The actin nucleator Spire cooperates with Rab11 to initiate nascent dendrite branches.

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1 Abstract

Dendrites form arbors whose size, shape and complexity define how neurons cover their

receptive territories. Actin dynamics contribute to growth and remodelling of dendrite arbors.

Here we examined how Spire, a conserved actin nucleation factor, promotes formation of

new branches in vivo. In live imaging of Drosophila class IV dendritic arborisation (c4da)

neurons, Spire was observed at new sites of branch initiation, where it assembled new actin

polymer prior to filopodial outgrowth. For dendrite arborization, Spire required intact

structural domains to nucleate actin and target the secretory network, and Spire interacted

with Rab11 GTPase, a key regulator of recycling endosomes. Together, these findings

support a model that Spire cooperates with Rab11 to promote new dendrite branches by

linking localized actin assembly with intracellular trafficking of endosomes that deliver lipids

and cargoes to fuel protrusive outgrowth of nascent dendrites.

Keywords: dendrite, neuron, development, nervous system, actin, Drosophila,

endomembrane system, secretory network, recycling endosome

17 Introduction

Different types of neurons are characterized by dendrites with distinct tree-like

branching patterns that influence the number, strength, and integration of sensory or synaptic

inputs into neurons (Grueber et al., 2005; Lefebvre et al., 2015; London and Hausser, 2005). A

major gap remains in our understanding of the spatiotemporal control of cytoskeletal

remodelling responsible for dendrite morphogenesis during development (Lefebvre, 2021).

Understanding how dendrites are shaped during development is essential to gain full insight

into the construction of neural circuits that underlie animal survival, behaviors, learning, and

memory (Luo, 2021). The growth and structural remodelling of dendrite arbors requires complex spatial and temporal regulation of actin dynamics (Konietzny et al., 2017), involving coordination of specific proteins to nucleate and elongate actin filaments (Rottner et al., 2017; Siton-Mendelson and Bernheim-Groswasser, 2017). Furthermore, to cope with their size and complexity, dendrites have specialized arrangements of secretory network organelles for the biogenesis of cargo-carrying vesicles and their transport to the cell surface (Kennedy and Hanus, 2019). Given the importance of actin and the secretory network for dendrite development and function, it is important to clarify how they are coordinated to initiate new dendrite branches in vivo (Lanoue and Cooper, 2019; Lefebvre, 2021).

New dendrite branches arise from actin-rich filopodia that rapidly extend from initiation sites along established branches (Lanoue and Cooper, 2019). Dendrite filopodia are structurally distinct from conventional filopodia, with an unusual network-like cytoskeletal organization characterized by both branched and linear filaments of mixed polarity (Korobova and Svitkina, 2010), suggesting involvement of multiple actin regulatory proteins with distinct activities. Few studies have identified specific actin regulators involved in forming new branches (Hou et al., 2015; Nithianandam and Chien, 2018; Shi et al., 2021; Sturner et al., 2022; Sturner et al., 2019; Zou et al., 2018), and none have pinpointed their regulation of actin to the location and timing of nascent branch outgrowth. In sensory neurons of living Drosophila larvae, the locations of dendrite filopodia initiation sites are pre-figured by patches of actin polymer (Andersen et al., 2005; Nithianandam and Chien, 2018; Sturner *et al.*, 2019), as has been proposed for dendrite filopodia in the mouse brain also (Willig et al., 2014). In Drosophila larvae, class IV dendritic arborization (c4da) neurons provide an excellent model to study the roles of actin regulators in the development of dendrite arbors in vivo (Grueber et al., 2002; Medina et al., 2006; Nagel et al., 2000). In c4da neurons, formation of new dendrites requires the Arp2/3 actin nucleator complex under control of the activator WAVE and the small GTPase

Rac1 (Sturner *et al.*, 2019). New dendrite formation also involves F-actin severing by Twinstar/Cofilin in the production of "blobs" of pre-assembled actin polymer, which move bidirectionally within dendrites, pause before filopodium outgrowth, and appear to contribute F-actin into the nascent branch (Nithianandam and Chien, 2018). It is unclear whether stationary actin patches and motile actin blobs are features of convergent or parallel processes to initiate dendrite branches (Pai and Moore, 2018). Moreover, the factor(s) that specify the location and timing of filopodial outgrowth from actin patches and blobs have not been defined.

Here we explored the role of Spire (Spir), a conserved multi-domain actin nucleation factor. We previously showed that knockdown of Spir with RNA interference (RNAi) in cd4da neurons led to reduced number of terminal dendrite branches and compromised the ability of these nociceptive neurons to elicit larval escape from noxious stimulus (Ferreira et al., 2014a). Spir is known to co-operate with Fmn-family formins, which are also actin nucleators, during Drosophila and mouse oogenesis (Manseau and Schupbach, 1989; Pfender et al., 2011; Quinlan et al., 2005; Vizcarra et al., 2011). Spir has four WASP homology 2 (WH2)-domains for actin nucleation, a KIND domain for interaction with Capu/Fmn, a modified FYVE (mFYVE) domain to target vesicles of the secretory network, and a SPIR-box with potential to interact with Rab GTPases (Kerkhoff et al., 2001; Quinlan *et al.*, 2005; Quinlan et al., 2007; Tittel et al., 2015), which play roles in vesicle sorting and transport (Kiral et al., 2018). Our findings indicate that Spir stimulates new actin polymer just prior to filopodial outgrowth and that Spir cooperates with Rab11 to promote new dendrite branches, supporting a model in which Spir and Rab11 link localized actin assembly with recycling endosomes that deliver lipids and cargoes to nascent dendrites.

Results

Spir is required for localized F-actin synthesis just prior to outgrowth of new dendrite branches.

The development of Drosophila c4da neuron dendrites begins in embryogenesis and continues in larval stages, with arbors growing in the larval body wall between muscles and epithelial cells (Grueber *et al.*, 2002). To reveal actin dynamics leading up to the protrusion of dendrite filopodia, we acquired time-lapse movies (5 minutes (min) each) in second instar (L2) larvae, capturing F-actin (labeled with LifeAct::GFP) within c4da neurons (labeled with ppk-CD4::tdTom) (Fig. 1A, B). In control animals (+/+ and *spir^{2F}*/+ heterozygotes) LifeAct::GFP was seen in stationary puncta that appeared *de novo* at the site shortly before initiation (Fig. 1A) or in pre-formed actin blobs that moved to the branching site prior to branch initiation (Fig. 1B). Instances where a new filopodium grew from a site where an actin punctum existed in the first frame of the movie were disregarded because the movie did not capture the origin of the actin punctum. Like the LifeAct::GFP signal that arose de novo at branch initiation points, the LifeAct::GFP signal from pre-formed actin blobs became more intense just prior to branch initiation and then, upon outgrowth, LifeAct::GFP signal extended into the protruding nascent branchlet (Fig. 1A, B). The intensity increase of LifeAct::GFP was specific to branch initiation points; it did not occur at nearby puncta.

To confirm expression of the actin nucleator Spir in c4da neurons, we produced a *GAL4* line inserted in the *spir* locus (*spir^{GAL4}*) and used it to drive *UAS-mCD8::GFP*, which encodes a fluorescent reporter targeted to the plasma membrane. *spir^{GAL4}* was expressed in c4da neurons marked by ppk-CD4::tdTom and other sensory neurons in the larval body wall (Fig. 1C). We confirmed this using immunohistochemistry (IHC) with newly generated anti-Spir sera (Fig. S1A), consistent with our previous research (Ferreira *et al.*, 2014a).

