Mutations in the *Caenorhabditis elegans* U2AF Large Subunit UAF-1 Alter the Choice of a 3’ Splice Site *In Vivo*

Long Ma, H. Robert Horvitz*

Howard Hughes Medical Institute, Department of Biology, Massachusetts Institute of Technology, Cambridge, Massachusetts, United States of America

Abstract

The removal of introns from eukaryotic RNA transcripts requires the activities of five multi-component ribonucleoprotein complexes and numerous associated proteins. The lack of mutations affecting splicing factors essential for animal survival has limited the study of the *in vivo* regulation of splicing. From a screen for suppressors of the *Caenorhabditis elegans* unc-93(e1500) rubberband Unc phenotype, we identified mutations in genes that encode the *C. elegans* orthologs of two splicing factors, the U2AF large subunit (UAF-1) and SF1/BBP (SFA-1). The uaf-1(n4588) mutation resulted in temperature-sensitive lethality and caused the unc-93 RNA transcript to be spliced using a cryptic 3’ splice site generated by the unc-93(e1500) missense mutation. The sfa-1(n4562) mutation did not cause the utilization of this cryptic 3’ splice site. We isolated four uaf-1(n4588) intragenic suppressors that restored the viability of uaf-1 mutants at 25°C. These suppressors differentially affected the recognition of the cryptic 3’ splice site and implicated a small region of UAF-1 affecting the splicing of an unknown gene. Our observations provide *in vivo* evidence that UAF-1 can act in regulating 3’ splice-site choice and establish a system that can be used to investigate the *in vivo* regulation of RNA splicing in *C. elegans*.

Introduction

Eukaryotic genes contain intervening introns that are spliced from transcribed pre-mRNAs to generate functional coding mRNAs [1,2]. Alternative splicing results in distinct mRNAs that encode proteins with distinct functions, increases the proteome size and is believed to be important to the biological complexity of metazoans [1,3,4]. In *C. elegans*, mRNA transcripts of at least 13% of predicted genes are alternatively spliced [5]. In humans, most genes are alternatively spliced [6,7]. A dramatic example of alternative splicing is provided by the *Drosophila* gene *Dscam* (*Down syndrome cell adhesion molecule*), which through alternative splicing could potentially generate over 30,000 isoforms [8], some of which have been shown to play important roles in immune responses [9] and neuronal arborization [10–12]. Mutations affecting the splicing process or splicing machinery cause numerous human diseases [13,14].

Pre-mRNA splicing involves five small nuclear ribonucleoprotein particles (snRNPs) and numerous associated factors [1,2,15]. The U1 snRNP recognizes the 5’ splice donor site through base-pairing between the U1 snRNA and the 5’ splice site of the target intron [16]. The recognition of the 3’ splice acceptor site is achieved by SF1/BBP (splicing factor one/branch-point binding protein) and the large and small subunits of U2AF (U2 auxiliary factor) [17–23]. In mammals, SF1/BBP binds a weak consensus branch-point sequence, the U2AF large subunit binds a long polypyrimidine sequence and the U2AF small subunit binds the 3’ splice site YAG [19,21,24–26]. The yeast *Saccharomyces cerevisiae* lacks a U2AF small subunit and a polypyrimidine sequence in its introns, and the recognition of a 3’ splice site is achieved by binding of SF1/BBP to a highly conserved consensus branch-point sequence [17,24,27,28]. In the nematode *Caenorhabditis elegans*, there is no consensus branch-point sequence or long polypyrimidine sequence, and the recognition of a 3’ splice site is achieved by the binding of the U2AF large and small subunits to a consensus UUUUCAGR sequence in which “AG” is the 3’ splice site [23,29].

Splicing is also regulated by many Arginine-Serine-rich RNA-binding SR proteins [30–33] and hnRNP RNA-binding proteins [4]. These splicing factors recognize enhancer or silencer sequences in exons and introns to regulate the specificity and efficiency of splicing [4]. The genetic interactions among splicing factors and how signaling events regulate splicing efficiency and specificity are only partially understood.

*C. elegans* is a genetically tractable organism and has been used to study a broad variety of biological problems. Our laboratory has analyzed a set of genes, *unc-93, sup-9* and *sup-10*, that encode components of a presumptive *C. elegans* two-pore domain K+ channel, which is a genetically tractable organism and has been used to study a broad variety of biological problems.
Author Summary

Eukaryotic genes contain intervening intronic sequences that must be removed from pre-mRNA transcripts by RNA splicing to generate functional messenger RNAs. While studying genes that encode and control a presumptive muscle potassium channel complex in the nematode *Caenorhabditis elegans*, we found that mutations in two splicing factors, the U2AF large subunit and SF1/BBP, suppress the rubberband Unc phenotype caused by a rare missense mutation in the gene unc-93. Mutations affecting the U2AF large subunit caused the recognition of a cryptic 3′ splice site generated by the unc-93 mutation, providing in vivo evidence that the U2AF large subunit can affect splice-site selection. By contrast, an SF1/BBP mutation that suppressed the rubberband Unc phenotype did not cause splicing using this cryptic 3′ splice site. Our genetic studies identified a region of the U2AF large subunit important for its effect on 3′ splice-site choice. Our mutagenesis analysis of *in vivo* transgene splicing identified a positional effect on weak 3′ splice site selection and nucleotides of the endogenous 3′ splice site important for recognition. The system we have defined should facilitate future *in vivo* analyses of pre-mRNA splicing.

channel complex and regulate muscle activity [34–37]. Rare gain-of-function (gf) mutations in any of these three genes cause abnormal body-muscle contraction and are thought to activate the SUP-9 K′ channel. The gf mutant animals are defective in egg laying, sluggish and exhibit a rubberband phenotype: when prodded on the head, the animal contracts and relaxes along its entire body without moving backwards. Complete loss-of-function (lf) mutations of unc-93, sup-9 and sup-10 do not cause any obvious abnormalities [35,36]. The SUP-9 protein is similar to the mammalian Two-pore Acid Sensitive K′ channels TASK-1 and TASK-3 [34]. sup-10 encodes a novel single-transmembrane domain protein without identified mammalian homologs [34], unc-93 encodes a multiple transmembrane-domain protein that defines a novel family of proteins conserved from *C. elegans* to mammals [34,37]. A mammalian UNC-93 homolog, UNC-93b, plays important roles in the innate immune response, probably by regulating signals mediated through Toll-like receptors [38–42].

Previous genetic screens for genes that affect the activities of unc-93, sup-9 and sup-10 were not designed to identify genes essential for fertility or animal survival. To seek such essential genes, we performed a clonal genetic screen for suppressors of the locomotion defect caused by the *unc-93* gf mutation *e1500*. In this paper, we describe our studies of two suppressors identified from this screen and the establishment of a reporter system for *in vivo* analysis of RNA splicing in *C. elegans*. We suggest that the U2AF large subunit affects 3′ splice site recognition and that some aspect of the function of the putative UNC-93/SUP-9/SUP-10 two-pore domain potassium channel complex depends on an unidentified gene the processing of which requires the functions of the U2AF large subunit and SF1/BBP.

Results

A clonal screen identified two new *unc-93(e1500)* suppressor genes essential for survival

Rare gf mutations in the *C. elegans* genes *unc-93*, *sup-9* and *sup-10* cause a rubberband Unc phenotype, while lf mutations in these genes result in a phenotypically wild-type phenotype [35,36,43]. Previous screens for suppressors of the rubberband Unc phenotype were not designed to identify genes essential for animal survival [35,36,43,44]. We performed a clonal genetic screen to seek new suppressors of the rubberband Unc phenotype caused by the *unc-93(e1500)* mutation, with the goal of identifying mutations that also cause sterility or lethality (see Materials and Methods). We screened about 10,000 F1 progeny (about 20,000 mutagenized haploid genomes) of P1 animals mutagenized with EMS (ethyl methanesulfonate) and isolated the suppressors *n4588* and *n562*. *n4588* causes embryonic lethality at 25°C, and *n562* causes sterility at all temperatures. By mapping these mutations, we found that *n4588* and *n562* are not alleles of any previously characterized suppressors of the rubberband Unc phenotype (see Materials and Methods).

*n4588* is a missense mutation in *uaf-1*, which encodes the *C. elegans* ortholog of the U2AF large subunit splicing factor

*n4588* is a strong recessive suppressor of the locomotion defect and rubberband phenotype of *unc-93(e1500)* animals (Table 1). *n4588* is closely linked to a mutation that causes a recessive temperature-sensitive (ts) lethal phenotype and results in embryonic lethality at 25°C (see Materials and Methods) (data not shown). At 20°C the lethal phenotype was incompletely penetrant. At 15°C *n4588* animals appeared similar to wild-type animals. We mapped the ts-lethal phenotype of *n4588* animals to an 80 kb region on the left arm of LG III (see Materials and Methods). By determining the sequences of the coding exons of four of eight genes located within this 80 kb interval, we found a point mutation determining the sequences of the coding exons of four of eight Unc phenotype genes located within this 80 kb interval, we found a point mutation

Expression of *uaf-1a* in body-wall muscles rescued the suppression of *unc-93(e1500)* by *n4588*

To test whether the point mutation found in the *uaf-1a* isof orm caused the suppressor activity of *n4588*, we generated transgenic animals expressing a UAF-1a::GFP fusion protein under the control of a *myo-3* myosin promoter, which drives transgene expression in body-wall muscle cells [49]. This *uaf-1a* cDNA, which encodes a predicted full-length UAF-1 protein, restored the Unc phenotype when expressed in *uaf-1a(n4588) unc-93(e1500)* animals (Figure 1B and Table 2). A predicted short *uaf-1* isof orm, *uaf-1b*, which contains only part of the second RRM domain and the C-terminal UHM domain, failed to restore the *Unc* phenotype (Figure 1B and Table 2). Expression of these *myo-3*-driven transgenes (*uaf-1a* and *uaf-1b*) in wild-type animals did not cause a rubberband Unc phenotype or any other visible abnormality (data not shown). Introducing stop codons or the *n4588* T180I
mutation into the full-length uaf-1a cDNA abrogated its rescuing activity (Table 2). Heat-shock-driven expression of a transgene expressing the full-length uaf-1a cDNA under control of a heat-shock promoter [50] partially rescued both the suppression of unc-93(e1500) by uaf-1(n4588) and the ts-lethality caused by uaf-1(n4588) (Table 2 and data not shown), suggesting that the T180I mutation also caused the ts-lethal phenotype. Feeding unc-93(e1500) animals with uaf-1 RNAi-expressing bacteria (Figure 1B and Materials and Methods) also partially suppressed the Unc phenotype (Table 2), suggesting that normal expression of uaf-1 is required for the rubberband Unc phenotype caused by unc-93(e1500).

