The C. elegans homeodomain gene unc-42 regulates chemosensory and glutamate receptor expression

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SUMMARY

Genes that specify cell fate can influence multiple aspects of neuronal differentiation, including axon guidance, target selection and synapse formation. Mutations in the unc-42 gene disrupt axon guidance along the C. elegans ventral nerve cord and cause distinct functional defects in sensory-locomotory neural circuits. Here we show that unc-42 encodes a novel homeodomain protein that specifies the fate of three classes of neurons in the Caenorhabditis elegans nervous system: the ASH polymodal sensory neurons, the AVA, AVD and AVE interneurons that mediate repulsive sensory stimuli to the nematode head and anterior body, and a subset of motor neurons that innervate head and body-wall muscles. unc-42 is required for the expression of cell-surface receptors that are essential for the mature function of these neurons. In mutant animals, the ASH sensory neurons fail to express SRA-6 and SRB-6, putative chemosensory receptors. The AVA, AVD and AVE interneurons and RME and RMD motor neurons of unc-42 mutants similarly fail to express the GLR-1 glutamate receptor. These results show that unc-42 performs an essential role in defining neuron identity and contributes to the establishment of neural circuits in C. elegans by regulating the transcription of glutamate and chemosensory receptor genes.

Key words: unc-42, Homeodomain, Mechanosensory, Axon pathfinding, Caenorhabditis elegans

INTRODUCTION

Neural development requires the generation of a diverse population of neuron types distinguished by morphology, connectivity patterns and the expression of distinct combinations of neurotransmitters, receptors and ion channels. Even the relatively simple nervous system of the C. elegans hermaphrodite is made up of 118 different classes of neurons (White et al., 1986). Cell fate specification in the nervous system is complex, requiring the combinatorial action of multiple transcriptional regulators (reviewed in Bang and Goulding, 1996; Ruvkun, 1997; Sengupta and Bargmann, 1996; Tanabe and Jessell, 1996; Doe and Skeath, 1996). Extensive studies in invertebrates and vertebrates have identified genes that act at early stages of neuronal fate determination and patterning of the nervous system, but the mechanisms that generate specific neuronal subtypes are still poorly understood.

One important group of transcriptional regulators defined by genetic mutations are the paired-like homeobox proteins. Members of this class contain homeodomains closely related to the homeodomains of the Prd/Pax gene family (Frigerio et al., 1986), but lack the paired domain. The neuronal paired-like homeoproteins regulate particular neuronal traits in subsets of neurons, and thus are candidates to act downstream of transcriptional regulators that play more general roles in determining whether a cell assumes a neuronal fate. The C. elegans UNC-4 protein, for example, regulates synaptic specificity of one class of motor neuron (Miller et al., 1992; White et al., 1992). The VA motor neurons of unc-4 mutants receive inappropriate synaptic inputs from interneurons that normally synapse onto another class of motor neuron. Yet, other aspects of VA differentiation appear normal, including their ability to make appropriate neuromuscular synapses. Phox2A, a mouse homeobox protein of this class, is required for specific aspects of noradrenergic cell fate, including neurotransmitter synthesis and expression of Ret, the receptor for glial derived neurotrophic factor (GDNF) (Morin et al., 1997).

In this paper, we describe the characterization of unc-42. We show that unc-42 encodes a novel homeodomain protein that is related to UNC-4 and other C. elegans paired-like homeodomain proteins, but is expressed by a different subset of neurons. Cells that require unc-42 function include the AVA, AVD and AVE interneurons that control backward movement and the polymodal ASH sensory neurons that mediate aversive responses to mechanical stimulation, chemorepellents and high osmolarity. Our analysis indicates that unc-42 mutations eliminate expression of two putative chemoreceptors, SRA-6.
and SRB-6, by the ASH neurons, while other general neuronal traits are not affected. We show that unc-42 mutants also fail to express the GLR-1 glutamate receptor in many of the interneurons and motor neurons that form the neural circuitry for nose touch. Our results demonstrate that the neural circuits for forward and backward motion in C. elegans are regulated by separate developmental programs and reveal a potential role for UNC-42 as a direct transcriptional regulator of glutamate receptor and chemosensory receptor expression.

MATERIALS AND METHODS

Strains and genetics

Strains were grown at 20°C and maintained as described by Brenner (1974). In addition to the standard wild-type strain (N2), strains with the following mutations were used in this work:

- LGII: gmt13 [srb-6-gfp + rol-6] (N. Hawkins, personal communication; Troemel et al., 1995).
- LGII: ncl-1(e1865).
- LGV: unc-42(e270), unc-42(e419), unc-42(e623), unc-42(gm23), smg-4(mal16).

Chromosomal aberrations: eT1(III,V) (Rosenbluth and Baillie, 1981); dpy-29(V) (Rosenbluth and Baillie, 1985).

Extrachromosomal arrays: gmx10 [pRB18::rol-6(dn)], gmx18[pRB22 + rol-6(dn)], gmx71 [sra-6-gfp + rol-6(dn)] (Wightman et al., 1997; Troemel et al., 1995).


Mosaic analysis

The method of Herman (1984) was used for genetic mosaic analysis. We constructed a strain that was mutant for unc-42(e270) and the cell-autonomous marker ncl-1 (Kenyon, 1986; Hedgecock and Herman, 1995), and carried cdp11, a free chromosomal duplication containing wild-type copies of both genes (Hunter and Wood, 1992). Cells that lose the duplication and are mutant for ncl-1 have enlarged nucleoli and can be identified by Nomarski optics. To analyze the defects in locomotion and the response to light body touch, we identified Unc non-Mec and Mec non-Unc F1 mosaic hermaphrodites and determined the point in the cell lineage where loss of the duplication occurred.

