The *C. elegans* peroxidasin PXN-2 is essential for embryonic morphogenesis and inhibits adult axon regeneration

Jennifer R. Gotstein\(^1\), Ryann E. Swale\(^2\), Tetsuko Fukuda\(^1\), Zili Wu\(^3\), Claudiu A. Giurumescu\(^1\), Alexandr Goncharov\(^3\), Yishi Jin\(^3,4\) and Andrew D. Chisholm\(^{1,2,4,*}\)

**SUMMARY**

Peroxidasins form a highly conserved family of extracellular peroxidases of unknown cellular function. We identified the *C. elegans* peroxidasin PXN-2 in screens for mutants defective in embryonic morphogenesis. We find that PXN-2 is essential for specific stages of embryonic morphogenesis and muscle-epidermal attachment, and is also required postembryonically for basement membrane integrity. The peroxidase catalytic activity of PXN-2 is necessary for these developmental roles. *pxn-2* mutants display aberrant ultrastructure of the extracellular matrix, suggesting a role in basement membrane consolidation. PXN-2 affects specific axon guidance choice points in the developing nervous system but is dispensable for maintenance of process positions. In adults, loss of *pxn-2* function promotes regrowth of axons after injury, providing the first evidence that *C. elegans* extracellular matrix can play an inhibitory role in axon regeneration. Loss of function in the closely related *C. elegans* peroxidasin *pxn-1* does not cause overt developmental defects. Unexpectedly, *pxn-2* mutant phenotypes are suppressed by loss of function in *pxn-1* and exacerbated by overexpression of wild-type *pxn-1*, indicating that PXN-1 and PXN-2 have antagonistic functions. These results demonstrate that peroxidasins play crucial roles in development and reveal a new role for peroxidasins as extracellular inhibitors of axonal regeneration.

**KEY WORDS:** Epidermis, Extracellular matrix, Axon guidance, Genetic suppression, Leucine-rich repeat, Laser axotomy, *Caenorhabditis elegans*

**INTRODUCTION**

Peroxidasins are unusual secreted enzymes that contain both a peroxidase catalytic domain and multiple motifs found in extracellular matrix (ECM) proteins. The first peroxidasin was isolated biochemically from conditioned media of *Drosophila* Kc cells (Nelson et al., 1994). Most animal genomes encode at least one peroxidasin-like protein. The in vivo functions of peroxidasins have not been determined, although they have been proposed to act in basement membrane biogenesis, tissue development and innate immune defense (Nelson et al., 1994). Peroxidasins contain an animal peroxidase catalytic domain (O’Brien, 2000). Animal peroxidases contain a heme group as a cofactor (Daiyasu and Toh, 2000; Furtmüller et al., 2006). The founding member of the animal peroxidase family is the neutrophil enzyme myeloperoxidase (MPO), which catalyzes the production of hypochlorous acid from hydrogen peroxide and chloride anion. Hydrogen peroxide is a relatively inert form of active oxygen and the action of MPO converts it into more reactive oxygen species with putative bactericidal roles. MPO is made in neutrophils, where it is either targeted to azurophilic granules or secreted extracellularly (Hansson et al., 2006). Expression of MPO by neutrophils is important for their function in innate immune defense against bacterial pathogens, and genetic MPO deficiency results in increased susceptibility to fungal infection in humans (Lehrer and Cline, 1969) and in a mouse model (Aratani et al., 1999). Other members of the animal peroxidase family, such as eosinophil peroxidase (EPO) and lactoperoxidase (LPO), are thought to have analogous roles in innate immune defense (Wang and Slungaard, 2006); the more distantly related thyroid peroxidase (TPO) functions in thyroid hormone synthesis (Ruf and Carayon, 2006). Other peroxidasins may act as extracellular bactericidal agents in exocrine secretions (Ihalin et al., 2006).

As well as these established roles in innate immunity, peroxidasins have been implicated in cell adhesion and formation of ECM. The extracellular oxidants generated by MPO can have both damaging and protective effects on the ECM (Rees et al., 2008), including inactivation of matrix metalloproteases (Wang et al., 2007) and formation of dityrosine cross-links (Heinecke et al., 1993). Other peroxidasins are thought to promote cell-ECM adhesion. A crayfish cell adhesion protein was found upon purification to encode an MPO-like protein, named peroxinectin (Johansson et al., 1995). MPO itself promotes integrin-mediated adhesion of neutrophils (Johansson et al., 1997).

Among animal peroxidase domain-containing proteins, the peroxidasins are likely to be more stably associated with ECM because they are defined by the presence of other motifs typical of extracellular proteins, including leucine-rich repeats (LRRs) and immunoglobulin (Ig) domains. *Drosophila* Peroxidasin is expressed by blood cells (hemocytes) and some of their derivatives, such as plasmatocytes, and is deposited in basement membranes. Peroxidasin expression is widely used as a molecular marker for the early hemocyte lineage (Alfonso and Jones, 2002; Stofanko et al., 2008). Although the function of peroxidasin in *Drosophila* has not yet been assessed genetically, its expression in the blood cell lineage suggests that it could mediate some functions of blood cells. Hemocytes are migratory cells that deposit ECM and...
phagocytose dead or foreign cells. Hemocytes are crucial for a morphogenetic event known as condensation of the ventral nerve cord (VNC); if hemocyte migration is blocked, deposition of ECM components, including peroxidasin and type IV collagen, does not occur, leading to a failure of VNC condensation (Olofsson and Page, 2005).

To date, there has been no in vivo study of peroxidasin function. An amphibian peroxidasin is expressed during embryogenesis in specific organs, including the neural tube, otic vesicle, pronephros and tail-forming region (Tindall et al., 2005). By contrast, murine peroxidasin is more widely expressed (Homma et al., 2009). Human peroxidasin (PXDN) transcription is also widespread, whereas peroxidasin protein appears to be restricted to the cardiovascular system (Cheng et al., 2008). PXDN has been identified as a melanoma-associated antigen (Mitchell et al., 2000) and as a transcript that is upregulated in cells undergoing p53-induced apoptosis (Horkoshi et al., 1999). It is not yet known whether peroxidasin expression is functionally important in cancer or cell death.

The C. elegans genome encodes two highly related peroxidasins, PXN-1 and PXN-2. We show here that PXN-2 is essential for embryonic development and that it promotes basement membrane formation and maintenance of cell adhesion in postembryonic tissues. Adult pxn-2 mutants display enhanced axon regrowth after injury, suggesting that PXN-2 contributes to an inhibitory microenvironment for regeneration in C. elegans. By contrast, PXN-1 is not essential for development. Unexpectedly, we find that PXN-1 and PXN-2 have antagonistic roles in development, revealing complexity in the functions of this family of extracellular enzymes.