We isolated a uaf-1 deletion mutation, n5222Δ, which removes the fourth exon (encoding part of the first RRM and part of the second RRM of UAF-1a) of the uaf-1a isoform (Figure 1A) and is predicted to cause a frameshift after amino acid 229 if the third

Table 1. Suppression of unc-93(e1500) and sup-10(n983) by uaf-1 and sfa-1 mutations.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Bodybends/30 sec ±SD</th>
<th>Rubberband phenotype</th>
<th>n</th>
</tr>
</thead>
<tbody>
<tr>
<td>wild-type</td>
<td>20.4 ± 3.7</td>
<td>None</td>
<td>15</td>
</tr>
<tr>
<td>uaf-1(n4588)</td>
<td>23.1 ± 4.1</td>
<td>None</td>
<td>20</td>
</tr>
<tr>
<td>sfa-1(n4562)</td>
<td>26.5 ± 4.9</td>
<td>None</td>
<td>20</td>
</tr>
<tr>
<td>unc-93(e1500)</td>
<td>0.9 ± 1.2</td>
<td>Strong</td>
<td>15</td>
</tr>
<tr>
<td>uaf-1(n4588) unc-93(e1500)</td>
<td>21.0 ± 5.5</td>
<td>None</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588) unc-93(e1500)/uaf-1(n5222Δ) unc-93(e1500)</td>
<td>22.2 ± 2.4</td>
<td>None</td>
<td>20</td>
</tr>
<tr>
<td>unc-93(e1500); sfa-1(n4562)</td>
<td>13.5 ± 4.9</td>
<td>Weak</td>
<td>15</td>
</tr>
<tr>
<td>unc-93(n200)</td>
<td>15.6 ± 3.5</td>
<td>Weak</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588) unc-93(n200)</td>
<td>10.2 ± 2.2</td>
<td>Weak</td>
<td>20</td>
</tr>
<tr>
<td>unc-93(n200); sfa-1(n4562)</td>
<td>13.3 ± 2.5</td>
<td>Weak</td>
<td>20</td>
</tr>
<tr>
<td>sup-10(n983)</td>
<td>4.3 ± 1.9</td>
<td>Moderate</td>
<td>15</td>
</tr>
<tr>
<td>uaf-1(n4588); sup-10(n983)</td>
<td>24.5 ± 4.1</td>
<td>None</td>
<td>20</td>
</tr>
<tr>
<td>sfa-1(n4562); sup-10(n983)</td>
<td>18.8 ± 4.0</td>
<td>Weak</td>
<td>15</td>
</tr>
<tr>
<td>sup-9(n1550); sup-18(n1014)*</td>
<td>0.1 ± 0.4</td>
<td>Severe</td>
<td>15</td>
</tr>
<tr>
<td>sup-9(n1550); uaf-1(n4588) sup-18(n1014)*</td>
<td>0.1 ± 0.2</td>
<td>Severe</td>
<td>20</td>
</tr>
<tr>
<td>sup-9(n1550); sup-18(n1014)*; sfa-1(n4562)</td>
<td>1.0 ± 1.3</td>
<td>Severe</td>
<td>12</td>
</tr>
</tbody>
</table>

Locomotion and the rubberband phenotype were scored as described in Materials and Methods. Genotypes were as listed.

*sup-18(n1014) was included to allow the survival of sup-9(n1550) animals. SD: Standard deviation.

doi:10.1371/journal.pgen.1000708.t001

Figure 1. uaf-1 gene and proteins. (A) Genomic structure of the uaf-1 isoforms uaf-1a and uaf-1b (adapted from Wormbase WS189) [45]. The locations of the n4588 missense mutation and the n5222 deletion allele are indicated. Black boxes: coding exons. Open box: 3' UTR. Positions of start (ATG) and stop codons (TAA) are indicated. SL1 and SL2, splice leaders associated with the uaf-1a transcript [45]. (B) Predicted UAF-1 protein domains encoded by uaf-1a and uaf-1b cDNAs, the position of the T180I change caused by the n4588 mutation and the domains affected by the n5222Δ deletion are shown. RNAi fragment: the portion of the uaf-1a cDNA used within a dsRNA-expressing plasmid for RNAi. RS: Arginine-Serine rich domain. W: U2AF small subunit-interacting domain. RRM: RNA recognition motif. UHM: U2AF homology motif.

doi:10.1371/journal.pgen.1000708.g001
was not suppressed by (Table 1). The strongest rubberband mutant, \textit{93(e1500)} animals, was completely suppressed by \textit{unc-93} distinct in its suppression pattern from other known suppressors of \textit{uaf-1(n4588)} that \textit{93(n200)} these other mutations (Table 1). Neither the weak locomotion \textit{uaf-1a} and fifth exons of the \textit{uaf-1a} isoform are spliced together. \textit{uaf-1(n5222A)}+ animals grew and moved like the wild type, and \textit{uaf-1(n5222A)/+} did not suppress the rubberband Unc phenotype of \textit{uaf-1(n4588)} animals (data not shown). \textit{uaf-1(n5222A)} homozygous mutants arrested and died at the late L1 to early L2 larval stages (based on body size), which precluded examination of the rubberband Unc behavior of \textit{n5222A} homozygous animals (see Materials and Methods). \textit{uaf-1(n4588)}/\textit{uaf-1(n5222A)} suppressed the rubberband Unc phenotype of \textit{uaf-1(n4588)} animals as strongly as did homozygous \textit{uaf-1(n4588)} (Table 1). Similar to \textit{uaf-1(n4588)} homozygotes, \textit{uaf-1(n4588)}/\textit{uaf-1(n5222A)} animals died embryonically at 25°C (data not shown). These results establish that \textit{n5288} is an allele of \textit{uaf-1} and that reducing the dosage of the \textit{uaf-1(n4588)} allele by 50% does not affect the suppression of the rubberband Unc phenotype of \textit{uaf-1(n4588)} animals. These data suggest that \textit{uaf-1(n4588)} causes either a reduction/loss of \textit{uaf-1} activity or an altered \textit{uaf-1} activity that is antagonized by the wild-type \textit{uaf-1} gene (see Discussion).

\textit{uaf-1(n4588)} differentially suppressed different rubberband Unc mutants

Locomotion defects similar to those caused by \textit{unc-93(e1500)} are also caused by the \textit{unc-93(n200)} mutation [36] and by \textit{gf} mutations in the genes \textit{sup-9} and \textit{sup-10} [35,43]. We tested whether the \textit{uaf-1(n4588)} mutation could suppress the Unc phenotype caused by these other mutations (Table 1). Neither the weak locomotion defect nor the weak rubber band Unc defect caused by \textit{unc-93(n200)} was suppressed by \textit{uaf-1(n4588)} (Table 1). \textit{sup-10(n983)}, which causes a rubberband Unc phenotype that is more severe than that of \textit{unc-93(n200)} animals but less severe than that of \textit{unc-93(e1500)} animals, was completely suppressed by \textit{uaf-1(n4588)} (Table 1). The strongest rubberband mutant, \textit{sup-9(n1550)} [43], was not suppressed by \textit{uaf-1(n4588)} (Table 1). These data suggest that \textit{uaf-1(n4588)} is an allele-specific suppressor of \textit{unc-93} but not a gene-specific suppressor of the rubberband Unc mutants and is distinct in its suppression pattern from other known suppressors of \textit{unc-93}, \textit{sup-9} and \textit{sup-10} (see Discussion).

Null mutations of \textit{unc-93}, \textit{sup-10} and \textit{sup-9} do not cause visible abnormalities in a wild-type background [35,36]. We tested whether these genes might function redundantly with \textit{uaf-1}, by generating double mutants containing \textit{uaf-1(n4588)} and null mutations of \textit{unc-93}, \textit{sup-10} or \textit{sup-9}. We found that such double mutant animals grew and behaved indistinguishably from \textit{uaf-1(n4588)} single mutant animals (Table S1), suggesting that \textit{unc-93}, \textit{sup-10} and \textit{sup-9} are not functionally redundant with \textit{uaf-1}. To examine whether \textit{uaf-1(n4588)} can suppress \textit{gf} mutations affecting other two-domain potassium channels, we generated double mutant animals containing the \textit{uaf-1(n4588)} mutation and the \textit{unc-93(n5222D)} [51] (J. Thomas, personal communication), \textit{egl-23(n601D)} [52] (J. Thomas, personal communication) or \textit{twk-18(n1913D)} [53] mutations. The behavioral defects of these mutants were not suppressed by \textit{uaf-1(n4588)} (Table S1).

To determine if the expression of \textit{unc-93}, \textit{sup-9}, \textit{sup-10} or any of the other genes known to interact with these genes is reduced in \textit{uaf-1(n4588)} animals, we examined \textit{unc-93}, \textit{sup-10}, \textit{sup-9} and \textit{sup-18} [35] (I. Perez de la Cruz and H.R.H., unpublished results) and \textit{sup-11} [54] (E. Alvarez-Saavedra and H.R.H, unpublished results) mRNA levels. Like if mutations in \textit{unc-93}, \textit{sup-10} and \textit{sup-9}, if mutations in \textit{sup-18} and \textit{gf} mutations in \textit{sup-11} can suppress the rubberband Unc phenotype caused by \textit{gf} mutations in \textit{unc-93}, \textit{sup-9} and \textit{sup-10}. Using real-time qRT–PCR, we found no obvious reduction of the mRNA levels of these five genes (Figure S1). We also examined the expression of \textit{UAF-1} protein using western blotting [45] and found no apparent difference in \textit{UAF-1} protein levels. To examine whether \textit{uaf-1(n4588)} altered the splicing of \textit{unc-93(e1500)} exon 9 by recognizing a cryptic 3’ splice site generated by the \textit{unc-93(e1500)} missense mutation

We tested whether the splicing of \textit{unc-93} is altered by \textit{uaf-1(n4588)}. We examined the splicing of each exon of \textit{unc-93} in wild-

