Syndapin promotes pseudocleavage furrow formation by actin organization in the syncytial Drosophila embryo

Aparna Sherlekar and Richa Rikhy*
Biology, Indian Institute of Science Education and Research, Pashan, Pune 411008, India

ABSTRACT Coordinated membrane and cytoskeletal remodeling activities are required for membrane extension in processes such as cytokinesis and syncytial nuclear division cycles in Drosophila. Pseudocleavage furrow membranes in the syncytial Drosophila blastoderm embryo show rapid extension and retraction regulated by actin-remodeling proteins. The F-BAR domain protein Syndapin (Synd) is involved in membrane tubulation, endocytosis, and, uniquely, in F-actin stability. Here we report a role for Synd in actin-regulated pseudocleavage furrow formation. Synd localized to these furrows, and its loss resulted in short, disorganized furrows. Synd presence was important for the recruitment of the septin Peanut and distribution of Diaphanous and F-actin at furrows. Synd and Peanut were both absent in furrow-initiation mutants of RhoGEF2 and Diaphanous and in furrow-progression mutants of Anillin. Synd overexpression in rhogef2 mutants reversed its furrow-extension phenotypes, Peanut and Diaphanous recruitment, and F-actin organization. We conclude that Synd plays an important role in pseudocleavage furrow extension, and this role is also likely to be crucial in cleavage furrow formation during cell division.

INTRODUCTION

Cleavage furrow formation during cell division requires a highly conserved set of cytoskeletal and membrane-trafficking proteins (D’Avino, 2009; Haglund et al., 2011; Cabernard, 2012; Fededa and Gerlich, 2012). Their positioning and initiation involve microtubules and the centralspindlin complex (Alsop and Zhang, 2003; Bringmann and Hyman, 2005; Crest et al., 2012). Rho-GTPase–activating protein (RacGAP50C) of this complex positions Rho-GTP exchange factor (RhoGEF) Pebble at contractile rings, and another RhoGEF recruits formins that assemble an actin scaffold for contractile-ring formation and/or furrow initiation (Barmchi et al., 2005; Grosshans et al., 2005; Watanabe et al., 2008, 2010, 2013). Formin activity also depends on the presence of a scaffold protein, Anillin, at the contractile ring (Watanabe et al., 2010; Saha and Pollard, 2012). Rac-GAP50C also accumulates Anillin at the furrow (D’Avino et al., 2008; Gregory et al., 2008), which is responsible for both septin and myosin II association at the contractile ring (Straight et al., 2005; Pieken and Maddox, 2010). Cytokinesis failure increases in Caenorhabditis elegans when embryos are depleted of both Rho kinase and Anillin/septins (Maddox et al., 2007), implying that they work together for robust furrow formation.

The cell division cycle is accompanied by drastic changes in cell shape that necessitate dynamic interplay between the membrane and actin cytoskeleton (Heng and Koh, 2010; Bezanilla et al., 2015). In the Drosophila syncytial embryo, nuclear division cycles 10–13 are rapid and involve dynamic pseudocleavage furrow ingestion and retraction between adjacent dividing nuclei. These furrows serve to prevent spindle cross-talk across compartments during metaphase of each cycle (Foe and Alberts, 1983; Kellogg et al., 1988) and organize the embryo into discrete polarized functional units (Frescas et al., 2006; Mavrakis et al., 2009; Daniels et al., 2012). Furrow
positioning and initiation at this stage requires RhoGEF2 for recruiting Rho1 and the formin Diaphanus (Dia) (Barmchi et al., 2005; Grosshans et al., 2005; Crest et al., 2012). Microtubules are required for furrow positioning (Bringmann and Hyman, 2005; Crest et al., 2012), while furrow ingression involves dynamic growth of actin filaments through Profilin and the action of anticapping proteins (like Ena/VASP; Grevengoed et al., 2003; Bezanilla et al., 2015). The syncytial cycles are followed by massive elongation of furrows to form individual cells in a process called cellularization, during which membrane extension is fueled by flattening of apical microvilli and Rab11-mediated endocytosis (Lecuit and Wieschaus, 2000; Pelissier et al., 2003; Figard et al., 2013) and driven by an actomyosin contractile ring that, apart from actin and myosin II, also comprises Anillin, septins, RhoGEF2, and Dia (Lecuit, 2004; Royou et al., 2004). Although contractile rings first form only during cellularization in early developing Drosophila embryos, the syncytial pseudocleavage furrows contain most of the proteins present in the contractile ring such as Rho1, RhoGEF2, Dia, Anillin, and septins (Fares et al., 1995; Field and Alberts, 1995; Afshar et al., 2000; Foe et al., 2000; Cao et al., 2008).