To study how complete loss of *spir* affects actin accumulation and dendrite arborization, we examined *spir¹* and *spir²F* mutants, which harbor point mutations causing premature stop codons predicted to truncate the Spir protein within the KIND domain (Fig. 1D) (Wellington et al., 1999). We studied these mutant alleles in combination with a deficiency (*spir^Df*) to control for effects of genetic background in homozygotes. Using antiserum directed to an epitope C-terminal to these mutations, we confirmed that *spir* mutants lack Spir expression with IHC in larval sensory neurons (Fig. S1A), and with western blot analysis of adult brain lysates (Fig. S1B). In *spir* mutants, overall levels of LifeAct::GFP expression in dendrites appeared lower than in controls, consistent with our previous observations upon Spir knockdown with RNAi (Ferreira *et al.*, 2014a). However, the LifeAct::GFP signal remained strong enough to monitor actin at sites of new branch initiation with time-lapse imaging.

In contrast to controls, in *spir²F/spir^Df* mutant larvae we observed no instances where actin polymer appeared *de novo* prior to branch initiation (Fig. 1F). All new dendrite filopodia stemmed from pre-formed actin blobs that moved to the initiation site (Fig. 1E). We measured LifeAct::GFP fluorescence intensity at branch initiation sites. In controls (+/+) the signal in both actin blobs and stationary actin puncta increased roughly two-fold on average in the 60s prior to outgrowth and remained at the elevated intensity for at least 60s afterward (Fig. 1G). In contrast, in *spir²F/spir^Df* mutants the intensity of LifeAct::GFP in actin blobs did not increase prior to branch initiation or afterward (Fig. 1E,G).

Localization of Spir in developing dendrites, and requirement of Spir for new branch formation.

Using IHC to examine *spir¹/+* controls, we found that the cell bodies and proximal dendrites of c4da neurons in L3 larvae were immunopositive for Spir (Fig. S1A), but we did not detect Spir in distal dendrites with our new antisera. However, upon over-expressing a

UAS-Spir::GFP transgene (Fig. 1D) in c4da neurons with *ppk-GAL4,* the anti-Spir serum

strongly labelled the cell body and discrete puncta in proximal and distal dendrites (Fig. S1C).

The coordinates of Spir::GFP puncta were plotted relative to the skeletonized centerlines of

CD4-tdTom labeled dendrites. Spir::GFP puncta were seen in all dendrite shafts, some branch

points (28%), but few branch tips (6%) (Fig. S1D,E). Consistent with this, most Spir::GFP

puncta were found along dendrite shafts (57%) and at branch points (36%) (Fig. S1F).

Time-lapse movies (~1 frame/2 sec for >5 min, L2 larvae) showed a pattern for the GFP

tag on Spir::GFP (Fig. 1H) that was like what we observed in fixed L3 larvae (Fig. S1E).

Interestingly, some Spir::GFP puncta remained stationary while others were steadily motile or

moved in a saltatory manner with occasional pauses (Fig. S1F). Motile puncta were often

smaller and rounder, while stationary puncta could be larger and irregular in shape.

Every nascent branch we observed in our movies from control larvae (+/+, L2) had a

Spir::GFP punctum stationed precisely at (68% of branches) or near (< 1 µm, 32% of branches)

the initiation site prior to outgrowth (Fig. 1J). These puncta were seen to arrive from elsewhere

(30%, Fig. 1H, K) or were already at that site in the first frame of the movie (70%, Fig. 1I, K).

The interval of time from the appearance or arrival of a Spir::GFP punctum at the initiation site

until outgrowth showed a broad range (Fig. 1K). Spir::GFP intensity did not typically increase

prior to outgrowth but, in some instances (12%), a motile punctum of Spir::GFP combined with

one already stationed at the future initiation site. Spir::GFP puncta at or near (< 1 µm) branch

initiation sites were stably maintained throughout the process of filopodial outgrowth,

stabilization, or retraction, and Spir::GFP signal appeared to invade the filopodia as they grew

(Fig. 1I).

Terminal branches that existed at the beginning of each movie were monitored for their

subsequent dynamics in controls (+/+) and *spir²F/spirDf* mutants. Neither of these genotypes

affected the percentage of pre-existing branches that either extended, retracted, did both, or

remained static (Fig. S2A-D). We also compared the protrusive characteristics of nascent

branches in instances where actin (labelled with LifeAct::GFP) appeared de novo (seen in +/+

only) or after arrival of motile actin blobs (seen in +/+ and $spir^{2F}/spir^{Df}$ mutants). In both

genotypes, typical growth involved saltatory extensions and pauses. There were no differences

in the mean speed of outgrowth, the proportion of time spent paused between extensions, or

the maximum length of protrusion (Fig. S2E-G).

Importantly, the number of terminal dendrites/μm^2 was reduced in $spir^{2F}/spir^{Df}$ mutants

compared to heterozygous controls (Fig. 2A), as quantified per μm^2 in the first frame of each

of the time-lapse movies. Based on Spir::GFP localization and because Spir did not exhibit

obvious control over the dynamics of pre-existing terminal branches, we focused on new

branches. We found that the proportion of new branches formed during each movie was

reduced in $spir^{2F}/spir^{Df}$ mutants (Fig. 2B). Movies of c4da neurons expressing LifeAct::GFP

also showed that $spir$ mutants had reduced terminal dendrites/μm^2 (Fig S3A), fewer new

branches per movie (Fig. S3B), and no effect on branch dynamics (Fig. S3C-F), confirming

independently that Spir specifically influences the formation of new branches.

Consequences of Spir function for dendrite arborization in c4da neurons.

To explore Spir's role at initiation sites for nascent terminal dendrites, we compared

control heterozygotes ($spir^{2F}/+$) to $spir$ mutants ($spir^{2F}/spir^{Df}$) or $spir$ mutants rescued with

either Spir::GFP or Spir^{ABCD}::GFP. Spir^{ABCD}::GFP contains a series of 4 triple-alanine

substitutions in the WH2 domains that greatly diminish the ability of Spir to polymerize F-

actin *in vitro* (Quinlan *et al.*, 2005). In time-lapse movies of L2 larvae, the correct number of

terminal dendrites/μm^2 was rescued by expressing intact Spir::GFP in c4da neurons but not by

expressing Spir^{ABCD}::GFP (Fig. 2, indicating a role for Spir to establish the correct number of

terminal branches that depends on its ability to polymerize F-actin. The proportion of new

branches in each movie appeared to be rescued partially by Spir::GFP but also by

Spir^{ABCD}::GFP (Fig. 2B). We note the arbors were monitored for only 5 min in these movies,

a short window in an arborization process that takes several days. To gain a full view of the

effects of Spir on dendrite arborization, we examined images of fully developed c4da arbors in

L3 larvae (Fig. 2C), measuring the number of terminal dendrites (Fig. 2D), total arbor length

(Fig. 2E), and the area of the dendritic field (Fig. 2F). Compared to heterozygous controls, we

found that *spir* mutants (*spir^1/spir^{Df}* or *spir^{2F}/spir^{Df}*) had far fewer terminal branches (Fig. 2D).

