

Supplemental information

Table S1. Mutant alleles and transgenes used in this study

A. Mutant alleles

Allele	Reference
<i>sax-7(nj48)</i>	(Sasakura et al., 2005)
<i>dma-1(wy686)</i>	(Liu and Shen, 2012)
<i>mnr-1(wy758)</i>	This study

B. Integrated transgenes

Allele	Chromosome	Constructs	Co-injection marker
<i>wyIs378</i>	X	pOL020, pOL090	
<i>wyIs369</i>	IV	pOL071	<i>Pmyo-2::mCherry</i>

C. Extrachromosomal arrays

Allele	Constructs	Co-injection marker
<i>wyEx3869</i>	pRP13	<i>Pmyo-2::mCherry</i>
<i>wyEx4003</i>	Engineered fosmid WRM063aC06	<i>Podr-1::gfp</i>
<i>wyEx5668</i>	pXD65	<i>Podr-1::gfp</i>
<i>wyEx5776</i>	Engineered fosmid WRM0618aD06	<i>Podr-1::gfp</i>
<i>wyEx5134</i>	pXD13+pXD26+pOL036	<i>Podr-1::rfp</i>
<i>wyEx5781</i>	pXD38+pXD86+pOL036	<i>Podr-1::gfp</i>
<i>wyEx5937</i>	pXD86	<i>Pmyo-2::mCherry</i>
<i>wyEx5950</i>	pXD20+pXD97	<i>Podr-1::gfp</i>
<i>wyEx5946</i>	pXD105+pXD106	<i>Podr-1::gfp</i>
<i>wyEx5948</i>	pXD86+pXD97+pXD105+pXD106	<i>Podr-1::gfp</i>
<i>wyEx4897</i>	pOL036+pOL057	<i>Podr-1::rfp</i>
<i>wyEx5938</i>	pXD103	<i>Podr-1::gfp</i>
<i>wyEx6039</i>	pXD118	<i>Podr-1::rfp</i>
<i>wyEx4286</i>	pOL035	<i>Podr-1::rfp</i>
<i>wyEx5790</i>	pXD46+pOL036	<i>Podr-1::gfp</i>
<i>wyEx6034</i>	pXD91+pOL036	<i>Podr-1::rfp</i>

Table S2. Plasmids used in this study

A. Plasmids

Plasmid	Description	Note
pOL020	<i>ser2prom3::myr-gfp</i>	
pOL035	<i>ser2prom3::dma-1::gfp</i>	
pOL036	<i>ser2prom3::myr-mCherry</i>	
pOL057	<i>Pdpy-7::sax-7s::gfp</i>	
pOL071	<i>Pnhr-81::sax-7s</i>	
pOL090	<i>Prab-3::myr-mCherry</i>	

pRP13	<i>Pdpy-7::sax-7s</i>	A gift of Oliver Hobert. (Pocock et al., 2008)
pXD13	<i>Prab-3::cfp</i>	
pXD20	<i>Pmec-17::BFP</i>	
pXD26	<i>Pdpy-7::sax-7s::yfp</i>	
pXD38	<i>Pmec-17::sax-7s::yfp</i>	
pXD46	<i>Pdpy-7::sax-7sΔIg</i>	All 4 Ig domains of SAX-7 deleted by yeast recombineering using primers 5'-ttctgtcacaagtttgaaccacgcagagtgaacagccacaggaacatcattcacgtactgctctgttgg -3' and 5'-gatgttctgtggctgttca-3' (Kevin R. et al., 1997)
pXD65	<i>Pdpy-7::mnr-1</i>	cDNA of mnr-1 cloned with primers 5'-ATGATGATATCAATACTATTGGTTT -3' and 5'-TTAAAGTAGGTAGATCATTAGGAG -3'
pXD86	<i>Pmec-17::mnr-1</i>	
pXD91	<i>Pdpy-7::sax-7sΔFnIII</i>	All 5 FnIII domains of SAX-7 deleted by yeast recombineering using primers 5'-aacatcctaaattgaatttga -3' and 5'-ctaaattggatcaagttgaaaaggaaatcaaaattcaatttaaggatgttggtgaaacgacgaaaacgt -3' (Kevin R. et al., 1997)
pXD97	<i>Pmec-17::sax-7s</i>	
pXD103	<i>Pdpy-7::mnr-1ΔTM</i>	
pXD105	<i>Punc-47::mnr-1</i>	
pXD106	<i>Punc-47::sax-7s</i>	
pXD118	<i>Pdpy-7::mCherry::mnr-1</i>	