MATERIALS AND METHODS

Genetics and strain construction

C. elegans strains were maintained on NGM agar plates at 20-22°C following standard procedures. Bristol N2 was used as wild type for all crosses and scoring. In addition to the pxn mutants described below, we used the following mutations: dpy-7(e88), unc-9(e111), spon-1(ju430s), rrf-3(pk1426), nDf19, and transgenes Pac-2-GFP (jul676), Pacr-2-GFP (jul14) (Huang et al., 2002), Pmec-4-GFP (zds5), Pphp-1-GFP (zds13) (Clark and Chiu, 2003), Pcsra-6-GFP (oys143), Pmyo-3-memYFP (trls10) (Dixon et al., 2006), HIM-4::GFP (hls23) (Vogel and Hedgecock, 2001) and MUP-4::GFP (juls172) (Hong et al., 2001).

The pxn-2 mutations js328, js358, js379, js403, js432, js436 and js445 were isolated in a semi-clonal screen for ethyl methanesulfonic acid (EMS)-induced mutants with defects in embryonic elongation and muscle detachment (M. Ding, W.-M. Woo and A.D.C., unpublished). pxn-2(tm346), provided by S. Mitani (Tokyo Women’s Medical University), comprises a 630 bp deletion and a 6 bp insertion and is predicted to result in deletion of residues Q748 to K877 and termination of translation in the peroxidase domain. pxn-1(ok785) is a 1084 bp deletion predicted to cause premature stop codon. js445 mutants (not shown). We performed RNA interference (RNAi) on the four largest genes in the K09C8 region and found that RNAi of K09C8.5-pxn-2 phenocopied the js432 phenotypes, when performed in the sensitized rrf-3 or eru-1 backgrounds, but not in N2. We confirmed the pxn-2 gene structure by sequencing cDNAs yk448b10 and yk643e10. The pxn-2 transcript extends over 7.1 kb, contains 21 exons, and encodes a 1328 amino acid polypeptide of a predicted 151 kDa. To identify the molecular lesions of pxn-2 alleles we amplified mutant DNAs by PCR and sequenced them at the UC Berkeley DNA Sequencing Facility. For feeding RNAi of lam-3 we used Ahringer library clone I-5G24 (Kamath et al., 2003).

Phenotypic analysis

We quantitated the penetrance of lethal and epidermal morphology defects as previously described (George et al., 1998). We collected time-lapse differential interference contrast (DIC) ‘four-dimensional’ (4D) movies as described (Hudson et al., 2006). At least ten embryos were recorded per genotype. We scored muscle detachment and axon guidance as described (Woo et al., 2008). Drug sensitivity and egg-laying assays followed standard procedures (Hart, 2006). All drugs were obtained from Sigma. Statistical tests used Prism (GraphPad, La Jolla, CA).

For electron microscopy, we fixed worms using high-pressure freezing and freeze substitution in tannic acid and osmium in acetone, as described (Weimer, 2006). Five ju432 and six L4 stage ju358 animals were fixed and sectioned in the head and anterior body regions. Femtosecond laser axotomy was performed with the laser in MHz mode, as described (Wu et al., 2007).

Molecular biology and transgenes

To generate pxn-2 transcriptional reporters we amplified 1.8 kb 5′ to the pxn-2 ATG by PCR (see Table S1 in the supplemental material) and linked it to a GFP fragment amplified from plasmid pPD95.75 using duplex PCR (Hobert, 2002). The resulting PCR products were injected at 50 ng/μl with the co-injection marker Ptx-3-RFP (Hobert et al., 1997) to generate transgenes juEx1100-1063; all four displayed indistinguishable expression. Ppxn-1-GFP transcriptional reporters juEx2492-juEx2495 (in Fig. 7B) were used to generate duplex PCR, amplifying 3 kb 5′ to the pxn-1 ATG. Confocal images and time-lapse movies were taken on a Zeiss LSM510 confocal microscope and processed with Zen Software.

A near full-length pxn-2 cDNA, yk643e10, was kindly provided by Y. Kohara (National Institute of Genetics, Mishima, Japan). yk643e10 contains the entire ORF except for the first 25 bp. The Ppxn-2-PXN-2 cDNA minigene pCZ792 was generated by inserting the 1.8 kb pxn-2 promoter fragment into yk643e10, using NorI and DraI sites introduced by PCR. Pjuz792 was injected at 1 ng/μl (juEx2142), 5 ng/μl (juEx2163) and 50 ng/μl (juEx2140), all with Ptx-3-RFP.

To generate YFP-tagged PXN-2 we used Gateway cloning (Invitrogen) to insert a PXN-2 cDNA lacking its N-terminal signal sequence into the vector pCZGY20, which contains the KAL-1 secretion signal sequence followed by Venus YFP (Hudson et al., 2006). We then injected the 1.8 kb pxn-2 promoter to create Ppxn-2-YFP::PXN-2 (pCZGY926). Ppxn-2-YFP was injected at 50 ng/μl with the Ptx-3-RFP marker to generate arrays juEx2492-2495; images in Fig. 3 are of juEx2492. To visualize YFP expression we used anti-GFP immunostaining, as described (Woo et al., 2008). To overexpress PXN-2 we injected pCZGY926 at 100 ng/μl and generated arrays juEx8908-2910. Unlike most juEx2492 embryos, embryos transgenic for these high-concentration arrays displayed YFP fluorescence visible under the dissection microscope.

For site-directed mutagenesis we used the QuickChange Kit (Stratagene) or oligoligation of digested plasmids from the Ppxn-2-PXN-2 cDNA minigene (pCZ792). The following clones and transgenic lines were generated: pCZ794 (H755A: juEx2490, juEx2491), pCZ795 (ΔLRR, deletion of residues 20-268; juEx2540, juEx2543-2545), pCZ797 (ΔLg, residues 293-602; juEx2541-2542). We confirmed all constructs by sequencing and injected them at 25-50 ng/μl to create transgenes. YFP-tagged versions of the H755A and ΔLg clones were created by subcloning the mutated regions into pCZGY926. The resulting clones were injected at 50 ng/μl to create juEx2898 [YFP::PXN-2 (H755A)] and juEx2899 [YFP::PXN-2ΔLg].

