Shared receptors in axon guidance: SAX-3/Robo signals via UNC-34/ Enabled and a Netrin-independent UNC-40/DCC function

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Published online 15 October 2002; doi:10.1038/nn956

The *C. elegans* SAX-3/Robo receptor acts in anterior–posterior, dorsal–ventral and midline guidance decisions. Here we show that SAX-3 signaling involves the *C. elegans* Enabled protein UNC-34 and an unexpected Netrin-independent function of the Netrin receptor UNC-40/DCC. Genetic interactions with gain- and loss-of-function mutations suggest that *unc-34* and *unc-40* act together with *sax-3* in several guidance decisions, but the *C. elegans* Netrin gene *unc-6* does not act in the same genetic pathways. Within the migrating axon, *sax-3, unc-34* and *unc-40* all act cell-autonomously. Our results support a role for UNC-34/Enabled proteins in SAX-3-mediated repulsion, and show that UNC-40/DCC can potentiate SAX-3/Robo signaling via a mechanism that may involve direct binding of the two guidance receptors. A combinatorial logic dictates alternative functions for UNC-40/DCC, which can act in attraction to UNC-6/Netrin, repulsion from Netrin (with UNC-5), or repulsion from Slit (with SAX-3).

Growth cones of developing neurons navigate through their environments by responding to attractive and repulsive guidance cues¹. Several conserved families of ligands and receptors participate in axon guidance, including UNC-6/Netrin and its receptors UNC-40/DCC/Frazzled and UNC-5, Slit and its receptor Robo/SAX-3, Ephrins and the Eph receptors, and Semaphorins and their receptors Neuropilin and Plexin^{2–6}. Although the cytoplasmic domains of most guidance receptors lack obvious similarity to one another, these domains define the guidance functions of the receptors. Thus, when the cytoplasmic sequences of UNC-40/DCC/Frazzled and SAX-3/Robo are fused to heterologous ligand-binding domains, they can drive axon attraction or repulsion, respectively^{7,8}.

The function of a particular guidance receptor can vary depending on the cell and its environment. For example, UNC-40/DCC is required for attraction to UNC-6/Netrin, but some cells that express UNC-40 are not attracted to Netrin, suggesting that UNC-40 requires additional cofactors to mediate attractive guidance⁹. In addition to its role in attraction, UNC-40 also potentiates repulsion from Netrin mediated by the UNC-5 receptor^{10,11}. This potentiation occurs through a direct interaction between the UNC-40 and UNC-5 cytoplasmic domains that is stimulated by Netrin binding¹². There are also Netrin-independent functions of UNC-40 in cell and axon migration^{13–16}.

We are studying mechanisms of axon repulsion mediated by *C. elegans sax-3*, a member of the Robo family of guidance receptors. The nematode, fly and human SAX-3/Robo proteins are

transmembrane receptors with five immunoglobulin domains, three fibronectin type III domains, and cytoplasmic domains from 377 to 733 amino acids in size^{17,18}. *Drosophila Robo* and *C. elegans sax-3* mutants have defects in repulsion of axons from the ventral midline^{17–21}. In *Drosophila*, the secreted Robo ligand Slit is expressed at the midline, where it acts to repel Robo-expressing axons²². *C. elegans sax-3* mutants also have defects in long-range cell migrations, in the formation of the nerve ring in the head, and in ventral axon guidance in the body²³. A *C. elegans* Slit homolog, *slt-1*, is a ligand for *sax-3* in several guidance decisions²⁴. Vertebrate Robos and Slits act in repulsion from midline structures and at other locations^{25–29}.

Genetic screens in *C. elegans* and *Drosophila* have led to the identification of several genes that are candidate downstream components of axon guidance signaling pathways^{30–32}. One of these genes, *enabled*, was identified in *Drosophila* as a genetic suppressor of lethal mutations in the tyrosine kinase *abl*³³; subsequent analysis of *ena* mutants revealed axon guidance defects in the *Drosophila* nervous system³⁴. Dose-dependent interactions between *ena*, *abl*, and genes for receptor tyrosine phosphatases (RPTPs) suggested that these proteins act in a common regulatory pathway for axon guidance³⁵.

We show here that the *C. elegans* Enabled protein UNC-34 is a mediator of SAX-3 signaling in repulsive guidance from SLT-1. Robo and Enabled also act together in *Drosophila* midline guidance³⁶. We also report the unexpected finding that SAX-3

	wild type	sax-3	unc-34
Cell migration			
CAN cells	posterior migration	stop short ¹	stop short ²
Ventral nerve cord			
PVQ interneurons	do not cross midline	cross midline ³	cross midline
glr-1 interneurons	ventral	lateral ³	lateral ⁴
HSN motor neurons	anterior to head	anterior to head	terminate ⁵
Dorsal/ventral guidanc	e		
AVM axon	ventral guidance	guidance defect ¹	guidance defect
VD and DD axons	dorsal guidance	dorsal guidance	guidance defect
Nerve ring			
ceh-23 sensory neurons	nerve ring	anterior misguidance ¹	nerve ring
glr-1 interneurons	nerve ring	anterior misguidance ¹	nerve ring

interactions between SAX-3 and *C. ele*gans EVH1 domain–containing proteins.

