>
<td>UGT2B10 (22%)</td>
<td>glucuronosyltransferase</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG17324</td>
<td>N/A</td>
<td>UGT2A1 (25%)</td>
<td>glucuronosyltransferase</td>
</tr>
<tr>
<td>d05779</td>
<td>+++</td>
<td>CG18375</td>
<td>N/A</td>
<td>PPP1R3B(27%)/PPP1R3L (27%)</td>
<td>p53 binding protein, apoptosis</td>
</tr>
<tr>
<td>d09885</td>
<td>++</td>
<td>CG34379</td>
<td>SHRROD1 (15%)/</td>
<td>SHRROD3 (10%)</td>
<td>F-actin binding</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG5889</td>
<td>N/A</td>
<td>TDRD5 (15%)</td>
<td>nucleic acid binding</td>
</tr>
<tr>
<td>f04424</td>
<td>+++</td>
<td>CG11450</td>
<td>nel</td>
<td>ATOH8(37.7%)</td>
<td>transcription factor</td>
</tr>
<tr>
<td>d02492</td>
<td>+++</td>
<td>CG10776</td>
<td>wishful thinking (wft)</td>
<td>BPRII (37%)</td>
<td>BMP type II receptor</td>
</tr>
<tr>
<td>d09170</td>
<td>+++</td>
<td>CG5361</td>
<td>N/A</td>
<td>ALPL (28%)</td>
<td>Alkaline phosphatase</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG2603</td>
<td>(Fmr1)</td>
<td>FXR2 (46.6%)</td>
<td>miRNA binding</td>
</tr>
<tr>
<td>d09801</td>
<td>+</td>
<td>CG18127</td>
<td>Edylons-induced protein 75B (Evp57B)</td>
<td>PPARg (35%)</td>
<td>nuclear hormone receptor</td>
</tr>
<tr>
<td>f02477</td>
<td>++</td>
<td>CG1927</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>f02601</td>
<td>+</td>
<td>CG1927</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>f02684</td>
<td>+++</td>
<td>CG2134</td>
<td>batholess (baf)</td>
<td>FGFR2(48.8%)</td>
<td>FGFR receptor</td>
</tr>
</tbody>
</table>

### Suppressor

<table>
<thead>
<tr>
<th>Enhancer insertion</th>
<th>NMU Phenotype</th>
<th>Corresponding Gene</th>
<th>Gene Name (Symbol)</th>
<th>Human Homolog (% of identities)</th>
<th>Annotated Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>d00184</td>
<td>+++</td>
<td>CG4520</td>
<td>raptor</td>
<td>raptor (44%)</td>
<td>mTOR binding protein</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG4317</td>
<td>Multiple inositol polyphosphoinositide phosphatase 2 (Mip2)</td>
<td>MIP1 (24%)</td>
<td>phosphoinositol phosphatase</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG5605</td>
<td>Nephrin 1 (Neph1)</td>
<td>Nephrin (38%)</td>
<td>metachondiopeltase</td>
</tr>
<tr>
<td>e02359</td>
<td>+++</td>
<td>CG10701</td>
<td>moesin (Moe)</td>
<td>moesin (75.3%)</td>
<td>cytoskeleton association</td>
</tr>
<tr>
<td>d05478</td>
<td>+</td>
<td>CG12796</td>
<td>Nkx2</td>
<td>Nkx2 (69%)</td>
<td>mitosikeiosis, cell cycle</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG1422</td>
<td>p15</td>
<td>USO1(67.1%)</td>
<td>protein transport, vesicle docking</td>
</tr>
<tr>
<td>f03415</td>
<td>++</td>
<td>CG9998</td>
<td>cut up (cut)</td>
<td>DYNL2 (97.8%)</td>
<td>cytoskeleton motor</td>
</tr>
<tr>
<td>d10703</td>
<td>++</td>
<td>CG1697</td>
<td>rhomboid-4 (rh-4)</td>
<td>RBB6L3 (28%)</td>
<td>EGF signaling activation</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG1561</td>
<td>N/A</td>
<td>N/A</td>
<td>contains a kinase domain</td>
</tr>
<tr>
<td>c05057</td>
<td>+++</td>
<td>CG1336</td>
<td>Atm</td>
<td>ATR (25%)</td>
<td>transcription factor responsive to ER stress</td>
</tr>
<tr>
<td>d02302</td>
<td>+++</td>
<td>CG11200</td>
<td>DHR5X (32%)</td>
<td>DHR5X (32%)</td>
<td>catenary/ reductase (NAPDH)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG8920</td>
<td>N/A</td>
<td>TRD7 (23%)</td>
<td>lupon domain/nuclear acid binding</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG13968</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>e0818</td>
<td>+</td>
<td>CG12714</td>
<td>TBCEL (40%)</td>
<td>TBCEL (40%)</td>
<td>tubulin polymerization</td>
</tr>
<tr>
<td>f05459</td>
<td>+</td>
<td>CG13775</td>
<td>N/A</td>
<td>RASD2 (40%)</td>
<td>GTPase activity</td>
</tr>
<tr>
<td>f02650</td>
<td>++</td>
<td>CG10561</td>
<td>N/A</td>
<td>SMOX (27%)</td>
<td>polyamine oxidase</td>
</tr>
</tbody>
</table>

