Regulation of *C. elegans* presynaptic differentiation and neurite branching via a novel signaling pathway initiated by SAM-10

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**SUMMARY**

Little is known about transcriptional control of neurite branching or presynaptic differentiation, events that occur relatively late in neuronal development. Using the *Caenorhabditis elegans* mechanosensory circuit as an in vivo model, we show that SAM-10, an ortholog of mammalian single-stranded DNA-binding protein (SSDP), functions cell-autonomously in the nucleus to regulate synaptic differentiation, as well as positioning of, a single neurite branch. PLM mechanosensory neurons in *sam-10* mutants exhibit abnormal placement of the neurite branch point, and defective synaptogenesis, characterized by an overextended synaptic varicosity, underdeveloped synaptic morphology and disrupted colocalization of active zone and synaptic vesicles. SAM-10 functions coordinately with Lim domain-binding protein 1 (LDB-1), demonstrated by our observations that: (1) mutations in either gene show similar defects in PLM neurons; and (2) LDB-1 is required for SAM-10 nuclear localization. SAM-10 regulates PLM synaptic differentiation by suppressing transcription of *prk-2*, which encodes an ortholog of the mammalian Pim kinase family. PRK-2-mediated activities of SAM-10 are specifically involved in PLM synaptic differentiation, but not other *sam-10* phenotypes such as neurite branching. Thus, these data reveal a novel transcriptional signaling pathway that regulates neuronal specification of neurite branching and presynaptic differentiation.

**KEY WORDS:** Synapse differentiation, Neurite branching, Branch positioning, Transcriptional regulation, SAM-10, *C. elegans*

**INTRODUCTION**

Chemical synapses are the primary intercellular signaling unit in the nervous system. After reaching target area, axons form synapses to innervate their postsynaptic partners. The stereotypic growth pattern of axons, including branching, and precise assembly of synapses are crucial in building the complex neuronal networks of the brain. Ultrastructurally, mature synapses consist of precisely juxtaposed specialized pre- and postsynaptic subcellular structures. The presynapse consists of a cluster of synaptic vesicles that surround an electron-dense cytomatrix, the active zone, for exocytosis of transmitters. The postsynapse is highly enriched in neurotransmitter receptors and many associated scaffolding proteins, which serve to anchor the receptors in proximity to the presynaptic release site. Synapses are very stable, yet plastic. As the likely cellular site of both learning and memory, the pre- and postsynapse have the dual potential of being exceedingly stable structures, but also retain the ability to change dynamically to alter synaptic strength. Therefore, understanding the molecular mechanisms underlying assembly of synapses is crucial to understanding both brain development and function.

Studies have shown that presynaptic differentiation is regulated by intra- and extracellular signals. One type of regulatory mechanism that has been well described involves local acting post-transcriptional signals that are crucial for synaptogenesis in a variety of systems. For example, PHR (Pam/Highwire/RPM-1) proteins are evolutionarily conserved E3 ubiquitin ligases, which regulate synaptic structure and function in mice, flies and worms (Burgess et al., 2004; Nakata et al., 2005; Schaefer et al., 2000; Wan et al., 2000; Zhen et al., 2000). RPM-1, the *C. elegans* PHR, functions coordinately with the F-box protein FSN-1 to regulate synaptic differentiation by silencing the DLK-1/MKK-4/PMK-3 MAP kinase pathway at the neuromuscular junction (NMJ) (Liao et al., 2004; Nakata et al., 2005; Zhen et al., 2000). Likewise, the *Drosophila* highwire gene was also found to regulate synaptogenesis at NMJs (Wan et al., 2000). More recently, a ubiquitin-signaling pathway mediated by Cdc20-APC was shown to regulate presynaptic differentiation in mammalian neurons (Yang et al., 2009).

The use of post-translational regulation such as ubiquitin-mediated protein degradation in synaptic development provides a mechanism to overcome the difficulty of transmitting signals across extended distances between the synapse and the soma. However, regulation at the transcriptional level is also likely to play crucial roles in synaptic differentiation (Diaz, 2009; Kalinovsky and Scheiffele, 2004). In a screen for genes induced by membrane depolarization in mouse cortical neurons, Npas4 was identified as a transcription factor regulating inhibitory synapse development in an activity-dependent manner (Lin et al., 2008). In *Drosophila*, mutations in multiple components of a TGFβ/BMP signaling pathway have been identified that regulate the size of presynapses via a retrograde signaling pathway that acts via phosphorylated and nuclearly-localized SMAD (McCabe et al., 2004). Furthermore, the use of post-translational regulation such as ubiquitin-mediated protein degradation in synaptic development provides a mechanism to overcome the difficulty of transmitting signals across extended distances between the synapse and the soma. However, regulation at the transcriptional level is also likely to play crucial roles in synaptic differentiation (Diaz, 2009; Kalinovsky and Scheiffele, 2004). In a screen for genes induced by membrane depolarization in mouse cortical neurons, Npas4 was identified as a transcription factor regulating inhibitory synapse development in an activity-dependent manner (Lin et al., 2008). In *Drosophila*, mutations in multiple components of a TGFβ/BMP signaling pathway have been identified that regulate the size of presynapses via a retrograde signaling pathway that acts via phosphorylated and nuclearly-localized SMAD (McCabe et al., 2004). Furthermore, these pathways are probably modulated at many different levels, because mutants such as spinster (Sweeney and Davis, 2002) and nervous wreck (O’Connor-Giles et al., 2008), which encode genes that regulate endocytic trafficking also display synaptogenesis defects. These studies suggest that synaptogenesis is finely tuned...
by distinct mechanisms. Although an increasing number of intrinsic signals have been implicated in regulating synaptic development, it is not yet fully understood how neurons program synaptic differentiation at the transcriptional level: namely, how neurons become competent for synaptogenesis.