Analysis of unc-42 heterozygotes and sDf29 heterozygotes

To determine if unc-42 heterozygotes exhibit HSN pathfinding defects, wild-type males were mated to dpy-6(e11); unc-42 double mutants. HSN axon morphology was examined in F1 cross progeny and dpy-6(e11)/+ control animals by anti-serotonin staining (Gariga et al., 1993a). Self-progeny exhibit the short, dumb phenotype of dpy-6 and are easily distinguished from unc-42/+/ heterozygotes that have a wild-type body type. To examine pathfinding defects in deficiency hemizygotes, we analyzed animals that contained sDf29, a deletion chromosome that uncovers the unc-42 gene, balanced by eT1 (dpy-18(e364)III/eT1; unc-46(e177)sDf29 V/eT1). eT1 is a reciprocal translocation of chromosomes II and V that breaks within the unc-36 gene, generating viable translocation homoygotes that are Unc. To examine HSN axon morphology in sDf29/+ animals, 200 non-Unc-36 hermaphrodites were transferred to a separate plate and stained with anti-serotonin (Gariga et al., 1993a).

Cloning unc-42

unc-42 mapped genetically to the right of her-1 on chromosome V. her-1 is located on cosmID C12G5 on the C. elegans physical map (Trent et al., 1991). Both her-1 and unc-42 are removed by the small chromosomal deletion, sDf29. The right end-point of sDf29 was mapped to cosmid T07C12 by RFLP analysis of wild-type and sDf29 genomic DNA. Rescue of the Unc and Mec phenotypes and ventral cord pathfinding defects of unc-42 was obtained when mutant worms were injected with either of two YACs that bridge the region, Y1D1 and Y42F5 (Coulson et al., 1986). All germline transformation experiments were conducted as described by Mello et al. (1991). Y42F5 and Y1D1 YAC DNA were purified by pulsed-field gel electrophoresis, treated with β-agarase (USB) and concentrated in Centricon-30 microconcentrators (Amicon). unc-42(e270) smg-4(mal16) hermaphrodites were injected with 5 μg/ml of YAC DNA plus 20 μg/ml of rol-6(su1006dm) DNA (pRF4) as a dominant selectable marker.

Y42F5 was used to construct a Lambda FIXII phage library. Genomic DNA from yeast carrying the Y42F5 YAC was partially digested with Sau3AI and ligated into the Lambda FIXII vector using the Lambda FIXII/XhoI vector system from Stratagene. 60,000 plaques from the Y42F5 Lambda FIXII library were screened with three DNA probes generated by random priming (Feinberg and Vogtenstein, 1983). Probes were made from purified Y1D1 and Y42F5 YAC DNA and B15.1, a circular deletion derivative of Y42F5 generated as described by Miller et al. (1993) and isolated by the method of Devenish and Newlon (1982). DNA was prepared from 59 λ clones that hybridized with all three probes and tested in pools of 5-6 for rescuing activity. unc-42(e270) hermaphrodites were injected with DNA from the Lambda FIXII phage clones at concentrations of 50 μg/ml with 100 μg/ml of rol-6(su1006) DNA. A single 16.8 kb phage clone, λRB162, rescued the unc-42 mutant phenotypes. Subclones of λRB162 were constructed in pBluescript KS+ and used to identify a minimal rescuing region of 7.8 kb.

Isolation, PCR and cloning of unc-42 cDNAs

A 4.2 kb SalI-EcoRI genomic fragment from the unc-42 minimal rescuing region was used to screen 500,000 plaques of a λgt10 C. elegans cDNA library (gift of L. Miller and B. Meyer). Three cDNA clones were identified; all contained inserts of approximately 1.2 kb and showed the same pattern of restriction sites. Inserts were amplified by PCR using primers to λgt10 flanking sequence (5′CCGGATCCCTTCGCTGGTTAAGTCCAAG3′ and 5′GGGGATCCGGTATGGGACTTTCCAGG3′) and ligated into pBluescript KS+. Two additional cDNA clones were generated by RT-PCR (primers: 5′GGAAGCTGCAATGGCAGCTAACTGGC3′ and 5′GGGGTGCTACTAGATGGAAGAGG3′). Complete double-strand sequence obtained for the cDNAs indicated that they were identical.

Northern blot hybridization

Poly(A)+ RNA from embryonic and mixed stage cultures of C. elegans was prepared as described by Garriga et al. (1993b). Electrophoresis, blotting and probing of the RNA was performed by standard molecular biology techniques (Sambrook, 1989). An unc-42 cDNA clone was used to produce an RNA probe that hybridizes to the C-terminal two-thirds of the unc-42 transcript.

Sequence of genomic and unc-42 mutant DNA

C. elegans genomic sequence for the unc-42 region was obtained using the transposon-mediated method of Strathmann et al. (1991) and assembled using AssemblyLIGN software (Kodak). Double-strand sequence was generated for overlapping subclones of λRB162 that constituted the minimal rescuing region of unc-42 in germline transformation experiments. This region was sequenced subsequently by the C. elegans genome project. unc-42 corresponds, in part, to the predicted gene F58E6.10.

For analysis of unc-42 mutant alleles, genomic DNA from mutant strains was amplified by single-worm PCR and ligated into pBluescript KS+. For each mutant strain, double-strand sequence was obtained for two or three subclones constructed from DNA amplified in independent PCR reactions. Single mutant worms were prepared
Worms prepared for immunofluorescence were viewed and photographed with Ektachrome T160 film using a Zeiss microscope and filters #487910 and #487915. Photographs were scanned into a computer graphics file with a Nikon scanner and annotated with the Adobe Photoshop graphics program.