As perhaps expected with such significant loss of branches, total arbor length was also reduced

(Fig. 2E). Dendritic field was not reduced in *spir^1/spir^{Df}* mutants, but 4 out of the 15 cells in

spir^{2F}/spir^{Df} mutants had fields that were unusually small, and so the average for cells of this

genotype was reduced compared to controls (Fig. 2F). When these 4 cells were removed from

the analysis to mitigate the potential effect of their small fields, the remaining *spir^{2F}/spir^{Df}*

mutant cells continued to display far fewer terminal branches than controls (Fig. S4A, B).

We also used modified Sholl analysis (Ferreira et al., 2014b; Sholl, 1953) to plot the

density profiles of dendrites within an arbor as a function of distance from the cell soma (Fig.

2G). The peak of maximum branch density (critical value) was significantly reduced in both

spir^1/spir^{Df} and *spir^{2F}/spir^{Df}* mutants (Fig. 2H and Fig. S4D). Selective expression of a *UAS-*

Spir::GFP transgene in c4da neurons with *ppk-GAL4* (Fig. 2C) fully rescued the number of

terminal branches in *spir^{2F}/spir^{Df}* mutants (Fig. 2D), and the Sholl critical value (Fig. 2H, Fig.

S4D). However, Spir::GFP did not fully rescue total arbor length (Fig. 1E, Fig S4C). It is

unlikely that incomplete rescue is due to inadequate Spir::GFP expression. Western blots (Fig

S1B) and IHC (Fig. S1C) showed the transgene was expressed at similar, and even higher,

levels compared to endogenous Spir. Thus, there is a possibility that additional cell types,

perhaps the surrounding epidermis or muscle cells of the larval body wall where Spir appeared

to be expressed (Fig. S1A, B), contribute to total arbor length. We conclude that Spir acts

within c4da neurons to establish the correct number of terminal dendrite branches, likely by

initiating the filopodial outgrowth necessary for nascent branches.

Each domain of Spir is required for dendrite arborization.

We next sought to determine the importance of the four identified protein domains of

Spir by testing if disruptive mutations in Spir::GFP (Fig. 1D) could rescue the correct numbers

of terminal branches in c4da neurons of *spir* mutants. In addition to the ABCD mutation in the

WH2 domains, we tested Y232K, a missense substitution in the KIND domain known to

abolish the interaction between Spir and the formin Cappuccino (Capu) in oocytes (Quinlan,

2013; Vizcarra *et al.*, 2011). We also tested ΔSB, a 20 aa deletion of the entire Spir-box domain

which has sequence similarity to the Rab effector protein Rabphilin3a suggesting it interacts

with Rab GTPases (Kerkhoff *et al.*, 2001). Finally, we tested C5,6S, a substitution of serine

residues for 2 key cysteines in the so-called modified FYVE (mFYVE) domain. FYVE

domains interact in lipid membranes with Phosphatidylinositol 3-phosphate (PtdIns3P), a

prominent component of the membranes in the endosomal system (Marat and Haucke, 2016).

The mFYVE domain in Spir binds less specifically to negatively charged lipids, including

PtdIns3P, and is required to localize to intracellular membranes (Tittel *et al.*, 2015).

The impact of each mutation was determined by expressing the transgenes in c4da

neurons (with *ppk-GAL4*) of *spir^{2F}/spir^{Df}* mutants. Compared with the intact Spir::GFP control,

none of these transgenes (Spir^{Y232K}::GFP, Spir^{ABCD}::GFP, Spir^{ΔSB}::GFP or Spir^{C5,6S}::GFP)

rescued the number of terminal dendrites per neuron (Fig. 3A), nor the Sholl critical value (Fig.

3B, Fig. S5A). When each of these transgenes was expressed in all neurons with *nSyb-GAL4*,

western blots of adult head lysates showed that none were expressed at lower levels than intact

Spir::GFP (Fig. 3C, D and Fig. S5B), whose levels were clearly enough to support rescue of

function. These results demonstrate that each domain contributes to Spir's role in controlling

dendrite branching.

The effect of each mutation (Y232K, ABCD, ΔSB, or C5,6S) on the distribution of

Spir::GFP in c4da neurons was examined in $spir^{2F}/spir^{Df}$ animals. Spir::GFP was found in

puncta at dendrite branch points, shafts and at branch tips (Fig. 3E), as it is in control animals

(Fig. 1H and Fig. S1E). None of the Y232K, ABCD, or C5,6S mutations had a dramatic effect

on this pattern of distribution (Fig. S5C). In contrast, Spir^{ASB}::GFP accumulated near the cell

soma and formed a more continuous than punctate pattern (Fig. 3E). Though this might be

explained in part by unusually high expression levels (Fig. 3C,D and Fig. S5B), these results

suggest that the SB domain is required for proper localization of Spir within c4da arbors.

Spir and Rab11 cooperate for dendrite arborization.

The pattern and motility of Spir::GFP puncta within dendrites of c4da neurons was

reminiscent of elements of the secretory network, where Rab GTPases including Rab11 and

Rab4 are key regulators of vesicle and cargo trafficking (Kiral *et al.*, 2018). Rab11 is associated

with the trans-Golgi network, post-Golgi, and recycling endosomes (Sonnichsen et al., 2000).

Upon co-expression in c4da neurons, Spir::GFP and Rab11::mCherry appeared to co-localize

within dendrites (Fig. 4A). Spir::GFP also appeared to co-label punctae with Rab4-mRFP in

dendrites (Fig. S6A), a marker of early endosomes. We focused on Rab11 because previous

studies show functional links between Spir and Rab11, in both oocytes and cultured cells

(Kerkhoff *et al.*, 2001; Pylypenko et al., 2016; Schuh, 2011). Rab11 is involved in regulated

movement of recycling endosomes towards the plasma membrane (Lasiecka and Winckler,

2011) and has been shown to traffic receptors and trans-membrane proteins necessary for

neurite outgrowth and remodelling (Eva et al., 2010; Park et al., 2004).

To test whether Spir and Rab11 can physically associate with one another *in vivo*, Spir-

tdTom was co-expressed with either Rab11::GFP or Capu::GFP (a positive control) in all

neurons using the *nSyb-GAL4* driver. From lysates of adult heads, co-immunoprecipitation (co-

IP) with anti-GFP labelled beads revealed that Spir::tdTom associates (Fig. 4B) with both

Rab11::GFP and Capu::GFP but not with Rab6-GFP (negative control, data not shown). This

suggests that Spir selectively associates with Rab11 in protein complexes in neurons.

We tested whether loss of Rab11 would affect the distribution of Spir::GFP, using *ppk-*

GAL4 to drive the expression of a Rab11-dsRNAi in c4da neurons. Compared to controls (Fig.

S6B), knockdown of *Rab11* mRNA in c4da neurons resulted in reduced numbers of branches

(Fig. S6C), as published previously (Kramer et al., 2019). However, the distribution of

Spir::GFP within arbors was seemingly unaffected by loss of *Rab11* (Fig. S6C), suggesting

that Rab11 is not required for Spir localization within c4da neurons.