C. elegans has three predicted EVH1 domain proteins: a single Enabled homolog on chromosome V (overlapping the predicted gene Y50D4C.1; Methods) and two other EVH1-containing proteins on chromosome III (B0280.2) and IV (C07G1.4). To ask whether the C. elegans Enabled protein affects cell and axon migrations, we disrupted its function using double-stranded RNA-mediated interference37. RNAi of Y50D4C.1 in wildtype C. elegans resulted in cell migration defects in the CAN neuron, a withered tail phenotype, and an uncoordinated (Unc) phenotype (data not shown). Similar CAN migration and withered tail phenotypes are observed in sax-3 mutants. These defects are also observed in unc-34 mutants, which map to the same region of chromosome V as Y50D4C.1, suggesting that Y50D4C.1 might correspond to unc-34. Indeed, unc-34 encodes the C. ele-

function is potentiated by a Netrin-independent function of the Netrin receptor UNC-40. Our results suggest that SAX-3, UNC-34 and UNC-40 may interact in complexes that drive repulsive guidance.

RESULTS

Overlap in sax-3/Robo and unc-34/Ena phenotypes

A conserved proline-rich motif in the cytoplasmic domains of *C. elegans* SAX-3, *Drosophila* Robo1 and human Robo1 receptors resembles a consensus binding site for EVH1 domains, domains characteristic of Enabled proteins and their family members¹⁸. This motif, designated CC2, has a core of seven conserved prolines flanked by hydrophobic amino acids (in SAX-3, FIPP-SNP). The evidence implicating Enabled in *Drosophila* axon guidance and the presence of this recognition site led us to study

gans Enabled homolog and the allele *unc-34(gm104)* has been identified as a molecular null allele (M. Dell and G. Garriga, pers. comm.).

To ask whether *unc-34* has a role in *sax-3* signaling, we first compared the mutant phenotypes of *sax-3* and *unc-34* mutants. *sax-3* and *unc-34* mutants share a highly penetrant defect in the posterior migration of the CAN neurons (**Table 1**)^{17,38,39}. We observed that they shared several other defects that were not previously described. These include inappropriate midline crossing by the two PVQ axons (37% penetrance in *unc-34(gm104)*, n = 114; 55% in *sax-3(ky123)*¹⁷, n = 70), inappropriate lateral axon migrations of *glr-1*-expressing interneurons (S. G. Clark and C.I.B., unpub. data), and defects in ventral migration of the AVM sensory axons²³ (**Fig. 1a–l; Table 1**). However, other phenotypes of *sax-3* and *unc-34* mutants were not identical: only

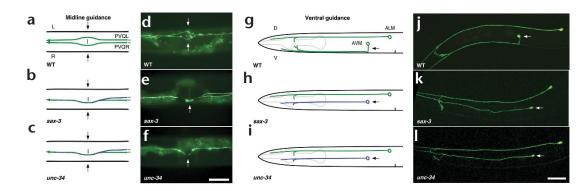


Fig. 1. *unc-34* and *sax-3* mutants share axon guidance phenotypes at the ventral midline and in ventral guidance. (**a**–**f**) Ventral views of ventral cord axons expressing *sra-6:gfp* in wild-type (**a**, **d**), *sax-3* (**b**, **e**) or *unc-34* (**c**, **f**) backgrounds. (**a**, **d**) In wild-type animals, axons from the two PVQ interneurons extend in the ventral nerve cord where they are restricted to the ipsilateral nerve cord. (**b**, **e**) In a *sax-3(ky123)* mutant animal, the PVQ axons cross the midline. Here both PVQ axons run on the right side of the vulva (arrows). (**c**, **f**) In an *unc-34(gm104)* mutant animal, the PVQ axons also cross the midline (arrows). (**g**–**I**) Ventral guidance phenotypes visualized by *mec-4:gfp* in wild-type (**g**, **j**), *sax-3* (**h**, **k**) or *unc-34* (**i**, **I**) mutant back-grounds. (**g**, **j**) In wild-type animals, AVM (*arrow*) grows ventrally to the ventral cord, and then extends anteriorly to the nerve ring. (**h**, **k**) In *sax-3(ky123)* animals in which AVM fails to grow ventrally and extends directly anteriorly. (**i**, **I**) *unc-34* mutants also have ventral guidance defects in AVM. Anterior is left in all panels. Scale bars, 20 m.

Fig. 2. unc-34 double mutant analysis in AVM ventral guidance. (a) Organization of guidance cues for AVM ventral guidance in C. elegans. SLT-1 is expressed dorsally in muscle (red), whereas UNC-6 is expressed ventrally in the ventral nerve cord (blue). AVM (green) expresses both SAX-3 and UNC-40 guidance receptors. (b) Quantitation of ventral guidance defects in sax-3, slt-1, unc-6, unc-40 and unc-34 single and double mutants. * Defects greater than those of the unc-6 or unc-40 single mutant (P < 0.01).

sax-3 mutants have anteriorly misrouted sensory axons in the nerve ring¹⁷, and only *unc-34* mutants exhibit misguidance of motor axons and premature termination of axons in the ventral nerve cord³⁹. We conclude that sax-3 and unc-34 mutants share some, but not all, axon and cell migration defects.

sax-3 and unc-34 act in a common genetic pathway

We used genetic criteria to test the involvement of unc-34 in sax-3 signaling. If two genes act exclusively in the same pathway, a double mutant should be similar to the strongest single null mutant. The phenotype of the strong sax-3(ky123) allele, which lacks the start and signal sequence of SAX-3, served as the presumed sax-3 null phenotype. A strong sax-3 phenotype is also caused by the *sax-3(ky200ts)* mutant at 25°C. The strong *slt-1(eh15)* allele, which truncates SLT-1 near the N terminus, was used to inactivate SLT-1 function²⁴, and the unc-34(gm104) null allele was used.