---

Figure 7. **Modifiers of Smn phenotypes.** Listed are the insertions that enhance (top) or suppress (bottom) Smn\(^{73789}\)-dependent lethality. Due to the site of transposon insertion, unambiguous gene assignments were not possible in all instances (shaded). Strains whose designations begin with “d” or “f” contain GAL4 responsive elements (UAS), whereas strains beginning with “c” or “e” are not GAL4-inducible. Gene assignments were determined using FlyBase (http://www.flybase.org/). Human homologs were determined using NCBI BLAST, NCBI UniGene (NCBI) (http://www.ncbi.nlm.nih.gov/sites/entrez?db = unigene) or ENSEMBL genome browser (http://www.ensembl.org). Annotated functions were determined based on FlyBase, NCBI Entrez Gene and SMART (http://smart.embl-heidelberg.de/). Modification of the NMJ morphology between muscles 6 and 7 in the A2 segment was assayed in the elavGAL4 pWIZ[UAS-Smn-RNAi]\(^{73789}\) background in trans with all identified modifiers using the pre-synaptic (Horseradish peroxidase) and post-synaptic (GluRIIA) markers (see Materials and Methods). In the three cases that did not show significant phenotypic alteration, additional pWIZ[UAS-Smn-RNAi]\(^{113}\) allele was also used (see text). The degrees of change observed in GlurIIA staining were categorized as follows: +++, strong; +++, moderate; ++, weak; N.E., No Effects.

doi:10.1371/journal.pone.0003209.g007
Figure 8. *wit* overexpression in neurons exacerbates *Smn*-dependent NMJ defects. A gain-of-function mutation of *wishful thinking* (*wit*), *wit*^{d02492}, was identified as an enhancer in our screen. To further investigate the interaction between *wit* and *Smn* at the NMJ, we used the neuron-specific driver, *elavGAL4* to express WIT in neurons. (A–F) The morphology of the NMJ, as judged by bouton numbers, between muscles 6 and 7 in the A2 segment was observed in different genetic backgrounds using the pre-synaptic (*Synaptotagmin*) and post-synaptic (*Discs large*) markers, shown in green and red, respectively. The following genotypes were examined: (A) *elavGAL4/+, (B) elavGAL4, Smn^{73Ao/+, (C) elavGAL4, Smn^{f01109/+, (D) elavGAL4/UAS-wit2A, (E) elavGAL4, Smn^{73Ao/UAS-wit2A, (F) elavGAL4, Smn^{f01109/UAS-wit2A, (G) Bouton counts for genotypes from (A–F and wild-type). Consistent with previous reports, neural induced expression of the UAS-wit2A transgene had no obvious effect on NMJ bouton number. A synergistic effect was observed upon the addition of a single *Smn* allele (*Smn^{73Ao} or *Smn^{f01109}*/*) to this background, leading to a reduction of NMJ bouton numbers. The phenotype was more severe in the *Smn^{f01109}* background. *Smn^{f01109}* showed an approximate 50% reduction in bouton numbers while *Smn^{73Ao}* reduced the bouton count by 20%. *elavGAL4, Smn^{73Ao/+, (B) and *elavGAL4, Smn^{f01109/+/+ (C) individuals display no significant reduction in NMJ bouton numbers compared to wild-type (G). Bouton counts were determined as above. Error bars are s.e.m.; * P < 0.02 was determined by the ANOVA multiple comparisons test to wild-type and all controls. *n* was 15–20 animals for each genotype. Bouton numbers for each genotype were normalized to the ratio of muscle areas. Scale bars represent 20 μm.