Finally, we used a genetic interaction approach to test whether Spir might operate in

the same molecular pathway as Rab11 to control dendrite branching. The arbors of c4da

neurons in trans-heterozygotes for mutant alleles of both *spir* and *Rab11* were compared to

control heterozygotes for either mutation alone (Fig. 4C). We observed reduced numbers of

terminal branches (Fig. 4D) and reduced arbor length (Fig. 4E) only in the trans-heterozygotes

but dendritic field was unaffected (Fig. 4F). The Sholl profile also revealed reduced branching

(Fig. 4G). Together, these results provide evidence that Spir and Rab11 interact with one

another functionally in neurons. We cannot say if the interaction is direct or indirect, but we

conclude that they act in a common molecular pathway to regulate dendrite branching.

Discussion

We found that Spir promoted the formation of new dendrite branches in vivo by

stimulating localized assembly of actin polymer in the seconds leading up to filopodial

outgrowth. Intact domains for actin assembly (KIND, WH2) and for targeting Spir to the

secretory network (mFYVE) were essential for Spir function in dendrite arborization. In

addition, an intact Spir-box was essential to control the localization and levels of Spir

expression in dendrites. The Spir-box has the potential to mediate interactions with Rab

GTPases, and here we found physical and genetic interactions to link Spir function with Rab11.

Rab11 is a key regulator of recycling endosomes. Together our data indicate that Spir and

Rab11 collaborate to stimulate dendrite branch formation. An appealing model is one in which

Spir and Rab11 cooperate to deliver lipids and cargoes through the secretory network to fuel

protrusive outgrowth of nascent dendrites. Further experiments will be required to test this

model.

Newly formed branches in control animals were pre-figured either by the appearance

of actin polymer *de novo* or by the arrival of pre-formed actin blobs, in roughly equal

proportions. In *spir* mutants, there were fewer new branches, and none stemming from

initiation sites with *de novo* actin polymer, indicating that Spir is a critical factor controlling

the frequency of new dendrite formation from such sites. Although present and active at

initiation sites stemming from pre-formed actin blobs, Spir was dispensable for branch

initiation from at least some of them. From this we infer redundancy with other molecular

mechanisms for branch initiation, perhaps involving actin synthesized by the Arp2/3 complex

which has been shown to transiently localize to branch initiation sites in c4da neurons (Sturner

et al., 2019).

Spir::GFP overexpression was not sufficient to induce ectopic branching in the rescue

assay (Fig. 2D) nor in +/+ animals (data not shown), and there was a variable interval between

the stationing of Spir at a branching site and filopodial outgrowth. These findings suggest that

Spir activity is tightly regulated. It may require stoichiometric amounts of additional partners

to engage the switch that signals the initiation step. The KIND domain mutation Y232K is

known to abolish the interaction between Spir and Capu, and there is some genetic evidence

that Spir and Capu interact for dendrite branching in class 3 da (c3da) neurons (Sturner *et al.*,

2022), but it remains unclear whether Capu is required in c4da neurons for dendrite

arborization. In unpublished data, we built a *capu^{GAL4}* line that did not label c4da neurons, and

RNAi lines targeting Capu did not reduce terminal branch number when expressed in c4da

neurons. Spir might cooperate with another formin in c4da neurons such as Formin3. Formin3

is required for c4da dendrite arborization (Das et al., 2021), and its ortholog INF2 has been

reported to interact with mouse Spir-1 in mammalian cells (Manor et al., 2015). It is possible

that Spir employs different mechanisms to polymerize actin in dendrites of different neuronal

cell types, and further research will be required to identify a partner or determine if Spir could

nucleate actin on its own in neurons, as has been shown *in vitro* (Quinlan *et al.*, 2005). It is

worth noting that the KIND domain also binds intramolecularly to the mFYVE domain (Tittel

et al., 2015). If Spir functions independently of another formin, perhaps the KIND mutation

(Y232K) and mFYVE (C5,6S) mutations affect the intramolecular interaction thereby

disrupting Spir function in dendrites.

It is not known if Spir orthologs are involved in dendrite arborization in mammals, but

it is intriguing that mRNA for murine orthologs of Spir (Spir-1 and Spir-2) are expressed in the

developing CNS and adult brain (Pleiser et al., 2010; Schumacher et al., 2004). A distinct

tandem WH2 domain actin nucleator, Cordon-bleu, has been demonstrated to promote dendrite

branch initiation in cultured hippocampal neurons and slice preparations of cerebellar Purkinje

neurons (Hou *et al.*, 2015).

Why might Spir proteins nucleate localized actin polymer just prior to the emergence

of nascent dendrites? Short actin filaments generated by Spir proteins and formins provide

tracks for myosin-V motors in long-range, microtubule-independent transport of Rab11-

labeled endosomes to the plasma membrane of oocytes (Holubcova et al., 2013; Schuh, 2011)

and in dispersal of Rab27a-labeled melanosomes in melanocytes (Alzahofi et al., 2020).

Interestingly, the human ortholog of myosin Vb has been shown to bind directly to the

orthologs of both Spir and Rab11 (Pylypenko *et al.*, 2016). Similarly, Spir could contribute to

an actin pool for myosin-V-mediated delivery of Rab11 vesicles to nascent dendrites, supplying

lipids and proteins required for their initiation and protrusive growth. This actin pool could

allow for the subsequent invasion of microtubules into these nascent branches, perhaps

mediated by myosin-6(Yoong et al., 2020), to enable microtubule-dependent long-distance

transport of cargo-carrying vesicles. This idea is consistent with our observation that Spir does

not appear to regulate the dynamics or maintenance of pre-existing terminal dendrites in c4da

neurons, implicating microtubules and perhaps other actin nucleators in these processes.

Further experiments will be required to further elucidate the mechanism and molecular partners

relevant to Spir-mediated dendrite branching, and the stimuli that activate Spir function at

branch initiation sites in vivo.

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Author Contributions

M.Q. and D.J.v.M conceived the project and designed experiments with input from all other

authors. D.H., C.M., C.H., T.F., Y.O., W.S., performed experiments and analyzed all data.

D.J.v.M wrote the manuscript with input from all other authors.

Declaration of interests

The authors declare no competing interests.

Figure Legends

Figure 1: Spir is required for localized F-actin synthesis just prior to new branch outgrowth. (A, B) Filmstrips (Supplemental Videos 1 and 2, 1 frame/6.5s) of new dendrite branch formation in a c4da neuron (labeled with ppkCD4::tdTom) of a control (+/+) L2 larva. LifeAct::GFP (driven by *ppk-GAL4*) reveals actin polymer within dendrites, and arrows point to instances where a punctum of F-actin was seen either to appear *de novo* (A) or to pre-exist prior to branch initiation (B). In all instances of either type, LifeAct::GFP signal intensified just prior to branch initiation. Scale bar = 2μm. (C) *spir^{GAL4}*-driven mCD8::GFP in c4da neurons (ppkCD4::tdTom) including ddaC (arrowhead), and other sensory neurons in the body wall of an L3 larva. Scale bar=25μm. (D) Diagram showing Spir protein domains (KIND, WH2, SB, and mFYVE), the locations *spir^{2F}* and *spir^{1}* mutations, and the names of the disruptive mutations (Y232K, ABCD, ΔSB, and C5,6S) introduced into Spir::GFP. (E) Filmstrip (Supplemental Video 3, 1 frame/6.5s), showing new dendrite branch formation in a *spir^{2F}/spir^{Df}* L2 larva. Pre-formed actin polymer (arrow) moved to the initiation site, but