### Table 2. \textit{uaf-1a} and \textit{sfa-1} transgenes rescued the suppression of the rubberband Unc phenotype of \textit{unc-93(e1500)} animals by \textit{uaf-1(n4588)} and \textit{sfa-1(n4562)}.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Phenotype</th>
<th>Rescued lines/Total lines</th>
</tr>
</thead>
<tbody>
<tr>
<td>\textit{uaf-1(n4588)} \textit{unc-93(e1500)}</td>
<td>Strong Unc</td>
<td>NA</td>
</tr>
<tr>
<td>\textit{uaf-1(n4588)} \textit{unc-93(e1500)}; \textit{nEx[nmyo-3\textit{uaf-1a cDNA::gfp}]}</td>
<td>Non-Unc</td>
<td>NA</td>
</tr>
<tr>
<td>\textit{uaf-1(n4588)} \textit{unc-93(e1500)}; \textit{nEx[nmyo-3\textit{uaf-1b cDNA::gfp}]}</td>
<td>Non-Unc</td>
<td>0/4</td>
</tr>
<tr>
<td>\textit{uaf-1(n4588)} \textit{unc-93(e1500)}; \textit{nEx[nmyo-3\textit{uaf-1a cDNA:G178O;puf, Q182Ochre::gfp}]}</td>
<td>Non-Unc</td>
<td>0/7</td>
</tr>
<tr>
<td>\textit{uaf-1(n4588)} \textit{unc-93(e1500)}; \textit{nEx[psg-18\textit{uaf-1\textit{a cDNA::gfp}]}</td>
<td>Non-Unc</td>
<td>0/2</td>
</tr>
<tr>
<td>\textit{uaf-1(RNAi)} \textit{unc-93(e1500)}</td>
<td>Moderate Unc</td>
<td>5/13</td>
</tr>
<tr>
<td>\textit{unc-93(e1500)}; \textit{sfa-1(n4562)}</td>
<td>Weak Unc</td>
<td>NA</td>
</tr>
<tr>
<td>\textit{unc-93(e1500)}; \textit{sfa-1(n4562)}; \textit{nEx[nmyo-3\textit{sfa-1 cDNA::gfp}]}</td>
<td>Weak Unc</td>
<td>NA</td>
</tr>
<tr>
<td>\textit{unc-93(e1500)}; \textit{sfa-1(n4562)}; \textit{nEx[nmyo-3\textit{uaf-1\textit{a cDNA::gfp}]}</td>
<td>Strong Unc</td>
<td>6/6</td>
</tr>
<tr>
<td>\textit{unc-93(e1500)}; \textit{sfa-1(RNAi)}</td>
<td>Weak Unc</td>
<td>NA</td>
</tr>
</tbody>
</table>

A wild-type \textit{uaf-1a} cDNA expressed in body-wall muscles rescued the suppression of \textit{unc-93(e1500)} by \textit{uaf-1(n4588)}. A \textit{gf} cDNA for the shorter \textit{uaf-1a} isoform, \textit{uaf-1b}, failed to rescue. Introducing stop codons or the \textit{n5288} T180I mutation into the \textit{uaf-1a} cDNA abrogated the rescuing activity. Inducing \textit{uaf-1} expression with heat-shock partially rescued the suppression of \textit{unc-93(e1500)}. Reducing \textit{uaf-1} expression by RNAi partially suppressed the rubberband Unc phenotype of \textit{unc-93(e1500)}. A wild-type \textit{sfa-1} \textit{cDNA} expressed in body-wall muscles of \textit{unc-93(e1500)}; \textit{sfa-1(n4562)} animals restored the rubberband Unc phenotype. Reducing \textit{sfa-1} expression by RNAi partially suppressed the rubberband Unc phenotype. Total lines: number of stable independent transgenic lines that expressed the transgenes. Rescued lines: number of transgenic lines that the rubberband Unc phenotype of \textit{unc-93(e1500)} was restored. Non-transgenic animals were used for comparison. NA: Not applicable. doi:10.1371/journal.pgen.1000708.t002
type, uaf-1(n4588), unc-93(e1500), uaf-1(n4588) unc-93(e1500), unc-93(n200) and uaf-1(n4588) unc-93(n200) animals by RT–PCR (Figure 2). Every exon other than exon 9 of the unc-93 gene was spliced similarly in all genotypes examined (Figure 2A and 2B). However, we had difficulty in consistently amplifying a cDNA band from uaf-1(n4588) unc-93(e1500) animals (data not shown) using the PCR primer pairs at the 3’ end of exon 8 and the 5’ end of exon 9 (indicated in black in Figure 2A). We therefore used a new pair of PCR primers that should amplify a larger region between exons 8 and 9 (indicated in red in Figure 2A). With the new pair of PCR primers, we found that in unc-93(e1500) animals the region between exon 8 and 9 corresponded to a weak but consistent RT–PCR product of a reduced length (Figure 2C, lane 3, lower arrow), and this RT–PCR product was seen only in samples from unc-93(e1500) mutant animals (Figure 2C, lower arrow). In uaf-1(n4588) unc-93(e1500) animals, the RT–PCR product of reduced length was the most prominent product (Figure 2C, lane 4, lower arrow). We determined the sequence of this RT–PCR product and found that it was a consequence of an alternative splicing event that utilized a cryptic 3’ splice site in exon 9. This cryptic 3’ splice site was generated by the unc-93(e1500) missense mutation, which has a G-to-A transition that changes amino acid 388 from Gly to Arg [37] (Figure 2E). Quantification using Taqman RT–PCR (see Figure 4A for probe designs) indicated that the alternatively spliced exon 9 was about 1.3% of all spliced unc-93 exon 9 in unc-93(e1500) animals and 68% in uaf-1(n4588) unc-93(e1500) animals (Figure 4B). Both non-quantitative (Figure 2C) and quantitative RT–PCR (Figure 4B) analyses failed to detect alternatively spliced

Figure 2. uaf-1(n4588) dramatically alters unc-93(e1500) but not unc-93(+) exon 9 splicing. (A) Genomic structure of the unc-93 gene. Exons of unc-93 are indicated by black boxes and introns by thin lines. The part of exon 9 that was removed by alternative splicing in uaf-1(n4588) unc-93(e1500) exon 9. (B) RT–PCR experiments to examine the splicing of unc-93 mRNA. En–En+1 (arrows) indicates the junction of two adjacent exons. Genotypes of each sample are indicated at the top. Small arrowheads indicate primer dimers, which form variably in RT–PCR experiments and are template-independent. (C) A weak alternatively spliced unc-93 exon 9 was detected in unc-93(e1500) animals (lane 3, lower arrow). In uaf-1(n4588) unc-93(e1500) animals (lane 4, lower arrow), this alternative spliced product was dramatically enhanced. The diagrams on the left illustrate the splicing events responsible for the generation of each band. The upper band reflects the splicing seen in wild-type unc-93, while the lower band reflects the use of a cryptic 3’ splice site generated by the unc-93(e1500) missense mutation. Red arrows indicate the positions of PCR primers. Genotypes of each sample are listed at the top. (D) Reducing UAF-1 levels with RNAi did not cause increased splicing at the cryptic 3’ splice site found in unc-93(e1500) exon 9. (E) Partial genomic sequences of unc-93 intron 8 (lowercase letters) and exon 9 (uppercase letters) in the wild type (above) and in unc-93(e1500) mutants (below). The G-to-A nucleotide change of the e1500 mutation is indicated with an arrow. The AG sequence (red) forms a cryptic 3’ splice site that is recognized by the splicing machinery in uaf-1(n4588) animals.

doi:10.1371/journal.pgen.1000708.g002
The alternatively spliced unc-93 transcript is predicted to encode a truncated protein lacking 12 amino acids in one of the predicted transmembrane domains [37] (data not shown). To test whether the alternatively spliced unc-93 transcript in uaf-1(n4588) unc-93(n1500) animals encoded a functional UNC-93 protein, we expressed the cDNA in the body-wall muscles of sub-9(n1550); unc-93(k12Δ) animals [34,44] and found that this transgene did not restore the rubberband Unc phenotype (Table S2). By contrast, expression of the wild-type unc-93 cDNA in these animals restored the severe rubberband Unc phenotype. These results suggest that the alternatively spliced unc-93 transcript encoded a lf UNC-93 protein or possibly a dominant-negative UNC-93 protein.

To test the latter possibility, we expressed either unc-93 wild-type cDNA or the alternatively spliced unc-93 cDNA in the body-wall muscles of unc-93(e1500) animals (Table S3). Consistent with previous observations that unc-93(n1500)/+ animals have better locomotion than unc-93(e1500) animals [36,37], overexpression of wild-type unc-93 cDNA dramatically improved the locomotion of unc-93(e1500) animals (Table S3). If the alternatively spliced unc-93 transcript encoded an UNC-93 protein that could interfere with the endogenous UNC-93 function and cause the suppression of the rubberband Unc phenotype by uaf-1(n4588) (68% alternatively spliced unc-93 transcript), the transgene should also suppress the Unc phenotype of unc-93(e1500) animals. However, expression of the alternatively spliced unc-93 transcript in the body-wall muscles did not suppress the Unc phenotype of unc-93(n1500) animals (Table S3), suggesting that the alternatively spliced unc-93 transcript caused a loss of unc-93 function and did not interfere with endogenous unc-93 function.

To examine whether reducing UAF-1 expression, like the uaf-1(n4588) mutation, would alter the splicing of unc-93(e1500) exon 9, we fed animals with bacteria expressing dsRNA targeting uaf-1 and assessed unc-93 exon 9 splicing. As shown in Figure 2D and Figure 4B, reducing UAF-1 did not increase the relative level of alternatively spliced unc-93(e1500) exon 9. The RNAi treatment did significantly reduce the level of UAF-1 protein (Figure S2). That reducing uaf-1 expression with RNAi did not cause altered splicing of unc-93(e1500) exon 9 similarly to that by the uaf-1(n4588) mutation is consistent with the hypothesis that uaf-1(n4588) does not reduce the function of UAF-1α but rather alters the function of UAF-1α, which leads to the recognition of the cryptic 3’ splice site of unc-93(e1500) exon 9 (see Discussion).

However, it is possible that uaf-1(n4588) reduces uaf-1 function and that uaf-1(RNAi) does not reduce uaf-1 function as much.

uaf-1(n4588) suppressed the rubberband Unc phenotype of sup-10(n983) animals but did not suppress the rubberband Unc phenotype of unc-93(n1500) and sup-9(n1550) animals (Table 1). Quantitative RT–PCR did not indicate reduction of sup-10 mRNA in uaf-1(n4588) animals (Figure S1). We examined whether the sup-10(n983) transcript was alternatively spliced in uaf-1(n4588) mutants. uaf-1(n4588) did not cause the appearance of a sup-10 cDNA band different in size from the full-length sup-10 cDNA (Figure S3A). We determined the sequences of the sup-10 cDNA RT–PCR products from wild-type, sup-10(n983), uaf-1(n4588) and uaf-1(n4588); sup-10(n983) animals and found that an alternatively spliced sup-10 transcript (data not shown).