*doi:10.1371/journal.pone.0003209.g008*
Figure 9. Loss of mad function enhances Smn NMJ defects. (A–F) The morphology of the NMJ, as judged by bouton numbers, between muscles 6 and 7 in the A2 segment was observed in different genetic backgrounds using the pre-synaptic (Synaptotagmin) and post-synaptic (Discs large) markers, shown in green and red, respectively. The following genotypes were examined: (A) wild-type, (B) Smn73A0/+ , (C) Smn f01109/+ , (D) mad12/+ , (E) Smn73A0/mad12 and (F) Smn f01109/mad12. (G) Bouton counts for genotypes in (A–F). Introduction of mad12 into either a Smn73A0/+ or a Smn f01109/+ background dominantly reduces the Smn-dependent NMJ bouton count. Error bars are s.e.m.; *P<0.02 was determined by the ANOVA multiple comparisons test to wild-type and all controls. n was 15–20 animals for each genotype. Bouton numbers for each genotype were normalized to the ratio of muscle areas. Scale bars represent 20 μm.

doi:10.1371/journal.pone.0003209.g009
These genes, apart from their intrinsic value in providing insight into the role of SMN at the NMJ, may also define novel therapeutic targets.

Previous studies based primarily on the analysis of the Smn\textsuperscript{73A0} allele demonstrated that reduced Smn activity causes lethality and NMJ morphological defects [15]. We corroborated these observations through the examination of several extant and novel Smn mutations of varied severities, including several GAL4-inducible Smn RNAi alleles generated for this study. These hypomorphic strains reduce SMN expression levels to different degrees in a
manner formally analogous to decreased SMN levels observed in SMA patients. Additionally, these strains may model the dosage-dependent nature of SMA [1,2] as the developmental arrest associated with these animals correlates with the extent of morphological abnormalities observed at the NMJ.

Figure 11. A dad null allele rescues Smn NMJ defects. (A–D) The morphology of the NMJ, as judged by bouton numbers, between muscles 6 and 7 in the A2 segment was observed in different genetic backgrounds using the pre-synaptic (Synaptotagmin) and post-synaptic (Discs large) markers, shown in green and red, respectively. The following genotypes were examined: (A) wild-type, (B) Smn73Ao/Smn01109, (C) dad271-68 homozygotes and (D) Smn73Ao dad271-68/Smn01109 dad271-68. (E) Bouton counts for genotypes in (A–D). Smn73Ao/Smn01109 individuals display strongly reduced NMJ bouton numbers while dad271-68 homozygotes have a greater than two-fold of bouton numbers relative to the Smn73Ao/Smn01109 animals. The Smn73Ao dad271-68/Smn01109 dad271-68 double mutants behave like dad271-68 homozygotes. Error bars are s.e.m.; n is 15–20 animals for wild-type and Smn73Ao/Smn01109. n is 30 for dad271-68/dad271-68 and Smn73Ao, dad271-68/Smn01109, dad271-68. *P<0.002 by the ANOVA multiple comparisons test. Bouton numbers for each genotype were normalized to the ratio of muscle area. Scale bars represent 15 μm.