LifeAct::GFP signal did not intensify prior to outgrowth. Scale bar = 2μm. (F) Proportion of

newly formed terminal branches in L2 larvae that had either *de novo* F-actin or pre-formed F-

actin prior to branch initiation in c4da neurons. Graph shows mean ± SEM, comparing controls

(+/+, n=50 new branches) with *spir* heterozygotes (*spir^{2F}*/+, n=18 new branches) and *spir*

mutants (*spir^{2F}*/*spir^{Df}*, n=8 new branches). (G) Fold change of F-actin intensity (LifeAct:GFP)

at branch initiation sites, from 60s before branch formation to 60s afterward, comparing control

(black) and *spir* mutants (red). Graphs (F, G) show mean ± SEM. (H, I) Filmstrips

(Supplemental Video 5, 1 frame/~4s and Supplemental Video 6, 1 frame/~7s) of control (+/+)

L2 larva, where Spir::GFP (arrows) was observed to move to the initiation site of a new

dendrite branch (H), or was already stationed at the site at the beginning of the movie (I). Scale

bars = 2μm. (J, K) For newly formed dendrite branches, the distance of the closest Spir::GFP

puncta to the site of branch initiation was measured (J), and the time from observation of a

stationary Spir::GFP punctum at the site to filopodial outgrowth was recorded (K).

Figure 2: Spir is required to initiate new branches within dendrite arbors of c4da

neurons. (A, B) Dendrite parameters from time lapse movies of control heterozygotes

(*spir^{2F}*/+, n= 10), *spir* mutants (*spir^{2F}*/*spir^{DF}*, , n= 13, or *spir* mutants rescued with either

Spir::GFP (n= 10) or Spir^{ABCD}::GFP (n= 8), where graphs show mean ± SEM. Dunnett's test

was used for multiple post hoc comparisons, and asterisks in each graph (A, B) indicate

significant changes compared to *spir^{2F}*/+ heterozygous controls (**P<0.01, ***P<0.001). (A)

Number of terminal branches per μm^2 of area in first frame of each movie. (ANOVA ($F_{(3, 39)}$

= 10.52, p < 0.0001). (B) Proportion of new/total branches in each movie (ANOVA ($F_{(3,40)}$ =

3.346, p = 0.0284). (C) Dendrite arbors of c4da neurons (ddaC) visualized with *ppk-*

CD4::tdTom in a *spir* heterozygote control (left), a *spir* mutant (middle), and a *spir* mutant

rescued with *ppk-Gal4* expressing Spir::GFP (right). (D-H) Dendrite parameters per ddaC

neuron in L3 larvae (n=15 for each genotype, graphs show mean ± SEM. Asterisks indicate significant changes compared to $spir^{2F/+}$ heterozygous controls. (D) Total number of terminal dendrites per ddaC neuron (ANOVA $(F(4, 70) = 11.30, p < 0.0001)$. (E) Total length of dendrite arbor (mm) (ANOVA $F(4, 70) = 15.12, p < 0.0001$). (F) Dendritic field ($mm^2$) (ANOVA $(F(4, 70) = 3.352, p = 0.0144)$. (G, H) Sholl analysis of entire ddaC neurons labelled with *ppk-CD4::tdTom*. (I) Sholl profiles, with dotted line indicating critical value for controls ($spir^{2F/+}$) (J) Sholl critical value (ANOVA $(F(4, 70) = 8.936, p < 0.0001)$.

Figure 3: Structure-function to reveal Spir domains required for dendrite arborization and Spir localization. (A-B) Dendrite parameters in L3 larvae, comparing *spir* mutants ($spir^{2F/Df}$) with animals rescued with Spir::GFP, or Spir:GFP with domain-specific mutations (n=15 for each genotype, graphs show mean ± SEM). Asterisks indicate significant changes compared to $spir^{2F}/Df$ mutants. (A) Total number of terminal dendrites per ddaC neuron (ANOVA $(F(5, 83) = 2.269, p = 0.0550)$. (B) Sholl critical value (ANOVA $(F(5, 84) = 3.552, p = 0.058)$. (C) Anti-GFP and anti-Actin western blot analysis from adult head lysates. Expected size of Spir::GFP is 142 kDa, and endogenous Actin is 42 kDa. (D) Relative band intensities on western blots (n=3) of Spir::GFP constructs (anti-GFP) normalised to anti-Actin. Spir$^{\Delta SB}$::GFP is present at significantly higher levels than Spir::GFP (Friedman test $(Q (4) = 10.40, p = 0.0053)$, with Dunn's post-hoc tests, where all genotypes were compared to Spir::GFP. (E) *ppk-GAL4*-driven Spir::GFP or Spir$^{\Delta SB}$::GFP in a *spir* mutant background. White boxes in left panels indicate areas magnified in panels to their right. Scale bar=50μm. Compared to the punctate distribution of Spir::GFP in ddaC dendrites, Spir$^{\Delta SB}$::GFP accumulates in a continuous pattern in dendrites proximal to the cell soma (white arrowhead), where GFP expression is also seen to be unusually high.

Figure 4. Spire interacts with Rab11 in c4da neurons. (A) *ppk-GAL4*-driven Spir::GFP and Rab11::mCherry. Cell bodies of ddaC neurons are indicated (white arrowheads). Co-localization is observed at branch points (e.g., orange arrowhead) and dendrite shafts (e.g., blue arrowhead). Scale bar=50μm. (B) Spir::tdTom co-IPs with either Capu::GFP (left) or Rab11::GFP (right) from adult head lysates. (C) Dendrites of c4da neurons labelled with ppk-CD4::tdTom in *spir²F/+* heterozygotes (left), *Rab11^Bi* heterozygotes (middle), and trans-heterozygotes for both (right). (D-F) Dendrite arbor parameters in *spir* heterozygotes (*spir²F/+*, n=15), *Rab11* heterozygotes (*Rab11^Bi/+*, n=17), and trans-heterozygotes (*spir²F/+; Rab11^Bi /+*, n=15), where graphs show mean ± SEM. Asterisks indicate significant changes compared to *spir²F/+* heterozygous controls (*P<0.05). (D) Total number of terminal dendrites (ANOVA ($F_{(2, 44)}$ = 4.745 p = 0.0136). (E) Total length of dendrite arbor (mm) (ANOVA ($F_{(2, 44)}$ = 5.443, p =0.0077). (F) Dendritic field (mm²) (ANOVA ($F_{2, 44}$ = 0.8512, p=0.4338). (G) Sholl profiles.