One confounding factor in defining synaptogenesis is that synaptic differentiation is a late step in the differentiation of neurons. Numerous signaling pathways including many transcriptional pathways have been described; their disruption severely affects neuronal development before synaptogenesis is even initiated. For example, neuronal cell-fate specification along both the rostralcaudal and dorsoventral axes in the brain is regulated by a large number of extensively studied transcription factors and less thoroughly characterized associated factors. One such factor is Single-stranded DNA-binding protein (SSDP), which was originally isolated as a nuclear protein that specifically binds to the single-stranded polyuridylic region of the chicken n2 (1) collagen promoter (Bayarsaikhan et al., 1998). SSDP interacts biochemically with Lim domain binding protein 1 (LDB-1), which, in turn, binds to a variety of Lim homeobox transcription factors (LimHD) (Agulnick et al., 1996; Chen et al., 2002; van Meyel et al., 2003). The similarity of the embryonic lethal phenotypes of ldb1, ssdp1 and some limHD mutants have lead to the current hypothesis that SSDP functions in a complex with LDB1 and LimHDS to regulate neuronal cell fate (Enkhamdakh et al., 2006; Nishioka et al., 2005). However, biochemical studies suggest that SSDP may also function to execute transcriptional activities independently of LDB1 (Wu, 2006).

Whereas SSDP is clearly required for late stage embryonic brain development, no studies have addressed whether SSDP is involved in neurite branching or synaptic differentiation. Here we use the C. elegans mechanosensory system as a model to study these processes, and describe an evolutionarily conserved signaling pathway that cell-autonomously regulates the stereotopic pattern of neurite branching and presynaptic development. This pathway consists of two nuclear components, SAM-10 (encoding a C. elegans SSDP ortholog of SSDP) and LDB-1. Mutations in consists of two nuclear components, SAM-10 (encoding a Pim kinase gene. Overexpression of SAM-10/LDB-1 regulates synaptogenesis by downregulating disruption neurite branching spatial pattern and synapse defects are fully rescued by a transgene expressing the currently predicted Y48C3A.8a gene, the structure of which is based upon yk292a5, a 2031bp cDNA predicted to encode a 455 amino acid protein that includes a proline-rich domain. These data identified Y48C3A.8a as the predicted sam-10 genomic clone, the structure of which is based upon yk292a5, a 2031bp cDNA (Enkhmandakh et al., 2006) (see Fig. S5A in the supplementary material). The downstream gene Y48C3A.9 contained a proline-rich domain. We tested transgenic rescue of sam-10 mutant phenotypes using a clone encoding only Y48C3A.9, but we observed no rescue, suggesting that this prediction is incorrect (see Fig. S5B in the supplementary material). These two predicted genes actually define a single gene. sam-10 defects are fully rescued by a transgene expressing the currently predicted Y48C3A.8a gene, the structure of which is based upon yk292a5, a 2031bp cDNA predicted to encode a 455 amino acid protein that includes a proline-rich domain. These data identified Y48C3A.8a as sam-10.