F-BAR domain–containing proteins link membrane and cytoskeleton in various processes, including endocytosis, cell shape and polarity, cell motility, and cytokinesis (Roberts-Galbraith and Gould, 2010; Liu et al., 2015). The yeast orthologues of F-BAR protein Cip4 are known to recruit formins and influence their nucleation and elongation activities (Laporte et al., 2011; Yan et al., 2013; Graziano et al., 2014; Willet et al., 2015). In addition, Hof1 (Cip4 in Saccharomyces cerevisiae) coiled-coil domain binds Septin (Cdc10) and localizes it to the bud neck (Meitinger et al., 2013; Oh et al., 2013). Drosophila Cip4, however, is not essential for formin Dia recruitment to cellularization furrows, and its loss does not result in a defect in cellularization but its overexpression shows dia loss-of-function phenotypes (Yan et al., 2013). The F-BAR domain protein, Syndapin/Pacsin (Synd), initially identified as a binding partner for Dynamin and neuronal Wiscott-Aldrich syndrome protein (N-Wasp) via its SH3 domain, participates in endocytosis and actin remodeling (Roos and Kelly, 1998; Simpson et al., 1999; Qualmann and Kelly, 2000; Dharmalingam et al., 2009; Rao et al., 2010). Mammalian Synd1 binds to the actin nucleator Cordon bleu (Cobl) (Ahuja et al., 2007) and mediates its interaction with Arp2/3 to affect actin nucleation during neuromorphogenesis (Schwintzer et al., 2011). Synd, unlike other F-BAR proteins, directly binds and stabilizes F-actin (Kostan et al., 2000) and, unlike any N- or F-BAR protein, can generate a range of membrane curvatures much greater than its own intrinsic curvature (Frost et al., 2008; Ramesh et al., 2013). Drosophila Synd promotes expansion of the subsynaptic reticulum (Kumar et al., 2009b), which also requires actin-remodeling (Ramachandran et al., 2009). Drosophila Synd also binds to Anillin via its myosin-binding domain in vitro, localizes at the cytokinetic furrow (earlier than Drosophila Cip4) in D.Met-2 cells, and is important for cytokinesis during male meiosis in primary spermatocytes (Takeda et al., 2013). Together these studies suggest a role for Synd in coordinated membrane and actin remodeling during cleavage furrow formation. However, no analysis of its recruitment dynamics or functional analysis in organization of actin or actin-remodeling proteins with respect to furrow initiation or extension machinery has been carried out so far. In this study, we report that Synd is important for syncytial Drosophila pseudocleavage furrow extension; septin Peanut (Pnut) recruitment; and distinct Dia, Anillin, and actin localization. Most significantly, Synd can recruit actin remodeling proteins, organize actin, and result in furrow extension during pseudocleavage furrow formation in rhogef2-depleted embryos.

### RESULTS

**Synd is enriched at Drosophila syncytial pseudocleavage furrow tips**

The nuclear division cycle from interphase through metaphase in the Drosophila syncytial embryo is accompanied by extension of the pseudocleavage furrow; the furrow being shortest in interphase and longest in metaphase, when mitotic spindles attach chromosomes at the equator (Figure 1A). An antibody generated against the Synd SH3 domain (Kumar et al., 2009a,b) was used to study its localization in pseudocleavage furrows in wild-type syncytial Drosophila embryos (Figure 1B). We found that Synd localized to the apical and lateral membranes and was enriched at the furrow tip (FT), where it colocalized with Patj, a marker for the FT (Supplemental Figure S1A; Mavrakis et al., 2009). Fluorescence intensity ratios of Synd to Amphiphysin (Amph, used as a membrane marker) were significantly reduced in embryos expressing synd<sup>RNAi</sup> (driven by nanos-Gal4) or containing a transposon in the first intrinsic region of the synd gene (synd<sup>d</sup>) (Kumar et al., 2009a) in the trans-allelic combination of synd<sup>d</sup>/Df (Figure 1, C–E). synd<sup>d</sup>/Df had the highest embryo lethality at 24 h after egg deposition (Figure 1F), and we used this allelic combination for Synd depletion for all subsequent analyses. The antibody staining and lethality were rescued using the fluorescently tagged Ub-Syndapin::green fluorescent protein (Synd-GFP; Synd-GFP expressed with the ubiquitin promotor), indicating the functionality of this GFP-tagged Synd (Figure 1, B–D; Takeda et al., 2013). The Synd-GFP localization overlaps almost completely with Synd antibody staining (Supplemental Figure S1B).