Methods

***Drosophila* stocks and genetics:** Fly stocks were obtained from the Bloomington Drosophila Stock Centre (*spir¹*, *spir²F*, *spir^DfExel6046* (referred to as *spir^Df*), Mi05646, Mi05737, *UAS-capu::GFP*, *w^1118*, *UAS-mCD8::GFP*, *UAS-Rab11::GFP*, *UAS-Rab4::mRFP*, *UAS-Rab6::GFP*, *UAS-Rab11-dsRNA*, *UAS-LifeAct-GFP*. *ppk-GAL4* and *ppkCD4::tdTom* were gifts from Dr. Yuh-Nung Jan. *UAS-Rab11::mCherry* was a gift from Dr. Gregory Emery. *nSyb-GAL4* line was created by Dr Julie Simpson, for which we used 2nd chromosome insertions generated by Dr Stefan Thor. To create the lines *UAS-spir::GFP*, *UAS-spir::tdTom*, *UAS-spir^Y232K::GFP*, *UAS-spir^ABCD::GFP*, *UAS-spir^ASB::GFP*, *UAS-spir^C5,6S::GFP*, DNA constructs encoding full-length Spir or each of the 4 mutated versions (Kerkhoff *et al.*, 2001;

Quinlan, 2013; Quinlan *et al.*, 2005) were designed to add C-terminal GFP or tdTomato

(tdTom) fluorophores. These constructs were subcloned into the vector pMUH, then

microinjected by standard procedures (Bestgene, Inc) to target the VK00027 landing site in the

Drosophila genome with φc31-mediated transposition (Pfeiffer et al., 2010). *spir*^{GAL4} was

generated by inserting a so-called Trojan-GAL4 into the *spir* locus (Diao et al., 2015; Venken

et al., 2011). pT-GEM(0) a gift from Benjamin White (Addgene plasmid # 62891) was

microinjected (Bestgene, Inc) into MiMIC line, Mi05646 (Diao *et al.*, 2015; Venken *et al.*,

2011). The same plasmid was injected into MiMIC line Mi05737 to generate *capu*^{GAL4}.

Antibodies: To produce anti-Spir antisera, DNA encoding Spir amino acids 565-692

were cloned into pGEX-6P-1 to produce an IPTG-inducible C-terminal GST fusion proteins in

BL21 cells. The purified GST fusion protein was injected into two rabbits and the serum was

extracted according to approved protocols at the Comparative Medicine and Animal

Resources Centre (McGill University) and standards established by the Canadian Council on

Animal Care. Crude serum (500 µl) was then pre-absorbed by overnight incubation with 500

µl L3 larvae (*spir*^{1}/*spir*^{Df}) that had been fixed previously in 4% PFA. Another primary antibody

for IHC was Alexa-647-conjugated goat anti-HRP (1:800, Jackson ImmunoResearch

#123605021), while secondary antibody for anti Spir IHC was Alexa-647-conjugated goat anti-

rabbit (1:1000, Invitrogen, #A21244). For western blotting, membranes were incubated with

mouse anti-GFP (Clontech #632380), rabbit anti-DsRed (Takara #632496), mouse anti-Actin

(Sigma #A4700) or rabbit anti-Spire (directed at amino acids 565-692). For detection, HRP-

conjugated secondary antibodies (anti-mouse and anti-rabbit (both 1:3000, BioRad) were used

and revealed with chemiluminescence (Amersham ECL Western Blotting Detection Reagents).

Immunohistochemistry (IHC): Third instar larvae (L3) of either sex were dissected

in Sorensen phosphate buffer (pH 7.4) and fixed in 4% paraformaldehyde (in Sorensen's

buffer) for 10 minutes (min) at room temperature. Washes (3X over 20 min) were done with

Sorensen's buffer containing 0.2% Triton-X-100 (Sigma). Specimens were then blocked with Sorensen's buffer containing 5% normal goat serum (NGS), incubated at 4°C with primary antibodies overnight, washed as above, then incubated with secondary antibodies for 2 hours at room temperature. Anti-Spir antiserum for immunohistochemistry was directed at amino acids 1-91. Primary and secondary antibodies were diluted in Sorensen's buffer containing 5% NGS. After a final wash as above, specimens were then mounted with SlowFade Diamond Antifade Mountant (Invitrogen) for imaging.

Co-immunoprecipitation (co-IP) and western blotting: Lysates for co-IPs and western blots were made from adult heads aged 1-5 days after eclosion. For western blots, heads were mechanically crushed using a motorized pestle directly in 2X Laemmli buffer. For co-IPs, 100 heads were cut and collected on dry ice, then mechanically crushed using a motorized pestle in 100ul of lysis buffer containing 50mM Tris pH, 150mM KCl, 1mM MgCl2, 1mM EGTA, Roche protease inhibitor cocktail and 10% glycerol. Lysates were treated with 10% deoxycholic acid and 10% Triton X-100, then incubated overnight on a Nutator with anti-GFP bound agarose beads (Chromotek GFP-Trap® #gta). Lysates and beads were separated in a centrifuge, washed with a glycerol free buffer, and the complexes on the beads were dissociated directly in Laemmli buffer, then separated using standard SDS-PAGE and wet-transfer procedures.

Imaging: All imaging and quantification was of ddaC, the dorsal-most c4da neuron, in abdominal segments of the larval body wall. For static images, third instar (L3) larvae were dissected and prepared for IHC, or they were squished directly on the slide in 100% glycerol and prepared for imaging of native fluorescence (GFP, tdTom, mCherry, mRFP) within 10 minutes. Static images were taken with an Olympus Fluoview FV-1000/BX63 confocal microscope using either a 20X or 60X oil-immersion objective lens. All time-lapse imaging was done on L2 larvae, where eggs were initially collected for 4h on agar plates containing

grape juice and yeast. After 24h, hatched larvae of selected genotypes were transferred on a

fresh fly food plate to start timing. L2 larvae (65h ± 4h AEL) were mounted in a drop of

halocarbon oil in a polydimethylsiloxane (PDMS) microfluid device, and then imaged by live

confocal microscopy (Zeiss, Spinning Disk, Inverted Axio Observer Z1) with 63x objective

lens, at room temperature with Immersol W (Zeiss) between lens and coverslip. Using Zen

software (Zeiss), live imaging of fluorescent proteins GFP and tdTomato was performed for 5

min with 5s interval on average. If GFP only, then the interval was 2s on average. Only videos

obtained from larvae that were still alive and active after imaging were used for analysis. Each

video was then registered on ImageJ using StackReg plugin (Thevenaz et al., 1998) before

analysis.

Quantification of Lifeact::GFP and Spir::GFP localization: New branches

appearing in each movie were identified, and initiation sites were classified as having "de

novo" actin polymer if a punctum of LifeAct::GFP intensity appeared at the site and grew in

intensity until protrusion of the new branch. Initiation sites had "pre-formed" actin if motile

blobs of LifeAct::GFP were observed to arrive prior to branch outgrowth (motile). New

branches for which a LifeAct::GFP punctum was at the initiation site in the first frame of the

movie were not considered because it was uncertain when or how this actin arose there.

Consistent with a previous report (Nithianandam and Chien, 2018), we observed only a single

rare instance where a filopodium grew from an initiation site where LifeAct::GFP was not

detected.

To measure the association of Spir::GFP labeled punctae to either a dendrite shaft,

branch point, or tip, a custom routine was developed to extract this information from images

acquired with a 20X objective (2 to 4 images stitched together where necessary using the

Pairwise Stitching plugin (Preibisch et al., 2009). From maximum intensity projections (MIP)

of 10 c4da neurons (ddaC) labeled for the dendrite marker CD4-tdTom, signal from beyond

the cell of interest was cleared manually, the background was subtracted, and a MIP mask

created. This mask was then applied to the SpirFL:: GFP channel. Pixels outside the mask was

cleared. The MIP mask was skeletonized using Fiji's skeletonization plugin (Arganda-Carreras

et al., 2010) to obtain the location of shafts, branch points, and tips. A script from the

Neuroantomy update site was then used to determine which Spir::GFP punctae were associated

with such skeleton features. When a Spir::GFP punctum was 3 μm or less (snap-to distance)

from either a branch point or tip it was assigned to each, respectively. This snap-to distance

was selected because from a representative Spir:GFP image, 80% of the punctae had a diameter

of 3 μm or less. Additionally, no branch points or tips were 3 μm or less apart from one another.