To overexpress pxn-1 we injected the pxn-1(+/-) fosmid clones WRM0616aF08 and WRM0621bE07 at 25-30 ng/μl with Ptx-3-RFP to create juEx2911-2914 and juEx2915, respectively.
To generate transgenes in which the PXN-2 peroxidase domain had been replaced with that of PXN-1, we amplified exons coding for the *pxn-1* peroxidase domain and cloned them into the YFP::PXN-2 clone pCZGY926. Using restriction sites introduced by the PCR we cloned *pxn-1* peroxidase domain genomic DNA fragments into pCZGY926 cut with MseI and either *MluI* or *SbfI* to generate pCZGY1104 and pCZGY1105, respectively. The resulting transgenes are predicted to encode PXN-2::PXN-1 chimeric proteins consisting of the first 652 residues of PXN-2, 506 residues of PXN-1 peroxidase domain and the last 170 residues of PXN-2 (*MluI*, pCZGY1104), or the first 652 residues of PXN-1, 643 PXN-1 residues comprising the entire peroxidase domain and most of the C-terminus apart from the final 20 residues of PXN-2 (*SbfI*, pCZGY1105). These constructs were injected at 50 ng/µl and the transgenes displayed significantly reduced rescue activity compared with that of *pxn-2* genomic DNA (not shown) or a full-length *pxn-2* cDNA expressed under the control of a 1.8 kb *pxn-2* promoter (Fig. 1D).

Peroxidasins are secreted proteins that contain several LRRs, and two to four Ig domains and a heme peroxidase catalytic domain (Fig. 1B). The PXN-2 peroxidase domain contains all the key residues required for heme coordination and catalytic activity (Zamocky et al., 2008), and is 52% identical to the peroxidase domain of murine peroxidin (*Q3UQ28*) and 50% identical to that of *Drosophila* peroxidin. Overall, PXN-2 is most closely related to its ortholog in *C. briggsae* (CBG15737), followed by the other *C. elegans* peroxidin, PXN-1 (see below).

Three *pxn-2* mutants carry missense alterations in the peroxidase domain: the strongest viable allele, *ju358*, affects a non-conserved glutamate; *ju328* affects a conserved arginine; and *ju436* affects a semi-conserved histidine. The relatively minor change (R to K) in a side chain due to *ju328* may account for the comparatively weak effect of changing this conserved residue. To test whether the peroxidase catalytic activity of PXN-2 is important for its developmental functions, we mutated the 'distal histidine' of the peroxidase active site to alanine (*H755A*). Mutation of the equivalent side chain due to a semi-conserved histidine. The relatively minor change (R to K) in a side chain due to *ju328* may account for the comparatively weak effect of changing this conserved residue. To test whether the peroxidase catalytic activity of PXN-2 is important for its developmental functions, we mutated the ‘distal histidine’ of the peroxidase active site to alanine (*H755A*). Mutation of the equivalent side chain due to *ju328* may account for the comparatively weak effect of changing this conserved residue. To test whether the peroxidase catalytic activity of PXN-2 is important for its developmental functions, we mutated the ‘distal histidine’ of the peroxidase active site to alanine (*H755A*). Mutation of the equivalent side chain due to *ju328* may account for the comparatively weak effect of changing this conserved residue. To test whether the peroxidase catalytic activity of PXN-2 is important for its developmental functions, we mutated the ‘distal histidine’ of the peroxidase active site to alanine (*H755A*). Mutation of the equivalent side chain due to *ju328* may account for the comparatively weak effect of changing this conserved residue. To test whether the peroxidase catalytic activity of PXN-2 is important for its developmental functions, we mutated the ‘distal histidine’ of the peroxidase active site to alanine (*H755A*). Mutation of the equivalent side chain due to *ju328* may account for the comparatively weak effect of changing this conserved residue. To test whether the peroxidase catalytic activity of PXN-2 is important for its developmental functions, we mutated the ‘distal histidine’ of the peroxidase active site to alanine (*H755A*). Mutation of the equivalent side chain due to *ju328* may account for the comparatively weak effect of changing this conserved residue.
PXN-2 promotes late embryonic elongation and muscle attachment

Approximately 25-30% of animals mutant for the strong alleles 
ju379, ju445 and tm3464 arrested as unhatched eggs; the remainder
hatched and arrested as incompletely elongated L1 larvae. To
define when pxn-2 acts in morphogenesis we used time-lapse
recordings in multiple focal planes (4D movies). Most
pxn-2(tm3464) and pxn-2(ju445) mutants developed normally until just
after the twofold stage of epidermal elongation (Fig. 2A,B). For
tm3464 embryos, 7/11 displayed normal muscle contractions
starting at the 1.75-fold stage and elongated to twofold. Within ~15
minutes of reaching the twofold stage, the embryos developed
deformities in the epidermis; elongation continued with decreased
muscle twitching until the embryos arrested at ~2.5-fold
elongation. Other embryos ceased elongation at the threefold stage.
The deficiency nDf19 failed to complement pxn-2; embryos of
genotype pxn-2(tm3464)/nDf19 (see Materials and methods)
mostly resembled tm3464 homozygotes, suggesting that tm3464
eliminates pxn-2 function. A small fraction of ju379 or tm3464/Df
embryos displayed morphological defects before the twofold stage,
suggesting that PXN-2 might play a minor role in earlier
elongation. Most ju379 embryos elongated to the threefold stage
before arresting; pxn-2(ju432) mutants displayed milder defects
than those of the lethal alleles, beginning in late elongation after
the threefold stage. We conclude that PXN-2 function becomes
critical soon after the twofold stage of epidermal elongation.

The defects of pxn-2 embryos most closely resemble those of
animals lacking the basement membrane components type IV
collagen (EMB-9/LET-2) or F-spondin (SPON-1) (Gupta et al.,
1997; Woo et al., 2008). Unlike animals lacking integrins or
perlecan, muscle development appeared initially normal in
pxn-2 mutants. Perlecan itself displayed normal localization to muscle
quadrants, developing gaps in later elongation after muscle
detachment (Fig. 2D). pxn-2 mutants also displayed normal
localization of laminin (not shown), suggesting that PXN-2 is not
required for the initial stages of basement membrane assembly. We