**Behavioral tests**
Mechanosensory function for light body touch was assayed by the method of Chalfie and Sulston (1981), and nose touch was determined as described by Kaplan and Horvitz (1993).

**RESULTS**

**Mutations in unc-42 alter locomotion and disrupt multiple sensori-locomotor neural circuits**

The first three unc-42 alleles were identified based on the uncoordinated (Unc) phenotype conferred by the mutations (Brenner, 1974). Although mutant worms can move forward or backward spontaneously, this movement is slow and irregular. Mutant worms tend to kink ventrally and their head movement is restricted. These defects are likely to be the result of neural defects because muscle development and morphology are normal in unc-42 mutants (Waterston and Francis, 1985).

In additional assays for behavioral defects, we found that unc-42 mutants also exhibited severe defects in response to mechanical stimuli to the nematode head and anterior body. unc-42 mutants exhibited a distinctive mechanosensory (Mec) response to light touch along the body: mutant animals failed to back up when stroked along anterior body regions, but moved forward normally when touched along the posterior body (Table 1). The response to touch at the tip of the nose (Not) was also severely reduced in the mutants. Only 8% of unc-42 (e419) animals responded to nose touch, compared to 90% for wild-type worms (Table 1).

Nose touch and body touch are mediated through separate neural circuits defined by anatomy (White et al., 1986), cell killing experiments (Chalfie et al., 1985) and genetic analysis (Hart et al., 1995; Maricq et al., 1995). Wild-type animals respond to light strokes to the anterior part of the body by

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<th>Table 1. Mechanosensory defects in unc-42 mutants</th>
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unc-42 mutant adult hermaphrodites were tested for response to light touch along the anterior and posterior body (Mec) and to the tip of the nose (Not). Wild-type and glr-1(n2461) mutant adult hermaphrodites were tested as controls.

*50 animals for each strain were scored for anterior and posterior body touch, and nose touch. Light touch to the body was assayed by lightly stroking the side of the head or tail as described by Chalfie et al. (1985). Each animal was tested at least three times. Animals were scored as responding to anterior touch if they moved backward when touched along the head or anterior. Posterior touch was scored as normal if the animals moved forward or stopped backward movement when touched along the tail or posterior body. Nose touch was tested as described by Kaplan & Horvitz (1993). Animals were tested at least five times and were scored positive for nose touch if they stopped or moved backward in response to stimulus at the tip of the nose. Errors indicate the s.e.m.
backing up and to touch along the posterior body by moving forward. The ALMR, ALML and AVM neurons sense light touch along the anterior body, and the PLMR and PLML neurons sense touch along the posterior body. Anterior body touch requires the function of the AVA and AVD interneurons, which innervate type-A motor neurons, to drive backward movement, while posterior body touch requires the AVB and PVC interneurons, which innervate type-B motor neurons, to drive forward movement (Chalfie et al., 1985; White et al., 1986). The response to anterior body touch is dependent primarily on the AVD interneurons, probably via gap junctions with the ALM and AVM sensory neurons (Chalfie et al., 1985).

Avoidance to touch at the tip of the nose is detected primarily by the sensory neurons ASH and FLP (Kaplan and Horvitz, 1993). The ASH neurons also sense high osmolarity and volatile repellents (Bargmann et al., 1990; Troemel et al., 1995), and may be analogous to vertebrate nociceptors that detect several pain modalities (Besson and Chaouch, 1987; Kaplan and Driscoll, 1997). Although the ASH and FLP sensory neurons synapse with many of the same interneurons as the ALM and AVM mechanosensory neurons, nose touch employs a separate mode of synaptic transmission. ASH-mediated nose touch requires GLR-1, an AMPA-type glutamate receptor expressed by many postsynaptic targets of ASH and FLP including the AVA and AVD interneurons (Hart et al., 1995; Maricq et al., 1995). Mutations in glr-1 block the response to nose touch, but do not alter avoidance to body touch or high osmolarity, even though these responses are also mediated by the AVA and AVD interneurons. We found that mutations in unc-42 altered all of these behaviors. Nose touch and anterior body touch were severely diminished (Table 1), and osmotic avoidance was also reduced (data not shown).

**ASH differentiation is altered in unc-42 mutants**

To determine if developmental defects in the mechanosensory neurons could account for these behavioral defects, we first examined the morphology and differentiation of mutant ALM, AVM and ASH sensory neurons. UNC-86, a POU homeodomain protein required to specify ALM, AVM and FLP cell fate (reviewed by Ruvkun, 1997), was expressed normally in the mutants (data not shown). The axon trajectories of the unc-42 and wild-type ALM and AVM neurons were also indistinguishable when animals were stained with an antiserum to α-tubulin (Piperno and Fuller, 1985).

The ASH neurons and several other sensory neurons with ciliated endings take up lipophilic fluorescent dyes such as DiI. When unc-42 mutants were incubated in media containing DiI, the ASH neurons took up the dye normally, indicating that their ciliated ending were exposed. Although ASH axonal and dendritic morphology appeared normal in these animals (data not shown), we found that other markers for ASH differentiation were not expressed. The ASH neurons of unc-42(e419) mutants failed to express an srb-6-gfp transgene (Fig. 1), while the ADL

**Fig. 1. srb-6-gfp transgene expression in unc-42 mutant animals.** The ASH sensory neurons in unc-42 mutants fail to express gmIS13, an integrated srb-6-gfp transgene. (A,C) Diagram of the pattern of srb-6-gfp expression in the anterior of (A) wild-type and (C) unc-42 larvae. Circles depict the cell bodies on the left side. Solid circles represent the sensory neurons that express srb-6-gfp; the open circle represents ASH in an unc-42 mutant, which fails to express srb-6-gfp. (B,D) Fluorescence photomicrographs of left lateral views of (B) wild-type and (D) unc-42(e419) larvae showing expression of the srb-6-gfp transgene. Scale bar, 10 μm.