The number of punctae at branch points and tips was then divided by the total number of branch

points and tips, respectively, to obtain the percent of branch points and tips that were occupied

by Spir::GFP.

Dendrite morphometry: c4da neurons (ddaC) were imaged at 20X, with 1 image field

usually sufficient to capture the entire dendritic field of a neuron. However, in some cases 2

images were stitched together using the Fiji plugin Pairwise Stitching to generate an image of

the entire neuron (Preibisch et al., 2009). Maximum intensity projections of confocal z-series

image stacks were segmented as described previously (Ferreira et al., 2014a). Various Fiji

plugins were used to determine branching characteristics of neurons; Sholl Analysis to generate

Sholl profiles and extract Sholl related parameters (Ferreira et al., 2014b), Strahler Analysis to

assess the number of terminal dendrites (Ferreira et al., 2014b; Strahler, 1957), and Analyze

Skeleton for total arbor length. Dendritic field was determined by fitting a polygon around the

segmented neuron on Fiji, and measuring the area inside the shape (Schindelin et al., 2012).

Measuring dendrite dynamics: Pre-existing dendrites at the beginning of live imaging

movies were analyzed for the dynamics of their terminal branches using MTrackJ (Meijering

et al., 2012). Terminal branch length was compared by an observer every frame (every 5s on

average) for the entire duration (5 min) of each movie. Dendrites that extended, retracted, or

did both, or remained static were recorded, and these numbers were expressed as the percentage

of the total number of pre-existing dendrites at the beginning of each movie. Newly formed

dendrites were tracked in a similar manner (every 5s), and their numbers expressed as a

percentage of the total number of terminal branches seen at the beginning of each movie. To

measure their protrusive characteristics during outgrowth, mean speed was the average of the

speeds of growth for each frame (including extensions and pauses) until the branch stopped

growing altogether, or retracted, or the movie ended. The proportion of time the branch spent

paused during this period of saltatory outgrowth was calculated, as was the maximum length

of its protrusion.

Graphs and Statistics: Bar graphs and statistics were done using GraphPad Prism v9,

and displayed data is expressed as mean ± standard error. For comparisons of more than two

conditions, data were tested for normal distribution using D'Agostino & Pearson test and

analysed for statistical significance using one-way ANOVA (multiple groups). Following

ANOVA at $P<0.05$, Dunnett's post-hoc tests were performed. For the repeated measures of

western blots, Friedman test was applied then Dunn's post-hoc tests. To compare two

conditions, Student's t-test was used. Asterisks indicate the significance of *P*-values compared

to the indicated control group (*$P<0.05$, **$P<0.01$, ***$P<0.001$, ****$P<0.0001$).

Supplemental Information

Supplemental Figure S1: Spir expression and motility in dendrites (related to Figure 1).

(A) Co-labeling for endogenous Spir and horseradish peroxidase (HRP) in the body wall of an

L3 larva, using IHC. Spir expression observed in a c4da neuron (arrowhead, left panel) in a

spir^{1}/+ heterozygote, but not in a *spir$^{1/Df}$* hemizygous mutant (arrowhead, right panel). (B)

Anti-Spir western blot of lysates from dissected adult brains, comparing controls with *spir$^{1/Df}$*

mutants and with flies overexpressing Spir::GFP in all neurons with nSyb-Gal4. Expected mass of Spir::GFP is 142kDa, while that of Spir is 115kDa. The increased presence of Spir (115 kDa) upon overexpression of Spir::GFP likely arises from proteolytic cleavage of the GFP tag from Spir::GFP fusion protein. (C) ppk-Gal4 driven Spir::GFP expression is detected strongly with anti-Spir IHC in a c4da neuron cell soma (white arrowhead) and in puncta within at dendrite branch points (e.g., orange arrowhead), and dendrite shafts (e.g., blue arrowhead) Scale bars (A, B) = 50um. (D) High magnification view of Spir::GFP (native GFP, green) in c4da neuron dendrites (tdTom, magenta) of an L3 larva. Based on size, morphology and location, the types of Spir::GFP-positive puncta in dendrites include large, irregularly shaped puncta at branch points (e.g., orange arrowhead), and smaller, circular puncta in dendrite shafts (e.g., blue arrowhead) or at branch tips (e.g., yellow arrowhead). (E) Locations of Spir::GFP puncta observed in static images of c4da dendrite arbors at L3 (n=10 neurons). (F) Greyscale filmstrip (Supplemental Video 4, acquired at ~1 frame/2s) from a c4da neuron of an L2 larva, where the black arrowhead indicates progressive movement of a Spir::GFP-labelled punctum within a dendrite shaft. Scale bar: 5μm. Motile Spir::GFP puncta moved in both anterograde (64%) and retrograde (36%) directions from the cell soma, and sometimes were observed to switch from to the other. Some puncta appeared to pass one another, while others merged. Motile Spir::GFP particles were found to travel 0.6 um/s on average, and achieved a maximal speed of 1.1 um/s.

Supplemental Figure S2: Quantification of dynamics of terminal branches that pre-existed at onset of time-lapse movies (related to Figure 2). (A-D) Quantification of percentage of branches that extended (A, ANOVA ($F_{(3, 39)}$ = 0.1262, p = 0.9440), retracted (B, ANOVA ($F_{(3, 39)}$ = 0.8598, p = 0.47), extended and retracted in the same movie (C, ANOVA ($F_{(3, 39)}$ = 2.348, p = 0.0875) or remained static (D, ANOVA ($F_{(3, 39)}$ = 1.983, p = 0.1324). Graphs

show mean±SEM. (E-G) Protrusive growth characteristics of nascent branches in controls (+/+, n=14) and *spir* mutants (*spir²F/spir^Df*, n=7) in L2 larvae expressing LifeAct::GFP driven by *ppk-GAL4*, including mean speed (E, t-test ($t(21) = 1,757$, $p = 0,0951$)), time paused (F, t-test($t(21) = 0,7025$, $p = 0,4909$), and maximum protrusion length (G, t-test ($t(21) = 1,516$, $p = 0,1459$). Graphs show scatter plot for each branch, with mean ± SEM indicated (ns, not significant).

Supplemental Figure S3: Quantification of dynamics of newly formed and pre-existing terminal branches (related to Figure 2). (A-B) Dendrite parameters from time-lapse movies of c4da neurons (labeled with ppkCD4::tdTom) in L2 larvae expressing LifeAct::GFP driven by *ppk-GAL4*. Graphs show mean ± SEM, comparing controls (+/+, n=11) with *spir* heterozygotes (*spir²F/+*, n=8) and *spir* mutants (*spir²F/spir^Df*, n=11). Asterisks indicate significant changes compared to +/+ heterozygous controls (*P<0.05). (A) Number of terminal branches per μm^2 of area in first frame of each movie. (ANOVA ($F(2, 27) = 4.079$, $p = 0.0283$). (B) Proportion of new/total branches in each movie (ANOVA ($F(2, 27) = 3.376$, $p = 0.0491$). (C-F) For branches that pre-existed in the first frame of each movie, quantification of percentage of the number of branches that extended (C, ANOVA ($F(2, 27) = 0.0129$, $p = 0.9872$)), retracted (D, ANOVA ($F(2, 27) = 0.7537$, $p = 0.4803$)), extended and retracted in the same movie (E, ANOVA ($F(2, 27) = 1.979$, $p = 0.1577$)) or remained static (F, ANOVA ($F(2, 27) = 0.05392$, $p = 0.9476$).