We examined sax-3, slt-1 and unc-34 in detail for the ventral guidance of the AVM mechanosensory neuron, the bestcharacterized sax-3-dependent guidance decision. The AVM cell body lies on the lateral body wall; at the end of the first larval stage (L1), its axon grows ventrally to the ventral nerve cord, where it turns anteriorly and extends to the nerve ring (Fig. 1g and j; Fig. $(2a)^{40}$. The initial ventral guidance of the AVM axon is mediated in part by repulsion from SLT-1, which is expressed by dorsal muscles. In AVM, sax-3 is required for repulsion from SLT-1²³; in strong sax-3 or slt-1 mutants, 30-40% of AVM neurons fail in the initial ventral component of their trajectory and instead take an anterior path appropriate for the second part of their trajectory (Fig. 1h and k; Fig. 2b). On their own, unc-34 mutants had a mild defect in AVM ventral guidance (Fig. 1i and l; Fig. 2b). AVM defects in unc-34; slt-1 double mutants were

b 80% Ventral guidance defect SLT-1/Slit 60% 40% UNC-6/Netrin 20% Longitudinal section SLT-1/Slit 0% sax-3(ky123) sax-3(ky200) 25° unc-34(gm104); sax-3(ky200) 25° ž unc-34(gm104) slt-1(eh15) unc-34(gm104); slt-1(eh15) unc-6(ev400) unc-40(e1430) unc-6(ev400) slt-1(eh15) unc-34(gm104); unc-6(ev400) inc-34 (gm104); unc-40(e1430) UNC-6/Netrin Cross section

100%

а

similar to those of strong slt-1 single mutants, and a similar result was observed for unc-34; sax-3(ky200) (Fig. 2b). (The unc-34; sax-3(ky123) double mutants were not viable, precluding analysis of AVM axon guidance.) These results are consistent with a role for unc-34 in the slt-1/sax-3 guidance decision.

A second test for similar functions of sax-3 and unc-34 is to examine their effects when mutations are combined with mutations in an independent guidance pathway. Netrin/unc-6 and slt-1 guidance systems act in parallel to direct AVM ventral guidance: AVM is simultaneously repelled by dorsal SLT-1 and attracted to ventral UNC-6^{24,41}. In the strong unc-6(ev400) allele, 40% of AVM axons fail to grow ventrally¹⁴ (Fig. 2b). The defect in unc-6 slt-1 double mutants is enhanced to over 90%, suggesting a loss of all dorsal-ventral guidance information (Fig. 2b)²⁴. If unc-34 acts specifically in the slt-1 pathway, unc-34 mutants should act like slt-1 mutants to enhance the AVM ventral guidance defects of null mutants in unc-6. Indeed, the ventral guidance defects of unc-34; unc-6 mutants were much more severe than those of single mutants (Fig. 2b). Similar synergistic enhancement was observed in double mutants between unc-34 and the Netrin receptor unc-40. Because the unc-34 mutation has little effect on AVM on its own, but has a very strong effect in a genetic background

Fig. 3. Suppression of Slit gain-of-function pheno-

types by unc-34 and unc-40. (a) A wild-type ventral AVM axon projection (arrow) visualized with

mec-4:gfp. ALM (white arrowhead) is also visible

with this marker. Position of the vulva (red arrow-

head) is shown. (b) Expression pattern of the myo-3 promoter, as visualized by GFP. The myo-3 promoter drives expression in dorsal and ventral body

wall muscle cells. Position of the vulva (red arrowhead) is shown for comparison. (c) Posteriorly directed AVM axon (arrow) caused by misexpression of SLT-1 under the myo-3 promoter, with positions of ALM (white arrowhead) and the vulva (red

d a 30% Posterior axon defect 20% wт b 10% 0% 0-3::SLT-1 and the state

arrowhead) shown for reference. (d) Quantitation and a state of posterior axon phenotypes of an integrated myo-3:SLT-1 transgene (kyls218) in a variety of genetic backgrounds. Data shown ± s.e.m. *Strains that are significantly suppressed compared to myo-3:SLT-1 alone (P < 0.01). Scale bars, 20 m.

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		ercent anterior or posterior axons (D–V guidance)		
	Percent wild type		٥	
			Genotype	
wild type			100	0
sax-3(ky123)	67	33	0	383
unc-34(gm104)	97	3	-	252
unc-40(e271)	82	18	I	186
unc-6(ev400)	60	40	7	275
kyls218(myo-3:SLT-1)	68	32	13	213
kyls218; sax-3(ky123)	61	39	I *	223
kyls218; sax-3(ky123); mec-7:SAX-3	64	36	20	76
kyls218; unc-34(gm104)	75	25	3*	330
kyls218; unc-34(e951)	60	40	4*	167
kyls218; unc-34(e951); mec-7:UNC-34	60	40	П	154
kyls223(myo-3:SLT-1)	66	34	14	658
kyls223; unc-34(gm l 04)	76	24	*	146
kyls218; unc-40(e271)	24	72	I *	139
kyls218; unc-40(e1430)	39	61	*	166
kyls218; unc-40(e1430); mec-7:UNC-40	47	53	9	181
kyls213(myo-3:SLT-1)	63	37	9	225
kyls213; unc-40(e271)	28	72	0	39
kyls218; unc-6(ev400)	10	90	23	203
kyls218; unc-40(e1430); unc-6(ev400)	15	85	1*	133

Table 2. Suppression of myo-3:SLT-1 gain-of-function A-P phenotype by sax-3, unc-34 and unc-40.

