A Conserved LIM Protein That Affects Muscular Adherens Junction Integrity and Mechanosensory Function in Caenorhabditis elegans

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Abstract. We describe here the molecular and functional characterization of the Caenorhabditis elegans unc-97 gene, whose gene product constitutes a novel component of muscular adherens junctions. UNC-97 and homologues from several other species define the PINCH family, a family of LIM proteins whose modular composition of five LIM domains implicates them as potential adapter molecules. unc-97 expression is restricted to tissue types that attach to the hypodermis, specifically body wall muscles, vulval muscles, and mechanosensory neurons. In body wall muscles, the UNC-97 protein colocalizes with the β-integrin PAT-3 to the focal adhesion-like attachment sites of muscles. Partial and complete loss-of-function studies demonstrate that UNC-97 affects the structural integrity of the integrin containing muscle adherens junctions and contributes to the mechanosensory functions of touch neurons. The expression of a Drosophila homologue of unc-97 in two integrin containing cell types, muscles, and muscle-attached epidermal cells, suggests that unc-97 function in adherens junction assembly and stability has been conserved across phylogeny. In addition to its localization to adherens junctions UNC-97 can also be detected in the nucleus, suggesting multiple functions for this LIM domain protein.

Key words: LIM domains • UNC-97 • muscle development • adherens junction • touch neuron

The nematode Caenorhabditis elegans has proven to be a useful system to study the development of muscle (Moerman and Fire, 1997; Waterston, 1988). Myoblasts arise after the end of gastrulation (at ~290 min of embryonic development) and are defined by the accumulation of structural components such as myosin, vinculin, and integrin (Epstein et al., 1993; Coutu-Hresko et al., 1994). Myoblasts then migrate to their final positions, polarize, and flatten. In mid-embryogenesis (450 min), the muscle components organize into sarcomeres and attachment structures (Coutu-Hresko et al., 1994; see Fig. 1). These attachment structures, also termed dense bodies, are adherens junctions that provide a physical linkage between muscles and the hypodermis and are of critical importance to translate the mechanical movement of myofibrillar components to motion of the whole animal. These adherens junctions contain integrin heterodimers as central structural units that anchor cytoskeletal components to the extracellular matrix (Gettner et al., 1995). They also contain cytoskeletal adapter proteins such as vinculin, α-actinin, and talin (see Fig. 1) (Francis and Waterston, 1985; Barstead and Waterston, 1991; Moulder et al., 1996); thus, dense bodies are reminiscent of the structural composition of focal adhesions in tissue culture cells (Clark and Brugge, 1995). The regulatory steps that coordinate the assembly of adherens junction components into functional attachment structures that are capable of enduring and transmitting mechanical stress are largely undefined. We describe here a new LIM domain protein, UNC-97, that is required for assembly and stability of focal adhesion-like muscle attachment structures in C. elegans.

LIM domains are defined by the presence of two zinc coordinating, Cys/His-containing motifs and represent protein–protein interaction domains (Schmeichel and Beckham, 1994; Feuerstein et al., 1994; Dawid et al., 1998). Some LIM proteins (LIM-only) are comprised almost exclusively of LIM domains whereas other LIM proteins (LIM-plus) display LIM domains linked to other functional domains including homeodomains, kinase domains or other protein–protein interaction domains (Dawid et al., 1998). LIM domain proteins display considerable specificity in their sites of subcellular localization. LIM homeodomain proteins and the LIM-only proteins LMO1, -2, and -3 are transcriptional regulatory proteins that function in the nucleus (Dawid et al., 1998). On the other hand, the
LIM-only proteins zyxin and paxillin localize to actin stress fibers and focal adhesions, CRP family members localize to actin filaments and to the Z lines of myofibers in vertebrates (Turner et al., 1990; Crawford and Beckerle, 1991; Arber et al., 1997; Louis et al., 1997) and the Drosophila CRP family members, MLP60A and MLP84B, distribute along muscle fibers and to sites of muscle attachment (Stronach et al., 1996). Several of these cytoskeletal LIM proteins have been shown to display a remarkable dual subcellular localization; apart from its cytoskeletal localization, CRP3/MLP protein has also been reported to localize to the nucleus (Arber and Caroni, 1996), where it may participate in MyoD dependent transcriptional regulation (Kong et al., 1997). Moreover, although the LIM protein zyxin appears to be restricted to focal adhesions at steady-state levels, recent experiments have shown that it shuttles between focal adhesions and the nucleus (Nix and Beckerle, 1997).

The functional role of LIM proteins has mostly been addressed for those LIM proteins involved in transcriptional control. Mutations in LIM homeobox genes revealed their participation in lineage determination and neural differentiation in vertebrates and invertebrates (Dawid et al., 1998). Disruption of the LMO transcriptional regulator LMO1 causes haematopoietic lineage defects (Warren et al., 1994). Disruption of the LMO1 transcriptional regulator LMO1 causes haematopoietic lineage defects (Warren et al., 1994).

CRP3/MLP in the organization of myofibrillar structures (Stronach et al., 1996). Several of these cytoskeletal LIM proteins have been conserved throughout evolution. We find that CRP3/MLP protein has also been reported to localize to the nucleus (Arber and Caroni, 1996), where it may participate in MyoD dependent transcriptional regulation (Kong et al., 1997). Moreover, although the LIM protein zyxin appears to be restricted to focal adhesions at steady-state levels, recent experiments have shown that it shuttles between focal adhesions and the nucleus (Nix and Beckerle, 1997).

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Materials and Methods

Strains and Genetics

The strains used in this study are: HE110 [unc-97(su110)], mec-3(su298), mec-3(e1388), dpy-20(e1282), and N2 wild-type strain. Double mutant mec-3(su298); unc-97(su110) animals were constructed by first marking unc-97(su110)X with dpy-20(e1282)/XIV and then repelling dpy-20(e1282) with the closely linked mec-3(su298).

Polarized Light Microscopy

Polarized light images were obtained essentially as described in Waterston et al. (1980). In brief, single live adult hermaphrodites were placed in a drop of M9 buffer on a slide and then a coverslip was carefully lowered onto the animals. Excess liquid was wicked away until the animals were immobilized and then animals were rolled gently until a good view of body wall muscle was obtained. Animals were viewed using a Zeiss Axio-phot microscope (Carl Zeiss) equipped with polarizing optics.