Supplemental Figure S4: Dendrite parameters for c4da neurons in L3 larvae (related to Figure 2). (A-D) This is the same dataset shown in Fig. 2, except it was adjusted to control for dendritic field size by removing from the analysis four *spir²F/Df* c4da neurons with unusually small arbors (n=11). Graphs show mean ± SEM). Asterisks indicate significant changes

compared to $spir^{2F}/+$ heterozygous controls. (A) Dendritic field per ddaC neuron (mm^2)

(ANOVA ($F_{(4, 66)} = 1.912$, $p = 0.1189$. (B) Total number of terminal dendrites per ddaC

neuron (ANOVA ($F_{(4, 66)} = 9.328$, $p < 0.0001$). (C) Total length of dendrite arbor per ddaC

neuron (mm) (ANOVA ($F_{(4,66)} = 12.03$, $p < 0.0001$). (D) Sholl critical value (ANOVA ($F_{(4,}$

$_{66)} = 6.914$, $p = 0.0001$).

Supplemental Figure S5: Function, expression, and distribution of Spir::GFP bearing

domain-specific mutations (related to Figure 3). (A) Sholl profiles for entire ddaC neurons

labelled with ppk-CD4::tdTom. (B) Anti-GFP western blot from adult heads of animals

overexpressing in all neurons either intact Spir::GFP or Spir::GFP bearing domain-specific

mutations. One of three replicate blots, this blot is distinct from the one shown in Fig. 3C and

is shown in its entirety. The expected molecular weight of Spir::GFP is 142 kDa, and that of

GFP is 27 kDa, and so proteolytic cleavage of GFP is not apparent for most constructs. (C)

ppk-GAL4 drives the expression of Spir^{Y232K}::GFP or Spir^{ABCD}::GFP or Spir^{C5,6S}::GFP in a *spir*

mutant background. Punctate distribution of Spir::GFP is maintained for each of these

mutations. White boxes in left panels indicate areas magnified in panels to their right. Scale

bar=50μm.

Supplemental Figure S6: Expression, and distribution of Spir::GFP bearing domain-

specific mutations (related to Figure 4). (A) *ppk-GAL4*-driven expression of Spir::GFP and

Rab4::mRFP. Cell bodies of ddaC neurons are indicated (white arrowheads). Co-localization

of Spir::GFP with Rab4:mRFP is observed at branch points (e.g., orange arrowhead) and

dendrite shafts (e.g., blue arrowhead). (B, C) Distribution of Spir::GFP in c4da neurons in

controls (B) and upon expression Rab11-dsRNAi in c4da neurons with *ppk-Gal4* (C). White

boxes in left panels indicate areas magnified in panels to their right. Punctate distribution of

Spir::GFP within dendrite arbors of c4da neurons was seemingly unaffected by the knockdown

of Rab11. Scale bars=50μm.

Supplemental Video 1 – corresponding to Fig. 1A

Supplemental Video 2 - corresponding to Fig. 1B

Supplemental Video 3 - corresponding to Fig. 1E

Supplemental Video 4 - corresponding to Supplemental Fig. S1F

Supplemental Video 5 - corresponding to Fig. 1H

Supplemental Video 6 - corresponding to Fig. 1I

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Figure 1

A LifeAct::GFP / ppk-CD4::tdTom — 0s, 36s, 65s, 86s, 166s, 252s

B LifeAct::GFP / ppk-CD4::tdTom — 0s, 43s, 108s, 252s, 281s, 396s, 511s

C $spir^{GAL4}$ — mCD8::GFP, ppk-CD4::tdTom

D Spir::GFP — KIND (2F 1, Y232K) — WH2 (ABCD) — SB (ΔSB) — mFYVE (C5,6S) — GFP

E LifeAct::GFP / ppk-CD4::tdTom — 0s, 30s, 90s, 120s, 150s, 180s, 210s, 240s

F % of Nascent Dendrites with:
De novo F-Actin: +/+, $spir^{2F}$/+, $spir^{2F/Df}$
Pre-formed F-Actin: +/+, $spir^{2F}$/+, $spir^{2F/Df}$

G Fold change of LifeAct::GFP intensity at branch initiation site vs Time (s)
+/+ , $spir^{2F}$ / $spir^{Df}$
Branch Initiation

H Spir::GFP / ppk-CD4::tdTom — 0s, 30s, 180s, 360s, 390s

I Spir::GFP / ppk-CD4::tdTom — 0s, 28s, 43s, 57s, 71s

J % Newly formed branches vs Distance of Spir::GFP punctum from branch initiation site (mm). n=139

K

Spir::GFP puncta at branch initiation sites in time-lapse movies at L2 (n=61)	Occurrence	Time (s) from stationary punctum to branch outgrowth		
		Minimum	Maximum	Mean ±sd
Spir::GFP observed to move to site	30%	4	129	43 ± 41
Spir::GFP stationed at site in first movie frame	70%	8	229	88 ± 67

Figure 2

Figure 3

Figure 4

Figure S1

A *spir¹/+* | *spir¹/Df*
Spir HRP | Spir HRP

B
kDa | +/+ | *spir¹/Df* | *nSyb>*Spir::GFP
150 | | | Spir::GFP
100 | | | Spir
α-Spir

C *ppk>*Spir::GFP
Spir HRP

D Spir::GFP ppk-CD4::tdTom

E

Spir::GFP puncta in static images at L3			
	Occurrence		
	Shafts	Branch points	Tips
Spir::GFP occupancy of each location	100%	28%	6%
Proportion of total Spir::GFP puncta at each location	57%	36%	7%

F *ppk>*Spir::GFP
0s 10s 20s 30s 40s 50s 60s 70s

Figure S2

Figure S3

Figure S4

Figure S5

A

No. of Intersections (y-axis)
Distance from soma (μm) (x-axis)

- *spir²ᶠ/ᴰᶠ*
- *spir²ᶠ/ᴰᶠ* + Spir
- *spir²ᶠ/ᴰᶠ* + Spir^Y232K
- *spir²ᶠ/ᴰᶠ* + Spir^ABCD
- *spir²ᶠ/ᴰᶠ* + Spir^ΔSB
- *spir²ᶠ/ᴰᶠ* + Spir^C5,6S

B

α-GFP (Spir)

C

spir²ᶠ/ᴰᶠ, ppk-GAL4

Spir^Y232K::GFP — ppk-CD4::tdTom — ppk-CD4::tdTom — Spir^Y232K::GFP

Spir^ABCD::GFP — ppk-CD4::tdTom — ppk-CD4::tdTom — Spir^ABCD::GFP

Spir^C5,6S::GFP — ppk-CD4::tdTom — ppk-CD4::tdTom — Spir^C5,6S::GFP

Figure S6