Axons that fail to grow ventrally are classified as D–V guidance defective, and include both anterior and posteriorly guided axons. Asterisks denote double mutants that were significantly suppressed compared to myo-3:SLT-1 alone (P < 0.01).

that relies entirely on *slt-1/sax-3* signaling, these results place *unc-34* in the Slit pathway for AVM ventral guidance.

Additional evidence for a role of *unc-34* in SAX-3/Robo signaling was provided by its ability to suppress a gain-of-function of the *sax-3* pathway. SLT-1 is normally expressed in dorsal muscles. Ubiquitous muscle expression of SLT-1 under the *myo-3* promoter causes both dorsal–ventral defects and anterior– posterior defects in AVM axon guidance, whereas loss-of-function of *sax-3* or *slt-1* causes only dorsal–ventral defects in AVM (Fig. 3)²⁴. The anterior–posterior defects caused by *myo-3*: *SLT-1* are diagnostic of overactivated SAX-3/SLT-1 signaling, and provide a distinguishable gain-of-function phenotype for epistasis analysis. *sax-3* loss-of-function mutations are strong suppressors of the anterior–posterior defect of *myo-3*:*SLT-1*, as expected because loss of a receptor should suppress the effects of excess ligand (Fig. 3d)²⁴. Expression of *sax-3* within AVM using a *mec-7:SAX-3* transgene restored the *myo-3:SLT-1* posterior defect, indicating that *sax-3* acts cell-autonomously in AVM (Fig. 3d; Table 2).

Posterior AVM defects of *myo-3* :*SLT-1* animals were also suppressed by mutations in *unc-34* (Fig. 3d; Table 2). This epistasis result suggests that *unc-34* acts with *sax-3* downstream of *slt-1*. To ask whether this suppression reflected a function for UNC-34 within the AVM neuron, we isolated a full-length UNC-34 cDNA using RT-PCR. Expression of this *unc-34* cDNA in AVM caused reappearance of posterior guidance defects (Fig. 3d; Table 2), demonstrating that *unc-34* acts cell autonomously to potentiate *slt-1/sax-3* signaling.

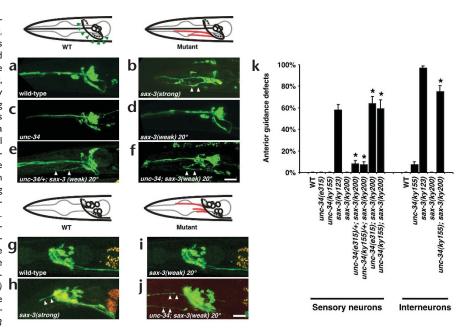
The shared CAN migration, midline guidance, and AVM guidance phenotypes of sax-3 and unc-34 contrast with the situation in the nerve ring, where sax-3 and unc-34 have different phenotypes. Sensory axons exit the nerve ring to take abnormal anterior trajectories in strong sax-3 mutants such as sax-3(ky123), but not in sax-3(ky200) at 20°C or in unc-34 null mutants (Fig. 4a-d). In a genetic background sensitized by weak mutations in one gene, mutation of a second gene in the pathway can synergize to yield a stronger phenotype. Removing a single copy of unc-34 in a sax-3(ky200) background at 20°C caused anterior sensory axon defects (Fig. 4e). Removing both copies of unc-34 in a sax-3(ky200) background had an even stronger effect, resulting in a defect that was comparable to that of sax-3 null mutants (Fig. 4f). Similar synergistic interactions were observed in interneuron axons in the nerve ring

observed with the marker *glr-1:GFP. unc-34* and *sax-3(ky200)* at 20°C had mild anterior axon defects, which were strongly enhanced toward the *sax-3* null phenotype in *unc-34; sax-3(ky200)* double mutants at 20°C (**Fig. 4g–k**). These results demonstrate that UNC-34 contributes to nerve ring axon guidance, a role not evident from analysis of *unc-34* mutants alone. They therefore reveal another function shared by *sax-3* and *unc-34*, and support the model that *unc-34* and *sax-3* function in a common guidance pathway.

unc-40 has a Netrin-independent signaling role

To seek additional components of the *sax-3* guidance pathway, we examined the functions of other axon guidance genes using the genetic assays described above. Surprisingly, we observed that