Table 1. pxn-2 allelic series and DNA lesions

<table>
<thead>
<tr>
<th>Allele</th>
<th>Embryonic lethal (%)</th>
<th>Larval lethal (%)</th>
<th>Adult Vab (%)</th>
<th>Adult non-Vab (%)</th>
<th>DNA change</th>
<th>Predicted effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>ju436</td>
<td>0.3</td>
<td>0</td>
<td>20.0</td>
<td>79.7</td>
<td>CAT→TAT</td>
<td>H739Y</td>
</tr>
<tr>
<td>ju328</td>
<td>2.5</td>
<td>2.5</td>
<td>23.7</td>
<td>71.3</td>
<td>AGA→AAA</td>
<td>R1178K</td>
</tr>
<tr>
<td>ju403</td>
<td>4.6</td>
<td>21.7</td>
<td>66.1</td>
<td>7.6</td>
<td>cagTT→cagCTT</td>
<td></td>
</tr>
<tr>
<td>ju432</td>
<td>12.5</td>
<td>16.1</td>
<td>33.5</td>
<td>37.9</td>
<td>GAAGct→GAAGata</td>
<td>Exon 2 splice acceptor</td>
</tr>
<tr>
<td>ju358</td>
<td>31.1</td>
<td>46.8</td>
<td>21.2</td>
<td>0.9</td>
<td>GAA→AAA</td>
<td>E853K</td>
</tr>
<tr>
<td>ju379/+</td>
<td>6.0</td>
<td>13.7</td>
<td>0</td>
<td>80.3</td>
<td>GGC→GGC</td>
<td>G1314S</td>
</tr>
<tr>
<td>ju445/+</td>
<td>5.2</td>
<td>15.2</td>
<td>0</td>
<td>(79.5)</td>
<td>aagAAT→aagAAT</td>
<td>Exon 5 splice acceptor</td>
</tr>
<tr>
<td>tm3464/+</td>
<td>4.25</td>
<td>11.8</td>
<td>0</td>
<td>(83.6)</td>
<td>630 bp deletion</td>
<td>Premature stop codon</td>
</tr>
</tbody>
</table>

Penetrance of lethal and morphological phenotypes was determined from counts of several complete broods (n>500 progeny for each genotype). Mutant strains are homozygous viable with the exception of ju379, ju445 and tm3464.

Fig. 2. pxn-2 mutant embryos are defective in late stages of epidermal elongation, in muscle attachment and in epidermal attachment structures. (A,B) Frames from 4D Nomarski DIC movies of embryogenesis in wild-type N2 (A) and pxn-2(tm3464) (B) C. elegans embryos. Elongation proceeds normally until the twofold stage in pxn-2 mutants. Between 20 and 40 minutes after the twofold stage, visible constrictions appear in the epidermis (arrow), and elongation ceases ~1 hour later, in most cases not extending to the threefold stage. (C) Early elongation rates are normal in pxn-2 mutants. Dot plot of times from comma stage to twofold as measured in time-lapse movies. Horizontal lines indicate the mean. WT, wild type. (D) In wild-type embryos, perlecan (UNC-52) (MH3 immunostaining) is localized to the basement membrane of muscle quadrants. In threefold pxn-2(tm3464) embryos this localization is retained except where muscles have detached from the epidermis, leaving gaps in the perlecan-staining bands (arrow). (E) In the wild-type larvae, MUP-4::GFP is localized to regularly spaced attachment structures in the epidermis. In pxn-2 mutant larvae, MUP-4::GFP is absent from regions of muscle detachment (arrow). Scale bars: 10 μm.
Functions of peroxidasin PXN-2

RESEARCH ARTICLE

3607

inferred that a weakened muscle-epidermal basement membrane attachment is broken by the force of muscle contraction, leading to defects in the epidermal cytoskeleton and subsequent failure to elongate. Indeed, in larvae, regions of detached muscle correlated with gaps in the pattern of epidermal cytoskeletal attachment structures, as visualized by components such as MUP-4 (Hong et al., 2001) (Fig. 2E), suggesting that muscle detachment results in local disorganization of the epidermal cytoskeleton.

**pxn-2 is expressed in epidermal cells from early embryogenesis onwards**

**pxn-2** transcriptional GFP reporters containing the 1.8 kb promoter sequence defined by rescue experiments (Fig. 1D) were expressed in the embryonic epidermis (Fig. 3). Expression was observed in epidermal precursors beginning in late gastrulation (~200 minutes after the first cleavage), which is ~4 hours before the elongation defects of **pxn-2** mutants become apparent at 450 minutes (Fig. 3A). **Ppxn-2-GFP** was expressed by most differentiated epidermal cells throughout embryonic, larval and adult development (Fig. 3B). In adults, **Ppxn-2-GFP** was expressed in vulval muscles (Fig. 3B) and in a small number of neurons, including PVQ (Fig. 3C).

To determine where PXN-2 protein is localized, we generated YFP-tagged PXN-2 transgenics. These transgenics fully rescued **pxn-2(ju358)** (Fig. 1D) and **pxn-2(tm3464)** (not shown), indicating that the YFP tag does not disrupt PXN-2 function. As with the **pxn-2** transcriptional reporters, GFP::PXN-2 was expressed in epidermal cells at all stages, in vulval muscles and in a few neurons. In early embryonic epidermal elongation, most YFP::PXN-2 appeared to be intracellular in epidermal cells, in the locations that likely correspond to compartments of the secretory pathway (Fig. 3D). By late elongation, YFP::PXN-2 was also found in longitudinal striations adjacent to body wall muscle quadrants (Fig. 3E). As such longitudinal structures are not found inside the epidermis these are likely to represent localization to the basement membrane between the epidermis and muscles. Consistent with this interpretation, YFP::PXN-2 localized close to endogenous basement membrane components such as perlecan (Fig. 3F). In larval and adult stages, YFP::PXN-2 was faintly visible throughout the epidermis, in vulval muscles and in PVQ neurons (not shown). Transgenes expressing YFP::PXN-2(H755A) and YFP::PXN-2(Δlg) were made by injection at the same concentration as wild-type YFP::PXN-2. Mutant fusion proteins were expressed within epidermal cells and showed a range of localization similar to the wild-type protein (Fig. 3G). Like the wild-type protein, some YFP-tagged PXN-2 accumulated within the epidermis; however, some punctate or striated staining, similar to that in the wild type, was also observed. These observations suggest that the failure of the H755A and Δlg transgenes to rescue is likely to be due to the requirement for peroxidase activity and the Ig domains for proper PXN-2 function. However, we cannot exclude the possibility that improper localization or processing also contributes to the failure to rescue.