Sequence Analysis

The unc-97(su110) molecular lesion was identified by PCR amplification of the F14D12.2 gene from unc-97(su110) mutant animals and subsequent DNA sequencing. BLAST searches identified unc-97 cDNAs in Y. Kohara’s (Mishima, Japan) cDNA collection (yk460db, yk457cl1, yk455g5, yk45flc10, yk403d5, yk267h9, yk114h11, yk184e5). yk184e5 was completely sequenced and found to encode a full-length clone. The nucleotide and protein coding sequence have been submitted to GenBank/EMBL/DDBJ under accession number AF035583. UNC-97 homologous proteins were identified using the BLAST search algorithm. The cDNA representing the Drosophila expressed sequence tag (EST) sequence was obtained from Genome Systems. The complete nucleotide and protein coding sequence for d-unc97 have been submitted to GenBank/EMBL/DDBJ under accession number AF078907. Sequence alignments and dendograms were constructed using the pileup algorithm in the GCG software package.

Fusion Gene Constructs

All three reporter gene constructs were constructed using a PCR fusion approach. First, two independent PCRs were performed, one amplifying the promoter and coding region (in the case of unc-97-prom::GFP just the promoter) from genomic DNA. The 3’ primer contained sequences overlapping with part of the green fluorescent protein (GFP)’s sequences on pPD95.75; the other PCR amplified GFP and the unc-54 3’-UTR from the pPD95.75 vector. The 5’ primer contained sequences overlapping with the genomic region targeted for fusion. The two PCR products were then fused by combining 1 μl of each PCR reaction and subsequent amplification with a set of nested primers, one at the beginning of the promoter, the other at the end of the unc-54 3’-UTR. For all the PCR reactions a mixture of Taq-polymerase and proofreading PwoI polymerase (Boehringer Mannheim, Indianapolis, IN) was used to ensure fidelity of the reaction. The fusion PCR product was injected at ~100 ng/μl into wild-type worms. The promoter sequence used for both unc-97 reporter constructs starts at −2168 5’ of the predicted ATG start codon (reaching almost to the preceding predicted gene). unc-97-prom::GFP is a translational fusion encompassing the first 21 amino acids of UNC-97. unc-97-GFP is a translational fusion encompassing the complete genomic coding sequence of unc-97 (see Fig. 4). Note that both reporter gene constructs reveal a similar set of expressing cells, arguing that none of the introns contain regulatory sites. The promoter sequence used for pin-2::GFP starts at ~2038 5’ of the predicted ATG start codon (reaching almost to the preceding predicted gene) and contains its complete, predicted genomic coding sequence.

Transgenic Animals and Rescue Analysis

Transgenic strains were constructed by injecting GFP reporter gene constructs as PCR products into N2 wild-type animals. No coinjection marker was used; transgenic animals were identified by their green fluorescence. The extrachromosomal GFP reporter gene arrays were integrated using a Stratalinker 1800 UV light source (Stratagene) at 300 J/m². The extrachromosomal GFP reporter gene arrays were integrated using a Stratalinker 1800 UV light source (Stratagene) at 300 J/m².

The transgenic strains used are: N2 Ex[unc-97::GFP], N2 Ex[unc-97-prom::GFP], mgls25 (integrated Ex[unc-97-GFP]), mgls26 (integrated Ex[unc-97-prom::GFP]); N2 Ex[pin-2::GFP, rol-6]. Rescue of unc-97(su110) was performed by making use of (a) the X-linkage of unc-97 and (b) an autosomally integrated, full-length unc-97-GFP copy; mgls25 heterozygous males were mated with unc-97(su110) hermaphrodites. There are two types of F1 male cross progeny from this cross. One type contains a chromosome from the father that has no integrated unc-97::GFP. This type of F1 male cross progeny is not fluorescent and display the uncoordinated (unc) phenotype.

1. Abbreviations used in this paper: EST, expressed sequence tag; GFP, green fluorescent protein; LIM, LIN-11, ISL-1, MEC-3; MEC, mechanosensory; PAT, paralyzed and arrested at twofold stage; RNAi, RNA interference; UNC, uncoordinated.

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notype, since it is hemizygous for unc-97(su110). The other type received a chromosome from the father that does contain an integrated unc-97::GFP (identified as fluorescent animals). If unc-97::GFP rescues, these fluorescent males should be non-unc. Indeed we found male animals of both phenotypes: nonfluorescent unc as well as fluorescent non-unc, thus demonstrating rescue specific for the animals that carry the unc-97::GFP containing array.

**Antibody Staining and GFP Expression Analysis**

Fixation of animals for antibody staining was performed as described by Finney and Ruvkun (1990). In brief, animals were freeze-cracked by two rounds of freezing and thawing in dry-ice/ethanol and fixed in 3% paraformaldehyde, 80 mM KC1, 20 mM NaCl, 10 mM EGTA, 5 mM spermidine, 15 mM Pipes, pH 7.4, 23% methanol for 3 h at 4°C. Animals were washed twice in Tris/Triton buffer (100 mM Tris/HC1, pH 7.4; 1% Triton X-100, 1 mM EDTA), antigens reduced in Tris/Triton buffer + 1% β-mercaptoethanol for 1 h at 37°C. After washing once in borate buffer (33.3 mM boric acid, 16.6 mM NaOH, pH 9.5), antigens were oxidized in borate buffer + 0.3% hydrogen peroxide for 15 min at room temperature. After washing once in borate buffer, samples were blocked in antibody buffer (1× PBS, pH 7.4, 1% BSA [fraction V, 96–99%; Sigma, St. Louis, MO], 0.5% Triton X-100, 0.05% sodium azide, 1 mM EDTA) for at least 15 min. Antibodies used were: monoclonal mouse anti-pat-3 antibody MHZ25 (Francis and Waterston, 1985), monoclonal mouse anti-vinculin antibody MHZ4 (Francis and Waterston, 1985), and mouse polyclonal anti-unc-52 antibody GM1 (Moerman et al., 1996). MHZ4 and MHZ25 were used at 1:250, GM1 at 1:50, and incubated overnight at 4°C. Secondary antibodies (FITC- or TRITC-coupled) were incubated for 6–12 hours at 4°C. DNA was stained using 4',6-diamidino-2-phenylindole (DAPI) at 10 µg/mL.