B. Engineered fosmids

Construct	Original fosmid
<i>Psax-7::sax-7::gfp::sl2::mCherry</i>	WRM063aC06
<i>Pmnr-1::mnr-1::gfp::sl2::mCherry</i>	WRM0618aD06

Table S3. S2 cell aggregation assay

A. Plasmids used in S2 cell transfection

Plasmid	Description
pAWG	<i>Pactin::gfp</i>
pAWR	<i>Pactin::rfp</i>
pXD49	<i>Pactin::sax-7s::gfp</i>
pXD54	<i>Pactin::dma-1::rfp</i>
pXD85	<i>Pactin::mnr-1::gfp</i>
pXD53	<i>Pactin::sax-7s::HA</i>
pXD95	<i>Pactin::dma-1 ecto-domain::myc</i>
pXD84	<i>Pactin::mnr-1::Flag</i>

pXD130	<i>Pactin::sax-7sΔIg::gfp</i>
pXD116	<i>Pactin::sax-7sΔFnIII::gfp</i>

B. S2 cell aggregation assay

Green cells	Red cells	Result
GFP (pAWG)	DMA-1::RFP (pXD54)	No aggregation
SAX-7::GFP(pXD49)	RFP (pAWR)	No aggregation
MNR-1::GFP(pXD85)	RFP (pAWR)	No aggregation
SAX-7::FP(pXD49)	DMA-1::RFP (pXD54)	No aggregation
MNR-1::GFP(pXD85)	DMA-1::RFP (pXD54)	No aggregation
SAX-7::GFP(pXD49) + MNR-1::GFP(pXD85)	DMA-1::RFP (pXD54)	Aggregation
SAX-7ΔIg::GFP(pXD130) + MNR-1::GFP(pXD85)	DMA-1::RFP (pXD54)	Aggregation
SAX-7ΔFnIII::GFP(pXD116) + MNR-1::GFP(pXD85)	DMA-1::RFP (pXD54)	No aggregation

Supplemental figure legends

Figure S1. Phylogenetic analysis of MNR-1 and schematic structures of SAX-7, MNR-1 and DMA-1 proteins. Related to Figure 1.

(A) Phylogenetic tree of *C. elegans* MNR-1 and its orthologues in other species. (B) Schematic of SAX-7, MNR-1 and DMA-1 proteins. Ig: Immunoglobulin domain. FnIII: Fibronectin III domain. F: FERM binding motif. A: Ankyrin binding motif. P: PDZ binding motif. LRR: Leucine rich repeat. LRR-NT: LRR N-terminal domain. LRR-CT: LRR C-terminal domain.

Figure S2. SAX-7 was expressed and localized early in development independent of MNR-1 or PVD dendrites. Related to Figure 2 and Figure 3.

(A-B) SAX-7 was expressed and subcellularly localized in hypodermal cells in (A) L2 and (B) L3 stages. (C-E) The expression and localization of SAX-7 did not depend on MNR-1 or PVD dendrites. (C) Fluorescent image showing disrupted PVD morphology in *mnr-1(wy758)* mutant. (D) SAX-7 localization in the hypodermal cells revealed by *Pdpy-7::sax-7s::gfp* was not altered in *mnr-1(wy758)* mutants despite the largely abnormal PVD structure. (E) Overlay of (C) and (D). Scale bar: 10μm

Figure S3. MNR-1 was partially secreted. Related to Figure 5.

(A) Expressing MNR-1 without its transmembrane domain partially rescued the “T” formation phenotype of *mnr-1(wy758)*. (B) Full length MNR-1 tagged with mCherry at its N-terminus could be detected in the ceolomocytes. Arrowheads: Ceolomocytes.

Figure S4. PVD dendrites in *dma-1* mutants did not follow PLM and ALM neurons expressing SAX-7 and MNR-1. Related to Figure 6.

(A-C) PLM overexpression of SAX-7 and MNR-1 failed to alter dendritic morphology in *dma-1(wy686)* mutants. (A) PLM and ALM neurons labeled by *Pmec-17::sax-7::yfp*. (B) Dendritic structure of *dma-1(wy686)* mutant worms was unaltered by overexpression of SAX-7 and MNR-1. No additional T's were formed when 2° PVD dendrites made contact with the PLM and ALM neurons. (C) Overlay between (A) and (B). Scale bar: 10 μm.

Figure S5. DMA-1 was the neuronal receptor for SAX-7 and MNR-1. Related to Figure 6.