Molecular biology
Plasmid DNA clones were constructed using standard molecular biology techniques. Y48C3A.9 (pNM1865) plasmid was constructed by inserting into pBlueScript SK(+) the KpnI/Smal site the Y48C3A.9 PCR product (primers: GTCTCCTCCTCCTCAGTTGACCCACCGGA and GACCTGACAGACATTGTTGATG) digested by Bmg1KpnI. sam-10 genomic clone (pNM2165) was constructed by two steps: (1) the PCR product of sam-10 3' end genomic region by Y48C3A.9 and containing the Y48C3A.9 sequences (primers: CAAAAGTGCAGCGCTCAATGCGCATTA and ATGATGCTCTAATCTCCCGAG) was inserted into Y48C3A.9 plasmid using KpnI and Nael; and (2) the resulting clone was modified by replacing the small promoter region with a long promoter by PCR (primers: AAGACCCGACATAACAGCAG and ATGTCATCGAGAGATCAATGAAGTCCGAG) using the Nhel and SacI. A rab-3p:sam-10 cDNA (pNM2120) was constructed by replacing the eGFP sequence in a rab-3p:eGFP rim 3' plasmid (pRB100) excised using AgeI and SacI with AgeI/SacI digested PCR product of a sam-10 cDNA (primers: ATACAGCGCAGCACTAGAGCGTACGAGAAGTCCGAG) using the Nhel and SacI. A rab-3p:sam-10 cDNA (pNM217) plasmid was constructed by replacing the rab-3 promoter in rab-3p:sam-10 cDNA with the gfp-1 promoter amplified from worm genomic DNA by PCR (primers: TGATAGAATCGCTACGACTGAG and AGTGACTAGACCGTCGCTTTCGCTTTCTCCTCGG) and inserted using PstI and AgeI. A mec-7p:sam-10 cDNA (pNM2112) was
constructed by replacing the rab-3 promoter in rab-3p:sam-10 cDNA with the mec-7 promoter amplified from genomic DNA by PCR (primers: ACTGAAATCTCGAGATACGCAAGACAGCTCGCTG and CATTCTGTACGATCGGCAAGAGGTGACGTAATCTGCGTGGTCGTGAAAGCAGCAGG) using AgeI and Agel. A sam-10::mCherry-sam-10 (pNM2168) plasmid was generated by inserting an mCherry PCR product [primers: ATAGTCAGCTGATCTGTGGTGAAGGCGGAAGTGTCGATGTCGTTGACGAGCAGCTGCAACAGG] and CATCTCTGAAGCTAGCGACTTGCTACGCTGTGCTCAT (template: UAS mCherry (pNM1413, a gift from the R. Wong lab)] into the sam-10 genomic clone (pNM2165) at the Nhel site in frame. A rab-3p:prk-2 cDNA (pNM2374) plasmid was constructed by replacing the eGFP region of prkAB100 with a PCR product of prk-2 cDNA (primers: ATACAGCCGCGCTATGAGAAGCTGGCTTCAGCACG and AAGAGCGGCTTGCAGTAGTCCTGCGAGAAGACGCCG) from first strand cDNA using Agel and SacI. A mec-7p::prk-2 cDNA (pNM2489) plasmid was constructed by replacing the rab-3 promoter region of pNM2374 plasmid with a PCR product of the mec-7 promoter from the worm genomic DNA prep (primers: ACCTGCAGCCCGGGG-AAAATTGATACGTACAGCACG and ATACAGGGTGCTGCTAGGTGGTTGTCGTGAAATTGGAAGCCTG) using restriction sites of XmaI and NotI.

Light microscopy

Transgenic animals were imaged on an Olympus BX60 equipped with an EXFO 120 mercury bulb using epifluorescence using standard GFP and RFP filter set. All images were taken with a Retiga EXi CCD camera using OpenLab software and processed using Adobe Photoshop.

Quantification of synaptic varicosity extension

Size of PLM synaptic varicosities was quantified using a three-point scale based upon their length. More than 95% of wild-type varicosities have a similar size: ~5 μm long. We defined these varicosities as ‘normal’. Varicosities two times longer (~10 μm) than normal varicosities were defined as ‘medium extension’. Varicosities even longer (~15 μm) were defined as ‘severe extension’. Scoring of animals for an individual experiment was performed by a single investigator blinded to the genotype of tested animals.

Microarray assay

Animals were grown on fresh 8P plates (Wormbook.org) until gravid. Eggs were collected by bleaching and hatching in M9 buffer overnight. L1 animals were fed on fresh food for 2 hours at room temperature, harvested and separated from worm debris using a 25 μm mesh. RNA was isolated using a standard Trizol protocol. RNA preps were stored at -80°C.

Quality of RNA preps was first estimated using Agilent 2100 Bioanalyzer. RNA was then reverse transcribed using the Genisphere Array 350 kit, which contains Total RNA preps from C. elegans. The microarray dataset has been deposited in NCBI's Gene Expression Omnibus, (GEO accession number: GSE25285).

Real-time RT-PCR assay

Total RNA preparations for the microarray assays were used for real-time RT-PCR. Reverse transcription was conducted using SuperScript III First-Strand kit (Invitrogen, Carlsbad, CA, USA). Real-time RT-PCR was run on an Applied Biosystems Prism 7000 Sequence Detection System, using SYBR GREEN kit (ABI, Foster City, CA, USA). Gene specific primers were designed with Primer Express 3.0 (ABI). Each sample was tested in triplicate. Relative changes of transcripts were analyzed by 2^ΔΔCT method (Livak and Schmittgen, 2001), using levels of act-1 transcripts as reference.

RESULTS

The C. elegans mechanosensory neuronal circuit provides an in vivo model for observing the bona fide pattern of synaptic differentiation (White et al., 1986). This circuit mediates responses to mechanical stimuli, for example light touches, through gap junctions (Chalfie et al., 1985). Situated in the tail ganglia, PLMs are two of the six mechanosensory neurons, each with a long anterior-orientated neurite that runs in close apposition to the hypodermis (Chalfie and Sulston, 1981) and ends posterior to the ALM somata (Gallegos and Bargmann, 2004), the anterior analogs of PLMs (see Fig. S1 in the supplementary material). Each PLM neurite branches into the nerve ring, resulting in a single ‘synaptic branch’ that enters the ventral nerve cord (VNC).

All PLM chemical synapses with interneurons are located along the synaptic branch. These synapses appear at the light level as large synaptic varicosities. Ultrastructurally, they consist of a cluster of chemical presynapses.

The ALM neurons are located in the mid-body and extend anterior neurites toward the nose tip. Each ALM also extends a branch from the anterior neurite into the nerve ring, where it forms synaptic varicosities onto postsynaptic partners (see Fig. S1 in the supplementary material).