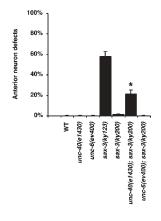
Fig. 4. Genetic interactions between sax-3 and unc-34 in the nerve ring. Phenotypes of sensory axons (a-f), as visualized with the ceh-23:gfp marker, and interneurons (g-j), as visualized with the **a** glr-1:gfp marker. (a) Wild-type nerve ring, in which sensory axons extend ventrally from their cell bodies into the nerve ring (green arrowheads). Anterior processes are sensory dendrites. (b) sax-3(ky123), a strong loss-of-function mutant. Nearly all axons (schematic, red axons) travel anteriorly beyond the normal confines of the ring. (c) unc-34 animals have no axon guidance defects in the nerve ring (although some axons terminate prematurely within the nerve ring). (d) sax-3(ky200ts) at the permissive temperature (20°C). Sensory axons are normal. (e) sax-3(ky200ts) unc-34/+ at the 9 permissive temperature (20°C). One axon grows anteriorly beyond the confines of the nerve ring. (f) sax-3(ky200ts) unc-34 at the permissive temperature (20°C). A highly disorganized, anterior nerve ring reminiscent of the strong sax-3



phenotype. (g) Wild-type animals, in which interneuron axons extend within the nerve ring *en route* to or from the ventral cord. (h) *sax-3(ky123)* animal. *glr-l*-expressing axons leave the nerve ring to travel anteriorly. (i) *sax-3(ky200ts)* at the permissive temperature (20°C). Interneuron axons are normal. (j) *sax-3(ky200ts) unc-34* at the permissive temperature (20°C), with anterior axon phenotype reminiscent of the strong *sax-3* phenotype. (k) Quantitation of anterior guidance defects in the nerve ring. *Double mutants that are enhanced compared to *sax-3(ky200ts)* alone (P < 0.01). Data shown ± s.e.m. for proportions. White arrowheads, aberrant trajectories. Scale bars, 20 m.

mutations in the Netrin receptor *unc-40* strongly suppressed anterior–posterior AVM defects in the *myo-3:SLT-1* strain (Fig. 3d; Table 2). Because the anterior–posterior defects are a specific result of SLT-1 misexpression, this result suggested that the gain-of-function SLT-1 phenotype requires the UNC-40 guidance receptor in addition to the SAX-3 guidance receptor. Expression of *unc-40* in touch neurons under the *mec-7* promoter was sufficient to restore posterior AVM axons to *unc-40; myo-3:SLT-1* animals (Fig. 3d; Table 2). These results indicate that *unc-40* acts cell-autonomously in AVM to modulate SLT-1 responses.

Mutations in *unc-6/Netrin* did not suppress the gain-offunction SLT-1 phenotype, suggesting that UNC-40 does not act as a Netrin receptor in this context (Fig. 3d; Table 2). In *Drosophila*, neurons expressing the *unc-40* homolog *frazzled* can bind Netrin and present it to developing axons⁴². If UNC-40 binds and redistributes the UNC-6 protein, mutations in *unc-40* could

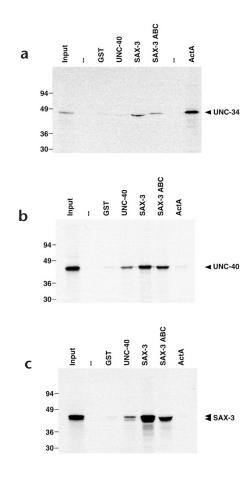


cause *unc-6*-dependent defects in pathfinding. To ask if the suppression of *myo-3:SLT-1* by *unc-40* was secondary to a redistribution of UNC-6, we examined an *unc-40; unc-6 myo-3:SLT-1* triple mutant. The triple mutant phenotype was identical to that of *unc-40; myo-3:SLT-1* (Fig. 3d). Thus the ability to suppress *myo-3:SLT-1* is not due to UNC-6 redistribution and is an *unc-6*-independent function of *unc-40*.

To test whether *unc-40* is involved in other *sax-3*-dependent guidance pathways, we examined the enhancement of nerve ring axon guidance defects in animals harboring the weak *sax-3(ky200)* allele. *unc-40* mutants did not have anterior guidance defects in the nerve ring. However, *unc-40; sax-3(ky200)* mutants at 20°C showed a substantial enhancement of anterior nerve ring phenotypes compared to *sax-3(ky200)* alone, yielding a phenotype similar to that of strong *sax-3* mutants (Fig. 5). No enhancement was observed in *unc-6(ev400) sax-3(ky200)* double mutants (Fig. 5). Thus, the nerve ring defect, like the *myo-3:SLT-1* defect, results from a Netrin-independent function of *unc-40*.

In summary, like *unc-34/Enabled* mutations, *unc-40/DCC* mutations suppressed a SLT-1 gain-of-function defect in AVM guidance and enhanced weak *sax-3* loss-of-function defects in the nerve ring. Neither of these *unc-40* functions was shared with *unc-6*.

Fig. 5. Genetic interactions between *sax-3* and *unc-40* in the nerve ring. Like *unc-34*, *unc-40* mutations have no anterior axon guidance defects in the nerve ring on their own; however, a contribution of *unc-40* to anterior nerve ring guidance is revealed in a sensitized *sax-3(ky200ts)* background. *Double mutants that are enhanced compared to *sax-3(ky200ts)* alone (P < 0.01). Data shown ± s.e.m.



UNC-34 and UNC-40 can bind SAX-3

To ask whether SAX-3, UNC-40 and UNC-34 could interact directly, we used *in vitro* binding assays to ask whether UNC-34 and UNC-40 proteins can bind SAX-3. *In-vitro* translated UNC-34 associated with a bacterially expressed GST:SAX-3 protein, but not with a GST:UNC-40 protein or with GST alone (Fig. 6a). Full-length UNC-34 also bound ActA (Fig. 6a), a *Listeria* protein that is a ligand for the EVH1 domains of vertebrate Enabled/VASP family members⁴³. UNC-34 has several unusual amino acid substitutions compared to other EVH1 domain proteins, but these results confirm that it acts as a typical ActA-binding EVH1 protein.