The expression of the unc-97::GFP reporter gene was either monitored in live animals or by fixing animals as described below for antibody staining. The fixation procedure used does not interfere with the fluorescent signal of GFP. We found that in several instances subcellular structures (such as the nuclear staining) could be better observed in fixed animals, although they were also clearly visible in the live animals, thus excluding fixation artifacts.

**RNA Interference**

The probable null phenotype for the unc-97 gene was generated using RNA interference as described by Fire et al. (1998). The template for the sense and antisense unc-97 RNA transcripts was the complete unc-97 cDNA, subcloned into the Bluescript vector, which was amplified using Bluescript specific primers flanking the T3 and T7 primer sites. Sense and antisense RNA was produced from this PCR product in separate transcription reactions using T7 and T3 primers and commercially available RNA synthesis kits. The RNA was resuspended in water, the antisense and sense templates were mixed to a final concentration of ~1-5 µg/µl and injected into the gonad. Scoring of the phenotype was done by allowing single injected animals to lay eggs at 20°C from hour 24 to hour 48 postinjection (see figure). The progeny derived from the hour 0 to hour 24 postinjection egg lay (which usually has not received as much RNA as the later progeny) also contained rescues, these fluorescing males should be non-unc. Indeed we found male animals of both phenotypes: nonfluorescent unc as well as fluorescent non-unc, thus demonstrating rescue specific for the animals that carry the unc-97::GFP containing array.

**Mechanosensory Assays**

For each genotype 30–100 individual animals were scored by touching the animals with a thin hair 10 times, five times at the anterior and five times at the posterior. Normally, animals respond by backing up away from the touch. The responsiveness of every single animal was recorded so that, for example, six responses out of 10 touches were recorded as 60% responsiveness. Note that although unc-97(su110) display an uncoordinated phenotype associated with an almost immobile appearance, those mutant animals are still capable of responding to touch by backing up.

**Whole Mount In Situ Hybridization of Drosophila Embryos**

w118 embryos were collected over a 17-h period and then prepared for whole mount in situ hybridization as described in Lehmann and Tautz (1993). The hybridization reaction proceeded for 12 h at 65°C in the following buffer, pH 4.5, 50% formamide (UltraPure; GIBCO BRL, Gaithersburg, MD), 5× SSC, 100 µg/ml tRNA, 100 ng/ml sonicated salmon sperm DNA (denatured), 50 µg/ml heparin (Sigma), and 0.1% Tween-20, plus the appropriate riboprobe at a concentration of 0.25 ng/ml. After hybridization, samples were washed several times over a 2-h period at 65°C. For detection of probe, samples were incubated with a 1:5000 dilution of anti-digoxigenin Fab fragments (Boehringer Mannheim), presorbed against fixed Drosophila embryos, either overnight at 4°C or 2 h at room temperature, and then processed according to the manufacturer’s instructions.

Full-length digoxigenin-labeled RNA probes, corresponding to the sense and antisense strands of the d-pinch cDNA, were prepared using the Boehringer Mannheim Genius kit according to the manufacturer's instructions. The full-length probes were hydrolyzed to a size of ~100 bp by treatment with carbonate buffer (60 mM Na2CO3, 40 mM NaHCO3, pH 10.2) at 60°C for 1 h.

**Results**

**unc-97 Is Required for the Maintenance of C. elegans Adherens Junctions**

The X-linked unc-97 gene was identified by Zengel and Epstein (1980) and is defined by a single recessive allele, su110. Adult animals homozygous for the su110 mutation are limp, egg laying-defective, and show movement defects that vary from slow moving to paralyzed animals. This probably reflects the degree of disorganization of the vulval and body wall muscles. Zengel and Epstein (1980) reported that unc-97 mutants have shallow, easily disrupted muscle sarcomeres. Using polarized light microscopy we also find that mutant muscle cells are fragile, but if animals are handled carefully intact sarcomeres can be observed (Fig. 2 A). As can be seen in Fig. 2 A (top left panel), when handled gently, unc-97(su110) muscle largely resembles wild-type muscle. Sarcomere dimensions and overall organization are similar between unc-97(su110) and wild-type muscle, but the dense bodies in su110 animals are never as clearly defined as in wild-type animals. Fig. 2 A (bottom four panels) illustrates the range of defects that can be observed within individual muscle cells of su110 animals. These panels are all of cells where the sarcomeres had already become disorganized. The combination of coverslip pressure and slight rolling of an unc-97(su110) animal will also lead to the collapse of the sarcomere structure. Under similar conditions sarcomeres within wild-type muscle cells do not collapse. Anchorage of the sarcomere complex to the plasma membrane is therefore weak and easily disrupted in unc-97(su110) animals.

The lability of the sarcomeres as observed by polarized light microscopy prompted us to analyze the structural integrity of the muscle attachment structures in more detail. To this end, we determined the subcellular localization of two defined components of these muscle–hypodermal adherens junctions. Immunohistochemistry with a β-integrin/PAT-3 monoclonal antibody (Gettner et al., 1995) revealed that the dense bodies do not for the most part show up as rows of discrete spots in unc-97 mutants, but instead appear primarily as diffuse stripes running parallel to the M line (Fig. 2 B). Similarly, vinculin, which normally localizes exclusively to dense bodies (Barstead and Waterston, 1991), shows a diffuse stripe-like appearance in unc-97 mutants (Fig. 2 B); the diffuse stripes do not always run in parallel, but occasionally fuse to one another. Due to the
presence of M lines in the anti-PAT-3–stained animals, the fusion of these stripes can more easily be observed using anti-vinculin stained antibodies. These observations are consistent with UNC-97 playing a role in determining the structural integrity of adherens junctions, perhaps through clustering integrin or other dense body-associated proteins.

The *C. elegans* proteoglycan perlecan, encoded by the unc-52 gene, localizes to the basement membrane underlying the muscle (Francis and Waterston, 1991; Rogalski et al., 1993). Staining with anti–UNC-52 antibodies reveals staining at periodicities corresponding to the sites of the dense bodies and M-line structures (Fig. 2 B) (Francis and Waterston, 1991). In unc-97(su110) mutant animals, the periodicity of the staining is abrogated; instead, UNC-52 appears more diffuse (Fig. 2 B). The effect of the intracellular UNC-97 protein on the localization of the extracellular UNC-52 protein demonstrates that the correct localization of extracellular matrix components depends on the structural integrity of the muscular integrin complexes.