Synd distribution in metaphase furrows of nuclear cycles 11–13 was measured in living embryos expressing Synd-GFP in the synd<sup>d</sup>/Df background (Figure 1G and Supplemental Movie S3). Synd-GFP localized to the apical and lateral pseudocleavage furrow membranes and was progressively enriched at the FT in cycles 12 and 13 (Figure 1, G and H). This increase correlated with increase in furrow length with each nuclear cycle (Holly et al., 2015). To assess Synd dynamics at the FT compared with the apical membrane, we used fluorescence recovery after photobleaching (FRAP) in these embryos during cycle 13 metaphase in the apical and FT membrane. The FRAP recovery data were fit to a one-phase exponential association equation (for diffusion-uncoupled FRAP); the recovery plateau obtained was higher at the metaphase FTs as compared with the apical region, with a mobile fraction of ~80% as compared with 60% (Figure 1, I–K). This difference of mobile fraction was not seen for the GFP-tagged pleckstrin homology (PH) domain of general receptor for phosphoinositides-1 (GRP1; tGPH; Britton et al., 2002; Supplemental Figure S1, D and E). Thus Synd shows increased mobile fraction at the FTs in long metaphase furrows.

**synd mutants have shorter and disorganized pseudocleavage furrows**

To study Synd’s role in the dynamics of furrow formation, we imaged developing embryos containing tGPH as a plasma membrane marker to compare furrow lengths in orthogonal sections. We compared pseudocleavage furrow dynamics in control tGPH embryos at five time points in cycle 13: 1) end of prophase (pro-metaphase), when the nuclei are the largest and furrows start to ingress (3.8 ± 0.4 μm; denoted as I); 2) beginning of metaphase (after ~3 min), when the nuclear envelope breaks down (furrow length: 8.3 ± 0.6 μm; II); 3) middle of metaphase (III); 4) end of metaphase (~6 min), when the furrow is the longest (10.2 ± 0.8 μm; IV); and 5) anaphase, when the furrow starts to retract (~7 min; V) (Figure 2, A and B, and Supplemental Movie S1). The tGPH; synd<sup>d</sup>/Df furrows in prometaphase had a length similar to that of...
FIGURE 1: Synd is enriched at the pseudocleavage FT. (A) Pseudocleavage furrow extension visualized in syncytial nuclear cycle 13 with membrane marker Gap43-Venus (green) and histone-RFP (red). (B) Synd antibody/Synd-GFP (green) and Amph (magenta) are localized at metaphase (DNA, blue) furrow tip in wild-type embryos. (C–F) Synd immunostaining and embryo viability is reduced in mutants and rescued by Synd-GFP. Synd immunostaining ratio to Amph is reduced in syndRNAi (60%, n = 15) and synd1d/Df (85%, n = 40) embryos in metaphase as compared with Synd-GFP (25%, n = 16) (C and D) and in a box plot using Syndapin:Amphiphysin fluorescence intensity ratios (E, n = 3; 15 furrows each, ****, p < 0.0001, n.s., not significant by nonparametric Mann-Whitney U-test). Mean ± SD of 24 h embryo lethality shows the highest lethality in synd1d/Df, which is reversed by Synd-GFP (n = 3; 100 embryos/genotype), p < 0.0001 (F). (G and H) Synd FT association increases across syncytial cycles. Synd-GFP fluorescence in Synd-GFP; synd1d/Df embryos in metaphase across nuclear cycles (n.c.) 11, 12, and 13 in the apical, lateral, and FT membranes (G) is quantified in a scatter plot (a.u., arbitrary units, n = 3; 10 membrane ROIs, ****, p < 0.0001, n.s. not significant, one-way ANOVA and Tukey’s multiple-comparison test) (H). (I–K) Synd shows increased mobile fraction at the FT compared with the apical membrane. Photobleaching (black ROI, ∼2.5 μm²) of Synd-GFP was performed in apical or FT membranes; images at key time points are shown (I). FRAP occurs to a greater extent at the FT membrane (n = 5 embryos/region) (J). The immobile fraction from individual FRAP curves in H is shown in a scatter plot (K, n = 5; **, p < 0.01, nonparametric Mann-Whitney U-test). Scale bar: 10 μm.