**Fig. 2. glr-1-gfp transgene expression in unc-42 mutant animals.** The AVA, AVD and AVE interneurons and RMD and RME motor neurons of unc-42 mutants fail to express mulsI, an integrated glr-1-gfp reporter transgene (Hart et al., 1995). (A,C) Diagram of the pattern of glr-1-gfp expression in the nematode head in (A) wild-type and (C) unc-42 L1 larvae. 34 cells in the head express glr-1-gfp in wild-type worms (Hart and Kaplan, 1995; Maricq et al., 1995). Circles depict the position of cell bodies on the left side. Solid circles represent the cells that express glr-1-gfp; open circles represent cells that are present but fail to express the GFP reporter in unc-42 mutants. (B,D) Fluorescence photomicrographs of left lateral views of (B) wild-type and (D) unc-42(e419) larvae showing expression of the glr-1-gfp transgene. Cells in the head that continue to express GLR-1 in the mutants are the URY, SMD, AVB, RIM, AVG, RIG and RIS neurons. Scale bar, 10 μm.
and ADF sensory neurons expressed this transgene normally. ASH neurons of unc-42 mutants also failed to express an sra-6-gfp transgene (Wightman et al., 1997; data not shown). sra-6 and srb-6 encode seven-transmembrane receptors that may function as chemoreceptors for the detection of volatile repellents (Troemel et al., 1995).

**Differentiation of the AVA, AVD and AVE interneurons and the RME and RMD motor neurons is altered in unc-42 mutants**

Failures in ASH function could account for behavioral defects mediated solely by ASH, but cannot account for the defects in body touch or locomotion, or the severity of the nose-touch defects of unc-42 mutants. If the ASH neurons of wild-type animals are killed by laser microsurgery, worms can still respond to nose touch 37% of the time (Kaplan and Horvitz, 1993). By contrast, unc-42 mutants respond to nose-touch stimuli only 10% of the time (Table 1). These results predict that cells in addition to ASH contribute to the nose-touch defects of the mutants.

To determine if unc-42 mutations also disrupted interneuron function, we tested whether unc-42 mutants expressed a transcriptional glr-1-gfp reporter transgene. glr-1 encodes an AMPA-type glutamate receptor expressed by all interneurons of the forward and backward locomotory circuit, as well as by a subset of head motor neurons (Hart et al., 1995, Maricq et al., 1995). We could not detect glr-1-gfp expression in the AVA, AVD and AVE interneurons in living mutants or in mutant worms that were fixed and stained with an anti-GFP antiserum to enhance GFP detection (Fig. 2). Identical results were obtained for unc-42 mutants that express a functional GLR-1 receptor tagged with GFP (nuIs25; Rongo et al., 1998). These interneurons receive synaptic input from ASH and FLP and provide output to motor neurons that control backward movement. The cell bodies of the interneurons were still present in the mutants, based on Nomarski microscopy of live animals and staining of fixed worms with DAPI (data not shown). However, we were unable to determine if the morphology of the interneuron axons along the ventral cord is normal in unc-42 mutants because individual markers for these neurons are not available.

The expression of the glr-1-gfp transgene was unaffected in AVB and PVC, interneurons that control forward motion (Fig. 2). Thus, the loss of GLR-1 receptor expression by the AVA, AVD and AVE interneurons contributes to the severe nose-touch phenotype of unc-42 mutants.

Mutations in unc-42 also disrupted glr-1-gfp expression in the six RMD and two RME motor neurons, which innervate head muscles (Fig. 2). The RME neurons are involved in foraging behavior, and the RMDs mediate a head withdrawal response to touch along the side of the nose that is also dependent on glr-1 (Hart et al., 1995). Because head mobility is defective in glr-1 mutants, we did not test mutant animals for defects in head withdrawal.

**unc-42 encodes a novel homeodomain protein**

Altered expression of late differentiation genes in several unc-42 mutant neurons suggested that unc-42 may act to regulate gene expression. We cloned unc-42 by transformation rescue (see Materials and Methods) and determined that it encodes a novel homeodomain protein of the paired-like class. The unc-42 gene structure is depicted in Fig. 3A. Northern blot analysis of mixed stage C. elegans RNA using an RNA antisense probe generated from the unc-42 cDNA revealed a single transcript of 1.2 kb (Fig. 3B). Sequence analysis of unc-42 cDNAs predicted a protein product of 263 amino acids (Fig. 4A).

To confirm that this gene is unc-42, we sequenced four of the mutant unc-42 alleles. The e419 and gm23 mutations are both GC to AT transitions that insert amber stop codons at position 10 and 48 of the homeodomain, respectively. The e270 mutation converts a conserved valine to glutamic acid at position 47 of helix three (Fig. 4B, top). The weak allele gm18 is a missense mutation in the region immediately C-terminal to the homeodomain (data not shown).