**unc-97 Defines a New Family of LIM Domain Proteins**

_unc-97(su110)_ was mapped to linkage group X in the lon-2 dpy-7 interval by Zengel and Epstein (1980). The cosmid F14D12 maps to this interval and contains a predicted LIM domain protein (F14D12.2; Fig. 3, A and B). Sequencing of this predicted gene from the mutant strain revealed that unc-97(su110) harbors a G→A splice site mutation at the last intron–exon boundary, which is predicted to disrupt the structural integrity of the last LIM domain of the UNC-97 protein (Fig. 3 A). A genomic PCR fragment containing the predicted unc-97 gene rescues the uncoordinated phenotype of unc-97(su110) (Materials and Methods). Taken together, these results demonstrate that the _unc-97_ gene is encoded by the predicted LIM domain containing protein F14D12.2.

Eight independent unc-97 cDNA clones were present in Y. Kohara’s EST collection library. We completely sequenced the largest cDNA clone and found it to represent a likely full-length clone containing a poly-A tail and an in-frame stop codon 5′ of the putative ATG start codon. The open reading frame (Fig. 3 C) was similar to the predicted gene structure; no evidence for alternative splice forms was detected in the other 7 cDNA clones. The UNC-97 protein encoded by the open reading frame (GenBank/EMBL/DDBJ accession number AF035583) consists entirely of 5 LIM domains (Fig. 3, B and C). Database searches revealed the presence of highly related proteins from other species, including the human PINCH
protein (Rearden, 1994), another predicted C. elegans protein, which we termed pin-2 (for PINCH-related gene 2) and several ESTs from mice, humans, and Drosophila (Fig. 4 D). To address cross-species conservation in more detail, we obtained the cDNA corresponding to the Drosophila EST, and after fully sequencing the transcript, found it to contain the entire open reading frame (GenBank/EMBL/DDBJ accession number AF078907). Like the other family members, Drosophila PINCH is a LIM-only protein comprised of five LIM domains and contains a significant sequence identity (on the order of 60%) to UNC-97 in each of its LIM modules (Fig. 3 C).

We propose to term this new family of LIM proteins the PINCH family after its founding member, PINCH (Rearden, 1994; renamed to h-PINCH-1 in Fig. 3). The PINCH family can be clearly distinguished from other multiple LIM domain-containing subfamilies (Fig. 3 D) and is defined by the following features: (a) all sequenced members consist exclusively of five LIM domains; (b) the spacing between the Zn-coordinating amino acids, a variable parameter in different LIM domain proteins, is with two exceptions invariant in the PINCH family; and (c) the Zn-coordinating amino acids in each LIM domain are with two exceptions invariant. Most notably, the first Zn finger of the last LIM domain of all PINCH family members is characterized by the highly unusual replacement of a His in the Cys-Cys-His-Cys LIM domain consensus motif by a Cys residue.

Expression of C. elegans unc-97 and Its Drosophila Homologue d-pinch in Muscle

To monitor the expression pattern of UNC-97, we fused the transcriptional regulatory regions of the unc-97 gene to GFP and analyzed its expression in transgenic C. elegans. A translational fusion protein, encoding all exons and introns of unc-97 reveals a similar set of expressing cells (see below). In both larvae and adult animals, unc-97 is expressed in two different cell types, muscles and neurons (Fig. 4). Strong expression is detectable in body wall muscle cells and vulval muscle cells, whereas no expression can be detected in pharyngeal muscles, intestinal muscle, or the anal depressor muscle. Weak expression can be observed in the anal sphincter muscle (data not shown). In the nervous system, unc-97 is expressed in the six mechanosensory receptor neurons ALML/R, PLML/R, AVM, and PVM (Fig. 4), which are responsible for sensing light touch (Chalfie et al., 1985). Intriguingly, a common theme of all the unc-97–expressing cell types is their attachment via the extracellular matrix to the hypodermis. We next exam-
ined unc-97 expression at earlier developmental stages to determine its onset of expression in development. We found that in embryos, unc-97 expression can first be observed at mid-embryogenesis at ~300 min of development (Fig. 4).

In an effort to deduce some conserved function among PINCH family members, we characterized the expression pattern of the Drosophila homologue of UNC-97, d-pinch. We generated a developmental profile and expression pattern for d-pinch by whole mount RNA in situ hybridization on 0–17-h embryos (Fig. 5). D-pinch transcripts were first detected in stage 10 embryos, where it is expressed in the visceral and body wall muscle. By stage 13, the expression has increased, and some pharyngeal muscle staining is also detected. Of particular interest is the intense expression of the transcripts at the sites of gut constriction. In late-stage 16 embryos, when the myotendinous junction is just beginning to form, we detect d-pinch transcripts in the epidermal tendon cells, as well as the aforementioned muscle lineages (Fig. 5). At this time of development, the heart musculature has differentiated as well; however, no d-pinch expression is seen in this muscle lineage.

Like unc-97-expressing cells, d-pinch-expressing cells are attached to extracellular matrix components via integ-
The timing of d-pinch expression in these cells is consistent with the expression of integrin subunits as well. A very striking example of coexpression is the temporal pattern of d-pinch and the integrin subunit $\alpha_{5\beta1}$ in tendon cells. By late stage 16, high levels of $\alpha_{5\beta1}$ are detected in the tendon cells with no other epidermal expression of the transcript (Wehrli et al., 1993); it is at this embryonic stage that we first detect d-pinch transcript in tendon cells.

**Adherens Junction and Nuclear Localization of UNC-97 in Muscle**

The complete coding sequence of unc-97 was fused to GFP to reveal the subcellular localization of UNC-97. The unc-97::GFP fusion gene rescues the unc-97(su110) mutant phenotype (Materials and Methods) and is thus likely to reveal a functionally relevant subcellular localization. In adult body wall muscles UNC-97 is located in discrete spots and lines along the body wall muscle (Fig. 6). Double labeling with an antibody directed against the C. elegans $\beta$-integrin PAT-3 (Gettner et al., 1995) revealed a colocalization of UNC-97 with PAT-3 at dense bodies and along the M lines (Fig. 6, see also Fig. 1). Containing with anti-vinculin antibodies, which also stain dense bodies, confirms that UNC-97 is part of the integrin complex at muscle-hypodermal attachment sites (data not shown). Taken together with the requirement of unc-97 for the integrity of dense bodies shown in Fig. 2, the localization of UNC-97 to dense bodies suggests that UNC-97 acts at the dense bodies to ensure the integrity of this type of adherens junction.