FIGURE 2: synd mutant embryos have short and disorganized pseudocleavage furrow membranes. (A and B) synd mutants have shorter metaphase furrow lengths. Time-lapse orthogonal views in tGPH control and synd\textsuperscript{1d/Df} embryos are shown at 0, 3, 5, 6, and 7 min (corresponding to I, II, III, IV, and V) in syncytial cycle 13 (A). Graph shows significantly decreased furrow lengths in synd\textsuperscript{1d/Df} (B, mean ± SEM, n = 3; 5 furrows/embryo). (C and D) synd mutants have loosened metaphase furrow membranes. Surface and orthogonal views of longest metaphase furrows from tGPH expressing control, synd\textsuperscript{1d/Df}, and Synd-GFP; synd\textsuperscript{1d/Df} embryos in cycles 12 and 13 (C). synd\textsuperscript{1d/Df} embryos show increased width (arrows) in Line scan-intensity profile across lateral furrow membranes compared with control and Synd-GFP–expressing embryos (D). (E–G) synd mutants have decreased x,y displacement in the syncytial cycle. Time-lapse surface views are shown at 1, 4, and 7 min from tGPH containing control and synd\textsuperscript{1d/Df} embryos in cycle 13 (yellow line indicates track selected for kymograph generation) (E and F). The average displacement in a scatter plot is not significantly different (n = 3; 4 furrows/embryo, p > 0.05, n.s., not significant) but variance is increased in synd\textsuperscript{1d/Df} (G). ****, p < 0.0001, F-test used to compare variances. Unpaired t test (two-tailed) with Welch’s correction used to compare means. Scale bar: 10 μm; kymograph scale bar: x = 2.5 μm; y = 100 s.
also much shorter than that of the control (7.9 ± 0.4 μm) at 7 min. These furrow extension–retraction dynamics were rescued in synd mutant embryos containing Synd-GFP (Figure 2, A and B, and Supplemental Movies S2 and S3). We found that furrow dynamics measured in embryos expressing different PH domains (tGPH, PHPLCδ-CFP) and in Synd-GFP; synd1d/Df embryos were indistinguishable from each other (unpublished data).

The furrow membrane in Synd-depleted embryos appeared “loosened” or ruffled as compared with a sharp, distinct furrow in tGPH and Synd-GFP; synd1d/Df rescue embryos (Figure 2, A and B, and Supplemental Movies S2 and S3). This was depicted with a line scan across the metaphase lateral furrow membrane that revealed broader peaks in cycles 12 and 13 in mutant embryos as compared with focused peaks in tGPH and rescue embryos. The furrow plasma membrane moves laterally and synchronously in the x,y plane during the syncytial cycles, and we reasoned that this displacement will be affected if the furrow membranes are shorter and loosened. Previous studies in Xenopus embryos have also shown that loose membranes in planar cell polarity and septin mutants during collective cell migration exhibited increased undulating behavior in kymographs (Kim et al., 2010).

A plot of the mean syncytial furrow-membrane displacement showed a significantly higher variance in synd-depleted embryos as compared with control. Also, the displacement of adjacent furrows occurred asynchronously in mutant embryos (Figure 2, F and G). Thus Synd is required for appropriate furrow elongation, and its deficiency not only causes defects in furrow extension but also membrane ruffling and correlates with an altered displacement and asynchrony in lateral membrane movement.

synd mutants show a loss of Pnut and mislocalization of Dia on the pseudocleavage furrow

Defects in furrow extension prompted us to check the effect of synd mutant on key players of cleavage furrow initiation/extension. Because actin remodeling is likely to be the main downstream driver of furrow ingestion in the syncytial embryo (Webb et al., 2009), and Synd can directly bind and stabilize actin (Kostan et al., 2014), we first used fluorescent phallolidin to check F-actin levels and distribution (Figure 3A). F-actin levels were unaffected in synd embryos. However, F-actin staining also revealed “looseness” in the lateral furrow membrane as shown by tGPH (Figure 2), and this was rescued with Synd-GFP.