To test whether uaf-1(n4588) can affect the splicing of all genes known to be alternatively spliced, we tested for genetic interactions between uaf-1(n4588) and unc-52(e669); unc-52 encodes the C. elegans ortholog of human basement membrane-specific heparan sulfate proteoglycan core protein, and mutations affecting unc-52 cause adult paralysis [55,56]. The Unc phenotype of unc-52(e669) can be suppressed by lfs mutations of smu-1 and smu-2, genes that encode C. elegans homologs of mammalian splicing factors [57–59]. The unc-52(e669) mutation causes a pre-mature stop in unc-52 exon 17 [60], and smu-1 and smu-2 mutations suppress unc-52(e669) by removing exon 17 and generating an alternatively spliced and functional transcript [58]. The unc-52(e444) mutation causes a pre-mature stop in unc-52 exon 18, which is not removed in smu-1 and smu-2 mutant animals, leading to a transcript with a premature stop codon. Double mutants containing the unc-52(e444) mutation and the smu-1 or smu-2 mutations display an Unc phenotype [58]. We examined the Unc phenotypes of unc-52(e669); uaf-1(n4588) and unc-52(e444); uaf-1(n4588) animals and found that uaf-1(n4588) did not suppress either unc-52(e669) or unc-52(e444) (Table S1), implying that the uaf-1(n4588) mutation did not affect the alternative splicing of unc-52(e669) exon 17 and thus does not affect all cases of alternative splicing non-specifically.

n4562 is a nonsense mutation in sfa-1, which encodes the C. elegans ortholog of the splicing factor SF1/BBP

The mutation n4562 was also isolated from our clonal screen as a suppressor of the rubberband Unc phenotype of unc-93(e1500) animals. The suppressed phenotype was recessive, and n4562 caused a completely penetrant recessive sterility that was temperature independent and was tightly linked to its suppressor activity (see Materials and Methods). Like uaf-1(n4588), n4562 suppressed unc-93(e1500) and sup-10(n983) but did not suppress unc-93(n1500) or sup-9(n1550) (Table 1). Therefore, n4562 is also an allele-specific suppressor of unc-93 gf mutations but not a gene-specific suppressor for the rubberband Unc genes.

We mapped n4562 to the right of LG IV (see Materials and Methods). No known suppressors of unc-93(e1500) are located in this region. The genes uaf-2, encoding the C. elegans U2AF small subunit ortholog [61] and Y116A8C.32, encoding the SF1/BBP (splicing factor 1/branch-point binding protein) ortholog [62], are located in this genomic region and are expressed from the same operon together with three other genes (Wormbase WS189, Y116A8C.32, Y116A8C.32, Y116A8C.32). Orthologs of UAF-2 and SF1/BBP function with the ortholog of UAF-1 to regulate pre-mRNA splicing [2], leading us to consider these two genes as candidates for being mutated by n4562. We determined the DNA sequences of coding regions of uaf-2 and Y116A8C.32 from n4562 animals and identified a nonsense mutation in Y116A8C.32, which we named sfa-1 (sfa, splicing factor) (Figure 3A). n4562 changed amino acid 458 from a Cys (TGT) to an opal stop (TGA) codon in a conserved C2HC-type zinc finger domain of the predicted SFA-1 protein (Figure 3A and 3B). This mutation is predicted to cause the expression of a truncated SFA-1 protein. We rescued the suppression of unc-93(e1500) by sfa-1(n4562) by expressing in body-wall muscles an SFA-1::GFP fusion protein driven by the myo-3 promoter [49] (Table 2). Feeding unc-93(e1500) animals with bacteria expressing dsRNA targeting sfa-1 partially suppressed the rubberband Unc phenotype (Table 2).

We isolated an sfa-1 deletion mutation, n5223A, which removes the third and fourth exons and a majority of the fifth exon (Figure 3A). Together these regions are predicted to encode most (101 aa) of the U2AF large subunit-interacting domain (118 aa) of SFA-1 [62]. n5223A is predicted to cause a frameshift after amino acid 188 if the second exon and the residual fifth exon are spliced together. sfa-1(n5223A) caused recessive embryonic lethality, and sfa-1(n5223A)+ did not suppress the rubberband Unc phenotype of unc-93(e1500) animals (data not shown). sfa-1(n5223A)n5223A+ similarly caused embryonic lethality (data not shown), suggesting that the lethal phenotype of sfa-1(n5223A) homozygotes is caused by...
the \textit{sfa-1(n5223\textDelta)} mutation. The embryonic lethality caused by \textit{sfa-1(n5223\textDelta)} and \textit{sfa-1(n4562)/sfa-1(n5223\textDelta)} precluded the use of \textit{n5223\textDelta} for an analysis of the rubberband Unc phenotype, because our behavioral assays are performed with young adults (see Materials and Methods).

\textbf{sfa-1(n4562)} did not cause alternative splicing of \textit{unc-93(e1500)} exon 9 at the cryptic 3' splice site

To test whether, like \textit{uaf-1(n4588)}, \textit{sfa-1(n4562)} caused alternative splicing of \textit{unc-93(e1500)} exon 9, we used RT--PCR to examine the splicing of \textit{unc-93(e1500)} exon 9. As shown in Figure 3C and Figure 4B, \textit{sfa-1(n4562)} did not cause increased alternative splicing of \textit{unc-93(e1500)} exon 9. We tested the effect of \textit{sfa-1(n4562)} on \textit{unc-93(e1500)} exon 9 splicing by reducing \textit{sfa-1} expression using RNAi (Figure 3D). \textit{sfa-1(RNAi)} did not increase exon 9 alternative splicing (Figure 3D and Figure 4B).

Because (1) the \textit{sfa-1(n4562)} mutation causes a recessive sterile phenotype, which is less severe than the recessive embryonic lethality caused by \textit{sfa-1(n5223\textDelta)}, (2) \textit{sfa-1(RNAi)} phenocopies \textit{sfa-1(n4562)} in the suppression of the rubberband Unc phenotype of \textit{unc-93(e1500)} animals, and (3) \textit{sfa-1(RNAi)} phenocopies \textit{sfa-1(n4562)} in affecting the splicing of \textit{unc-93(e1500)} exon 9, we propose that \textit{sfa-1(n4562)} is a partial \textit{lf} allele of \textit{sfa-1} and that the suppression of the rubberband Unc phenotype of \textit{unc-93(e1500)} animals by \textit{sfa-1(n4562)} is likely caused by reduced \textit{sfa-1} function.

\begin{figure}
\centering
\includegraphics[width=\textwidth]{figure3.png}
\caption{\textbf{sfa-1 gene and protein.} (A) Predicted \textit{sfa-1} gene structure (adapted from Wormbase WS189) [62]. The locations of the \textit{n4562} nonsense mutation and the \textit{n5223} deletion allele are indicated. SL2: splice leader associated with the \textit{sfa-1} transcript [62]. (B) Partial sequence alignment of the conserved zinc finger domains of SF1/BBP orthologs from \textit{C. elegans}, \textit{D. melanogaster} and human. The accession numbers, the accession numbers and the Cys458opal mutation are indicated. (C) Total RNAs were prepared from animals with the indicated genotypes, and RT--PCR experiments were performed to detect the splicing of \textit{unc-93} exon 9. \textit{sfa-1(n4562)} did not increase the alternative splicing of \textit{unc-93(e1500)} exon 9. Genotypes are listed at the top. (D) Total RNAs were prepared from wild-type or \textit{unc-93(e1500)} animals treated with control or \textit{sfa-1 RNAi} and RT--PCR experiments were performed to detect the splicing of \textit{unc-93} exon 9. Reducing SFA-1 by RNAi did not increase the alternative splicing of \textit{unc-93(e1500)} exon 9. RNAi treatments are listed at the top.}
doi:10.1371/journal.pgen.1000708.g003
\end{figure}
To examine whether sfa-1(n4562) affects the alternative splicing of unc-93(e1500) exon 9 caused by the uaf-1(n4588) mutation, we generated uaf-1(n4588); sfa-1(n4562) animals with or without unc-93(e1500). Most uaf-1(n4588); sfa-1(n4562) animals (with or without unc-93(e1500)) died embryonically, and the few that hatched arrested at the L2 larval stage (based on body size) (Figure S4). We failed to obtain a sufficient number of animals for RT–PCR analysis.

We also examined sup-10 splicing in sfa-1(n4562) animals and failed to detect alternative splicing of the sup-10 transcript (Figure S3B).

Intragenic suppressors of uaf-1(n4588) ts-lethality differentially affected the alternative splicing of unc-93(e1500) exon 9

The ts-lethality of uaf-1(n4588) offered a genetic approach to seek new regulators of RNA splicing by screening for suppressors of the ts-lethal phenotype. We performed a genetic screen for suppressors of uaf-1(n4588) ts-lethality at 25°C. From this screen, we isolated four intragenic suppressors, n5120, n5123, n5125 and n5127 (Table 3) and seven extragenic suppressors (see Materials and Methods). To date we have characterized only the intragenic suppressors. uaf-1(n5123) caused an I180F (ATT-to-TTT) change at the same residue mutated by n4588 (T180I) (ACT-to-ATT) (Table 3 and Figure 5) and eliminated the suppression of the

Table 3. Intragenic suppressors of uaf-1(n4588).

<table>
<thead>
<tr>
<th>Alleles of uaf-1</th>
<th>Mutations in UAF-1</th>
<th>Viability at 25°C</th>
</tr>
</thead>
<tbody>
<tr>
<td>n4588</td>
<td>T180I</td>
<td>Lethal</td>
</tr>
<tr>
<td>n5123</td>
<td>T180F</td>
<td>Viable</td>
</tr>
<tr>
<td>n4588 n5120</td>
<td>V179M, T180I</td>
<td>Viable</td>
</tr>
<tr>
<td>n4588 n5125</td>
<td>P177L, T180I</td>
<td>Viable</td>
</tr>
<tr>
<td>n4588 n5127</td>
<td>M157I, T180I</td>
<td>Viable</td>
</tr>
</tbody>
</table>

List of allele numbers and changes of amino acids caused by intragenic suppressors of uaf-1(n4588).

doi:10.1371/journal.pgen.1000708.t003
locomotion defect of unc-93(e1500) (Table 4). uaf-1(n4588 n5120) is predicted to cause a V179M (GTG-to-ATG) change in addition to the n4588 T180I mutation (Table 3 and Figure 5), and uaf-1(n4588 n5120) weakly suppressed unc-93(e1500) (Table 4). uaf-1(n4588 n5125) is predicted to cause a P177L (CCA-to-CTA) change in addition to the n4588 T180I mutation (Table 3 and Figure 5), and uaf-1(n4588 n5125) also weakly suppressed unc-93(e1500) (Table 4). uaf-1(n4588 n5127) is predicted to cause an M157I (ATG-to-ATA) change in addition to the n4588 T180I mutation (Table 3 and Figure 5) and was still a strong suppressor of unc-93(e1500) (Table 4). That the unc-93(e1500) suppressor activities of uaf-1(n4588 n5120), uaf-1(n4588 n5125) and uaf-1(n4588 n5127) were caused by uaf-1 mutations was confirmed by the observation that transgenes expressing uaf-1a (Figure 1A) in the body-wall muscles rescued the unc-93(e1500) suppressor phenotype of these mutants (Table 4). We quantified the splicing of unc-93(e1500) exon 9 in animals containing these uaf-1 mutations using Taqman RT–PCR. As shown in Figure 4B, these uaf-1 mutations exhibited differential effects on the splicing of unc-93(e1500) exon 9. uaf-1(n5123) had no apparent effect (1.6% alternative splicing vs. 1.3% for unc-93(e1500) alone). uaf-1(n4588 n5120) and uaf-1(n4588 n5125) weakly (4% and 2.8%, respectively) and uaf-1(n4588 n5127) moderately (25%) increased the alternative splicing of unc-93(e1500) exon 9 (Figure 4B). None of these mutations affected this splicing event as much as did uaf-1(n4588) (68%) (Figure 4B).