The UNC-40 cytoplasmic domain associated with GST: SAX-3 (Fig. 6b). This binding interaction is evolutionarily conserved, as vertebrate DCC and Robo can bind one another⁸. *In-vitro* translated UNC-40 also associated with GST:UNC-40 (Fig. 6b), consistent with observations that vertebrate DCC can dimerize⁴⁴. Similarly, *in-vitro* translated SAX-3 associated with GST:SAX-3 as well as with GST:UNC-40 (Fig. 6c). These results show that SAX-3 and UNC-40 have the potential to form homomeric and heteromeric complexes, and suggest that the observed genetic interactions could be mediated by direct interactions among SAX-3, UNC-34 and UNC-40 proteins.

DISCUSSION

Our results demonstrate that axon guidance by SAX-3, the *C. elegans* Robo protein, is potentiated by UNC-34/Enabled and UNC-40/DCC. The UNC-34/Enabled function is similar to a reported role of *Drosophila* Enabled in Robo function at the midline³⁶. Our results extend these observations to a variety of non-

Fig. 6. SAX-3, UNC-34 and UNC-40 proteins can associate in vitro. (a) UNC-34 associates in vitro with the SAX-3 cytoplasmic domain, but not with either GST alone or the UNC-40 cytoplasmic domain. UNC-34 also associates with the Listeria protein ActA. Arrow, band corresponding to full-length 35[S]-labeled UNC-34 probe. (b) The UNC-40 cytoplasmic domain associates with itself and with the SAX-3 cytoplasmic domain in vitro, but not with GST alone or with Listeria ActA protein. Arrow, band corresponding to 35[S]-labeled UNC-40 cytoplasmic domain probe. (c) The SAX-3 cytoplasmic domain associates with itself and with the UNC-40 cytoplasmic domain in vitro, but not with GST alone or with Listeria ActA protein. Double arrow, bands corresponding to 35[S]labeled SAX-3 cytoplasmic domain probe. Input, 1/20th of input probe; -, blank, GST, GST alone; UNC-40, GST fused to the UNC-40 cytoplasmic domain (amino acids 1106-1415); SAX-3, GST fused to the SAX-3 cytoplasmic domain (amino acids 898-1273); SAX-3 ABC, GST fused to a subdomain of the SAX-3 cytoplasmic domain (amino acids 978-1224); ActA, GST fused to the Listeria protein ActA. In all cases, 35[S]-labeled probe was incubated with GST fusion proteins, coprecipitated with glutathioneagarose beads, separated by SDS-PAGE and autoradiographed.

midline axon guidance decisions. The UNC-40/DCC function is unexpected, and suggests that SAX-3/Robo and UNC-40 cooperate in a guidance process that is distinct from the known roles of UNC-40 in Netrin responses.

unc-34/Ena acts in repulsive axon guidance

unc-34 and *sax-3* both affect midline axon guidance as well as longitudinal cell migrations. In addition to these shared mutant defects, four results suggest that *unc-34* interacts with *sax-3*. First, *unc-34* mutants in double-mutant combinations have defects in AVM ventral guidance that are diagnostic of reduced SLT-1/SAX-3 activity. Second, loss of *unc-34* function suppresses SLT-1 gain of function phenotypes. Third, *unc-34* mutations enhance nerve ring defects in a weak *sax-3* mutant. Fourth, UNC-34 can bind the SAX-3 cytoplasmic domain. SAX-3 and Robo share little overall sequence similarity in their intracellular domains, but these genetic and biochemical interactions are conserved between *Drosophila* and *C. elegans*, providing strong support for their biological relevance³⁶.

The involvement of Enabled proteins in actin polymerization suggests a role for UNC-34/Enabled as an effector that links SAX-3 to the actin cytoskeleton^{43,45}. In addition, mammalian Enafamily proteins can inhibit cell motility, consistent with roles of SAX-3 in axon repulsion⁴⁶. However, our experiments do not formally distinguish whether UNC-34 acts upstream or downstream of SAX-3 (though both act downstream of SLT-1), so it is possible that UNC-34 acts as a regulator and not an effector of SAX-3.

The phenotypes of *unc-34* mutants are considerably weaker than those of *sax-3* mutants in AVM ventral guidance and in the nerve ring. Therefore, UNC-34 cannot be the sole mediator of SAX-3 activity. Evidence from *Drosophila* also suggests that additional factors, including kinases, phosphatases, *son of sevenless* and calmodulin pathways, may contribute to Robo-mediated guidance^{36,47,48}. Conversely, UNC-34 has SAX-3-independent roles in guidance. *unc-34* mutants have defects in motor neuron guidance that resemble those of *unc-5* mutants, which lack the repulsive Netrin receptor. *unc-34* also suppresses an UNC-6-dependent, UNC-5 gain-of-function axon guidance defect¹⁰. Thus *unc-34* acts in two different repulsive guidance of UNC-6/Netrin (mediated by UNC-5).

Netrin-independent UNC-40 function in SAX-3 signaling It has long been appreciated that *C. elegans unc-40* has functions that are independent of *unc-6/Netrin*^{13–16}. Our observations

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demonstrate an UNC-6-independent function of UNC-40 in SAX-3 signaling. Mutations in *unc-40* but not *unc-6* suppress SLT-1 gain-of-function phenotypes in AVM and enhance weak *sax-3* loss-of-function mutations in the nerve ring. Thus, in two different cell types and two different genetic assays, UNC-40 had the properties expected of a component in the SAX-3 guidance pathway. Such a role is further supported by the direct interaction between UNC-40 and SAX-3 cytoplasmic domains.