PLM presynaptic differentiation and neurite branch positioning are defective in sam-10 mutants

sam-10 (Synaptic vesicle tag abnormal in mechanosensory neurons) was isolated in a compound microscope screen for mutants with defects in the morphology of PLM synaptic varicosities visualized with the synaptic marker SNB-1::GFP (A.M.S., PhD thesis, Washington University, MO, USA, 2001). We also observed presynaptic defects (increased number of synaptic puncta and synaptic vesicle accumulation) in DD motoneurons using SNB-1::GFP (JsIs1075) (see Fig. S2 in the supplementary material), indicating that sam-10 mutations affect synaptogenesis in different classes of neurons. To further define synaptogenesis defects of sam-10 (JsIs94) mutants, we used reporters for synaptic vesicle (RAB-3) and active zone (ELKS) components. Using RAB-3::GFP (JsIs821) to mark synaptic vesicles (Nonet et al., 1997), we observed that PLM synapses developed inappropriately: synaptic varicosities in sam-10 mutants are extended along the VNC, and varicosities are morphologically irregular (Fig. 1A,B,C; see Fig. S3 in the supplementary material). We never observed wild-type varicosities in sam-10 mutants at any developmental stage.

As expected, we found that active zones in wild-type animals colocalized well with synaptic vesicles in PLM synaptic varicosities, using TagRFP::ELKS (JsIs1075) as an active zone marker (Fig. 1B). By contrast, we found that colocalization of active zone markers (ELKS) and synaptic vesicles was disrupted in sam-10 mutants (Fig. 1C,D; see Fig. S3 in the supplementary material). To test if ELKS puncta represent active zones in sam-10 mutants, we examined localization of SYD-2, another active zone marker. We found that ELKS and SYD-2 colocalized well in sam-10 mutants (see Fig. S4 in the supplementary material), confirming that ELKS labeling identifies active zones in these animals. These data suggest that sam-10 synapses are not properly differentiated.

We also found that the PLM synaptic branch point in wild-type animals was posterior to the vulva but, in sam-10 mutants, the branch point was frequently anterior to the vulva (Fig. 4A). Thus, sam-10 mutations seem to specifically affect the spatial pattern of PLM neurite branching, but not branching frequency (data not shown).

In PLM neurons, altered colocalization of synaptic components was accompanied by overextension of the synaptic branch (Fig. 1A,B,C; see Fig. S3 in the supplementary material). The branches extended two- to threefold further in the ventral cord than in the wild
type and they displayed more irregular ‘rough’ morphology. To assess whether overextension of the PLM synaptic branch is the primary cause of the colocalization defect, we examined varicosities formed in the nerve ring by the anterior mechanosensory neurons, ALM (Fig. 1E). In the nerve ring of wild-type animals, each ALM neurite formed about five synaptic varicosities along its synaptic branch; these varicosities were evenly distributed and smooth (Fig. 1F). In sam-10 mutants, the synaptic branch extended normally into the nerve ring, and synaptic varicosities formed in the nerve ring, but individual synaptic varicosities were irregularly spaced and misshapen, although not obviously extended (Fig. 1G). Similar to PLM synaptic varicosities, colocalization of active zones and synaptic vesicles in the nerve ring was perturbed (Fig. 1G,H). These data demonstrate that mutations in sam-10 disrupt presynaptic differentiation in C. elegans mechanosensory neurons, and that misalignment of synaptic components is not simply due to altered morphology of the synaptic branch.

In addition to the defects described above, sam-10 mutants exhibited moderate uncoordinated movement (Unc), a small decrease in body size (Dpy), a defect in egg laying (Egl), and slow growth (Gro). However, they responded well to light touch (non-Mec). As the primary functional output of mechanosensory neurons is via gap junctions (Bounoutas et al., 2009; Chalfie et al., 1985), these data suggest that mechanosensory neurons are adequately differentiated and that they have formed functional gap junctions with interneurons. Consistent with the behavioral results, we found that, in js94 mutants, PLM neurons were superficially normal in position, polarity and neurite guidance when visualized using a cytosolic monomeric RFP (mRFP) marker (js973). These observations indicate that the defects in PLM neurons in sam-10 mutants refer specifically to later events in neuronal development.

Fig. 1. Mechanosensory neuron synaptic differentiation is defective in sam-10(js94). (A) Diagram of PLM neurites, synaptic branches and synaptic varicosities. (B,C) Somatic varicosities in PLM are labeled by the synaptic vesicle marker GFP-RAB-3 (green) and the active zone marker TagRFP-ELKS (red). (D) Quantification of TagRFP-ELKS and GFP-RAB-3 marker colocalization in PLM. Fisher’s exact test: **P<0.01 (relative to wild type); §P<0.05 (relative to sam-10), n=30 per group. (E) Diagram of ALM neurites, synaptic branches and synaptic varicosities. (F,G) Somatic varicosities in ALM are labeled by the synaptic vesicle marker GFP-RAB-3 (green) and the active zone marker TagRFP-ELKS (red). (F) Wild-type varicosities are regularly shaped. (G) An extended, irregular shape of varicosities is often observed in sam-10(js94) mutants. ELKS puncta lacking RAB-3 are indicated (arrows). (H) Quantification of TagRFP-ELKS and GFP-RAB-3 marker colocalization in ALM. Fisher’s exact test, *P<0.01 (relative to wild type); §§P<0.01 (relative to sam-10), n=30 per group. Scale bar: 5 μm in B,C,F,G. A, anterior; P, posterior; D, dorsal; V, ventral.