In the vulval muscles UNC-97 also localizes at sites of muscle attachment to the hypodermis (Fig. 6). 56% ($n = 32$) of the unc-97(su110) animals display a protruding vulva (p-vul) phenotype (Fig. 7), which could be ascribed to defects of these attachment sites in the absence of full unc-97 function. Structural defects of the vulval muscle attachments could explain the egg laying–defective phenotype of unc-97(su110), which is manifested by an accumulation of eggs in the gonad (data not shown).

Surprisingly, we also found UNC-97 to localize to the nuclei of muscle cells (Fig. 6). UNC-97 appears in discrete dots in muscle nuclei. We have not analyzed these dots in detail, however, their subnuclear localization appears to be somewhat variable. In many cases, these spots do not appear to be confined to submembraneal structures of the nuclear envelope, but appear to localize throughout the nucleoplasm (Fig. 6). In younger animals, however, particularly in embryos, we observe these subnuclear dots to be more concentrated towards the periphery of the nucleus (Fig. 7, A–C).

**RNA Interference of unc-97 Causes an Embryonic Arrest Phenotype**

Using the full-length unc-97::GFP fusion protein, we analyzed the developmental progression of UNC-97 expression and localization. In accordance with results from the promoter fusion (see above), we observe UNC-97 expression from $\sim$300 min of embryonic development onward (Fig. 7, A–C). This is about the time when myoblasts adopt their final identity, as judged by the onset of expression of structural muscle components, but is before the positioning of muscles into quadrants (Epstein et al., 1993; Coutu-Hresco et al., 1994). Upon formation of the muscle quadrant and the onset of muscle elongation, UNC-97 expression becomes stronger and its localization into discrete nuclear spots becomes visible (350–420 min; comma stage). This is about the stage when muscle components are first assembled into sarcomeres. Due to the strong punctate nuclear pattern it is hard to discern whether UNC-97 localizes to the newly formed dense bodies at this early stage. Discrete punctate UNC-97::GFP localization to dense bodies, which is clearly discernible from the punctate nuclear localization, can be observed around the time of hatching. Although most of the embryonic UNC-97::GFP signals can be accounted for by body wall muscle localization, some additional signals appear in the head and tail,
The early embryonic expression of UNC-97 in muscle prompted us to study its involvement in embryonic muscle development. Early defects in muscle development caused by the loss of the dense body components β-integrin/pat-3 or vinculin/deb-1 function have been shown to cause a specific developmental arrest phenotype, termed Pat phenotype (paralyzed, arrested elongation at twofold) (Barstead and Waterston, 1991; Williams and Waterston, 1994). unc-97(su110) mutant animals do not display such a phenotype; however, the molecular nature of the (su110) allele (Fig. 3) strongly suggests that this mutation does not lead to a complete loss of unc-97 function. To address this issue, we thus determined the probable loss-of-function phenotype of unc-97 using RNA interference (RNAi). This technique has been shown to effectively decrease the expression of both maternally and zygotically expressed genes and, in many cases, has been shown to phenocopy the null phenotype of a gene (Fire et al., 1998). We found that unc-97 RNAi causes a characteristic developmental arrest phenotype, which shows all the hallmarks of the Pat phenotype (Fig. 7, D and E). Embryos grow to the twofold stage, but arrest body elongation. The pharynx occasionally develops, but the embryo is paralyzed. Several embryos hatch, but are misshapen and then die (Fig. 7, D and E). Nonessential phenotypes could be observed upon injection of control double-stranded (ds) RNA. The Pat phenotype of unc-97 RNAi is similar to the loss-of-function phenotype of β-integrin/pat-3 and vinculin/deb-1, both factors which colocalize with UNC-97 at adherens junctions. Taken together, these data indicate that unc-97 is essential for early stages of muscle development.

UNC-97 expression is maintained in muscles throughout the postembryonic life of the animal (data not shown). Also, its dual subcellular localization in muscle nuclei and muscle attachment sites is not altered in development. These observations suggest that UNC-97 is continuously required to maintain the structural integrity of muscle attachment sites during growth and in the adult. The sarcomere fragility of unc-97(su110) described above clearly supports this notion. Conditional alleles of unc-97 will be required to address this issue in more detail.

unc-97 Functions in Mechanosensation

The subcellular localization of UNC-97::GFP in touch neurons is more diffuse than in muscles (Fig. 8 A). Although UNC-97 appears to be concentrated in submembranous regions, it can be found throughout the cytosol as well as throughout the nucleus (Fig. 8 A). Occasionally we observe a concentration of UNC-97::GFP in the periphery of the touch neuron nuclei in what appear to be ring like structures (data not shown). The nuclear staining profile of UNC-97::GFP in neurons thus appears to be distinct from that in muscles, suggesting that UNC-97 associates with cell type–specific and nonubiquitous subnuclear domains. We investigated whether unc-97 is required for the function of mechanosensory neurons. In behavioral touch assays we found that the partial loss-of-function allele unc-97(su110) displays no mechanosensory touch defectiveness on its own (Fig. 8 B). However, we find that this partial loss of unc-97 function strongly enhances the mechanosensory defect of a partial loss-of-function mutation in mec-3, a LIM homeobox gene required for mechanosensory function (Way and Chalfie, 1988). Although the strong mec-3 allele e1338 is completely touch insensitive, mec-3(u298) mutant animals retain some responsiveness to touch (Fig. 8 B). Examining a unc-97(su110); mec-3(u298) double mutant, we found that this partial responsiveness is almost completely abolished by the partial reduction unc-97 gene activity (Fig. 8 B). This experiment reveals that unc-97 contributes to the function of mechanosensory neurons. Due to the arrested lethal phenotype
of a complete loss of unc-97 function as determined by RNAi (Fig. 7), we could not address the null phenotype of unc-97 in touch neurons. Genetic mosaic experiments will address this issue in the future.