To test whether uaf-1(n4588) could suppress the Unc phenotype of unc-93(e1500) independently of unc-93 splicing, we generated transgenic animals that overexpressed in the body-wall muscles a full-length unc-93 cDNA containing the e1500 gf mutation. Since this cDNA generates a fully spliced form of unc-93 mRNA, if alternative splicing of unc-93(e1500) accounted for the suppression of the rubberband Unc phenotype, overexpressed unc-93(e1500)

![Figure 5. uaf-1 mutations define a UAF-1 region that affects the recognition of different 3' splice sites. Comparison of the sequences of the U2AF small subunit between the RS domain and the first RRM domain from C. elegans, D. melanogaster and human. The mutations caused by the uaf-1(n4588), uaf-1(n5120), uaf-1(n5123), uaf-1(n5125) and uaf-1(n5127) mutations are indicated with arrows. RS: Arginine-Serine rich domain. W: U2AF small subunit-interacting domain. RRM: RNA recognition motif. UHM: U2AF homology motif. Black box: region of UAF-1a that might regulate the recognition of 3' splice sites.](image)

![Image](image)

**Table 4. Intragenic suppressors of uaf-1(n4588) suppress unc-93(e1500) differently.**

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Bodybends/30 sec±SD</th>
<th>Rubberband phenotype</th>
<th>n</th>
</tr>
</thead>
<tbody>
<tr>
<td>wild-type</td>
<td>20.4±3.7</td>
<td>None</td>
<td>20</td>
</tr>
<tr>
<td>unc-93(e1500)</td>
<td>9.7±1.2</td>
<td>Strong</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n5123) unc-93(e1500)</td>
<td>0.6±0.8</td>
<td>Strong</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n5125)</td>
<td>19.1±3.1</td>
<td>None</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5120) unc-93(e1500)</td>
<td>4.9±2.0</td>
<td>Moderate</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5125) unc-93(e1500)</td>
<td>21.6±2.8</td>
<td>None</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5120) unc-93(e1500); Transgene #1</td>
<td>1.3±1.8</td>
<td>Strong</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5120) unc-93(e1500); Transgene #2</td>
<td>0.9±1.4</td>
<td>Strong</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5120) unc-93(e1500); Transgene #3</td>
<td>0.3±0.6</td>
<td>Strong</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5125) unc-93(e1500)</td>
<td>5.4±2.1</td>
<td>Moderate</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5125) unc-93(e1500); Transgene #1</td>
<td>19.5±3.3</td>
<td>None</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5125) unc-93(e1500); Transgene #2</td>
<td>0.6±0.9</td>
<td>Strong</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5125) unc-93(e1500); Transgene #3</td>
<td>1.3±1.6</td>
<td>Strong</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5125) unc-93(e1500); Transgene #3</td>
<td>0.8±1.4</td>
<td>Strong</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5127) unc-93(e1500)</td>
<td>21.5±3.6</td>
<td>Weak</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5127) unc-93(e1500); Transgene #1</td>
<td>22.1±4.0</td>
<td>None</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5127) unc-93(e1500); Transgene #2</td>
<td>1.3±1.7</td>
<td>Strong</td>
<td>20</td>
</tr>
<tr>
<td>uaf-1(n4588 n5127) unc-93(e1500); Transgene #2</td>
<td>0.7±1.4</td>
<td>Strong</td>
<td>20</td>
</tr>
</tbody>
</table>

To confirm that the suppression of unc-93(e1500) was caused by mutations in uaf-1, transgenes that express a wild-type uaf-1a cDNA in the body-wall muscles (nExP[pmyo-1::uaf-1a cDNA::gfp]) were introduced into the strains of the genotypes indicated and independent stable transgenic lines were established and scored. For the uaf-1(n4588 n5120) unc-93(e1500), uaf-1(n4588 n5125) unc-93(e1500) and uaf-1(n4588 n5127) unc-93(e1500) genotypes, three independent lines were scored. Locomotion and the rubberband phenotype were assessed as described in Materials and Methods. SD: Standard deviation.

doi:10.1371/journal.pgen.1000708.0004
Table 5. uaf-1(n4588) and sfa-1(n4562) partially suppress the rubberband Unc phenotype caused by overexpression of unc-93(e1500) cDNA in body-wall muscles.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Bodybends/30 sec/SD</th>
<th>n</th>
</tr>
</thead>
<tbody>
<tr>
<td>uaf-1(n4588); Transgene #1</td>
<td>7.8±3.9</td>
<td>15</td>
</tr>
<tr>
<td>wild-type; Transgene #1</td>
<td>3.7±2.9</td>
<td>15</td>
</tr>
<tr>
<td>uaf-1(n4588); Transgene #2</td>
<td>4.6±2.3</td>
<td>15</td>
</tr>
<tr>
<td>wild-type; Transgene #2</td>
<td>2.9±2.0</td>
<td>15</td>
</tr>
<tr>
<td>sfa-1(n4562); Transgene #3</td>
<td>8.2±2.1</td>
<td>15</td>
</tr>
<tr>
<td>wild-type*; Transgene #3</td>
<td>4.8±3.1</td>
<td>15</td>
</tr>
<tr>
<td>sfa-1(n4562); Transgene #4</td>
<td>10.5±3.0</td>
<td>15</td>
</tr>
<tr>
<td>wild-type*; Transgene #4</td>
<td>6.5±4.4</td>
<td>15</td>
</tr>
</tbody>
</table>

The same nucleotides at positions −3 to −1 (CAG), our mutagenesis analysis focused on nucleotides −7 to −4 (Figure 6B), which are variable and are known to be critical for recognition and binding by the U2AF complex [29,63–65]. We named each of 16 transgene constructs 1–16 (Figure 6B–6E).

We examined the splicing of a transgene (Figure 6B and 6E, No. 1) containing the same I8 and E9 as unc-93(e1500). In wild-type animals the splicing mimics that of the endogenous unc-93(e1500), with very little splicing at E9 (Figure 6B, 1.8%, compare to 1.3% in Figure 4B). Splicing of the same transgene (No. 1 in uaf-1(n4588) mutants occurred almost exclusively at E9 (>99%) (Figure 6B); endogenous splicing of unc-93(e1500) was qualitatively but not quantitatively similar, occurring mostly at E9 (68%) (Figure 4B). These results suggest that the splicing of mutated unc-93 transgenes could provide important information concerning the in vivo recognition of 3’ splice sites.

We replaced E9 with the sequence of I8 (Figure 6B, No. 2). In both wild-type and uaf-1(n4588) animals, splicing occurred mostly at the new E9 (97% and 98%, respectively) (Figure 6B and 6E). When I8 was replaced with the sequence of E9 (Figure 6B, No. 3), splicing again occurred mostly at E9 in both wild-type and uaf-1(n4588) animals (97% and >99%, respectively) (Figure 6B and 6E). These results suggest that the sequence that surrounds the original E9 is preferred by the splicing machinery in both wild-type and uaf-1(n4588) animals when two identical 3’ splice sites are present. We next switched the positions of I8 and E9 (Figure 6B, No. 4). In the wild type most splicing (>99%) occurred at the new E9 (Figure 6B and 6E). Similarly, in uaf-1(n4588) animals, most splicing (80%) occurred at the new E9 (Figure 6B and 6E, No. 4).

When I8 was replaced with the sequence of E9 (Figure 6B, No. 3), splicing again occurred mostly at E9 in both wild-type and uaf-1(n4588) animals (97% and >99%, respectively) (Figure 6B and 6E). These results suggest that the sequence that surrounds the original E9 is preferred by the splicing machinery in both wild-type and uaf-1(n4588) animals when two identical 3’ splice sites are present. We next switched the positions of I8 and E9 (Figure 6B, No. 4). In the wild type most splicing (>99%) occurred at the new E9 (Figure 6B and 6E). Similarly, in uaf-1(n4588) animals, most splicing (80%) occurred at the new E9 (Figure 6B and 6E, No. 4).

However, that a significant amount of splicing (20%) occurred at the new I8 in uaf-1(n4588) animals (Figure 6B and 6E, No. 4) suggested that the mutant UAF-1 can efficiently recognize the original E9 sequence even at the I8 position, which is normally a less favorable position.

The pattern of alternative splicing in cell culture can depend on the promoter used [66]. unc-93 is expressed in body-wall muscles [34,37]. We tested whether a different muscle-specific promoter would alter the splicing pattern of transgene No. 1 by expressing the transgene under the control of a myo-3 promoter [49] (Figure 6B and 6E, No. 5). We found almost identical splicing patterns of the transgene driven by the myo-3 promoter and the unc-93 promoter (Figure 6B and 6E, compare No. 1 and No. 5), suggesting that the alternative splicing of unc-93(e1500) involves a mechanism that is not promoter-specific.

We examined the effects of base substitutions at I8. Replacing I8 with the C. elegans consensus 3’ splice site TTTTTag [29,63–65] caused splicing to occur exclusively (100%) at the new I8 in both wild-type and uaf-1(n4588) animals (Figure 6C and 6E, No. 6). To identify the nucleotides required for the recognition of I8 in wild-type animals, we substituted each base from −7 to −4 of I8 with a G (Figure 6C, No. 7 to No. 10). G is the least used nucleotide from −7 to −4 of the highly conserved TTTTTag site significantly compromised binding of the U2AF complex to this site [29]. A G substitution at −7 (No. 7), −5 (No. 9) and −4 (No. 10) of I8 all dramatically reduced splicing at the new I8 (to the level of 15%, 0%, and 0%, respectively; Figure 6C and 6E) in wild-type animals, suggesting that these nucleotides are critical for the recognition by wild-type UAF-1. However, a G substitution at −6 (Figure 6C and 6E, No. 8) did not cause a significant change of splicing at the new I8 (which is 96% compared to 98% of No. 1), suggesting this nucleotide is not essential for recognition by wild-type UAF-1. We also substituted the A at −6 with a C to generate an I8 more...
similar to E9 (Figure 6C and 6E, No. 11). Splicing at this I8 (No. 11) was similar to that of transgenes No. 1 and No. 8 in wild-type animals, consistent with the notion that this base is not essential for the recognition by wild-type UAF-1. For all the transgenes with single-base substitutions of I8, splicing (Figure 6C and 6E, No. 7, 8, 9, 10 and 11) in uaf-1(n4588) animals is similar to that of transgene No. 1 (Figure 6B and 6E), suggesting that none of the substitutions significantly increased the affinity of I8 for mutant UAF-1.