sam-10 encodes the C. elegans ortholog of mammalian SSDP

Genetic mapping narrowed the sam-10 mutation to an interval between snp_Y48C3A[9] and snp_Y48C3A[24] on chromosome II. Sequencing of predicted gene coding regions in this interval revealed a nucleotide transition (G→A) in the second exon of predicted Y48C3A.8a. The identity of Y48C3A.8a as sam-10 was confirmed by transgene rescue of the Sam, Gro, Unc, Dpy and Egl phenotypes. The sam-10 phenotype was rescued by transgenic expression of a clone containing a 7 kb promoter region and the entire Y48C3A.8a coding region, but not by clones containing either a 4 kb deletion of the distal part of the promoter, or a deletion of the C-terminal portion of the Y48C3A.8a coding region (see Fig. S5 in the supplementary material; see Materials and methods for details).

Y48C3A.8a encodes a 455 amino acid protein orthologous to SSDP, which is highly conserved in Drosophila and mammals (Fig. 2A). Proteins of the SSDP family (Bayarsaikhan, 2002) contain two conserved domains: a Forward domain that probably mediates interactions with other proteins such as LDB-1 (van Meyel et al., 2003) and a proline-rich transcriptional activating domain. The sam-10(js94) mutation introduces an early termination codon (Trp73→STOP) in the middle of the Forward domain (Fig. 2A) and probably represents a null allele of the sam-10 gene.

SAM-10 functions cell autonomously to regulate PLM synaptic differentiation

Presynaptic differentiation can be influenced by cues derived from different sources including the presynaptic cell, postsynaptic partner(s) or neighboring support cells. To determine where SAM-10 functions to regulate presynaptic differentiation, we tested for
rescue of PLM synaptic defects by expressing sam-10 in different tissues using a transgenic approach. We found that pan-neuronal expression of sam-10 driven by the rab-3 promoter rescued PLM defects (three of four transgenic lines), suggesting that SAM-10 functions in neurons. We then assessed whether SAM-10 functions in the pre- or postsynaptic cells. When sam-10 was expressed in postsynaptic partners under the glr-1 promoter, no rescue was observed (zero of three transgenic lines). However, when we expressed sam-10 in mechanosensory neurons using a mec-7 promoter, PLM defects were fully rescued (three of three transgenic lines). Additionally, we noticed that sam-10 expression in mechanosensory neurons did not rescue other sam-10 defects including the Unc, Dpy, Egl and Gro phenotypes (data not shown), indicating that these phenotypes are independent of the function of SAM-10 in PLM late neuronal specification. These data suggest that SAM-10 functions cell-autonomously to regulate PLM presynaptic differentiation.

**sam-10 is expressed broadly and localized in the nucleus of PLM**

To further define the molecular mechanism underlying SAM-10 function, we characterized its expression using an mCherry-sam-10 fusion transgene that fully rescues the sam-10(js94) phenotypes (see Fig. S5B in the supplementary material). The MCherry-SAM-10 signal was detected broadly throughout the animal with dense expression in the head ganglion, vulva and tail ganglion (Fig. 2B). This expression pattern was consistent with observed Unc, Dpy, Egl and Gro mutant phenotypes. Consistent with the cell-autonomous rescue described above, we observed sam-10 expression in PLM neurons. Furthermore, using GFP-RAB-3 as a nuclear-excluded marker in the PLM soma, we found that SAM-10 was nuclearly localized in the PLM (Fig. 4B).

Our previous studies demonstrated that PLM synaptic branching and synaptic differentiation occur in the L1 larval stage, shortly after hatching (Schaefer et al., 2000). With this temporal framework for PLM synaptogenesis, we tested how sam-10 expression correlated with this developmental time course. We first examined the developmental dynamics of sam-10 expression, and found that mCherry-SAM-10 signal became detectable as early as the 1.5-fold stage during embryogenesis (Fig. 3A). However, SAM-10 is not nuclearly localized at this stage. Using RAB-3-GFP as a marker for PLMs, we discovered that SAM-10 was not nuclearly localized until the late embryonic threefold stage, just before hatching (Fig. 3B). Thus, SAM-10 translocated into the nucleus in embryonic animals, well before PLM synaptic branches have even formed in early larval stage animals, indicating that SAM-10 nuclear localization is not driven by pre- and postsynaptic cell contact.

**SAM-10 and LDB-1 function coordinately to regulate PLM synaptic differentiation**

In vertebrates, LDB-1 binds SSDP and plays important roles in regulating SSDP activities (Chen et al., 2002; Enkhmandakh et al., 2006; Nishioka et al., 2005). We hypothesized that SAM-10 may function in concert with the *C. elegans* ortholog of LDB-1 in regulating PLM presynaptic differentiation. *Caenorhabditis elegans* ldb-1(ok896) deletion mutants exhibit early larval lethality. However, a small fraction of ok896 homozygous animals escape this lethality and grow up as sterile adults, allowing us to analyze PLM synaptogenesis in the ldb-1 mutant background. We found that these escapers displayed similar PLM developmental defects as sam-10(js94) mutants (Fig. 1D; Fig. 4A), including misalignment of active zones and synaptic vesicles, anterior branch points and varicosity extension. Thus, these two proteins probably function in the same signaling pathway to regulate PLM presynaptic differentiation. Moreover, using MCherry-SAM-10 as a reporter, we found that SAM-10 failed to translocate into the PLM nucleus in ldb-1 mutants and, instead, remained cytosolic (Fig. 4B,C). These data suggest that SAM-10 nuclear-localization, and thus its presumptive transcriptional activities, are ldb-1-dependent.