FIGURE 3: synd mutant embryos show Pnut loss from pseudocleavage furrow membranes. (A) F-actin distribution (green) in synd1d/Df reveals loose membrane and absence of F-actin puncta below cortex (77%, n = 33) compared with wild-type (3%, n = 50) and Synd-GFP; synd1d/Df (25%, n = 16) embryos. (B) synd1d/Df embryos show Pnut (green) loss (93%, n = 44) as compared with wild type (2%, n = 45) and Synd-GFP; synd1d/Df (30%, n = 14). Anillin localizes normally to the furrow tip membrane (magenta) (86%, n = 44) in metaphase. (C) RhoGEF2 (green) antibody distribution is unchanged in synd1d/Df (91%, n = 11) compared with wild-type embryos. (D) Dia (green) is uniformly distributed along the furrow membrane in synd1d/Df (90%, n = 50) compared with wild-type (3%, N = 50) and Synd-GFP; synd1d/Df (25%, n = 16) embryos. Yellow arrow indicates uniform Dia staining along length of furrow (D); scale bar is for all panels in A–D. Scale bars: 10 μm.
The short-furrow phenotype of synd mutant embryos phenotypically mimics anillin mutants that fail to recruit Pnut on furrow membranes (Silverman-Gavrila et al., 2008). Anillin recruits Pnut to the membrane via its PH domain (Oegema et al., 2000; Field et al., 2005; Liu et al., 2012; Kinoshita et al., 2015) and promotes stable intercellular bridge elongation before abscission (Renshaw et al., 2014). Pnut organizes actin into bundles at highly curved geometries like those in furrow canals during cellularization (Mavrakis et al., 2014). We thus looked at the effect of synd mutant on Pnut and Anillin in the syncytial embryo. Interestingly, we found that, in synd mutant embryos, Pnut association with the pseudocleavage furrow membrane was lost, a defect that was partially reversed by expression of Synd-GFP transgene (Figure 3B). However, Anillin was present on the furrow tip in synd\(^{d/d}\)/Df embryos (Figure 3D). Taken together, this suggests that Pnut recruitment to the membrane does not depend only on its binding to Anillin, but also on Synd and the Anillin-Synd-Pnut interaction is significant for pseudocleavage furrow formation.

Missing and short furrows are caused due to the absence of RhoGEF2 and Dia during syncytial divisions and cellularization (Afshar et al., 2000; Barmchi et al., 2005), implicating them in furrow initiation and extension. In syncytial embryos, RhoGEF2 is cytoplasmic in interphase and localizes to Fts in prophase (Barmchi et al., 2005). Rho1, the downstream RhoGTPase effector of RhoGEF2, is required for Dia recruitment to cellularizing furrows (Grosshans et al., 2005); however, there may be other RhoGEF2-independent mechanisms for Rho1 activation (Yoshida et al., 2009) that allow some Dia to still be recruited to the membrane in germ-line clone rhogef2 mutants (Supplemental Figure S2A and Supplemental Table S1) or RhoGTPase-independent mechanisms may be implicated in its recruitment (Yonetani et al., 2008; Ang et al., 2010). RhoGEF2 was unaffected in synd mutant embryos and localized to the metaphase furrow (Figure 3C), showing that Synd presence on the furrow membrane is not important for RhoGEF2 recruitment.

Dia was identified as a gene responsible for cytokinesis (Castrillon and Wasserman, 1994). It initiates furrow formation along with Adenomatous Polyposis Coli2 (APC2) in Drosophila syncytial embryos (Webb et al., 2009), and Dia and APC1 collaborate to increase actin nucleation (Jaiswal et al., 2013). In synd\(^{d/d}\)/Df embryos, Dia was present uniformly along the length of the furrow in sagittal views, unlike in wild type, where it was enriched at the FT. Dia enrichment at furrow tips was rescued with Synd-GFP (Figure 3D). Altogether we observed that, in synd mutants, Pnut was completely depleted from the furrow, while F-actin, Anillin, and Dia were present on the furrow membrane. These data suggest that Synd contributes to stable furrow formation by recruitment of Pnut and enrichment of Dia at the FT.