To test whether we could increase the recognition of E9, we replaced E9 with the highly conserved consensus 3’ splice site TTTTcag sequence [29,63–65] (Figure 6D and 6E, No. 12). As expected, in both wild-type and uaf-1(n4588) animals, splicing occurred exclusively at the new E9 (100% and 100%, respectively). We next changed each of the non-T bases to T from 27 to 24 of E9 (Figure 6D and 6E, No. 13, 14 and 15). A T at –7, –6 or –4 increased splicing at E9 in wild-type animals (Figure 6D and 6E, No. 13, 14 and 15) by 53%, 100% and 91% for positions –7, –6 and –4, respectively, suggesting these substitutions increased recognition of E9 by wild-type UAF-1. For all three of these transgenes, splicing in uaf-1(n4588) animals occurred exclusively at E9 (100% for all three) (Figure 6D and 6E, No. 13, 14, and 15), suggesting none of the T substitutions significantly reduced the recognition of E9 by mutant UAF-1.
We mutated the C at −6 of E9 to an A (Figure 6D and 6E, No. 16), generating a 3′ splice site with a 1→G substitution at −4 of transgene No. 2 (Figure 6B, 6D, and 6E). Splicing of this transgene occurred exclusively at B (100%) in wild-type animals (Figure 6D and 6E, No. 16). In uaf-1(n4588) animals, splicing at the new E9 was reduced (to 62%, Figure 6D and 6E, No. 16) compared to that at E9 of transgene No. 2 (100%, Figure 6B and 6E, No. 2).

Discussion

Regulation of unc-93 activity by uaf-1 and sfa-1 likely involves unknown genes and biological processes

The mechanism(s) of the suppression of the Unc phenotype caused by the unc-93(e1500) mutation by uaf-1(n4588) and sfa-1(n4562) remains to be determined. Four observations indicate that although uaf-1(n4588) causes alternative splicing of unc-93(e1500) exon 9, this alternative splicing is not the basis of the suppression. First, unc-93(e1500)/unc-93(?) heterozygous animals are as Unc as unc-93(e1500) homozygous animals [36], indicating that reducing unc-93 expression by 50% does not reduce the rubberband Unc phenotype. By contrast, uaf-1(n4588) n5127 reduced unc-93(e1500) expression by 25% (since there was 25% alternative splicing), and these animals were strongly suppressed. Also, in uaf-1(n4588) unc-93(e1500) animals, the unc-93(e1500) transcript was reduced by 68% (there was 68% alternative splicing), and these animals might have been expected to be slightly less Unc than unc-93(e1500)/unc-93(?) animals but instead were strongly suppressed. Thus, the level of reduction of the unc-93(e1500) transcript does not correlate with the level of the suppression of the unc-93(e1500) Unc phenotype by uaf-1(n4588) and sfa-1(n4562). Second, the strong rubberband Unc phenotype caused by overexpression of the unc-93(e1500)-specific cDNA in body-wall muscles was partially suppressed by uaf-1(n4588), suggesting that unc-93(e1500) splicing is not needed for uaf-1(n4588)-mediated suppression. Third, sfa-1(n4562) suppressed unc-93(e1500) without affecting the splicing of unc-93(e1500) exon 9, and sfa-1(n4562) partially suppressed the rubberband Unc phenotype caused by overexpression of the unc-93(e1500) cDNA in the body-wall muscles. Again, suppression can occur without affecting unc-93(e1500) mRNA splicing. Similarly, we did not identify an alternatively spliced sup-10 transcript in either uaf-1(n4588); sup-10(n983) or sfa-1(n4562); sup-10(n983) animals, suggesting that sup-10(n983) was suppressed by uaf-1(n4588) and sfa-1(n4562) by a mechanism other than alternative splicing of the sup-10 transcript. Fourth, reducing the expression of uaf-1 and sfa-1 by RNAi suppressed the rubberband Unc phenotype of unc-93(e1500) but did not cause altered splicing of unc-93(e1500) exon 9. Based on these arguments, we propose that uaf-1 and sfa-1 mutations suppress unc-93(e1500) and sup-10(n983) by affecting the splicing of one or more unidentified genes required for the expression of the unc-93(e1500) and sup-10(n983) rubberband Unc phenotype. We cannot exclude the possibility that the alternative splicing of unc-93(e1500) contributed to the suppression of unc-93(e1500) by uaf-1 mutations.

uaf-1 and sfa-1 mutants provide new approaches for the analysis of the in vivo functions of the U2AF large subunit and SF1/BBP

The SF1/BBP and U2AF proteins are critical splicing factors that regulate splicing by binding the branch-point sequence and the 3′ splice sites [1,2], respectively. Mutations that affect the U2AF subunits and SF1/BBP in the yeasts Saccharomyces cerevisiae and Schizosaccharomyces pombe and the fruit fly Drosophila melanogaster have significantly facilitated the understanding of the in vivo function and regulation of these splicing factors [17,27,67–70]. Studies of S. cerevisiae identified genetic and biochemical interactions between the U2AF large subunit and SF1/BBP [17,27], and studies of S. pombe provided in vivo evidence that the U2AF subunits are required for splicing [68,70]. In Drosophila null mutations of the U2AF large or small subunits cause lethality [67,69], hindering genetic analysis of these splicing factors. Similarly, in C. elegans, reducing the expression of uaf-1 or sfa-1 by RNAi causes lethality [61,62], suggesting that these genes are essential for animal survival. We identified mutations that affect uaf-1 and sfa-1 and allow the survival of animals in permissive conditions, such as at lower temperatures or when derived from heterozygous mothers. These mutations provide a valuable resource for analyzing the function and regulation of the U2AF large subunit and SF1/BBP genes in vivo in animals.

Mutations in UAF-1 alter the in vivo recognition of a 3′ splice site

The recognition of 3′ splice sites is achieved by interactions between SF1/BBP and the U2AF large and small subunits, which together bind specific intronic sequences [1,2]. However, it is not clear how these factors regulate the choice of the correct splice site when two or more potential 3′ splice sites are proximal in vivo. Distinguishing different 3′ splice sites is a critical aspect of alternative splicing.

The unc-93(e1500) missense mutation generates a new cryptic 3′ splice site (AG) within exon 9 (ACTGcaG). This site differs from
the consensus 3' splice site for *C. elegans* (TTTTCag) [29] and is more rarely used by *C. elegans* than is TTTTCag or the intron 8 endogenous 3' splice site (AATTcag) (Table S4). Based on *in vitro* studies, this cryptic site should not be or be more weakly recognized by UAF-1 compared to TTTTCag and probably the intron 8 site AATTcag [29]. In a wild-type background, the choice between the wild-type 3' splice site of unc-93(e1500) intron 8 and the cryptic non-consensus site in unc-93(e1500) exon 9 followed this prediction, as only 1.3% of the splicing events utilized this cryptic 3' splice site. Strikingly, however, the n4388 missense mutation in uaf-1 shifted this specificity, causing splicing to occur mostly at the cryptic site, generating 68% of aberrantly spliced transcripts. This result suggests that UAF-1 might play an important role in determining the choice among alternative 3' splice sites *in vivo* (see discussion below).

The n4388 mutation did not cause an apparent change of UAF-1 protein level, and reducing UAF-1 using RNai did not increase the relative amount of alternatively spliced exon 9, suggesting that uaf-1(n4388) might alter UAF-1 function. However, RNAi treatment did not abolish the expression of UAF-1 (Figure S2), and we might have failed to detect an effect of UAF-1 on the splicing of unc-93(e1500) exon 9 because of residual UAF-1 protein in RNAi-treated animals. Thus, the altered splicing of unc-93(e1500) exon 9 in uaf-1(n4388) unc-93(e1500) mutants might reflect the consequence of the absence of UAF-1 activity. It is also possible that uaf-1(n4388) causes both a loss of function and an altered function of UAF-1, which cause the suppression of the RNAi phenotypes of the unc-93(e1500) animals and the altered splicing of unc-93(e1500) transcript, respectively.

The other 14 introns of the unc-93 transcript appeared to be spliced similarly in wild-type and uaf-1(n4388) animals, suggesting that uaf-1(n4388) did not alter the recognition of most wild-type 3' splice sites. We also found that uaf-1(n4388) did not suppress the Unc phenotype caused by the uaf-1(n4388) animals, which can be improved its recognition by wild-type UAF-1 and the relative amount of alternatively spliced exon 9, suggesting that a G at position (Figure 6A, No. 1) is critical for its recognition by the mutant UAF-1.

First, we conclude that the location of a 3' splice site affects its recognition. We found that the location of E9 was preferred to that of I8 by both wild-type and mutant UAF-1 when identical 3' splice sites were present at the two locations (Figure 6B, No. 2 and 3). However, this positional effect was not absolute. When the high-affinity 3' splice site TTTTCag was placed at either of the two locations, the site with the TTTTCag was preferred by both wild-type and mutant UAF-1 (Figure 6, No. 6 and No. 12). That splicing using I8 and E9 (both are likely weak 3' splice sites, since there are fewer such sites in *C. elegans* introns than there are copies of the strong 3' splice site sequence TTTTCag (Table S4)) was more affected by position than was splicing using the sequence TTTTCag suggests that weak 3' splice sites might be preferably used for alternative splicing, and, strong 3' splice sites such as TTTTCag might be generally used for constitutive splicing. If so, we might identify alternatively spliced genes by searching apparently weak 3' splice sites and then performing RT-PCR analyses. That TTTTCag is strongly recognized by mutant UAF-1 is consistent with our finding that the uaf-1(n4388) mutation does not appear to affect the splicing of most other introns of unc-93 (Figure 2B), which have a 3' splice site identical or highly similar to TTTTCag (data not shown).