**PXN-2 maintains postembryonic cell-matrix adhesion of body muscles and pharyngeal cells**

*C. elegans* body wall muscles are attached to the epidermis via a basement membrane between the two tissues. **pxn-2** mutants displayed a progressive detachment of body muscles from the epidermis during larval development (Fig. 4A,B). To test whether forces due to body muscle contraction were causing progressive detachment, we paralyzed muscles using levamisole and found that this significantly suppressed muscle-epidermal and muscle-muscle detachment in **pxn-2(ju432)** (Fig. 4B). This result implies that the muscle-epidermal and muscle-muscle detachment defects of **pxn-2** mutants are in part due to a failure to maintain strong adhesive attachments. Levamisole suppressed epidermal morphology defects in the stronger mutant ju358, but only slightly suppressed muscle detachment (Fig. 4B). The inability of levamisole to significantly suppress detachment defects in ju358 mutants might be because in this more severe mutant the body muscles have become irreversibly detached during embryogenesis.
pxn-2 mutant adults also displayed highly penetrant defects in egg laying (Fig. 4C). In wild-type hermaphrodites, eggs are expelled by vulval muscle contraction stimulated by serotonergic HSN neurons (Schafer, 2006). Although HSN neurons were occasionally mispositioned in pxn-2 mutants (Fig. 4D), the primary cause of the Egl defect appears to be a defective attachment of vulval muscles (Fig. 4E). Consistent with this interpretation, the pxn-2 Egl phenotype was only marginally suppressed by treatment with exogenous serotonin or serotonin re-uptake inhibitors (Fig. 4F).

To test whether the muscle detachment phenotypes of pxn-2 mutants reflect a defect in the basement membrane, we examined ECM ultrastructure. Muscles and epidermal cells normally generate basement membranes that are 20-100 nm thick (Fig. 4H,G) (Kramer, 2005). By contrast, in pxn-2 mutants, we often observed a diffuse, apparently unstructured ECM within which were embedded multiple electron-dense basement-membrane-like laminae of similar thickness to normal basement membranes (black arrows). (I) Enlargement of boxed region in H, showing muscle finger surrounded by laminae (arrows). Scale bars: 10 μm in A,C; 500 nm in G,H.

pxn-2 mutants also displayed striking progressive defects in the morphology of the adult pharynx. Over the course of several days the shape of the anterior pharyngeal bulb became progressively distorted (Fig. 5A). ECM component HIM-4 (hemicentin) is normally localized to the pharyngeal basement membrane and tracks that tether the anterior pharynx to the epidermis (Fig. 5B). The pharyngeal basement membrane appeared normal. Within the expanded matrix muscle cells were extended finger-like projections with membrane plaques resembling those of dense bodies (Fig. 4I).

pxn-2 mutants also displayed highly penetrant defects in egg laying (Fig. 4C). In wild-type hermaphrodites, eggs are expelled by vulval muscle contraction stimulated by serotonergic HSN neurons (Schafer, 2006). Although HSN neurons were occasionally mispositioned in pxn-2 mutants (Fig. 4D), the primary cause of the Egl defect appears to be a defective attachment of vulval muscles (Fig. 4E). Consistent with this interpretation, the pxn-2 Egl phenotype was only marginally suppressed by treatment with exogenous serotonin or serotonin re-uptake inhibitors (Fig. 4F).

To test whether the muscle detachment phenotypes of pxn-2 mutants reflect a defect in the basement membrane, we examined ECM ultrastructure. Muscles and epidermal cells normally generate basement membranes that are 20-100 nm thick (Fig. 4H,G) (Kramer, 2005). By contrast, in pxn-2 mutants, we often observed a diffuse, apparently unstructured ECM within which were embedded multiple electron-dense basement-membrane-like laminae of similar thickness to normal basement membranes (black arrows). (I) Enlargement of boxed region in H, showing muscle finger surrounded by laminae (arrows). Scale bars: 10 μm in A,C; 500 nm in G,H.

pxn-2 mutants also displayed striking progressive defects in the morphology of the adult pharynx. Over the course of several days the shape of the anterior pharyngeal bulb became progressively distorted (Fig. 5A). ECM component HIM-4 (hemicentin) is normally localized to the pharyngeal basement membrane and tracks that tether the anterior pharynx to the epidermis (Fig. 5B). The pharyngeal basement membrane appeared normal. Within the expanded matrix muscle cells were extended finger-like projections with membrane plaques resembling those of dense bodies (Fig. 4I).

pxn-2 mutants also displayed striking progressive defects in the morphology of the adult pharynx. Over the course of several days the shape of the anterior pharyngeal bulb became progressively distorted (Fig. 5A). ECM component HIM-4 (hemicentin) is normally localized to the pharyngeal basement membrane and tracks that tether the anterior pharynx to the epidermis (Fig. 5B). The pharyngeal basement membrane itself was also aberrant (Fig. 5C,D), resembling the unstructured material seen near body wall muscles.

To further address whether PXN-2 promotes basement membrane function we tested whether reduction of pxn-2 function could sensitize animals to loss of function in other known basement membrane components. We grew pxn-2(ju432) worms on bacteria expressing dsRNA for laminin αA (encoded by lam-3) (Huang et al.,
lam-3 RNAi feeding had no effect in the wild-type (N2) background but significantly enhanced lethality and Vab phenotypes when performed on pxn-2(ju432) partial loss-of-function mutants (Table 2). pxn-2(ju432) also synergized with RNAi for α-integrin (pat-2; Table 2). The enhanced sensitivity of pxn-2 mutants to RNAi for basement membrane components or receptors supports a role for PXN-2 in basement membrane function.

**PXN-2 is required to guide specific axons but does not maintain process position**

Basement membranes form substrates for outgrowth and guidance of pioneer growth cones. To investigate the role of PXN-2 in neuronal development, we examined a panel of neuron types, including cholinergic and GABAergic motoneurons and mechanosensory neurons. Both types of motoneuron extend circumferential commissures across basement membrane to the dorsal cord. Motor axon outgrowth and commissural guidance were mostly normal in pxn-2 mutants. However, pxn-2 mutants were strongly defective in the left-right guidance of commissure outgrowth. In the wild type, 17/19 D neuron commissures extend on the right-hand side, whereas in 89% of ju358 mutants at least one D commissure (of 17 scored) extended on the incorrect, left-hand side ($n=53$; see Fig. 6A,B); in 13% of ju358 animals more than four commissures extended incorrectly. Cholinergic DA and DB motoneurons displayed less penetrant handedness defects (not shown). Thus, PXN-2 acts in selective axon guidance decisions but is not essential for axon outgrowth.