**The UNC-97–related LIM protein PIN-2 Is Expressed in Neurons and Intestine**

The now completely sequenced genome of *C. elegans* reveals the presence of a single other PINCH family member in *C. elegans*, which we termed PIN-2 (Fig. 3). Although it represents the most diverged member of the PINCH family, it clearly shares all the features of this family including the presence of five LIM domains and a characteristic signature of Zn-coordinating residues of the LIM domains (Fig. 4; PIN-2 shows 55.7% amino acid similarity to UNC-97 and 58.5% amino acid similarity to h-PINCH-1), pin-2 maps on LGIV, ~7 kb to the left of the cloned unc-31 gene; no candidate mutations have been mapped to this region.

We were motivated to look for the expression and subcellular localization of PIN-2 to address whether PIN-2 might perform a role in muscle development similar to UNC-97 or whether this diverged PINCH family member might be used in distinct cellular processes. A pin-2::GFP fusion gene construct (Fig. 9), which contains the full coding region of pin-2 and presumably reflects the authentic subcellular localization of PIN-2, is not expressed during early stages of embryogenesis; expression is first detectable in embryos shortly before hatching (data not shown). In early larval stages, PIN-2::GFP is expressed in two major tissue types, neurons and intestinal cells (Fig. 9). It does not reveal any overlap of expression with UNC-97. Notably, however, PIN-2 expression in the intestine might be somewhat related to the expression of *Drosophila d-pinch* in the visceral mesoderm that envelopes the gut. Neural expression of PIN-2::GFP is restricted to few neurons, arguing for a cell type–specific role of PIN-2. Moreover, whereas PIN-2::GFP expression fades in intestinal cells and is almost undetectable in adults, its expression is maintained in neurons throughout adulthood (data not shown), suggesting a role for PIN-2 in neural maintenance. PIN-2::GFP localizes uniformly throughout the cytoplasm and nucleus. In neurons, it localizes uniformly along axonal processes. PIN-2 appears to label varicosities of the ventral cord axon where it is expressed. The functional significance of this observation is unclear at the moment.

In summary, both the tissue type expression and the
subcellular distribution of the only two PINCH family members in *C. elegans*, UNC-97 and PIN-2 is strikingly different, thus arguing for a divergence in function of the genes.

**Discussion**

**PINCH Family Members across Phylogeny**

The invertebrate PINCH-like genes described here as well as several as yet uncharacterized vertebrate PINCH genes define a new family of LIM proteins that have been highly conserved across phylogeny. No other LIM domain family contains the same LIM domain architecture as the PINCH family. Considering the involvement of LIM domains in protein–protein interactions (see introduction), we propose that PINCH proteins represent adapter proteins capable of assembling multiprotein complexes. Within *C. elegans*, we identified two PINCH-like genes, unc-97 and pin-2. unc-97 is more closely related to the vertebrate PINCH genes. The function of unc-97 at focal adhesion sites appears to be conserved as well, since vertebrate PINCH-1 colocalizes with integrins to sites of cell–matrix contact (Tu et al., 1999).

Additional evidence that PINCH family members may function at focal adhesion sites comes from the analysis of *d-pinch* expression during *Drosophila* embryogenesis. *D-pinch* transcripts are expressed in both the body wall muscles and epidermal tendon cells, coincident with integrin subunit expression in those tissues (Bogaert et al., 1987; Leptin et al., 1989; Wehrli et al., 1993). The timing and tissue-specific expression of *d-pinch* suggests that it is involved in the terminal differentiation of muscles and tendon cells; one common feature of these cell types is their formation of adherens junctions. Integrin complexes are crucial for the stability of the junctions, as demonstrated by the dramatic muscle detachment phenotype seen in *myospheroid*β integrin mutants (Wright, 1960; Leptin et al., 1989; Volk et al., 1990). Based on the observation that the null unc-97 phenotype is very severe and phenocopies mutations in the *pat-3/β-integrin* gene, we predict that loss of *d-pinch* will also result in a severe disruption of muscle function.

The PIN-2 protein, which displays a high degree of similarity to UNC-97 in architectural composition, as well as primary sequence, is expressed in entirely different tissue types and, unlike UNC-97, displays a uniform subcellular distribution. Nevertheless, it is conceivable that, although deployed in different tissue types, distinct PINCH gene paralogues (such as UNC-97 and PIN-2) might fulfill a similar function. For example, integrin complexes in *C. elegans* are not only present in muscle cells but also in neu-

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**Figure 7.** unc-97 functions in muscle development. (A–C): UNC-97::GFP localization in live worms at embryonic stage ~300 min (A), ~400 min (comma stage) (B), and ~500 min (threefold “pretzel” stage) (C). (A’–C’) Corresponding DIC micrographs. White arrows in C, a muscle nucleus and dense bodies, respectively. Note UNC-97::GFP localization to the periphery of nuclei in A–C. (D–F): Loss-of-function phenotype of unc-97 as determined by RNAi. D and E show the progeny of animals subjected to unc-97 RNAi. Embryos either arrest and die at the twofold stage or die shortly after hatching (both categories were scored as arrested). Note that the pharynx develops relatively normally but that elongation of the rest of the animal is arrested. All these phenotypes are hallmarks of the pat phenotype (Williams and Waterston, 1994). Bottom, progeny of animals subject to RNAi with a control ds RNA derived from a new homeobox gene (Hobert, O., and G. Ruvkun, unpublished data), which displays no lethality.
rons, where they do not appear to localize in discrete spots (Baum and Garriga, 1997). It is possible that PIN-2 might be involved in neural integrin complex assembly and/or signaling. The expression of PIN-2 in the intestine could potentially indicate a similarity to the expression of Drosohila d-pincho in the visceral mesoderm that envelopes the gut.

**UNC-97 and Muscle Development**

The structural components that anchor myofibers to the extracellular matrix, such as integrin, vinculin, talin, and α-actinin are remarkably conserved in C. elegans and resemble the protein composition of adherens junctions in other systems, such as focal adhesions in tissue culture cells (Waterston et al., 1980; Francis and Waterston, 1985; Waterston, 1988; Moerman and Fire, 1997). It is thus likely that the fundamental mechanisms required to assemble these structures are conserved as well. Based on our functional analysis of UNC-97 and the presence of highly related homologous molecules in flies and vertebrates, we suggest that members of the PINCH family of LIM-only proteins are a critical component of muscle attachment and adherens junction assemblies across phylogeny. Indeed, the mouse UNC-97 homologue PINCH-1 has recently been shown to colocalize with β1-integrins at focal adhesions (Tu et al., 1999). This interaction appears to be mediated by the ankyrin-repeat containing serine/threonine kinase ILK, which by direct association with both β1-integrins (Hannagan et al., 1996) and the mouse UNC-97
shown), we speculate that other LIM proteins besides highly related to the CRP proteins (T04C9.4; data not reported for the CRP3/MLP protein, whose loss-of-function causes disorganization of cardiac myofibers (Arber et al., 1997). We demonstrated here a similar requirement for the LIM-only protein UNC-97 in body wall muscles in C. elegans. Since the C. elegans genome contains a gene highly related to the CRP proteins (T04C9.4; data not shown), we speculate that other LIM proteins besides UNC-97 will also be involved in adherens junction assembly.