Second, we conclude that the nucleotides at −7, −5 and −4 were more important than the nucleotide at −6 for wild-type UAF-1 to recognize the sequence of I8 (Figure 6, No. 7 to No. 10). The nucleotides at −4 and −5 appear to be more important than that at −7. That the nucleotide at −4 is more important than the nucleotide at −6 also appears to be the case for splicing at E9 by wild-type UAF-1 (No. 15 and No. 16, compared to No. 2, Figure 6), which indicates that nucleotide substitution at −4 (No. 16) dramatically reduced splicing and nucleotide substitution at −6 (No. 15) had a minimal effect at E9 in wild-type animals.

Third, substituting individual non-T nucleotides with T in E9 improved its recognition by wild-type UAF-1. The original I8 (AATTcag) and E9 (ACTGcag) are both rare 3' splice sites compared to TTTTCag, which is found in about 26% of the approximate 40000 introns analyzed, and is the most commonly used 3' splice site in *C. elegans* (Table S4) [29,64]. I8 appears more frequently in introns than does E9 (Table S4), suggesting that E9 has a lower affinity for the wild-type UAF-1 than does I8. That the wild-type UAF-1 rarely recognized E9 even in the more favored position (Figure 6, No. 1) is consistent with this notion. We found that substituting any E9 non-T nucleotide with T could increase the recognition of E9 in wild-type animals (Figure 6, No. 13 to 15), and a T substitution at −6 and −4 had a much stronger effect than one at −7.

Fourth, we conclude that the T180I(n4388) mutation caused UAF-1 to be more tolerant of a G nucleotide at −4 of E9. In transgenes No. 11 and No. 16, a G substitution at −4 of E9 dramatically reduced splicing at E9 in wild-type animals but did not or only moderately affected splicing at E9 in uaf-1(n4388) mutants (Figure 6). The splicing of transgenes No. 1, No. 4 and No. 5 is consistent with this observation, implying that a G at −4 is more tolerated in uaf-1(n4388) animals than in wild-type animals. Based on these observations, we propose that the G nucleotide at position −4 of E9 is critical for its recognition by the mutant UAF-1.

**In vivo** functions of UAF-1 and SFA-1 probably remain to be discovered

**In vivo** studies have suggested functions for the U2AF large subunit beyond regulating pre-mRNA splicing. For example, *Drosophila* mutants with a temperature-sensitive U2AF large subunit are defective in the nucleus-to-cytoplasm export of...
intronless mRNAs at elevated temperatures [71], suggesting that lack of U2AF large subunit function can affect mRNA export in addition to pre-mRNA splicing. Studies of SF1/BBP suggest that this splicing factor might not be essential for splicing in vitro or in vivo. Biochemical depletion of SF1/BBP in extracts from HeLa cells [72] and S. cerevisiae [73] or genetic depletion of SF1/BBP in extracts from S. cerevisiae [73] did not significantly affect splicing in vitro. Reducing SF1/BBP expression by RNAi in HeLa cells does not affect the splicing of several endogenous genes and a reporter gene [74]. That uaf-1(n4588) and sfa-1(n4562) suppressed the Unc phenotype of unc-93(e1500) but had different effects on the splicing of unc-93(e1500) mRNA at the cryptic 3′ splice site suggests that uaf-1 and sfa-1 could have both distinct and shared in vivo functions in C. elegans. Specifically, the splicing of some genes might be affected similarly by uaf-1 and sfa-1, with other genes differentially affected. Alternatively, it is possible that uaf-1(n4588) has a stronger effect on the splicing of unc-93(e1500) exon 9, while sfa-1(n4562) has a weaker effect not detected in the experiments we performed.

The lack of conditionally viable mutants of the U2AF large subunit and SF1/BBP has impeded the analysis of the in vivo functions of these splicing factors in animals. The mutations we isolated affecting these two splicing factors should allow novel approaches for in vivo analyses of RNA splicing and of the functions of the U2AF large subunit and SF1/BBP in C. elegans. The transgene splicing system we developed provides an in vivo reporter assay for understanding the role of UAF-1 and possibly other splicing factors in regulating alternative 3′ splice site recognition.

Materials and Methods

Strains

C. elegans strains were grown at 20°C as described [53], except where otherwise specified. N2 (Bristol) was the reference wild-type strain. CB4856 (Hawaii) was used for mapping mutations using single-nucleotide polymorphisms [75]. Mutations used in this study include: LGI: sup-17(n403) [54]. LGII: sup-9(n1530), n2287 [34,43], unc-52(e444), e6609 [55,60]. LGIII: van-6(e697) and dpy-1(n1) [53]. LGIV: uaf-1(n4588), sfa-1(n4562), n5120, n5125, n5127, n5222A (this study), unc-93(hr12), n209, n1912, e1500 [36,37,44], sup-18(n1014) [35]. LGV: gk-23(n6019d) [52], dpy-4(e1166) [55], sfa-1(n4562), n3222A (this study). LGX: twk-18(e1913d) [53], unc-38(e6553d) [51] and sup-10(n983), n3564 [34,35]. The translocation n71 IVV with the dominant gfp marker qs41 [76] was used to balance the sfa-1 locus, and the translocation sc12(2023)/dpy-1(2170) [A. Rose, D. Baillie and D. Riddle, the Genetic Toolkit project] was used to balance the uaf-1(n5222A) locus.

Clonal screen to identify unc-93(e1500) suppressor genes essential for animal survival

Synchronized L4 unc-93(e1500) animals (P0) were mutagenized with EMS (ethyl methanesulfonate) as described [55]. F1 progeny from these animals were picked to single wells of 24-well culture plates with OP50 bacteria grown on NGM agar. F2 progeny were observed using a dissecting microscope to identify animals with improved locomotion. From ~10,000 F1 clones screened, 100 independent suppressed strains were isolated. 97 of the isolates, including two weak recessive sterile suppressors and 95 recessive fertile suppressors, were kept as frozen stocks for possible later study. Three stronger suppressors that caused or were closely linked to mutations that caused sterility (n4562) or ts-lethality (n4588 and n4562) were chosen for further analysis. The analysis of n4564 is ongoing.

Cloning of n4588 and n4562

We mapped n4588 to the left of dpy-1 on LGIII based on the suppression of unc-93(e1500) using standard methods. As the suppressor activity and ts-lethality were very closely linked, e.g., more than 500 n4588 unc-93(e1500)/+ unc-93(e1500) individuals failed to segregate Sup non-Let progeny, we then followed the phenotype of ts-lethality to further map n4588. We mapped n4588 to the right of nucd-105577 on BE0003N10 (cosmid BE0003N10 sequences refer to nucleotides of accession no. AC092690) using 10 Vab recombinants recovered after crossing vab-6(e697) n4588 hemaphrodites with males of the Hawaiian strain CB4856 [75] and to the left of nucleotide 13164 on Y92C3A (accession no. AC024874) using 37 Dpy recombinants recovered after crossing n4588 dpy-1(e1) hemaphrodites with males from the Hawaiian strain CB4856. We determined the coding sequences of four genes in this interval, uaf-1, vab-18, kbp-4 and par-2, and identified a missense mutation in the third exon of the uaf-1 isoform.

As the suppressor activity and sterility of n4562 were very closely linked, e.g., over 500 unc-93(e1500); n4562/+ individuals failed to segregate Sup non-Stc progeny, we followed the sterility phenotype to map n4562 to the right of dpy-1 on LG IV using standard methods. We next mapped n4562 to the right of nucleotide 37163 on Y43D4A (accession no. AL132846) using 234 Dpy recombinants recovered after crossing dpy-4(e1166) n4562 with males of the Hawaiian strain CB4856. The sequences of coding exons of sfa-1 and uaf-1, both located in this region, were determined, and a Cys458Opal (TGTTG-TGA) mutation was identified in sfa-1.

Isolation of deletion alleles

Genomic DNA pools from EMS-mutagenized animals were screened for deletions using PCR as described [77]. Deletion mutant animals were isolated from frozen stocks and backcrossed to the wild type at least three times. uaf-1(n5222A) removes nucleotides 9786 to 11082 of YAC Y92C3B. sfa-1(n5223A) removes nucleotides 207818 to 208925 of YAC Y116A8C.

Quantitative RT–PCR

Total RNA was prepared using Trizol according to the manufacturer’s instructions (Invitrogen), treated with RNase-Free DNase I (New England Biolabs) and followed by incubation at 75°C for 10 minutes to inactivate DNase I. First-strand cDNA was synthesized with random hexamer primers (New England Biolabs) using the Superscript II or III First-Strand Synthesis Kit (Invitrogen). Quantitative RT–PCR was performed using either a DNA Engine Opticon System (MJ Research) or a Mastercycler reaqlplex system (Eppendorf). For the SYBR green-based assay (DNA Engine Opticon System), each 30 μl PCR reaction contained 1 to 10 ng RT template, 0.5 mM PCR primers and 15 μl 2× SYBR Green PCR Master Mix (Applied Biosystems). Three independent samples of synchronized wild-type (N2) and uaf-1(n4588) L1 animals were prepared, and levels of control genes (rpl-26, gpd-2, act-1) and tested genes (myo-3, unc-93, sup-9, sup-10, sup-11, sup-18) were quantified from each biological replicate. For the Taqman probe-based assay (Mastercycler reaqlplex system), the probes (Figure 4A) were labeled at their 5′-ends with 6-carboxyfluorescein (FAM) and at their 3′-ends with Black Hole Quencher (BHQ-1) (Integrated DNA Technologies). Two independent samples of each genotype of animals of mixed stages were prepared, and levels of rpl-26 and unc-93 wild-type and alternatively spliced transcripts were quantified from each biological replicate. For RNAi-treated animals (see below), one
sample for each assay was quantified. PCR primers and Taqman probes are listed in Table S5.

Screen for suppressors of uaf-1(n4588)

Synchronized uaf-1(n4588) animals (P0) at the L4 larval stage grown at 15°C were mutagenized with EMS as described [55]. These P0 animals were allowed to grow to young adults at 15°C in a mixed population and bleached, and F1 progeny were synchronized at the early L1 stage by starvation in S medium [78]. The F1 animals were placed on 30 Petri plates (~1000 animals/plate) with NGM agar seeded with OP50 and permitted to grow to young adults at 15°C and then moved to 25°C. After six days at 25°C, the animals were grown at 20°C for six days and examined each day for the presence of living F2 animals. About 50,000 F1 progeny from a mixture of more than 10,000 P0 animals were screened. From the screen, we recovered 13 surviving F2 animals from 15 different F1 plates. Six of the 13 suppressors were intragenic suppressors (see Table S5). The other seven suppressors were extragenic suppressors, i.e., n5123/uaf-1 animals segregated n4588-like progeny. Some or all of the extragenic isolates could have been derived from the same P0 animal.