The alignment of the UNC-42 homeodomain with the homeodomains of related proteins is shown in Fig. 4B. The C. elegans homeoproteins most closely related to UNC-42 are CEH-10 and UNC-4" width="654" height="490" src="/images/38/38194194.jpg" data-type="image" data-page="2245" data-page-range="2245" data-image-id="38194194"><figcaption>Fig. 4A. Northern blot of poly(A)+ RNAs from mixed stage culture probed with an RNA antisense probe. (A) Structure of the unc-42 gene. At the top is a restriction map showing the positions of the SalI (S) and BamHI (B) sites. ATG and TAG are the predicted start and stop sites of translation, respectively. Boxes represent exons; V, introns; solid and open boxes, coding sequences; open boxes, homeodomain sequences; crosshatched boxes, 5' and 3' UTR sequences; dashed line, indication that we have not defined the precise 5' end of the mRNA. (B) Northern blot of poly(A)+ RNAs from a mixed stage culture probed with an unc-42 cDNA probe.</figcaption></figure>" width="654" height="490" src="/images/38/38194194.jpg" data-type="image" data-page="2245" data-page-range="2245" data-image-id="38194194">
also constructed and examined worms that carried unc-42-gfp transgenes (Materials and Methods).

We could detect UNC-42 expression with a mouse antiserum in several cells as early as 260 minutes of embryogenesis and in neurons at high levels in the head by comma stage, the time when these neurons extend axons and establish connections (Fig. 5A). Expression in head neurons continues into adulthood. UNC-42 expression was greatly reduced or missing in mutant unc-42(e419) embryos, while UNC-86 expression was not affected (data not shown). We found that expression of a transcriptional unc-42-gfp transgene, gmEx104, was also abolished in the mutants, suggesting that unc-42 regulates its own expression (data not shown). UNC-42 was strongly expressed in at least 20 pairs of neurons of the head (Fig. 5A), including the AVA, ABD and AVN interneurons, ASH sensory neurons, and RMS and SIB interneurons. The same expression pattern in the head was detected in animals that carry a transgene that encodes an UNC-42 protein tagged at its C terminus with GFP (gmEx186). This transgene retains unc-42 activity as it rescues the Unc and Mec phenotypes of unc-42 mutant worms (data not shown).

Antiserum to UNC-42 and the gmEx104 GFP reporter gene revealed low levels of unc-42 expression in hypodermis and additional neurons in the head (data not shown). Transient expression of UNC-42 protein was also detected in the DD motor neurons at hatching (data not shown) and at low levels in postembryonic ventral cord motor neurons derived from P11 (Fig. 5D). UNC-42 protein was not detected in descendants of

Fig. 4. The unc-42 gene encodes a paired-like homeodomain protein. (A) unc-42 nucleotide and predicted amino acid sequence (single letter code). Nucleotides and amino acids are numbered on the side, starting with the first nucleotide of the unc-42 cDNA. Arrowheads designate the positions of introns based on comparison of the cDNA and genomic DNA sequences. The homeodomain is underlined. (B) Comparison of the UNC-42 and related homeodomains. Predicted helices based on X-ray crystallography of the engrailed homeodomain (Kissinger et al., 1990) are underlined, engrailed-like proteins from other species: rat Cart-1 (L14018), mouse Arx (3142153) and UNC-30 (L37867), and CEH-10 (U19995), UNC-4 (U89245) and UNC-30 (L37867), and representative homeodomains of paired-like proteins from other species: rat Cart-1 (L14018), mouse Arx (3142153) and mouse Phox2a (X75014).

Nucleotide changes detected in three unc-42 alleles are shown at the top. Both unc-42(e419) and unc-42(gm23) are GC to AT transitions that insert amber stop codons at position 10 and 48 of the homeodomain, respectively. The unc-42(e270) mutation converts a conserved valine at position 47 of the recognition helix to glutamic acid.
unc-42 is expressed in a subset of interneurons, sensory neurons and motor neurons in C. elegans. Cell identifications were made based on cell positions in (L1) larvae and double staining glr-1::gfp transgenic worms with a rabbit antisera to GFP and mouse anti-serum to UNC-42. (A) Late stage (3½-fold) embryo stained with a mouse antiserum to UNC-42. The positions of the AVDL interneuron and the ASHL sensory neuron are indicated. Scale bar, 25 µm. (B) Expression of unc-42::gfp (gmEx104) transgene in the PVT interneuron of an L2 larva. PVT is a large, single interneuron located at the ventral midline of the pre-anal ganglion. (C) Diagram of the position of PVT in the tail. Scale bar, 10 µm. (D,E) UNC-42 is expressed in ventral cord motor neurons derived from P11. Wild-type adult hermaphrodites were double-stained with (D) rabbit anti-UNC-42 antisera to detect cells expressing UNC-42, and (E) DAPI to visualize the nuclei of all cells. Scale bar, 25 µm. (F) Lineage of the P11 blast cell. UNC-42 is not expressed in postembryonic motor neurons that are generated from P2-10 or P12, but is expressed by all three motor neurons derived from P11.

In the tail, unc-42::gfp (gmEx104) is strongly expressed in PVT (Fig. 5B).

unc-42 functions in AB.a for response to light body touch and in AB.p for locomotion

UNC-42 was expressed by AVA and AVD interneurons, which transmit stimuli from the ALM and AVM mechanosensory neurons and the ASH and FLP sensory neurons to motor neurons. To determine whether defects in the interneurons are responsible both for the sensory and locomotory defects of unc-42 mutants, we analyzed the behavior of animals that were mosaic for unc-42 function (Materials and Methods).