The su110 allele indicates that UNC-97 has an important role in maintaining sarcomere organization in growing and adult animals. Moreover, the RNAi (probable loss-of-function) experiment indicates an important regulatory role for UNC-97 during embryonic muscle development. However, it is unclear so far as to whether the embryonic defects caused by unc-97 RNA interference reflect a requirement for UNC-97 in the initial stages of assembly of the adherens junctions or reflects a requirement for UNC-97 in stabilizing adherens junctions after they are formed to resist the mechanical stress they are exposed to upon elongation of the animal. Since UNC-97 expression clearly coincides with the onset of expression of adherens junction components and their assembly into these structures, we favor a model in which UNC-97 is involved in the initial assembly of the adherens junction components and keeps residing in these structures to ensure their stability. We will address these issues in more detail in the future by isolating deletion alleles of unc-97, which will provide a better source for a detailed characterization of the embryonic phenotype than the dsRNA injected animals described here.

Although it is unclear how UNC-97 cooperates with β-integrins and other focal adhesion components such as vinculin to determine adherens junction integrity, the modular organization of UNC-97 into five LIM domains implicates UNC-97 in binding to multiple proteins. UNC-97 might be a scaffold or adapter protein onto which various different components assemble to form a functional muscle attachment site. Since defective myofibrils cause as a secondary consequence the destabilization of muscle attachment sites (Epstein, 1986), it is for example possible that UNC-97 serves as an anchor between myofibrils and membrane-anchored integrin components. In this model, dense body defects in unc-97(su110) mutant animals would not arise from direct defects in the dense body structure per se, but would represent a secondary consequence of the myofibril disorganization.

A Nuclear Function for UNC-97?

Our analysis of UNC-97 localization in a living, nonfixed animal, using a rescuing, i.e., functionally intact unc-97::GFP reporter gene, lends support for an authentic in vivo dual subcellular localization of this LIM protein. However, at this point it is unclear whether the nuclear localization of UNC-97 is indeed functionally significant. In contrast to the localization of UNC-97 to adherens junctions, which correspond to the site of action of UNC-97 as inferred from the unc-97 mutant phenotype, no such clear correlation exists to a possible nuclear function of UNC-97. However, our demonstration of a genetic interaction of unc-97 with the LIM homeodomain transcription factor mec-3 could be explained on the basis of a physical interaction between these proteins and could thus reflect a functional requirement for UNC-97 in the nucleus. LIM–LIM interaction have been previously described (Sadler et al., 1992) and the direct interaction of UNC-97 with MEC-3 could affect the transcriptional activity of the MEC-3 transcription factor. Alternatively, it is also entirely possible that the genetic interaction of unc-97 and mec-3 reflects an independent requirement for these genes in mechanosensory processes.

Although further experiments will need to address the physiological significance of UNC-97 in the nucleus, there are several attractive hypotheses regarding a potential nuclear function of UNC-97. As mentioned above, UNC-97 could be directly involved in gene regulatory events by interacting with specific transcription factors. The vertebrate LIM-only proteins CRP3/MLP and SLIM1/KyoT have been directly implicated in gene regulation via interaction with the transcription factors MyoD and RBP-J, respectively (Kong et al., 1997; Tanigushi et al., 1998), whereas the LIM-only protein LMO2 assembles higher order transcriptional activation complexes by bridging other transcription factors that are directly involved in DNA binding (Wadman et al., 1997). Alternatively, but not necessarily mutually exclusive, UNC-97 could represent a structural component of specific subnuclear domains. The localization of UNC-97 to discrete dots in muscle nuclei supports this hypothesis, although the nature of these dots is entirely unclear. Subnuclear domains of different types, such as speckles, coiled bodies, gems, and Kr bodies/nuclear domains have been described in various systems. Factors localizing to these domains are involved in distinct nuclear processes such transcriptional silencing and RNA processing (for review see Lamond and Earnshaw, 1998).

Lastly, in regard to the dual subcellular localization of UNC-97 it is also tempting to speculate that UNC-97 transmits a signal from attachment sites to the nucleus. Although we have not addressed the question whether UNC-97 dynamically shuttles between attachment sites and the nucleus, focal adhesion–nuclear shuttling has been recently demonstrated for the LIM protein zyxin (Nix and Beckerle, 1997). Recently, the mouse UNC-97 homologue PINCH-1 was shown to interact specifically with, and might serve as a substrate of, the integrin-linked kinase ILK (Tu et al., 1999), a serine-threonine kinase implicated in integrin signal transduction (Hannagan et al., 1996). This observation might point to a potential role for UNC-97 in integrin-mediated signal transduction.

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Hannigan, G.E., C. Leung-Hagesteijn, L. Fitz-Gibbon, M.G. Coppolino, G. Francis, G.R., and R.H. Waterston. 1991. Muscle cell attachment in *Caenorhabditis elegans*. *J. Cell Biol.* 114:465–479.

Lamond, A.I., and W.C. Earnshaw. 1998. Structure and function in the nucleus. *Science* 280:547–553.

Lehmann, R., and D. Tautz. 1993. In situ hybridization to RNA. In *Drosophila melanogaster: Practical Uses in Cell and Molecular Biology*. L.S.B. Goldstein and E.A. Fyrborg, editors. Academic Press, San Diego, CA. 575–598.

Lepiniec, L., T. Bogaert, R. Derivery, and M. Wilcox. 1989. The function of PS integrins during *Drosophila* development. *Cell*. 56:401–408.