RNA interference

Young adult animals (wild-type or unc-93(e1500)) were fed HT115(DE3) bacteria containing plasmids directing the expression of dsRNAs targeting either uaf-1 or sfa-1 on NGM plates with 1 mM IPTG and 0.1 mg/ml Ampicillin [79]. Surviving F1 progeny of the unc-93(e1500) animals (escapers) were examined for suppression of locomotion defects. Animals were washed from plates, rinsed three times with H2O, and resuspended in Trizol (Invitrogen) for preparation of total RNA or in 2× protein loading buffer (see Western blots, below) for SDS-PAGE analysis. We generated the DNA construct expressing dsRNA targeting uaf-1 (see below). The bacterial strain expressing dsRNA targeting sfa-1 was obtained from a whole-genome RNAi library [80], and the sequences of plasmids from single colonies of the strain were used to suppress of locomotion defects. Animals were washed from plates containing OP50 and permitted to grow to young adults at 20°C, and then moved to 25°C. After six days at 25°C, the animals were grown at 20°C for six days and examined each day for the presence of living F2 animals. About 50,000 F1 progeny from a mixture of more than 10,000 P0 animals were screened. From the screen, we recovered 13 surviving F2 animals from 15 different F1 plates. Six of the 13 suppressors were intragenic suppressors (see Table S5). The other seven suppressors were extragenic suppressors, i.e., n5123/uaf-1 animals segregated n4588-like progeny. Some or all of the extragenic isolates could have been derived from the same P0 animal.

Quantification of locomotion and the rubberband phenotype

L4 animals were picked 16–24 hrs before assaying and were grown at 20°C. Young adults were then individually picked to Petri plates containing NGM agar seeded with OP50, and bodybends were counted for 30 seconds using a dissecting microscope as described [81]. The rubberband phenotype was scored as described [43].

Western blots

Animals were washed from plates with H2O, rinsed three times with H2O, and resuspended in one volume of 2× SDS loading buffer (100 mM Tris.Cl [pH 6.8], 200 mM DTT, 4% SDS, 0.2% bromophenol blue, 20% glycerol), boiled for 5 minutes, and samples were then loaded onto 8% polyacrylamide gels containing SDS. Protein samples were transferred from polyacrylamide gels to Immobilon-P Transfer Membranes (Millipore). Primary and secondary antibody incubations were performed with 5% non-fat milk in TBST (25 mM Tris-HCl, PH 8.0; 125 mM NaCl, 0.1% Tween-20) at room temperature for one hour each. Signals were visualized using Chemiluminescence Reagent Plus (PerkinElmer Life Sciences) and X-ray film (BioMax XAR film, Kodak). Primary antibody was rabbit anti-UAF-1 (1:20000) [45]. Secondary antibody was HRP-conjugated goat anti-rabbit (1:3000) (BioRad).

Plasmids

To rescue the suppression of the Unc phenotype of uaf-1(n4588) by uaf-1(n4588) or sfa-1(n4582), uaf-1 and sfa-1 cDNAs were subcloned to vector pPD93.97 using BamH I and Age I restriction sites. uaf-1 cDNA was amplified with PCR using uaf-1a cDNA as template and subcloned to pPD93.97 using BamH I and Age I restriction sites. uaf-1a cDNA was subcloned to pPD93.97 (for heat-shock induced expression of uaf-1a cDNA) using BamH I and ScaI restriction sites. An Xho I/Spe I fragment of uaf-1a cDNA subcloned in a pGEM-TA easy vector (Promega) was subcloned to pPD129.36 (for the uaf-1a RNAi construct) using Xho I and Not I restriction sites. To test whether uaf-1(n4588) or sfa-1(n4582) mutations could suppress the Unc phenotype caused by ectopic expression of the unc-93(e1500) cDNA, unc-93(e1500) cDNA was subcloned to pPD93.97 using BamH I/blunt and Age I sites. To examine the effect of nucleotide substitutions on the recognition of the intron 3 endogenous 3’ splice site and the exon 9 cryptic 3’ splice site, we fused the genomic sequence between exon 8 and exon 9 of unc-93(e1500) in-frame with the GFP gene of pPD93.97 using BamH I and Age I sites. We replaced the nwy-3 promoter of pPD93.97 with a 2 kb promoter of unc-93 using PnuI and BamH I sites. Point mutations in uaf-1(stop codons), the unc-93(e1500) mutation or mutated transgenes were introduced using QuickChange II or III Site-Directed Mutagenesis Kit (Stratagene) with primers containing corresponding mutations. PCR was performed using Eppendorf Cyclers, and DNA products were resolved using agarose gels. DNA sequence determination was performed with an ABI Prism 3100 Genetic Analyzer. PCR primers are listed in Table S5.

Transgene experiments

Germline transgene experiments were performed as described [82]. Transgene mixtures generally contained 20 μg/ml 1 kb DNA ladder (Invitrogen), 20 μg/ml Arabidopsis genomic DNA and 10 μg/ml of the transgene of interest. When the transgene did not cause the expression of a GFP fusion protein, 10 μg/ml pPD93.36-GFP plasmid (expressing GFP in body-wall muscles) or 5 μg/ml pmyo-2:dsRED (expressing RFP in pharynx) was added to the injection mixture as a visible fluorescence marker to identify animals carrying the transgene.

Bioinformatics

We downloaded approximate 40,000 unique intronic sequences from WormMart (WormBase Release 195) and processed the sequences using BBEdit and MS Excel softwares. Identical 3’ splice sites (positions −7 to −1) were grouped and counted.

Supporting Information

Figure S1 uaf-1(n4588) does not reduce the mRNA levels of genes that genetically interact with unc-93. Real-time RT-PCR analyses of mRNA levels of constitutively expressed genes (act-1, gpd-2), a body wall muscle specific gene (nwy-3) and genes involved in the rubberband Unc phenotype (unc-93, sup-9, sup-10, sup-18, sup-11). The levels of endogenous rpl-26 mRNA of each sample were quantified in parallel real-time RT-PCR experiments and used as loading controls. Each data set represents the average of
duplicate experiments of three biological replicates of synchronized L1 animals. Error bars, standard errors.

Found at: doi:10.1371/journal.pgen.1000708.s003 (0.37 MB TIF)

Figure S2 uaf-1 RNAi reduces UAF-1 protein level. (A) Animals were fed bacteria expressing control empty vector or dsRNA targeting uaf-1. A western blot was prepared using a UAF-1 polyclonal antibody [45] and total protein extracted from these RNAi-treated animals. uaf-1(RNAi) dramatically reduced the protein level of UAF-1. (B) Coomassie blue staining indicated that the loading of total protein was similar among the samples. (C) Quantification using NIH ImageJ software of UAF-1 levels in wild-type or unc-93(e1500) animals treated with either control empty vector or uaf-1(RNAi). uaf-1(RNAi) treatment reduced UAF-1 levels in both wild-type and unc-93(e1500) animals (33% and 23% of the levels in animals treated with control empty vectors, respectively).

Found at: doi:10.1371/journal.pgen.1000708.s002 (0.30 MB TIF)

Figure S3 uaf-1(n4588) and sfa-1(n4562) do not cause obvious alternative splicing of the sup-10 transcript. (A) Total RNAs from animals of the indicated genotypes were prepared and RT-PCR experiments were performed to amplify the full-length sup-10 transcript with an abnormal size in the unc-93(e1500) animals treated with control empty vector or uaf-1(RNAi). uaf-1(RNAi) treatment reduced UAF-1 levels in both wild-type and unc-93(e1500) animals (33% and 23% of the levels in animals treated with control empty vectors, respectively).

Found at: doi:10.1371/journal.pgen.1000708.s001 (0.32 MB TIF)

Figure S4 uaf-1(n4588) and sfa-1(n4562) cause synthetic lethality. Anesthetized animals of the indicated genotypes were observed with Nomarski optics. For wild-type, uaf-1(n4588) and sfa-1(n4562), animals were photographed 24 hours after the mid-L4 stage (based on vulval invagination). For uaf-1(n4588) and sfa-1(n4562), double mutants, animals were observed each day for up to ten days after hatching.

Found at: doi:10.1371/journal.pgen.1000708.s000 (0.30 MB TIF)

Table S2 The alternatively spliced unc-93 transcript does not encode a functional UNC-93 protein product. Transgenes driving the expression of the alternatively spliced unc-93 cDNA (unc-93 cDNA(Δ)) did not rescue the suppression of sup-9(n1530) by the unc-93(Δ24) mutation, while transgenes expressing a wild-type unc-93 cDNA rescued the suppression.

Found at: doi:10.1371/journal.pgen.1000708.s005 (0.04 MB DOC)

Table S3 The alternatively spliced unc-93 transcript likely does not encode a dominant-negative UNC-93 protein product. Transgenes driving the expression of the unc-93 cDNA(Δ) did not suppress the rubberband Unc phenotype of unc-93(e1500) animals, while transgenes expressing a wild-type unc-93 cDNA suppressed the Unc phenotype. As loss of function of unc-93 results in phenotypically wild-type animals, the lack of suppression of unc-93(e1500) by the unc-93(Δ) transgenes suggests that the function of unc-93 was not antagonized by unc-93(Δ), indicating that the unc-93(Δ) cDNA does not encode a dominant-negative UNC-93 protein.

Found at: doi:10.1371/journal.pgen.1000708.s006 (0.02 MB DOC)

Table S4 Sequences and distributions of the three 3′ splice sites were analyzed. Approximate 40,000 unique introns were analyzed, and the numbers and ratios of all types of 3′ splice sites were calculated. The list here includes the three sites we analyzed in our mutagenesis experiments shown in Figure 6. TTTTcag is the most commonly used 3′ splice site.

Found at: doi:10.1371/journal.pgen.1000708.s007 (0.02 MB DOC)

Table S5 List of PCR primers and Taqman probes.

Found at: doi:10.1371/journal.pgen.1000708.s008 (0.03 MB DOC)

Acknowledgments

We thank current and ex-members of the Horvitz laboratory, especially H. Schwartz, B. Galvin, E. Alvarez-Saavedra, and J. Levin, for critical suggestions. We thank Na An for strain maintenance and E. Castor, E. Murphy, and T. Ljungars for technical support. We thank T. Blumenthal for providing the UAF-1 antibody and for constructive suggestions. We thank Y. Kohara and A. Kramer for providing cDNAs and A. Fire for providing the RNAi plasmids. Some nematode strains used in this work were provided by the Caenorhabditis Genetics Center, which is funded by the NIH National Center for Research Resources. Some genomic sequences and polymorphisms were identified by the WUSTL Genome Center.

Author Contributions

Conceived and designed the experiments: LM HRH. Performed the experiments: LM. Analyzed the data: LM HRH. Wrote the paper: LM HRH.

References


78. The Nematode Caenorhabditis elegans; WB and the Community of C. elegans Researchers Cold Spring Harbor Laboratory.