These results suggest that SAX-3/UNC-40 complexes are required for efficient axon guidance by SAX-3. SAX-3 can mediate guidance decisions without UNC-40, just as it can without UNC-34, but in their absence SAX-3 guidance is less efficient and more sensitive to perturbation. This proposed SAX-3/UNC-40 receptor complex is analogous in some respects to the UNC-5/UNC-40 complex that acts in repulsion from Netrin. UNC-5 can mediate repulsion on its own, but efficient repulsion from Netrin requires both UNC-5 and UNC-40 (refs. 10,12,14). Thus UNC-40 can assist two repulsive receptors, SAX-3 and UNC-5, in addition to its role in Netrin attraction. Unlike UNC-5/UNC-40, however, the proposed SAX-3/UNC-40 complex crosses ligand boundaries, by linking UNC-40 to Slit responses.

An interaction between UNC-40 and SAX-3 is also observed with their vertebrate counterparts, DCC and Robo⁸, where it is implicated in a different guidance decision. In *Xenopus* spinal cord neurons, Slit acting through Robo silences the ability of DCC to mediate turning toward Netrin, but those axons are not repelled by Slit. Thus Robo can act as a negative regulator of DCC in *Xenopus* or as a collaborator with UNC-40/DCC in *C. elegans*. We speculate that the outcome of the Robo/DCC interaction is regulated by other proteins that are present or absent in particular neurons at particular developmental stages. Mouse DCC mutants have more severe defects in spinal cord axon outgrowth than do Netrin mutants, suggesting a Netrin-independent role for DCC⁴⁹; perhaps this involves an interaction with Robo proteins.

The existence of a shared guidance complex such as SAX-3/UNC-40 could help explain why there is little similarity among cytoplasmic domains of different guidance receptors. SAX-3 does not need to have the same domains as UNC-40 if it can simply recruit UNC-40 into decisions when those domains are useful. For example, a SAX-3/UNC-40 complex could promote outgrowth and motility in certain regions of the growth cone, propelling it away from a source of repellent. We suggest that local interactions between guidance receptors optimize the ability of growth cones to perform local integration of guidance cues. Turning requires the growth cone to make a decision across its surface, and during turning different regions of the growth cone behave very differentlyone filopodium may be retracting as another advances. These local decisions may be best accomplished by integrating guidance decisions immediately at the level of the receptor, maximizing the interpretation of spatial information across the growth cone.

METHODS

Strains. Wild-type animals were *C. elegans* variety Bristol, strain N2. We used the following strains: CX3171 [*sax-3(ky200) X*], CX3198 [*sax-3(ky123) X*], CX5001 [*slt-1(eh15) X*], CB315 [*unc-34(e315) V*], CX4374 [*unc-34(gm104) V*], CX4345 [*unc-34(e951) V*], CX3099 [*unc-34(ky155) V*; *kyIs4 X*], NW434 [*unc-6(ev400) X*], CX5353 [*unc-40(e1430) I*], CB271 [*unc-40(e271) I*], CX5088 [*zdIs5 I*; *dpy-20(e1282) IV*; *myo-3:SLT-1(kyIs213)*], CX5078 [*zdIs5 I*; *dpy-20(e1282) IV*; *myo-3:SLT-1(kyIs218) X*], CX5083 [*zdIs5 I*; *dpy-20(e1282) IV*; *myo-3:SLT-1(kyIs218)*], CX2627 [*kyIs4(ceh-23:GFP) X*], CX5334 [*oyIs14(sra-6:GFP) V*; *lin-15(n765) X*] and CX4971 [*mcc-4:GFP(zdIs5)*], *sax-3(ky120)* deletes the start ATG and signal sequence of SAX-3. *sax-3(ky200)* encodes a P37S point mutation in the first immunoglobulin repeat¹⁷. *unc-34(gm104)* introduces an early

stop codon in the UNC-34 coding sequence. unc-34(e951) is a deletion that removes the EVH1 domain (M. Dell and G. Garriga, personal communication). slt-1(eh15) is a deletion that truncates SLT-1 after the first leucine rich repeat²⁴. unc-6(ev400), unc-40(e1430) and unc-40(e271) are canonical strong loss-of-function alleles^{9,14}. Strains were maintained using standard methods. Animals were grown at 20°C except for the sax-3(ky200) strain, which was grown at 20°C or 25°C as noted. M. Dell and G. Garriga provided unc-34 (gm104) and unc-34(e951) strains. Some strains were provided by the *Caenorhabditis* Genetic Center.

Double-mutant construction. Double mutants were constructed using standard genetic procedures. In general, *unc-34*, *unc-6* and *unc-40* were followed based on visible phenotypes, and *sax-3* and *slt-1* mutations were scored by PCR. Double Unc mutants were crossed to N2 to confirm segregation of the appropriate single mutants. *myo-3:SLT-1* homozygotes were selected based on expression of *str-1:GFP*, a marker present on the integrated *myo-3:SLT-1* array.