Louis, H.A., J.D. Pino, K.L. Schmechel, P. Pomies, and M.C. Beckerle. 1997. Comparison of three members of the cysteine-rich protein family reveals functional conservation and divergent patterns of gene expression. *J. Biol. Chem.* 272:27484–27491.

Moerman, D.G., and A. Fire. 1997. Muscle: structure, function and development. In *C. elegans* II: D.L. Riddle, T. Blumenthal, B.J. Meyer, and J.R. Priess, editors. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York. 417–470.

Moerman, D.G., H. Hutter, G.P. Mullen, and R. Schnabl. 1996. Cell autonomous expression of perlecan and plasticity of cell shape in embryonic muscle of *Caenorhabditis elegans*. *Dev. Biol.* 173:228–242.

Moulder, G.L., M.M. Huan, R.H. Waterston, and R.J. Barstead. 1996. Talin requires β-integrin but not vinculin for its assembly into focal adhesion-like structures in the nematode *C. elegans*. *Mol. Cell. Biol.* 1:1181–1193.

Nix, D.A., and M.C. Beckerle. 1997. Nuclear-cytoskeletal shuttling of the focal contact protein, zyxin: a potential mechanism for communication between sites of cell adhesion and the nucleus. *J. Cell Biol.* 138:1139–1147.

Rearden, A. 1994. A new LIM protein containing an autoepitope homologous to “senescent cell antigen.” *Biochem. Biophys. Res. Commun.* 201:1124–1131.

Rogalski, T.M., B.D. Williams, G.P. Mullen, and D.G. Moerman. 1993. Products of the unc-52 gene in *Caenorhabditis elegans* are homologous to the core protein of the mammalian basement membrane heparan sulfate proteoglycan. *Genes Dev.* 7:1471–1484.

Sadler, I., A.W. Crawford, J.W. Michelsen, and M.C. Beckerle. 1992. Zyxin and cCRP: two interactive LIM domain proteins associated with the cytoskeleton. *J. Cell Biol.* 119:1573–1586.

Schmechel, K.L., and M.C. Beckerle. 1994. The LIM domain is a modular protein–binding interface. *Cell*. 79:211–219.

Stromach, E.E., S.E. Siegrist, and M.C. Beckerle. 1996. Two muscle-specific LIM proteins in *Drosophila*. *J. Cell Biol.* 134:1179–1195.

Sulston, J.E., E. Schierenberg, J.G. White, and J.N. Thomson. 1983. The embryonic cell lineages of the nematode *Caenorhabditis elegans*. *Dev. Biol.* 100:64–119.

Taniguchi, Y., T. Furukawa, T. Tun, H. Han, and T. Honjo. 1998. LIM protein Kvyt2 negatively regulates transcription by association with the RBP7/DNA-binding protein. *Mol. Cell. Biol.* 18:644–654.

Tu, Y., F. Li, S. Goicoechea, and C. Wu. 1999. The LIM-only protein PINCH directly interacts with the integrin-linked kinase (ILK) and is recruited to integrin-rich sites in spreading cells. *Mol. Cell. Biol.* In press.

Turner, C.E., J.R. Glennery, Jr., and K. Burridge. 1990. Paxillin: A new vinculin-binding protein present in focal adhesions. *J. Cell Biol.* 111:1059–1068.

Volk, T., L.I. Fessler, and J.H. Fessler. 1990. A role for integrin in the formation of sarcomeric architecture. *Cell*. 63:525–536.

Wadman, L.A., H. Osada, G.G. Grütz, A.D. Aguín, H. Westphal, A. Forster, and T.H. Rabbits. 1997. The LIM-only protein Lmo2 is a bridging molecule associating an erythroid DNA-binding complex which includes TAL1, E47, GATA-1 and Ldb1/LNL proteins. *EMBO (Eur. Mol. Biol. Organ.) J.* 16:3145–3157.

Warren, A.J., W.H. Colledge, M.B. Carlton, M.J. Evans, A.J. Smith, and T.H. Rabbits. 1994. The oncogenic cysteine-rich LIM domain protein rhb6 is essential for erythroid development. *Cell* 78:45–57.

Waterston, R.H. 1988. Muscles. In *The Nematode Caenorhabditis elegans*. W.B. Wood, editor. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York. 281–336.

Waterston, R.H., J.N. Thomson, and S. Brenner. 1980. Mutants with altered thoracic morphology. *Cell*. 17:341–350.

Way, J.C., and M. Chalfie. 1988. mec-3, a homeobox-containing gene that specifies differentiation of the touch receptor neurons in *Caenorhabditis elegans*. *Cell.* 51:929–940.

Wehrli, M., A. DiAntonio, I.M. Fearnley, R.J. Smith, and M. Wilcox. 1993. Integrin expression and cell identity in *Caenorhabditis elegans* embryos assemble into nascent structures distinct from thick filaments and multifilament assemblages. *J. Cell Biol.* 122:845–858.

Wefersten, R., X. Wang, D. Song, N.E. Cooke, and S.A. Liebhaber. 1994. Zyxin and nuclear-cytoplasmic shuttling of the focal contact protein, zyxin: a potential mechanism for communication between sites of cell adhesion and the nucleus. *J. Cell Biol.* 111:1059–1068.

Weil, M., A. DiAntonio, I.M. Fearnley, R.J. Smith, and M. Wilcox. 1993. Cloning and characterization of mec-3, a novel Drosophila melanogaster integrin. *Mech. Dev.* 43:21–36.

White, J. 1988. The anatomy. In *The Nematode Caenorhabditis elegans*. W.B. Wood, editor. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York. 81–122.

Williams, B.D., and R.H. Waterston. 1994. Genes critical for muscle development and function in *Caenorhabditis elegans* identified through lethal mutations. *J. Cell Biol.* 124:475–490.

Wright, T.R.F. 1960. The phenogenetics of the embryonic mutant, lethal myosphere. *Drosophila melanogaster.* *J. Exp. Zool.* 143:77–99.

Xiao, S.T., S.T. Wosnok, W.L. Kuo, M.R. Altherr, and D.S. Bredt. 1997. Actinin-associated LIM protein: identification of a domain interaction between PDZ and spectrin-like repeat motifs. *J. Cell Biol.* 139:507–515.

Zengel, J.M., and H.F. Epstein. 1980. Identification of genetic elements associated with muscle structure in the nematode *Caenorhabditis elegans*. *Cell Mol. Biol.* 1:73–97.