**RhoGEF2, Dia, Anillin, and Pnut are each necessary for the recruitment of Synd on the Drosophila syncytial pseudocleavage furrow**

Conversely, to test whether Synd recruitment depends on presence of proteins known to affect furrow formation, we imaged germ-line clone mutant embryos and/or RNA interference (RNAi) lines for rhogef2, dia, anillin, and pnut for Synd antibody localization and found that they are defective for localization of Synd (Figure 4, A and B). Each of these mutants also showed an apical accumulation of F-actin (Figure 4, A and B, Supplemental Figure S2, A and B, and Supplemental Table S1). Most interestingly, these mutants showed significantly reduced Pnut, implying a strong correlation between Synd and Pnut localization on the membrane (Supplemental Figure S2, A and B, and Supplemental Table S1). dia\(^{5}\) mutant embryos also showed a loss of Anillin and Pnut, as reported previously (Afshar et al., 2000), and anillin mutants in turn showed reduced levels of Dia (Supplemental Figure S2 and Supplemental Table S1). In pnut mutant embryos, Anillin was present, but levels were reduced on furrows (Supplemental Figure S2 and Supplemental Table S1). These observations together corroborate the role of Dia in Anillin and Pnut recruitment and also of Anillin in Pnut recruitment.

Because Synd was depleted in pnut mutants, Pnut was in turn depleted in synd (Supplemental Figure S2, A and B, and Supplemental Table S1), and Dia has been shown to be important for furrow initiation (Grosshans et al., 2005), we doubly depleted pnut and dia in synd mutants by combining pnut\(^{OP}\) and dia\(^{5}\) alleles in one copy each (heterozygous) with synd\(^{d/d}\)/Df to see whether the defects intensified. In each case, we obtained very few embryos, suggesting an increased severity as compared with synd\(^{d/d}\)/Df, dia\(^{5/5}\), and pnut\(^{OP/OP}\). Phalloidin revealed stronger defects, such as broader Fts in pnut\(^{OP/OP}\); synd\(^{d/d}\)/Df and missing furrows in dia\(^{5/5}\); synd\(^{d/d}\)/Dia that have been previously observed in dia\(^{5}\) germ-line mutants (Figure 4, A and B; Afshar et al., 2000; Grosshans et al., 2005). Thus the furrow phenotype of synd\(^{d/d}\)/Df was worsened by doubly depleting Dia or Pnut.

**Defects in pseudocleavage furrow extension and morphology in rhogef2\(^{RNAi}\) are reversed by Synd overexpression**

Because furrow-initiation/extension dynamics in pnut and rhogef2 mutant embryos are uncharacterized, we studied this in TGPH-containing embryos depleted for Pnut and RhoGEF2 and found that they phenocopied synd\(^{d/d}\)/Df embryos; the furrow length at 6 min (IV, when the furrow is the longest) was reduced compared with controls (Figure 5, A and B, and Supplemental Movies S4–S6). The pnut\(^{OP/+}\); synd\(^{d/d}\)/Dia combination had short furrows (II–IV) like synd\(^{d/d}\)/Df embryos. To check whether Synd and Pnut can promote furrow dynamics in the absence of RhoGEF2, we overexpressed Synd and Pnut in the rhogef2\(^{RNAi}\) background. A combination of Synd-GFP with rhogef2\(^{RNAi}\) showed a rescue (IV), and the furrows were longer than those observed in either TGPH-Synd-GFP; synd\(^{d/d}\)/Df embryos alone (I–III and V; Figure 5, A and B, Supplemental Figure 2B, and Supplemental Movie S7). Overexpression of Pnut in the rhogef2\(^{RNAi}\) background, however, did not abrogate the furrow length or loosened membrane phenotypes (Supplemental Figure S3, A–H). This shows that Synd could specifically rescue furrow extension in rhogef2\(^{RNAi}\)-expressing embryos.

Like synd mutant embryos, rhogef2\(^{RNAi}\) and pnut\(^{RNAi}\) mutant embryos had broad furrows and loosening of membrane along the edges revealed by a line scan across orthogonal sections in cycles 12 and 13 (Figure 5, C and D). Multiple kymograph analyses for lateral furrow membrane in the x,y plane showed significantly less mean displacement and therefore increased severity in rhogef2\(^{RNAi}\), pnut\(^{RNAi}\), and pnut\(^{OP/+}\); synd\(^{d/d}\)/Df combination mutants as compared with synd\(^{d/d}\)/Df (Figure 5G and Supplemental Figure 2G). Furrow displacement depends on Rhoge2 and Pnut, and synd mutant embryos show a significant defect in displacement along with lowering of Pnut in the pnut\(^{OP/+}\) background.