We were surprised to find that the Unc and Mec phenotypes were separable in the mosaic animals, reflecting distinct sites of unc-42 function. We could isolate mosaic animals that were Unc but not Mec, as well as animals that were Mec but not Unc (Fig. 6). AVA and AVD, the interneurons that mediate backward motion, are derived from the AB.a blastomere. The AVB and PVC interneurons that control forward movement, ventral cord motor neurons that innervate head muscles, and many of the neurons that regulate head movement are all descendants of the AB.p blastomere (Sulston et al., 1983). 11/11 mosaic worms that failed to respond to light touch to the anterior body, but moved normally, had lost wild-type unc-42 gene activity in AB.a (Fig. 6A). Six of these losses were in AB.aala, producing mosaic animals that had mutant AVD interneurons, wild-type AVM and ALM mechanosensory neurons and wild-type motor neurons. By contrast, 12/12 mosaic worms that were Unc, but responded to light touch, had lost wild-type unc-42 function in the AB.p lineage (Fig. 6B). A severe uncoordinated phenotype was observed only when all cells derived from AB.p were mutant for unc-42. Animals with single losses of wild-type gene function in AB.p descendants were wild type, and the animals with multiple losses in AB.p descendants exhibited only weak defects in locomotion.

These results are consistent with the results of laser killing experiments, which showed that most members of a single motor neuron class or multiple classes must be killed to generate a severe uncoordinated phenotype (Chalfie et al., 1985). Because motor neurons are generated at multiple points in the AB.p cell lineage (Fig. 6B), only early losses in the lineage would affect gene function in a significant number of ventral cord motor neurons. In addition, some of the motor neurons that innervate head muscles and interneurons that coordinate head movement also express UNC-42 and are derived from AB.p.

Genetic mosaic analysis supports the hypothesis that unc-42 acts cell-autonomously in the AVD interneurons for the response to body touch and is likely to act cell-autonomously in motor neurons for locomotion. However, we did not detect overt differentiation defects in ventral cord motor neurons. We examined the UD and DD motor neurons of unc-42 mutants for expression of the neurotransmitter GABA, but did not detect any significant abnormalities in the placement of ventral cord axons or commissures (data not shown). Expression of CHA-1 and UNC-17, markers for cholinergic motor neuron differentiation, were also unaffected in unc-42 animals (J. Duerr and J. Rand, personal communication).

unc-42(e270) and unc-42(gm23) mutations alter gene activity

We showed previously that unc-42 is required for correct formation of the left ventral nerve cord of C. elegans (Wightman et al., 1997). The C. elegans nerve cord is asymmetric, with only four axons in the left bundle and more than 40 axons extending along the right bundle (White et al., 1985). Severe unc-42 alleles exhibited defects in pathfinding by three of the four neurons that contribute axons to the left nerve cord bundle: the HSNL motor neuron, and the PVQL and AVKR interneurons. We also found that in 20-30% of e270 and gm23 hermaphrodites, but not in other unc-42 mutants, PVPR failed to pioneer the left nerve tract. The PVPR pioneering defect of gm23 and e270 hermaphrodites results in a more severe HSNL defect: 80-86% of the HSNL axons from gm23 and e270 hermaphrodites display pathfinding errors, whereas only 60-65% of the HSNL axons of other strong unc-42
hermaphrodites, such as e419, pathfind abnormally (Wightman et al., 1997).

In light of these findings, the prediction from molecular analysis that e419 is the best candidate for a null allele came as a surprise. The e419 allele is a nonsense mutation at the beginning of the homeodomain, whereas the e270 and gm23 alleles are missense and nonsense mutations, respectively, in the third helix of the homeodomain. These observations raised the possibility that the gm23 and e270 mutations not only eliminate, but also alter unc-42 function. In this model, altered unc-42 function results in aberrant PVPR pioneering. To test this hypothesis, we examined HSNL axon pathfinding in unc-42 heterozygous hermaphrodites. In 10% of e270/+ and 12% of gm23/+ worms, the HSNL axon crossed the midline and extended along the right ventral nerve cord (n=50). By comparison, less than 2% of the unc-42(e419)+/ worms or wild-type controls showed this defect in HSNL pathfinding (n=50). HSNL pathfinding was also normal in animals hemizygous for sdF29, a deficiency chromosome that deletes unc-42 (n=25).

### DISCUSSION

unc-42 belongs to a family of homeodomain proteins that regulate neuronal differentiation

unc-42 encodes a novel homeodomain protein of the paired-like class. A growing body of evidence suggests that homeoproteins of this class play essential roles in defining neuron subtype identity. Other members of this family include UNC-4, CEH-10 and UNC-30 in C. elegans, and Phox2a in vertebrates. UNC-4 controls the differentiation of the VA motor neurons of C. elegans by specifying synaptic input (White et al., 1992). In unc-4 mutants, the VAs receive input from the interneurons that normally synapse onto their sister cells, the VBs, but retain the wild-type VA pattern of axon projections and output to motor neurons. CEH-10 regulates migration and differentiation of the bipolar canal-associated neurons (CANs) and is closely related to Chx10 in mouse, a paired-like protein required for differentiation of bipolar neurons in the vertebrate retina (Forrester et al., 1998; Liu et al., 1994; Burmeister et al., 1996). The C. elegans gene unc-30 regulates differentiation of type-D motor neurons. In unc-30 mutants, type-D axonal morphology is altered, and the type-D motor neurons fail to make appropriate synaptic connections (J. White, personal communication) and to express their neurotransmitter GABA (McIntire et al., 1993a,b; Jin et al., 1994). Similarly, mice mutant for the paired-like homeodomain gene Phox2a exhibit defects in catecholamine biosynthesis and fail to express the Ret receptor for GDNF in specific tissues (Morin et al., 1997).