**Table 2. Synergism of pxn-2 with laminin and integrin RNAi**

<table>
<thead>
<tr>
<th>Genotype</th>
<th>RNAi</th>
<th>Lethality (%)</th>
<th>Vab adults (%)</th>
<th>n</th>
</tr>
</thead>
<tbody>
<tr>
<td>N2</td>
<td>L4440</td>
<td>0.4</td>
<td>0</td>
<td>719</td>
</tr>
<tr>
<td>N2</td>
<td>lam-3</td>
<td>0.16</td>
<td>0</td>
<td>616</td>
</tr>
<tr>
<td>N2</td>
<td>pat-2</td>
<td>0.0</td>
<td>47</td>
<td>251</td>
</tr>
<tr>
<td>pxn-2(ju432)</td>
<td>L4440</td>
<td>2.8</td>
<td>17.6</td>
<td>216</td>
</tr>
<tr>
<td>pxn-2(ju432)</td>
<td>lam-3</td>
<td>8.9*</td>
<td>53.2*</td>
<td>158</td>
</tr>
<tr>
<td>pxn-2(ju432)</td>
<td>pat-2</td>
<td>16*</td>
<td>44</td>
<td>291</td>
</tr>
<tr>
<td>pxn-1(ok785)</td>
<td>L4440</td>
<td>0.13</td>
<td>0</td>
<td>765</td>
</tr>
<tr>
<td>pxn-1(ok785)</td>
<td>lam-3</td>
<td>0.4</td>
<td>0</td>
<td>678</td>
</tr>
<tr>
<td>pxn-1(ok785)</td>
<td>pat-2</td>
<td>0.0</td>
<td>39*</td>
<td>261</td>
</tr>
<tr>
<td>rrf-3</td>
<td>L4440</td>
<td>9.0</td>
<td>0</td>
<td>367</td>
</tr>
<tr>
<td>rrf-3</td>
<td>lam-3</td>
<td>25.0</td>
<td>0</td>
<td>248</td>
</tr>
<tr>
<td>pxn-1(ok785) rrf-3</td>
<td>L4440</td>
<td>17</td>
<td>0</td>
<td>392</td>
</tr>
<tr>
<td>pxn-1(ok785) rrf-3</td>
<td>lam-3</td>
<td>13*</td>
<td>0</td>
<td>276</td>
</tr>
</tbody>
</table>

Embryonic and larval lethality were scored in the progeny of animals feeding on HT115 bacteria containing either the L4440 empty vector or the lam-3 RNAi clone. lam-3 RNAi is not effective in the N2 or rrf-3 background but strongly enhances pxn-2(ju432) lethality and adult Vab phenotypes (+, $P<0.05$; Fisher’s exact test). pat-2 RNAi causes adult Vab in the N2 background, slightly enhanced lethality in the pxn-2 background, and reduced Vab phenotypes in the pxn-1 background ($P<0.05$).
Some basement membrane proteins, such as SPON-1 and DIG-1, act postembryonically to maintain axons in their correct positions (Benard et al., 2006; Woo et al., 2008). To test whether PXN-2 might also maintain axon position, we examined the morphology of PVQ neurons in $pxn-2$ mutants. Both $ju432$ and $ju358$ mutants displayed inappropriate PVQ midline crossing at the L1 stage (Fig. 6C). However, the incidence of PVQ midline crossing defects did not increase during postembryonic development. Quantitation in L1 and L4 stage animals and in L4 animals reared on levamisole (Lev) plates. $n>45$ per group; ns, not significant (Fisher’s exact test). (E) (Left) Diagram of PLM neuron showing position of axotomy (X). (Right) Images of PLM regrowth 6 hours post-axotomy in wild type and $pxn-2(ju358)$; arrow, site of axotomy. Note the growth-cone-like structure in $pxn-2$. (F) Quantitation of PLM (zdIs5) regrowth in wild type and $pxn-2(ju358)$ at 6 and 24 hours. Sample size is indicated within the columns. $pxn-2$ mutants displayed increased regrowth at 6 hours (*, $P=0.02$; Mann-Whitney test). The increased regrowth of $pxn-2$ mutants at 24 hours is rescued by the $PXN-2(+)$ transgene $juEx2140$ (***, $P<0.001$; ANOVA and Tukey’s post-hoc test). (G) By 24 hours post-axotomy, the distal process of the ALM neuron retracts slightly in the wild type, whereas in $pxn-2(ju358)$ mutants the ALM distal process displays significantly increased regrowth. Dot plot, horizontal lines indicate the mean. $P=0.003$, Mann-Whitney test. Scale bars: 10 µm.

**Fig. 6. PXN-2 functions in selective motoneuron axon guidance choice, prevents midline crossing and inhibits touch neuron axon regrowth after laser axotomy.** (A) In wild-type L1 stage C. elegans ($Punc-25$-$GFP$, $juIs76$), commissures of motoneurons DD2-6 extend on the right-hand side. In $pxn-2(ju358)$, commissures frequently extend on the left-hand side (arrow, DD6 commissure). (B) Summary of D neuron commissure handedness defects. The number of commissures that extended incorrectly is shown ($n>50$ per genotype). (C) Wild-type PVQ axons are fasciculated in the posterior and separate in the anterior. In $pxn-2(ju358)$ animals, PVQ axons inappropriately fasciculate; $qys14$. (D) $pxn-2$ midline crossing defects do not increase during postembryonic development. Quantitation in L1 and L4 stage animals and in L4 animals reared on levamisole (Lev) plates. $n>45$ per group; ns, not significant (Fisher’s exact test). (E) (Left) Diagram of PLM neuron showing position of axotomy (X). (Right) Images of PLM regrowth 6 hours post-axotomy in wild type and $pxn-2(ju358)$; arrow, site of axotomy. Note the growth-cone-like structure in $pxn-2$. (F) Quantitation of PLM (zdIs5) regrowth in wild type and $pxn-2(ju358)$ at 6 and 24 hours. Sample size is indicated within the columns. $pxn-2$ mutants displayed increased regrowth at 6 hours (*, $P=0.02$; Mann-Whitney test). The increased regrowth of $pxn-2$ mutants at 24 hours is rescued by the $PXN-2(+)$ transgene $juEx2140$ (***, $P<0.001$; ANOVA and Tukey’s post-hoc test). (G) By 24 hours post-axotomy, the distal process of the ALM neuron retracts slightly in the wild type, whereas in $pxn-2(ju358)$ mutants the ALM distal process displays significantly increased regrowth. Dot plot, horizontal lines indicate the mean. $P=0.003$, Mann-Whitney test. Scale bars: 10 µm.