Characterization of neuronal phenotypes. Axons were visualized with integrated GFP transgenes and scored in live adult animals. Nerve ring sensory axons were visualized with an integrated *ceh-23:GFP* transgene (*kyIs4 X*), and nerve ring interneurons were visualized with an integrated *glr-1:GFP* transgene (*kyIs29 X*). The PVQ interneurons were visualized with an integrated *sra-6:GFP* transgene (*oyIs14 V*, gift of Piali Sengupta). AVM axons were visualized with an integrated *mec-4:GFP* transgene (*zdIs5*, gift of Scott Clark). Images were acquired using a Zeiss Axiocam cooled CCD or by confocal microscopy.

Isolation of the unc-34 cDNA. A full-length unc-34 cDNA was isolated by RT-PCR. BLAST searches identified a predicted open reading frame on chromosome V with homology to Enabled proteins. Primers were designed to the C. elegans trans-spliced SL1 leader sequence and to EVH1- and EVH2related sequences of the predicted open reading frame. RT-PCR reactions with these primers yielded a 1.4 kB cDNA encoding an Enabled-related protein of 468 amino acids, with an EVH1 domain, a central proline-rich domain, and an EVH2 domain (Genbank accession number, AF535160). This sequence partially overlapped with the gene Y50D4C.1 predicted by the C. elegans Genome Sequencing Project. Exons 1 and 2 of unc-34 were absent from the original Y50D4C.1 sequence and corresponded to bp 51182-51359 and 53745-54124 of the clone Y50D4C, respectively. unc-34 exon 3 is encoded by bp 55745-55841 of Y50D4C (labelled exon 2 in Y50D4C.1). unc-34 exon 4 is encoded by bp 58885-59306 of Y50D4C (partially overlapping predicted exon 5 of Y50D4C.1). unc-34 exons 5, 6 and 7 correspond to bp 61574-61817, 62854-62979 and 63921-64053 of Y50D4C (exons 7, 8 and 9 of Y50D4C.1).

Cell autonomy experiments. Transgenic strains were created using standard methods. The *mec-7* promoter was used to drive expression in AVM and five other neurons (ALML/R, PLML/R, PVM)⁵⁰. For *sax-3* cell autonomy experiments, a *mec-7:SAX-3* clone²³ was injected at 50 ng/ 1 into *lin-15* mutants with *lin-15* and *odr-1:RFP* coinjection markers and crossed into *zdIs5; sax-3(ky123) myo-3:SLT-1*. For *unc-34* cell autonomy experiments, the *unc-34* cDNA was cloned into the pPD96.41 *mec-7* promoter vector (gift of A. Fire and S. Xu). *mec-7:unc-34* was injected at 50 ng/ 1 into *lin-15* mutants with *lin-15* and *odr-1:RFP* and crossed into *zdIs5; unc-34(e951); myo-3:SLT-1*. A *mec-7:UNC-40* construct was provided by J. Culotti⁹. For *unc-40* cell autonomy experiments, *mec-7:UNC-40* was injected at 10 ng/ 1 with *odr-1:RFP* into *zdIs5 unc-40(e1430); myo-3:SLT-1*. Transgenic strains were analyzed for rescue of AVM phenotypes, with non array-bearing siblings serving as controls.

Generation of proteins for binding analysis. Expression vectors for *in vitro* translation of SAX-3, UNC-40 and UNC-34 probes were constructed in pCITE-4c (Novagen, Madison, Wisconsin). The following clones were generated: CITE:SAX-3(898–1273), CITE:UNC-40(1106–1415) and CITE:UNC-34(1–467). These were used to generate 35[S]-methionine-labeled probes by *in vitro* transcription/translation (TNT T7 Quick Coupled Transcription/Translation kit, Promega, Madison, Wisconsin). Expression vectors for GST-fusion proteins were constructed in pGEX-4T-1 (Amersham, Piscataway, New Jersey). The

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following GST-fusion proteins were produced: GST:SAX-3(898-1273), GST:SAX-3(978-1224), GST:UNC-40(1106-1415) and GST:ActA. GSTfusions were expressed in E. coli BL21-CodonPlus RIL (Stratagene, La Jolla, California), purified using glutathione agarose beads (Sigma), and quantitated by SDS-PAGE and Coomassie staining. For binding assays, 2 g of GST fusion protein was mixed with 20 l of 35[S]-methioninelabeled probe in 10 mM Tris 7.5, 150 mM NaCl, 0.1% Triton and 0.05% BSA. Samples were incubated for six hours at 4°C and then washed three times in the same buffer. BSA was omitted from the last wash. Bound proteins were separated by SDS-PAGE, soaked in Amplify (Amersham), dried down under vacuum and exposed to film.

Acknowledgments

We thank K. Prehoda, D. Lee, J. Zallen, S. Clark and Z. Gitai for discussions and ideas that facilitated this work, M. Dell and G. Garriga for communicating results before publication, S. Clark, P. Sengupta, A. Fire and J. Culotti for clones and strains, and C. Adler, T. Saxton, S. Shaham and E. Stein for comments on the manuscript. T.W.Y. was supported by a MIND Institute predoctoral fellowship and the UCSF MSTP. J.C.H. was supported by an HHMI predoctoral fellowship. C.I.B. and M.T.L. are Investigators of the Howard Hughes Medical Institute. This work was supported by the Howard Hughes Medical Institute.

Competing interests statement

The authors declare that they have no competing financial interests.

RECEIVED 6 AUGUST; ACCEPTED 11 SEPTEMBER 2002

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