doi:10.1371/journal.pone.0003209.g011

Our examination of Smn NMJ structure in Drosophila using pre- and post-synaptic markers, SYT and DLG, respectively, revealed significant losses of synaptic bouton numbers in multiple Smn backgrounds (Figure 4). Moreover, in these backgrounds, we also detected reduced post-synaptic GluRIIA expression (data not
shown), consistent with previous analyses of the Smn\(^{73Ao}\) NMJ [15]. Together, these results suggest that loss of SMN function in Drosophila causes aberrant neuromuscular synaptic structure, mimicking the pathology of SMA [1,54]. In addition, these structural abnormalities are consistent with the altered electrophysiological profile previously observed in Drosophila Smn\(^{73Ao}\) animals [15].

It should be noted that other glutamate receptor subunits display altered transcriptional profiles in a Smn\(^{73Ao}\) background; specifically the GluRIIA and GluRIIB transcript levels were decreased while GluRIC levels were increased [55]. Therefore, combining genetic and morphological analyses of pathological changes in synaptic structure with future electrophysiological studies will be necessary to understand more thoroughly the synaptic consequences of SMN loss in SMA.

A longstanding question in the pathology of SMA is the relative neuronal and muscle contribution of SMN function. The RNAi strains allowed us to reduce SMN function in a tissue-specific fashion and therefore, address this issue directly. We find that SMN is required in both neurons and muscle for normal NMJ morphology as GAL4-inducible RNAi reduction of SMN in neurons and muscle both show a decrease in NMJ bouton numbers (Figure 5) and GluRIIA staining (Figures S3 and S6 and data not shown). In addition, expression of SMN in either tissue is sufficient to partially rescue NMJ defects associated with loss of Smn function (Figure 4E–G). These results are consistent with previous reports in Drosophila, zebrafish and mouse [15,16,54,56,57,58,59] that indicate an interdependence of neuron and muscle SMN activity.

In contrast to a requirement for Smn in both muscle and neurons at the NMJ, we demonstrated that muscle specific reduction of Smn causes a more severe lethal phenotype (Figure 3B–C). We do not know the cause of the lethality. It is possible that the earlier onset of lethality observed for the line24BGAL4 reduction of SMN in neurons and muscle both show a decrease in NMJ bouton numbers (Figure 3) and GluRIIA staining (Figures S3 and S6 and data not shown). In addition, expression of SMN in either tissue is sufficient to partially rescue NMJ defects associated with loss of Smn function (Figure 4E–G). These results are consistent with previous reports in Drosophila, zebrafish and mouse [15,16,54,56,57,58,59] that indicate an interdependence of neuron and muscle SMN activity.

Current therapeutic strategies for treatment of SMA are based on the dosage dependent nature of the disease, focusing on drugs that increase SMN2 transcription and splicing efficiency [60,61].

Though these strategies might ultimately prove successful in treating SMA, complementary therapies may allow for the delivery of a combination of drugs as this has been shown to be successful in alleviating the symptoms of other diseases, such as AIDS [62]. Hence, the identification and, ultimately, the manipulation of genetic elements that affect SMN activity may be necessary to treat SMA effectively. Though previous biochemical studies provide valuable and fundamental knowledge of SMN function, our current understanding of SMN has been limited mainly to its binding partners and a few genetic modulators [12,19]. Thus, we performed a genome-wide genetic screen in Drosophila to identify novel components of the Smn genetic circuitry to broaden our knowledge of its function and to seek potentially novel therapeutic approaches beyond the augmentation of SMN2 expression.