Several of these homeoproteins appear to act as direct transcriptional regulators of late neuronal differentiation genes. Arix, the rat homolog of Phox2a has been shown to activate in vitro transcription from the promoter of the dopamine beta-hydroxylase and tyrosine hydroxylase genes, which encode dopamine biosynthetic enzymes (Zellmer et al., 1995). In C. elegans, UNC-30 may be a direct regulator of GAD and other genes required for GABAergic differentiation (C. Eastman and Y. Jin, personal communication).

unc-42 represents a new neuronal identity gene in C. elegans. UNC-42 protein can be detected in neuronal precursor cells at 260 minutes and by comma stage is expressed at high levels in a subset of the C. elegans embryonic nervous system. Although unc-42 is expressed by about 15% of C. elegans neurons, loss of unc-42 function in a few key neurons of the
mechanosensory circuit is responsible for many of the behavioral defects displayed by the mutants.

**unc-42 is required for ASH cell fate**

We found that UNC-42 is expressed at high levels in the ASH sensory neurons and is required for ASH development. unc-42 mutants are defective for multiple ASH-mediated behaviors and fail to express the putative chemoreceptor genes sra-6 and srb-6 (Troemel et al., 1995). It is unlikely, however, that loss of unc-42 function in the ASH neurons is sufficient to cause the severe defects in nose-touch avoidance seen in the mutants. 37% of wild-type animals still respond to nose touch when the ASH neurons are killed, whereas unc-42 mutants exhibit almost no response to nose touch, a phenotype seen in animals lacking both ASH and FLP (Kaplan and Horvitz, 1993). Because UNC-42 is expressed by ASH and the AVA and AVD interneurons, and not by FLP, the inability of the mutants to respond to nose touch is probably due to defects both in the ASH sensory neurons and the interneurons.

**unc-42 specifies AVA, AVD and AVE cell fate**

Distinct neural circuits regulate backward and forward movement in *C. elegans* (Chalfie et al., 1985). AVA and AVD interneurons transmit stimuli from anterior sensory neurons to motor neurons that control backward locomotion, and AVB and PVC interneurons transmit stimuli from posterior sensory neurons to motor neurons that elicit forward motion. Our results show that separate genetic programs control the development of the circuits for forward and backward motion, with unc-42 controlling the circuit for backward movement by regulating AVA, AVD and AVE interneuron differentiation.

The axons of the AVA, AVD and AVE interneurons extend around the nerve ring and along the right ventral nerve cord. They are exclusively postsynaptic in the nerve ring and receive input from diverse classes of mechanosensory and chemosensory neurons in the nose and head of *C. elegans* (White et al., 1986). For instance, the AVDs are synaptic targets of the ASH, FLP and ADL sensory neurons and form gap junctions with the AVM and ALM touch cells. Our results demonstrate that unc-42 plays an essential role in AVA, AVD and AVE differentiation. First, unc-42 mutations cause severe defects in behaviors that are mediated by AVA and AVD, such as nose touch and touch along the anterior body, but do not affect behaviors dependent on AVB and PVC. Second, genetic mosaic analysis indicates that unc-42 function for anterior body touch is required in the AB.a blastomere, which generates both AVD neurons and one of the AVA neurons. Third, unc-42 is expressed by the AVA, AVD and AVE interneurons, but not by the AVB and PVC interneurons. Finally, unc-42 mutations abolish expression of the GLR-1 glutamate receptor by the AVA, AVD and AVE neurons, but do not alter GLR-1 expression by AVB and PVC. Thus, unc-42 is required only for the function of the backward command interneurons.

**unc-42 regulates the GLR-1 mediated neural circuitry for nose touch**

The *C. elegans* GLR-1 glutamate receptor is related to mammalian AMPA class (GluR) receptor subunits and is expressed in about 40 interneurons and motor neurons (Hart et al., 1995; Maricq et al., 1995). Glutamate receptors play critical roles in nervous system function, but transcription factors that regulate glutamate receptor expression have not been identified. The defects in GLR-1 expression observed in unc-42 mutants raise the possibility that unc-42 is a direct regulator of glutamate receptors in *C. elegans*.

unc-42 mutations eliminated *glr-1-gfp* transgene expression in interneurons and motor neurons that are part of the circuitry for nose touch: the RMD motor neurons and the AVA, AVD and AVE interneurons. These neurons mediate two distinct avoidance behaviors to nose touch that are dependent on GLR-1: backward body movement and head withdrawal (reviewed by Kaplan and Driscoll, 1997). Backward movement is mediated through the AVA and AVD interneurons, which form gap junctions with body wall motor neurons. Head withdrawal requires the RMD motor neurons, which form gap junctions with the AVEs and receive input directly from the sensory neurons IL1, OLL and OLQ (White et al., 1986).

It is interesting that unc-42 mutations disrupt GLR-1 expression by neurons that are part of the neural circuitry for nose touch, but do not affect GLR-1 expression by other neurons. Similar results were observed for the control of GABA synthesis by *unc-30*. Although ectopic expression of *unc-30* can activate synthesis of the neurotransmitter GABA both in neurons and epithelial cells, *unc-30* is not a global regulator of GABAergic differentiation in *C. elegans* (Jin et al., 1994). *unc-30* is required for GABA biosynthesis in the DD and VD motor neurons that are part of the body wall circuitry, but does not control other GABAergic neural circuits in the head and tail of *C. elegans*. In a similar fashion, unc-42 does not act as a global regulator of GLR-1, but is required for GLR-1 expression only in neural circuitry for nose-touch responses.