**PXN-2 inhibits adult axon regrowth after injury**

The continued expression of PXN-2 in adult stages prompted us to test whether PXN-2 might influence the ability of mature axons to regrow after injury. We focused on the ALM and PLM mechanosensory (touch) neurons, which display robust regrowth in L4 and adult stages when severed proximally to the synaptic branches, but very little regrowth when severed distally to the synaptic branches (Wu et al., 2007). The developmental outgrowth of touch neurons was largely normal in $pxn-2$ partial loss-of-function mutants, although a small percentage of neurons displayed axon overgrowth (not shown). After laser axotomy, the proximal axon of PLM regrew significantly further in $pxn-2(ju358)$ mutants than in the wild type at 6 hours (Fig. 6E,F). In the wild type, 1/16 axons formed new growth cones at 6 hours, whereas 7/15 PLM processes had reformed growth cones at 6 hours in $pxn-2$ mutants ($P=0.015$, Fisher’s exact test). The total regrowth of PLM neurons by 24 hours in $pxn-2$ mutants was ~150% that of wild-type PLM neurons; this increased regrowth was fully rescued by the $pxn-2(+)$ transgene (Fig. 6E). When severed distally to the synaptic branch, $pxn-2$ mutant ALM neurons displayed significantly increased regrowth compared with the wild type (Fig. 6G). Thus, reduced $pxn-2$ function can promote regrowth in both regeneration-permissive and regeneration-inhibited situations.

**PXN-1 is not essential for development and acts antagonistically to PXN-2**

*C. elegans* encodes a second peroxidasin, PXN-1, which is closely related to PXN-2 (Fig. 1C). $pxn-1$ transcriptional reporters were expressed in the epidermis (Fig. 7B), in several classes of neuron, and in vulval and uterine muscles. The deletion $pxn-1(ok785)$ is predicted to truncate PXN-1 before the peroxidase domain, and
should cause a strong loss of function (Fig. 7A). \textit{pxn-1(ok785)} mutants did not display overt defects in epidermal morphogenesis or egg laying. RNAi of \textit{pxn-1} in sensitized backgrounds did not reveal obvious phenotypes (not shown), suggesting that \textit{pxn-1} is not essential for basement membrane formation.

We tested whether \textit{pxn-1} might function redundantly with \textit{pxn-2} by analyzing \textit{pxn-1}: \textit{pxn-2} double mutants. Unexpectedly, \textit{pxn-1(ok785)} significantly suppressed the lethal, morphological and egg-laying defects caused by multiple \textit{pxn-2} alleles (Fig. 7C,D). For example, whereas \textit{ju379} or \textit{tm3464} mutants arrest in embryonic or early L1 stages, \textit{ok785}; \textit{ju379} and \textit{ok785}; \textit{tm3464} double mutants arrested at later stages. Approximately 1% of \textit{ok785}; \textit{tm3464} animals developed to sterile adults (Fig. 7C). As \textit{pxn-1(ok785)} can ameliorate the defects of the deletion allele \textit{pxn-2(tm3464)}, the suppression is unlikely to be due to upregulation of residual functional \textit{pxn-2}, but suggests that \textit{pxn-1} and \textit{pxn-2} have antagonistic roles. Indeed, transgenes overexpressing \textit{pxn-1} did not cause morphological defects in a wild-type background yet significantly enhanced \textit{pxn-2} mutant phenotypes (Fig. 7D). To further test this antagonist interaction, we generated transgenes that overexpress YFP::\textit{pxn-2} in the wild-type background. These transgenic animals exhibited \textit{pxn-2}-like phenotypes that were strongly suppressed by RNAi for GFP (Fig. 7D), suggesting that overexpression of \textit{pxn-2} resulted in inhibition of endogenous \textit{pxn-2} activity. Consistent with this interpretation, effects of \textit{pxn-2} overexpression were fully suppressed by \textit{pxn-1(ok785)} (Fig. 7D).

To address the gene specificity of the suppression effects of \textit{pxn-1}, we examined \textit{pxn-1} double mutants with \textit{spon-1} (F-spondin), and found that \textit{pxn-1} significantly suppressed the morphological defects of a \textit{spon-1} mutant (Fig. 7D). \textit{pxn-1} mutants were also slightly resistant to the effects of \textit{pat-2} and \textit{lam-3} RNAi (Table 2).

To investigate the basis of the striking divergence in \textit{pxn-1} and \textit{pxn-2} functions, we expressed transgenes in which either all or part of the peroxidase domain of \textit{pxn-2} had been replaced with that of \textit{pxn-1}. The resulting YFP-tagged chimeric proteins were expressed at levels comparable to wild-type YFP::\textit{pxn-2} (not shown) and did not cause significant defects in a wild-type background (Fig. 7D). Chimera-expressing transgenes failed to rescue \textit{pxn-2}-null mutant phenotypes (not shown) and slightly enhanced the defects of \textit{pxn-2} partial loss-of-function mutants (Fig. 7D). As replacement of the \textit{pxn-2} peroxidase domain with that of \textit{pxn-1} slightly ameliorated their defects, the differences in \textit{pxn-1} function, which are suppressed by \textit{pxn-1} and by RNAi for GFP. Arrays expressing a \textit{pxn-2}:\textit{pxn-1} chimera (\textit{juEx2900}) slightly enhanced \textit{pxn-2}(\textit{ju342}); similar results were obtained for the chimera array \textit{juEx2905} (not shown). ***, \textit{P}<0.001; **, \textit{P}<0.01; *, \textit{P}<0.05; Fisher’s exact or \chi^2 test. (E) Approximately 1% of \textit{pxn-2}(\textit{tm3464}); \textit{pxn-1(ok785)} animals develop to sterile adults.

**DISCUSSION**

The functions of peroxidinas have remained enigmatic since their discovery in \textit{Drosophila} (Nelson et al., 1994). The results of our analysis of the developmental and behavioral defects of \textit{pxn-2} mutants are consistent with an essential role for \textit{pxn-2} in the formation and maintenance of basement membranes. We further find that reduced \textit{pxn-2} function allows increased axonal regeneration after injury in adults, providing the first evidence that the \textit{C. elegans} ECM contributes to an inhibitory environment during axon regrowth.

Although peroxidinas derive their name from the presence of the peroxidase domain, the unusual domain structure of peroxidinas raises the question of whether their peroxidase catalytic activity is important in the ECM, or whether they might have two independent functions. Mutation of the active site histidine in \textit{pxn-2} almost eliminated rescuing activity, indicating that catalytic activity is important for \textit{pxn-2} developmental functions. A \textit{C. elegans} dual oxidase, BLI-3, has both a peroxidase-dependent function in cuticle cross-linking and a peroxidase-independent role in the generation of reactive oxygen species (Chavez et al., 2009), reflecting the presence of a second catalytic oxidase domain in the protein. As peroxidinas have only a single catalytic domain, any peroxidase-independent functions presumably involve the LRR or Ig domains, which we also find are required for \textit{pxn-2} function. Peroxidinas contain a highly conserved cysteine-rich motif in their C-termini that is related to the Von Willebrand factor type C domain and is thought to promote trimerization (Nelson et al., 1994). Strikingly, missense alteration of
a semi-conserved glycine (G1314), as in the strong pxn-2 allele 
ju379, almost completely abolished PXN-2 function, supporting the
hypothesis that the C-terminus of peroxidasins is important for
function. Together, our data show that peroxidasins are functional
peroxidases that contribute to ECM formation via multiple domains.

pxn-2 mutants display disorganization of ECM and striking
expansion of matrix material. Similar stacking of basement-
membrane-like structures has been observed in some C. elegans
ECM mutants, such as dig-1 (Benard et al., 2006), whereas
expansion of ECM is occasionally observed in laminin αA (epi-1)
mutants (Huang et al., 2003). PXN-2 might promote the
consolidation of a less structured ECM precursor into mature
basement membranes. Taken together with the late onset of pxn-2
defects, these results suggest that PXN-2 plays a restricted role in
late matrix assembly or consolidation.