**SAM-10/LDB-1 functions independently of LimHD proteins**

Previous studies suggested that SSDP and LDB-1 function in a complex with LimHD to regulate different developmental pathways (Chen et al., 2002; Enkhmandakh et al., 2006; Nishioka et al., 2005). We tested whether such a complex might regulate PLM
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Gro and Unc, we found that (Fig. 5A). Severe PLM differentiation defects in mutants of all other known late aspects of PLM differentiation by testing loss-of-function therefore asked if other LimHD proteins are involved in regulating mec-3 gene transcription. We found that, although LDB-1, we examined the role of these genes in regulating further confirm that MEC-3 acts distinctively from SAM-10 and 1, disruptions of which showed no such differentiation defects. To made it difficult to examine PLM late specifications, and also various phenotypes observed in sam-10 and ldb-1 animals including Gro and Unc, we found that mec-3 mutant phenotypes were distinct (Fig. 5A). Severe PLM differentiation defects in mec-3 mutants made it difficult to examine PLM late specifications, and also indicated that MEC-3 functions differently from SAM-10 and LDB-1, disruptions of which showed no such differentiation defects. To further confirm that MEC-3 acts distinctively from SAM-10 and LDB-1, we examined the role of these genes in regulating mec-7 gene transcription. We found that, although mec-7 gene transcription is disrupted in mec-3 mutants (Duggan et al., 1998), it was not obviously affected in either sam-10 or ldb-1 mutants (Fig. 5A). We therefore asked if other LimHD proteins are involved in regulating late aspects of PLM differentiation by testing loss-of-function mutants of all other known C. elegans LimHD genes: lin-11, ttx-3, ceh-14, lim-4, lim-6, lim-7, lim-8 and lim-9 (Hobert and Westphal, 2000; Qadota et al., 2007). Surprisingly, none of them showed similar PLM synaptogenesis defects to sam-10 (Fig. 5B). These observations challenge the simple model of SSDP-LDB-1-LimHD acting as a functional module, and suggest that LimHDs are probably dispensable for the SSDP-LDB-1 function in regulating PLM differentiation.

**SAM-10 regulates PLM synaptic differentiation by suppressing prk-2 expression**

Previous studies and our observations of SAM-10 nuclear-localization suggest that SAM-10 might regulate PLM synaptogenesis by modifying gene expression. Therefore, we looked for downstream targets by analyzing the transcription profile changes induced by sam-10 mutations. Because PLM synaptic differentiation occurs during the early L1 stage (Schaefer et al., 2000), we assumed that transcript levels at this developmental stage would best represent the gene expression profile involved in PLM synaptogenesis. Among regulated genes revealed by our L1 larval stage microarray analysis (see Table S1 in the supplementary material), we focused on the gene prk-2, the expression of which is dramatically increased in sam-10(js94) mutants. This upregulation was further confirmed by real-time RT-PCR (Fig. 6A).

Previous studies suggested that the prk-2 gene is involved in regulating neuronal specification in C. elegans (Sieburth et al., 2005). We examined PLM synaptic morphology and neurite branch position in loss-of-function prk-2 alleles pk278 and ok3069 (see Fig. S6A in the supplementary material). Interestingly, prk-2 mutants seemed grossly normal in PLM synapse formation and neurite branch positioning (Fig. 1D,H; Fig. 6F,G, and data not shown). Thus, prk-2 is not required as a positive regulator of PLM synaptogenesis.

Because prk-2 transcription was increased in sam-10 mutants, defects in sam-10 mutants may result from prk-2 overexpression. If so, loss-of-function prk-2 mutations would be predicted to suppress these defects. We tested this hypothesis by analyzing the morphology of synaptic varicosities of ALMs and PLMs in a sam-10(js94); prk-2(pk278) double mutant background. We found that prk-2 loss-of-function mutations significantly suppressed synaptic defects caused by sam-10 mutations (Fig. 1D,H; Fig. 6B). Suppression by prk-2 mutations was incomplete, indicating that there are probably other SAM-10 regulated factors modifying synapse differentiation. Interestingly, prk-2 mutations did not suppress other sam-10 phenotypes (anterior branch points, Unc, Dpy or Gro) (see Fig. S6B in the supplementary material, and data not shown), suggesting that SAM-10 regulates these developmental events independently of prk-2 transcriptional regulation.