**unc-42 regulates multiple neural circuits for locomotion**

unc-42 mutants have complex movement defects that predict unc-42 function is required in more than one locomotory circuit. Both backward and forward movement are abnormal, and coordination of anterior body movement is particularly affected. Mutants cannot propagate a normal sinusoidal wave through the head, have difficulty backing up and often kink ventrally. Several observations argue that these behavioral defects are due to loss of unc-42 function in multiple classes of motor neurons, and possibly also to loss of function in interneurons that coordinate head and body wall movement. First, the uncoordinated phenotype of unc-42 mutants is more complex than the defects observed when any single class of ventral cord motor neuron is removed by laser microsurgery (Chalfie et al., 1985). Second, genetic mosaic analysis shows that unc-42 function must be lost at multiple positions in the ventral cord motor neuron lineage to generate a severely uncoordinated animal. Finally, unc-42 has a complex expression pattern, including the embryonic DD motor neurons, motor neurons derived from P11 and three of the four classes of motor neurons in the head that innervate both head muscles and anterior body wall muscles: the RMD, RME and SMB motor neurons. unc-42 is also expressed by the SIB and SAA interneurons that may function in the coordination of head and body wall muscles.

**gm23 and e270 alter unc-42 gene function**

Mutations in unc-42 disrupt axon pathfinding in the left ventral nerve cord bundle of *C. elegans* (Wightman et al., 1997). We did not detect UNC-42 protein in the PVP, PVQ or HSN
neurons in larvae or adults, suggesting that UNC-42 expression by these neurons may be transient or below detection with our reagents, or that the pathfinding defects of these neurons is non-autonomous. Our genetic analysis suggests that altered unc-42 activity in the e270 and gm23 mutants leads to PVPR axon pioneering defects. During embryogenesis, the PVPR neuron first extends its axon contralaterally across the midline and then anteriorly along the ventral epithelial surface to pioneer the left ventral nerve cord bundle (Durbin et al., 1987). This step is dependent on PVT (Wadsworth et al., 1996), an interneuron at the ventral midline that expresses unc-42-gfp. The additional pattern defects that we observe in gm23 and e270 mutants could occur if altered unc-42 activity affected PVT differentiation, disrupting interactions between the PVPR growth cone and PVT. Because UNC-42 protein is also expressed at low levels in epithelial cells that provide a substrate for the PVPR axon, another possibility is that epithelial defects disrupt PVPR axon guidance in gm23 and e270 mutants.

The e270 and gm23 mutations are in adjacent, highly conserved positions of the UNC-42 recognition helix. The e270 mutation converts valine 47 of helix 3 to glutamic acid, and gm23 replaces tryptophan 48 with a stop codon, eliminating the C-terminal half of the protein, including most of helix three and a putative activation domain. Residues 47-49 and 51 are invariant in all paired and paired-like homeodomains. Analysis of other homeoproteins has shown that residues at position 47 and 51 interact with the major groove of the DNA and are required for high-affinity binding (Gehring et al., 1994). Because the e270 and gm23 mutations are likely to greatly reduce DNA-binding affinity or specificity, these two alleles probably eliminate normal unc-42 function. This hypothesis is supported by the behavioral phenotypes of unc-42 homozygotes: the Unc and Mec defects are similar in gm23, e270 and e419 mutants. In addition, expression of a transcriptional unc-42-gfp fusion gene was abolished in adults in all three mutant strains (data not shown), suggesting that unc-42 regulates its own expression and that none of the mutant proteins is able to perform this function. However, low levels of UNC-42 protein can still be detected in some gm23 and e270 mutant animals stained with UNC-42 antisera (data not shown).

Two hypotheses can account for altered function produced by the gm23 and e270 lesions. Sequences N-terminal to the homeodomain and in helices 1 and 2 would be normal in both mutant proteins. These sequences have been shown to contribute to dimerization and DNA binding in other homeoproteins (see Gehring et al., 1994 for review). One possibility is the aberrant gm23 and e270 proteins sequester cofactors that are necessary for other processes. Alternatively, the binding specificity of the mutant proteins could be altered, causing them to bind to different DNA sequences and resulting in phenotypes distinct from those produced by loss of unc-42 function.

Dominant mutations have also been identified in other paired-like homeoproteins. An autosomal dominant form of cone-rod dystrophy (CORDII) in humans is caused by mutations in CRX (Freund et al., 1997; Swain et al., 1997). However, it is not known if the photoreceptor degeneration caused by these mutations is due to haploinsufficiency or altered gene activity.

The role of UNC-42 in neuronal differentiation
How does unc-42 act to specify neuronal fate? In unc-42 mutants, affected neurons were present and did not appear to adopt other neuronal fates. Affected neurons, however, fail to differentiate fully. The ASH phenotypes of unc-42 mutants are particularly informative. The mutant ASH neurons were grossly normal in morphology, extending a dendrite anteriorly to the nose and an axon to the nerve ring, the normal target for this class of sensory neuron. The mutant neurons were also able to take up DiI, indicating that their sensory endings were exposed to the environment. The cells, however, failed to express the putative chemosensory receptor SRR-6. Thus, unc-42 is required for the expression of some ASH differentiation traits, but it is not essential for determining ASH identity as a sensory neuron. Several models could account for our results. unc-42 may function primarily at a specific time late in neuronal differentiation. Alternatively, unc-42 may be required throughout neuronal development, and regulate specific traits in parallel with factors that determine more general features of neuron identity.

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