As with other peroxidases, peroxidasin can catalyze the
formation of dityrosine cross-links in vitro. Many extracellular
matrices, such as cuticles or egg shells, are strengthened by
peroxidase-catalyzed dityrosine cross-links (Andersen, 1964;
Konstandi et al., 2005; Wong and Wessel, 2008). In C. elegans,
dityrosine cross-linking is required for cuticle integrity and is
catalyzed by the dual oxidase-peroxidase Ce-Duox1/BLI-3 and the
peroxidase MLT-7 (Edens et al., 2001; Thein et al., 2009).
Although expressed in epidermis, PXN-2 does not appear to cross-
link cuticle, but might play an analogous role in the basement
membrane. Dityrosine cross-linking has been proposed as a
function for peroxidasins in basement membranes, yet dityrosine
itself has not thus far been directly detected in basement
membranes. It remains possible that peroxidasins provide oxidants
for other kinds of post-translational modifications. Vertebrate
fibrillar collagens are extensively cross-linked by lysyl oxidase
(Robins, 2007); however, C. elegans lacks fibrillar collagens
(Myllyharju and Kivirikko, 2004). An important future goal is to
identify the in vivo substrates of PXN-2 and other peroxidasins.

PXN-2 is essential for late steps in basement membrane
formation, and specifically where mechanically strong attachment
between tissues and ECM is required. pxn-2 mutants display
progressive dystrophy of the pharynx, reminiscent of fibrulin (fbl-
1) mutants (Muriel et al., 2005). However, pxn-2 mutants do not
display defects in gonadal development or integrity, which are
found in laminin or fibrulin mutants (Hesselson et al., 2004; Kubota
et al., 2004). Pharyngeal muscles are likely to require a
mechanically strong basement membrane to exert force against
during contraction. By contrast, basement membranes, such as
those of the intestine or gonad, might have a lesser need to
withstand muscle contractions and thus do not require PXN-2.

We find that loss of pxn-2 function influences the ability of
mature neurons to regenerate after injury. PXN-2 might interact
directly with axonal receptors during axon navigation.
Alternatively, PXN-2 could play an indirect role in that aberrant
ECM in pxn-2 mutants might constitute a more permissive
environment for regrowth. Extensive studies of vertebrate axon
regeneration have shown that ECM components can be regrowth
promoting or inhibiting (Busch and Silver, 2007). Our findings
raise the possibility that mammalian peroxidasins are extracellular
inhibitors of regrowth. Inhibitors of peroxidasin catalytic activity
could have therapeutic benefits in situations of axon injury.

Most animals express multiple peroxidasins, either as products
of multiple peroxidasin genes or from alternative splicing of a
single gene. Gene duplication can result in an initial redundancy of
function, followed by subfunctionalization if the duplicated genes
take on distinct roles in different tissues or at different times (Lynch
and Force, 2000; Tvrdík and Capecci, 2006). Although the two C.
elegans peroxidasins are closely related, our data suggest that pxn-
1 and pxn-2 have become subfunctionalized. PXN-1 might have
peroxidase-independent functions that could be mediated by
truncated proteins made in ok785 mutants, yet RNAi of pxn-1
failed to reveal developmental phenotypes. Partial redundancy of
function should be reflected in phenotypic enhancement in a double
mutant, yet pxn-1: pxn-2 double mutants display suppression of
pxn-2 mutant phenotypes. pxn-1 loss of function also suppressed
span-1 partial loss of function, consistent with PXN-1 acting as a
negative regulator of basement membrane assembly or function.

Elevated expression of peroxidasins, such as MPO, during
inflammation or tissue injury can degrade ECM as a result of an
overproduction of extracellular oxidants and consequent
inactivation of protease inhibitors (Wang et al., 2007). PXN-1
could play an analogous regulatory role in the C. elegans matrix.
Intriguingly, loss of pxn-1 function can enhance neurodegenerative
phenotypes caused by overexpression of the microtubule-binding
protein tau (MAPT) in C. elegans, implying that PXN-1 protects
against neurodegeneration (Kraemer et al., 2006). Further work
will be required to determine whether the neuroprotective effects
of PXN-1 are related to its role in regulating the ECM.

Acknowledgements
We thank Mei Ding and Wei-Meng Woo for collaboration in the elongation
screen; Lizhen Chen for constructing the zds5 rescue strain; members of our
labs for help and advice; Alan Zahler, Manny Ares and Emily Troxell for
discussions; and Mark Ellisman (National Center for Microscopy and Imaging
Research, UCSD) and Marilyn Farquhar (Department of Cellular and Molecular
Medicine, UCSD) for electron microscopy resources. Deletion alleles were
generously provided by the C. elegans Gene Knockout Consortium (ok785)
and the Japan National BioResource Project (tm3464). We thank B. Vogel (University of Maryland) for rh823. Z.W. and A.G. are Associates and Y.J. is an
Investigator of the Howard Hughes Medical Institute. This work was supported by
NIH award F32 GM090652 to C.A.G. and R01 awards GM54657 and
N557317 to A.D.C. Deposited in PMC for release after 6 months.

Competing interests statement
The authors declare no competing financial interests.

Supplementary material
Supplementary material for this article is available at
http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.049189/-/DC1

References
Alfonso, T. B. and Jones, B. W. (2002). gc2m promotes glial cell differentiation and
is required with glial cells missing for macrophage development in Drosophila. Dev.
Biol. 248, 369-383.

Andersen, S. O. (1964). The cross-links in resilin identified as dityrosine and

Severe impairment in early host defense against Candida albicans in mice deficient

architecture. Development 133, 3329-3340.


reactive oxygen species as a protective innate immune mechanism in

Identification and characterization of VPO1, a new animal heme-containing


protein, regulates axonal development and neuronal differentiation. Development
130, 3781-3794.