To further confirm that increased prk-2 expression is causal to the PLM synaptic phenotypes of sam-10, we tested whether overexpression of prk-2 in wild-type animals results in sam-10-like phenotypes. By overexpressing prk-2 pan-neuronally (using a rab-3p-prk-2 transgene) or in PLM neurons (using a mec-7p-prk-2
transgene), we found that prk-2 overexpression caused PLM neurite overextension defects similar to those of sam-10 mutants (Fig. 6C,D,E). Upon examining localization of synaptic vesicle and active zone markers, we found that the vesicle marker GFP-RAB-3 was broadly distributed throughout these extended varicosities, but the active zone marker remained punctate (see Fig. S6C,D in the supplementary material). Several possibilities could account for the fact that prk-2 overexpression did not precisely recapitulate the sam-10 PLM synaptic phenotype, including differences in the levels or temporal kinetics of PRK-2 expression, or the possibility that SAM-10 probably regulates additional signals besides PRK-2 to specify synapse differentiation. The Unc, Dpy, Gro and Egl defects seen in sam-10 mutants were not observed in prk-2 overexpressing animals. Taken together, these data suggest that downregulation of prk-2 gene expression by SAM-10 is a crucial specific step in synaptic differentiation in PLM neurons.

DISCUSSION

Even though distinct pathways of transcriptional regulation have been linked with synaptogenesis (Diaz, 2009; Kalinovsky and Scheiffele, 2004), a detailed understanding of how neurons modify gene expression to instruct neurite branch positioning and synapse differentiation is lacking. Using the C. elegans mechanosensory system as an in vivo model, we have identified a novel signaling pathway regulating synaptogenesis that is specifically mediated by LDB-1/SAM-10/PRK-2 (Fig. 7). However, PRK-2 seems not to be required for neurite branch positioning, a process also regulated by LDB-1/SAM-10. Elucidation of these molecular cascades reveal a new facet of the complex signaling networks that regulate synaptic differentiation and neurite branching.

SSDP regulates PLM neurite branch positioning and presynaptic differentiation intrinsically at the transcriptional level

Disruption of SSDP function results in embryonic lethality in Drosophila and mouse models (Chen et al., 2002; Enkhmandakh et al., 2006; Nishioka et al., 2005; van Meyel et al., 2003), limiting our ability to characterize its activities during later stages of development, including neurite branch positioning and synaptic differentiation. The survival of C. elegans sam-10 mutants allowed us to study the postembryonic functions of this protein. Our studies provide evidence that SAM-10 functions as an intrinsic signal in the nucleus to regulate neurite branch positioning and presynaptic differentiation (Fig. 7).

Regulation of the stereotypic pattern of neurite branching and growth is integral to a functional neuronal network. Owing to complexity of the mammalian nervous system, it is challenging to follow individual neurite branches, especially their spatial patterns, in vivo. Many studies on neurite branching have focused on the branching frequency. It is largely unknown how stereotypic
patterns of neurite branching are regulated. The consistent involvement in PLM specifications regulated by Caenorhabditis elegans positioning but not branching frequency (an in vivo model to study this process. We observed that SAM-10 synaptic components precedes pre-postsynaptic contacting. Further, we describe here occurs before pre- and postsynaptic contact, indicating that active transcription, translation and transport of synaptic components precedes pre-postsynaptic contacting. Further, we previously found that presynaptic specialization, characterized by active zone formation and synaptic vesicle accumulation, occurs within 30 to 60 minutes after pre- and postsynaptic contact (M. L. Nonet, unpublished observations), a time window allowing assembly of pre-existing synaptic components but not the synthesis and transport of new synaptic components. These observations suggest that at least some aspects of synapse development might be pre-programmed. Unlike the WNT and TGF-beta/BMP pathways, initiation of SAM-10 signaling appears to be independent of postsynaptic signals. We propose that SAM-10 signaling may function to pre-program PLM neuronal development for synaptogenesis.

**SAM-10 regulates PLM neurite branching and presynaptic differentiation coordinately with LDB-1, but independently of C. elegans LimHD orthologs**

SSDP-LDB-1-LimHD is hypothesized to function as a module to regulate many development processes, including neuronal development (Agulnick et al., 1996; Enkhmandakh et al., 2006; Mukhopadhyay et al., 2003; Nishioka et al., 2005; van Meyel et al., 2003). This complex is proposed based on the observations that: (1) LDB1 binds LimHD proteins; (2) LDB1 binds SSDP proteins; and (3) disruption of these components result in comparable embryonic lethality. However, no biochemical evidence directly shows the integrity of this complex. LDB1 has been shown to regulate neuronal development in Drosophila and mouse models. In mice, the ldb1 gene is expressed in the developing nervous system (Agulnick et al., 1996; Bulchand et al., 2003; Ostendorff et al., 2006). Detailed analysis revealed that reductions in ssdp expression or ldb1 ablation cause remarkably similar brain developmental defects, shown by various brain regional molecular markers such as Six2 (forebrain marker), En2 (mid-hindbrain boundary marker) and Krox20 (hindbrain marker) (Mukhopadhyay et al., 2003; Nishioka et al., 2005). Similar to its mammalian orthologs, Drosophila Chip (ortholog of LDB1) is expressed in the developing nervous system (Morcillo et al., 1997; van Meyel et al., 2000). Loss-of-function Chip mutations result in defective neurotransmitter production and axon guidance (van Meyel et al., 2000). Whereas LDB-1 activities are proposed to be associated with LimHD proteins, there is also some evidence to show that LDB1 may sometimes function independently of LimHD proteins. For example, during mouse late embryonic brain development, LDB1 shows a different expression pattern from the LimHD proteins (Bulchand et al., 2003). Similarly, Drosophila Chip appears to have broader activities than those mediated by interactions with LimHD proteins (Morcillo et al., 1997). These studies suggest that LDB1 functions with SSDP to regulate neuronal development, and that at least some aspects of this regulation are LimHD independent.