Since we observed that the severity/onset of Smn-dependent mortality (Figure 3) corresponds to the degree of NMJ defects (Figure 5), we reasoned the identification of enhancers and suppressors of Smn\(^{73Ao}\)-dependent lethality would be likely to yield genes that also function at the NMJ. Our genetic screen using an allele (Smn\(^{73Ao}\)) that encodes a point mutation seen in SMA patients [3] resulted in the identification of twenty-seven modifiers of Smn lethality. Though we recognize the genetic circuitry in Drosophila may differ from that which exists in humans, we expect there to be substantial overlap given the conservation of gene function across species.

Despite the essential role of SMN in snRNP assembly [12], an unexpected result of the screen was that none of the modifying insertions for which unambiguous gene assignments were made appear to function in RNA processing. Consistent with this notion, direct attempts to identify genetic relationships between SMN and known components of the SMN multimeric complex, including deficiencies that uncover the Drosophila Gemin homologs, did not affect the Smn\(^{73Ao}\) heterozygous phenotype (data not shown). One possible explanation is that removal of additional components of the SMN complex may not enhance Smn-related phenotypes since SMN activity is critical for the initial steps in SMN complex assembly. Hence, altering the activity of “downstream” or directly-interacting partners of the SMN in the SMN complex may not affect Smn-related phenotypes.

Though none of the unambiguously identified modifier genes have an obvious role in snRNP assembly; we did recover genes (wishful thinking, fmri1 and cutup) that have been shown previously to function at the NMJ [27,28,63,64]. Moreover, the majority of the remaining genes, which had no previously known NMJ function, also modified Smn NMJ phenotypes. Thus our genetic approach was efficient in identifying genes related to Smn NMJ function. This suggests that a similar approach utilizing a hypomorphic Smn allele (e.g. UAS-Smn-RNAi) that more closely approximates the dosage dependent nature of the human disease condition may identify additional members of the Smn genetic circuitry.

An analysis of the interacting loci according to molecular functions reveals an assortment of functional categories including cytoskeleton interaction proteins (now and ctp), transcription factors (net) and metabolic enzymes (CG17323 and CG10561). Identified interactors also include members of several signal transduction pathways (e.g. BMP (soil), FGF (btl) and Nuclear Hormone Receptor (Eip75B), raising the possibility that these evolutionarily conserved signaling pathways integrate with SMN or targets of SMN function(s). Though more detailed analyses of the nature of the links (synergistic or parallel) between these pathways and SMN are necessary, we provide strong evidence supporting a connection between BMP signaling and Smn at NMJ by testing additional upstream and downstream elements of this pathway. Our molecular genetic analysis clearly indicates that SMN influences BMP activity. It remains to be determined whether SMN acts in the muscle to influence retrograde BMP signaling through the WIT receptor, for example by regulating the activity of the WIT ligand (GBB). It is also possible that SMN functions cell-autonomously in the neurons to affect the activity of MAD or its antagonist, DAD. As the BMP signaling pathway has been implicated in other neurodegenerative diseases, including Duchenne Dystrophy and Marfan Syndrome [63], it is probable that BMP signaling also plays a role in the pathology of SMA in humans.

Similar to what is observed in SMA, our results confirm the susceptibility of the Drosophila NMJ to lower levels of SMN, and our screen has also identified several genes that modify Smn NMJ phenotypes. In other recent studies, micro-array based approaches analyzed the effect of reduced Smn levels on tissue-specific gene expression at a genome-wide level [52,55]. They identified genes
whose splicing are susceptible to reduced SMN function [52] and genes involved in general metabolic processes [53]. These screens are clearly a valuable means to assess the housekeeping function of Smn. However, unlike the genes recovered from our screen, most of which affect NMJ structure, it remains to be determined whether the genes identified through transcriptional profiling are involved in the development and/or maintenance of the NMJ. Thus, our genetic approach has uncovered elements, revealing a potential NMJ-specific role for Smn.