(A) PVD dendritic phenotype of *dma-1(wy686); mnr-1(wy758)* mutants were identical to that of *dma-1(wy686)* single mutants. (B) PVD dendritic phenotype of *dma-1(wy686); sax-7(nj48); mnr-1(wy758)* mutants were identical to that of *dma-1(wy686)* single mutants. (C) Over-expressing DMA-1 in PVD caused overbranching. (D-E) PVD morphology of *sax-7(nj48)* mutant (D) or *mnr-1(wy758)* mutant (E) was not altered by DMA-1 overexpression. Scale bar: 10 μm.

Figure S6. Structure-function analysis of SAX-7. Related to Figure 7.

(A) Summary of structure-function analysis of SAX-7. (B) SAX-7ΔIg could rescue the PVD dendrite phenotype of *sax-7(nj48)* mutant. Scale bar: 10μm (C) SAX-7ΔFnIII failed to rescue. (D) S2 cells transfected with *sax-7ΔIg::gfp* and *mnr-1::gfp* strongly aggregated with cells expressing DMA-1-RFP. Scale bar: 100 μm (E) Cells transfected with *sax-7ΔFnIII::gfp* and *mnr-1::gfp* failed to aggregate with cells expressing DMA-1-RFP. (F) Schematic representation of proposed model: SAX-7 and MNR-1 formed pre-patterned lines in hypodermal cell (left). When PVD 2° branches expressing DMA-1 reached the SAX-7 and MNR-1 enriched line (middle), 3° branches formed and grew along the pre-patterned line. Thus the precise location of branch formation and growth direction was specified through interaction between pre-patterned cell adhesion molecules and their neuronal receptor.

Movies S1-S4. Time-lapse movies of PVD dendrite development. Related to Figure 4.

- S1. Development of WT PVD.
- S2. Development of PVD dendrites in *sax-7(nj48)* mutant.
- S3. Development of PVD dendrites in *mnr-1(wy758)* mutant.
- S4. Development of PVD dendrites in *dma-1(wy686)* mutant

Supplemental experimental procedures

Fluorescence microscopy and confocal imaging

Images of fluorescent proteins were captured in live animals using a Plan-Apochromat 40x/1.3 objective on a Zeiss LSM710 confocal microscope (Carl Zeiss). Worms were immobilized on 2% agarose pads using a mixture of 225 mM 2,3-butanedione monoxime and 2.5 mM levamisole (Sigma-Aldrich). Z-stacks were collected and the maximum intensity projection was used for additional analysis.

S2 cell aggregation and co-IP assays

S2 cells were transfected with *Pactin::sax-7::gfp*, *Pactin::mnr-1::gfp*, *Pactin::sax-7::gfp* +*Pactin::mnr-1::gfp*, or *Pactin::dma-1::rfp*. Cells transfected with *Pactin::gfp* and *Pactin::rfp* were used as controls. 3 days after transfection, cells were washed with 5 ml phosphate buffered saline (PBS) and resuspended in S2 medium at 10^6 cell/ml. 500 μ L of green cells were mixed with 500 μ L red cells and rotated at 30 rpm for 3 hours at room temperature. 3 μ L of each mixture was immediately spotted on glass slides for imaging and quantification.

Similarly, for co-IP assays S2 cells were transfected with *Pactin::sax-7::HA*, *Pactin::mnr-1::FLAG*, both *Pactin::sax-7::HA* and *Pactin::mnr-1::FLAG*, or *Pactin::dma-1::ecto-myc*. 3 days after transfection, cells transfected with SAX-7 and/or MNR-1 were collected and lysed in lysis buffer (50mM Tris-HCl pH 7.4, 10mM MgCl₂, 150mM NaCl, 1mM EGTA, 10% Glycerol, 0.5% Nonidet P-40 and protease inhibitor (Roche)). Cultured medium from *Pactin::dma-1::ecto-myc* transfected cells was collected. The cell lysates or cultured medium containing the desired proteins were mixed with anti-HA antibody coated agarose beads (Sigma) and incubated at 4°C for 3 hours with rotation and washed thoroughly with lysis buffer. Proteins were eluted at 65°C using 2% SDS elution buffer and detected using western blot analysis with mouse antibody to HA (1:1000, Roche), rabbit antibody to Myc (1:2000, Santa Cruz Biotechnology), mouse antibody to FLAG (1:5000, Sigma) and HRP-conjugated goat antibodies to mouse or rabbit (1:20,000, Jackson Immuno Research).

Supplemental references

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