In this study, although we show that SSDP functions coordinately with LDB-1 to regulate PLM development, our phenotypic analyses suggest that this regulation is independent of known C. elegans LimHD proteins (Fig. 7). However, because mec-3 loss-of-function disrupts mechanosensory cell fate specification, a prelude to synapse formation, we cannot exclude the possibility that MEC-3 may play a role in PLM neurite branch positioning and presynaptic differentiation regulated by SAM-10/LDB-1.

**SAM-10 regulates PLM synaptic differentiation by suppressing prk-2 expression**

In searching for SAM-10 downstream targets, we have shown that SAM-10 regulates PLM synaptic differentiation by inhibiting prk-2 transcription. prk-2 encodes a C. elegans

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**Fig. 5. Caenorhabditis elegans LimHD genes tested are not involved in PLM specifications regulated by sam-10/ldb-1.**

(A) Distinctive phenotypes of mec-3, sam-10 and ldb-1 mutants.

(B) Effects of Lim-HD gene mutations on PLM synaptic branch positioning and synaptic varicosity extension. All varicosity extensions of lim mutants fall in the ‘medium extension’ class (see Materials and methods). lin-11(n389) causes a dramatic increase of varicosity extension. However, a close look revealed that this diffusion appears different from extended varicosities in sam-10(js54); they are more regular and even in shape and shorter than sam-10(js54) varicosities. Plus, we failed to detect UN-11 expression in PLM neurons, using lyIs32 (whole lin-11:gfp integrant 2013, a gift from Piali Sengupta). We believe that varicosity extension is probably due to VNC defects in lin-11(n389) (Hutter, 2003). Varicosity extensions in other mutants are similar to these in lin-11(n389), albeit at lower frequency as shown in the figure. mec-3 mutants are not scored for PLM synaptic varicosity morphology owing to defective PLM neuronal differentiation. ND, not determined.

<table>
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<tr>
<th>Gene</th>
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* Morphology at hatch
** Tested with /ldb1

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**Fig. 6.** SAM-10 regulates PLM synaptic differentiation by suppressing prk-2 expression. (A) Increased prk-2 transcription in sam-10(js94) revealed by microarray and real-time RT-PCR assays. act-1 is used as a control. Student’s t-test, *P<0.05, **P<0.01, four biological repeats for microarray assay, and three repeats for real time RT-PCR assay. Error bars represent s.d. (B) Loss-of-function prk-2 mutations suppress PLM synaptic defects of sam-10(js94) mutants. PLM synaptic varicosities in different genetic backgrounds are scored blindly by their length; length of wild-type varicosities (~5 μm) is defined as normal; twofold longer (~10 μm) as medium extension; and threefold longer or more (>15 μm) as severe extension (see also Materials and methods). Fisher’s exact test; **P<0.01; n=30 per group. (C-G) PLM synaptic varicosity pattern, represented by GFP-RAB-3, in wild-type (C), rab-3(pk278) transgenic (D), mec-7,prk-2 transgenic (E), prk-2(pk278) (F) and prk-2(ok3069) (G) animals. Arrows, PLM synaptic varicosities. Scale bar: 10 μm.

Fig. 7. Model of SAM-10 signaling pathway. SAM-10 is translocated into the nucleus in an LDB-1-dependent manner. In the nucleus, SAM-10 regulates PLM synaptic differentiation and neurite branch positioning, presumably by regulating gene expression. SAM-10 regulation of synaptic differentiation is mediated at least partially by suppressing prk-2 transcription.

Induction of LTP is accompanied by synaptic structural plasticity, which is characterized by a dramatic increase in the proportion of axon terminals contacting multiple dendritic spines (Toni et al., 1999). It is likely that pim kinase genes, as immediate early genes induced by LTP-production stimuli, are involved in inducing synaptic structural plasticity by regulating presynaptic varicosity remodeling. In *C. elegans*, PLM synaptic varicosity extension induced by prk-2 overexpression may be the result of cellular changes favoring formation of synaptic contacts with additional postsynaptic partners. Although *C. elegans* PRK-2 functions in de novo synaptogenesis and vertebrate Pim kinase functions in synaptic remodeling, these two processes probably share many features in common. Crucial to elucidating this molecular pathway will be identification of PRK-2 targets. Our system provides several genetic avenues to address this challenge.

Taken together, our observations suggest that the LDB-1/SAM-10/PRK-2 pathway represents a novel transcriptional mechanism that regulates synaptic differentiation in the *C. elegans* mechanosensory system (Fig. 7). However, it is not the first kinase pathway identified that regulates synaptogenesis. An RPM-1/MAP kinase also plays crucial roles in mechanosensory synapse development. That both signaling systems rely on kinases provides a simple mechanism for cross regulation of the two pathways. Whereas the severity and pleiotropy of the sam-10 mutants complicates direct assessment of interactions between these pathways, cell specific transgenic approaches should eventually permit this analysis. Further investigation of this novel pathway should provide a new perspective on regulation of presynaptic differentiation.

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