In this study, we have used Drosophila genetics to broaden our understanding of Smn at the neuromuscular junction and probe the genetic circuitry of Smn, illustrating the utility of a genetic approach in the identification of novel genes that impact Smn activity. Given the high degree of genomic conservation, use of full-length Smn

Hermann Aberle. To generate the (Figure 2A). These constructs were then introduced into portion after, but not including, the Tudor domain (C constructs) entire Tudor domain (N constructs) and the carboxy-terminal constructs), the amino-terminal portion up to and including the Smn through all but the final 44 bp of the 3

affecting nearby loci (93 bp upstream of the transcription start site

Materials and Methods

Drosophila stocks

All stocks were maintained on standard cornmeal/yeast/molasses/agar medium at 25°C. The Smn

P[EP-gy2]Y14384, w1118 and w111B alleles were obtained from the Bloomington Drosophila Stock Center (Bloomington, IN). The Smn

and Smn

alleles are from the Exelixis collection at Harvard Medical School. Dmd

and Mad

were gifts from Graeme Davis. P[UAS-wtU2A] transgenic animals were gifts from Hermann Aberle. To generate the P[UAS-FLAG-Smn] strains, a full-length Smn cDNA was cloned into the amino-terminal FLAG-tagged vector, FLAG-pUAST and introduced into w

animals. Several independent strains were isolated and subsequently tested for their ability to rescue Smn-dependent lethality in a homozygous Smn

background. The majority of homozygous Smn

mutants die between 2nd and 3rd larval stages, and less than 10% reach the 3rd instar larval stage. Expression of this construct using the ubiquitous actinGAL4 and tubulinGAL4 drivers partially suppressed this lethality, as 50% of the animals survived to the late pupal stage and 20% survived to the adult stage. The null allele of Smn, Df[3L]Smn

, was generated by imprecise excision of the P

1.626 excision events were isolated and 17 failed to complement Smn

including Df[3L]Smn

. Subsequent sequence analysis of Df[3L]Smn

determined the excision event removed almost the entire SMN transcript without affecting nearby loci (93 bp upstream of the transcription start site through all but the final 44 bp of the 3’ UTR). To generate the Smn RNAi constructs, three different portions of the Smn cDNA were cloned into the pWIZ vector: the entire cDNA (FL constructs), the amino-terminal portion up to and including the entire Tudor domain (N constructs) and the carboxy-terminal portion after, but not including, the Tudor domain (C constructs) (Figure 2A). These constructs were then introduced into w

embryos by germ-line transformation according to standard procedures (by the CBRC fly core facility, Massachusetts General Hospital). Multiple independent insertions were obtained for each construct, including the pWIZ[UAS-Smn-RNAi]24 and pWIZ[UAS-Smn-RNAi]24 transgenic strains that were used for the analyses conducted in this study. Detailed primer sets and methods used for sequencing Smn

and Smn

alleles are available upon request.

Exelixis screen

The screen we performed combined elements from standard F1 and F2 screens. This “combination screen” was identical to a standard F2 screen with the exception that the crosses were designed to identify synthetic lethal interactions with Smn in the F1. In this screen we utilized the Smn

alleles in cis with a ubiquitously expressed tubulinGAL4 driver (Lee and Luo, 1999). Initially, Smn

and tubulinGAL4 were crossed to the entire Exelixis mutant collection to identify insertions that elicit F1 synthetic lethality or reduced viability. From these results, we arbitrarily defined a strain to be a candidate enhancer as one that displayed a viability of less than 30%. In the second generation, F1 males from strains that failed to elicit synthetic lethality were crossed to Smn

TM6B virgin females were crossed to the entire Exelixis mutant collection to identify insertions that elicit F1 synthetic lethality or reduced viability. From these results, we arbitrarily defined a strain to be a candidate enhancer as one that displayed a viability of less than 30%. In the second generation, F1 males from strains that failed to elicit synthetic lethality were crossed to Smn

TM1, Me virgins to test for their ability to suppress homozygous Smn

larval lethality. In the F2 screen, candidate suppressors were identified by the presence of individuals bearing the marker ebony (e), which is visible in both pupae and adults.

Secondary genetic assays

We used several secondary genetic assays to evaluate candidate modifiers. Initially, all candidate enhancers were crossed to tubulinGAL4 e alone, to determine whether the observed effects on viability were Smn-dependent.

Resultant strains and all candidate suppressors were then crossed to stocks containing additional combinations of Smn alleles and GAL4 drivers to observe their effects on viability. These stocks included both Smn

and Smn

alone and in combination with the tubulinGAL4 or actinGAL4 drivers. The actinGAL4 driver alone was also tested. Twenty-seven strains modified Smn-dependent lethality. Of these, seventeen were classified as enhancers and ten as suppressors.

NMJ analysis of 27 Smn interactors

Strains containing all twenty-seven interactors in combination with the pWIZ[UAS-Smn-RNAi]24 were generated. These were tested for their ability to modify NMJ phenotype associated with elavGAL4 (neuronal) directed expression of pWIZ[UAS-Smn-RNAi]24 and pWIZ[UAS-Smn-RNAi]N11. GlurRIA morphometric analyses were performed as described previously [66].

Lethality assays

Fertilized eggs were collected on apple juice agar plates. Before collection, adults were allowed to lay for 2 hours. All the F0 strains were balanced by TM6B, Dfd:YFP, Tb or CyO Dfd:YFP, and the non-YFP embryos were collected using a fluorescence dissection scope (Zeiss). Fertilized embryos were then placed onto fresh apple juice plates containing yeast paste. Each plate contained 20–25 embryos to avoid over-crowding. The animals were allowed to grow into different developmental stages in controlled temperature (25°C) and their survival was determined by visual inspection.

Immunohistochemistry and microscopy

Primary antibodies were used at the following dilutions: monoclonal anti-DLG (1:500) (Developmental Studies Hybridoma Bank), polyclonal anti-Synaptotagmin (1:1000) (a gift from Hugo Bellen), polyclonal anti-SMN (1:250, NMJ staining), monoclonal anti-SMN (1:500, wing disc), polyclonal anti-pMAD (1:250) (a gift from Carl-Henrik Heldin). Anti-SMN monoclonal and polyclonal antibodies were generated by immunizing animals with purified full-length SMN protein with a 6xHis-tag fused to its carboxy-terminus (Cocalico Biologicals, Inc.). Texas-red conjugated anti-HRP (1:250), FITC- (1:40) and Cy5- (1:40) conjugated anti-rabbit and anti-mouse secondary antibodies were purchased from Jackson Immunoresearch Laboratories. For the NMJ analyses, 3rd instar larvae were dissected and fixed for 5 minutes in Bouin’s
fixative. Imaginal disc dissections were performed on 3rd instar larvae in phosphate-buffered saline (PBS). Discs were kept on ice until fixation in 3% paraformaldehyde in PBS. Stained specimens were mounted in FluoroGuard Antifade Reagent (Bio-Rad), and images were obtained with a Zeiss LSM510 confocal microscope.

Bouton numbers were counted based on the Discs large and Synaptotagmin staining in the A2 segment between muscles 6 and 7. The ratio of muscle area for the various genotypes was normalized to wild-type. GhuRIIA morphometric analyses were performed as described previously [66].

Supporting Information

Figure S1 Specificity of the anti-SMN antibodies. (A–C) Wing discs from 3rd instar larvae overexpressing the USAS-FLAG-Smn transgenic rescue construct using the vestigialGAL driver were stained with antibodies against the FLAG peptide (green) (A) and SMN (red) (B). (C) Merge of (A) and (B) showing the overlapping expression of SMN and FLAG within the vestigial expression domain. (D) Wild-type and (E) vestigialGAL pWIZ[UAS-Smn-RNAi]N4 3rd instar wing discs were stained with antibodies against SMN (green). (F) Western blots of a serial dilution of S2 cell extracts (1: 20 μg; 2: 40 μg; 3: 60 μg; 4: 80 μg total protein) using the polyclonal (left) and monoclonal (right) antisem against SMN recognize a single band of approximately 28 kD in size.

Found at: doi:10.1371/journal.pone.0003209.s001 (4.46 MB TIF)

Figure S2 SMN post-synaptic staining is abolished by muscle specific SMN knockdown. (A–F) The morphology of the NMJ between muscles 6 and 7 in the A2 segment was observed in different genetic backgrounds using antibodies against SMN (green) and the post-synaptic marker, Discs large (red). (A–C) Wild-type: anti-DLG (A), anti-SMN (B) and (C) merge of (A) and (B). (D–F) Transgenic animals containing hosa24BGAL4 and pWIZ[UAS-Smn-RNAi]N4 anti-DLG (D), anti-SMN (E) and (F) merge of (D) and (E). In this background, SMN staining is reduced (E).

Found at: doi:10.1371/journal.pone.0003209.s002 (4.46 MB TIF)

Figure S3 Pre-synaptic ghost bouton counts are elevated in Smn animals. The morphology of the NMJ between muscles 6 and 7 in the A2 segment was observed in different Smn backgrounds using the pre-synaptic (Synaptotagmin) and post-synaptic (Discs large) markers. Ghost bouton counts were determined by assessing the numbers of boutons that stained positive for Synaptotagmin and failed to stain for Discs large. All combinations examined [SmnN43/SmnN101, SmnN596/SmnN101 and SmnN109/SmnN109] displayed elevated numbers of pre-synaptic ghost boutons when compared to wild-type.

Found at: doi:10.1371/journal.pone.0003209.s003 (0.21 MB TIF)

Figure S4 pMad staining of vestigialGAL, UAS-Smn-RNAi transgenic animals. (A–B) 3rd instar wing discs of vestigialGAL pWIZ[UAS-Smn-RNAi]N4 animals are stained with antibodies against SMN (red) (A) and pMad (green) (B). pMad staining is reduced in the dorsoventral boundary of the wing disc where SMN expression is decreased (see Figure 10 for wild-type control).

Found at: doi:10.1371/journal.pone.0003209.s004 (1.37 MB TIF)

Figure S5 NMJ analysis of Smn enhancers. Modification of the NMJ morphology between muscles 6 and 7 in the A2 segment was assayed in the elavGAL pWIZ[UAS-Smn-RNAi]C24 background in trans with all identified modifiers using the pre-synaptic (Horseradish peroxidase (HRP)) and post-synaptic (GhuRIIA) markers (see Materials and Methods). In the three cases (f04448, d09001 and d00698) that did not show significant phenotypic alteration, the pWIZ[UAS-Smn-RNAi]N3 allele was also used. In this background, strain f04448 and d09001 enhanced, whereas d00698 showed no interaction (data not shown and Figure 7).

Found at: doi:10.1371/journal.pone.0003209.s005 (0.74 MB TIF)

Figure S6 NMJ analysis of Smn suppressors. Modification of the NMJ morphology between muscles 6 and 7 in the A2 segment was assayed in the elavGAL pWIZ[UAS-Smn-RNAi]C24 background in trans with all identified modifiers using the pre-synaptic (Horseradish peroxidase (HRP)) and post-synaptic (GhuRIIA) markers (see Materials and Methods).

Found at: doi:10.1371/journal.pone.0003209.s006 (0.78 MB TIF)

Acknowledgments

We wish to thank April Duckworth, Melanie Smith, and Waineshef Tefera for their technical supports. We want to thank Tom Barbs, Jevode Harris, John Satterlee, James Shrigl, and Amy Walker for discussion and sharing their unpublished results. We also wish to thank Margaret L. Winberg of the SMAF, Robert Lake, Pallavi Kashetrapal, Cecilia Lu and Catherine Dubreuil for critically editing the manuscript.

Author Contributions

Conceived and designed the experiments: HCHC DND TY MWK DVV. Performed the experiments: HCHC DND TY VS DVV. Analyzed the data: HCHC DND TY VS. Conceived and designed the experiments: HCHC DND TY MWK DVV.

References