In summary, we found that pnut and rhogef2 mutant embryos phenocopied the furrow-extension defects of synd mutant embryos and Synd overexpression could reverse the furrow defects in rhogef2 mutant embryos.

**Rab5 early endosome depletion in rhogef2 mutant embryos is not reversed by Synd overexpression**

Synd functions in Clathrin/Dynamin-mediated endocytosis and actin remodeling (Qualmann and Kelly, 2000; Edeling et al., 2009).
Therefore we evaluated the contribution of Synd’s role in endocytosis for metaphase furrow formation. First we analyzed the localization of Dynamin/Shibire in synd1/Df embryos. Dynamin levels in immunostained synd mutant embryos were unaffected and colocalized with Amph at the furrow tip. rhogef2RNAi showed a punctate distribution of Dynamin similar to that seen in shiRNAi (Figure 6A). shiembryos also showed reduced Synd distribution on the membrane (Figure 6B) that correlated with previously observed reduction in Pnut levels and loss of metaphase furrow formation (Rikhy et al., 2015).
Endocytosis occurs at the tip of the ingressing syncytial furrows and can be visualized in the form of tubules labeled with Amph (Sokac and Wieschaus, 2008a). Their formation depends on actin and Dynamin and correlates with the rate of furrow ingestion in cellularization (Oegema et al., 2000; Sokac and Wieschaus, 2008a, 2008b; Su et al., 2013). We quantified the length of tubules in control and mutant embryos. syndΔ/Δ embryos showed a significant decrease in length of tubules (Supplemental Figure S4, A and B). Synd-GFP expression in syndΔ/Δ embryos restored the tubule length defect comparable to wild type. shi mutant embryos at the restrictive temperature are reported to show an increase in length of tubules during cellularization (Sokac and Wieschaus, 2008a; Su et al., 2013); we also found a significant increase in their length compared with wild type in syncytial cycles (Supplemental Figure S4, A–C). In rhogef2ΔRNAi embryos, there was no significant change in the tubule length. When Synd-GFP was overexpressed in rhogef2ΔRNAi embryos, the tubule length increased slightly (Supplemental Figure S4, A–C). Rab5 early endosome vesicles increase when synd mutant but not in rhogef2 mutant embryos (Figure 6, C and D). Taken together, these data indicate that Synd-GFP expression rescued the Amh tubule length defect and Rab5 vesicle number in synd mutant embryos but did not rescue the Rab5 vesicle number in rhogef2 mutant embryos.

**Defects in recruitment of Pnut in rhogef2ΔRNAi are partially reversed by Synd overexpression**

Finally, we analyzed the localization of Dia, Anillin, Pnut, and F-actin to the pseudocleavage furrow membrane in rhogef2ΔRNAi embryos alone and with Synd overexpression (Figure 7, A–D). On overexpression with Synd-GFP in the rhogef2ΔRNAi background, we observed a rescue in Dia and Pnut localization to the pseudocleavage furrow membrane compared with rhogef2ΔRNAi embryos (Figure 7, A and B). F-actin localization to furrows was uniform, and its apical accumulation was lost (Figure 7C). To gain further insight into morphological defects in F-actin seen in rhogef2 and synd mutants, we used structured illumination by Airyscan and three-dimensional (3D) surface rendering. The maximum-intensity projection (MIP) and surface-rendered image (Surface) in wild type revealed long and short actin along with few punctate structures. In synd mutants, however, the long structures were lost, and F-actin was disorganized and punctate along the furrow. Likewise, in rhogef2ΔRNAi, actin was accumulated in disorganized patches, and there were no long structures. On overexpression of Synd-GFP in the rhogef2ΔRNAi background, we found long, organized structures at the furrow and can, in the process, rescue furrow structures into continuous structures can restore furrow actin organization and morphology in synd and rhogef2 mutant embryos.

**DISCUSSION**

Syndapins belong to the family of highly conserved F-BAR–domain containing proteins with diverse roles in membrane tubulation (Kumar et al., 2009a; Ramesh et al., 2013), Clathrin-mediated and bulk endocytosis (Qualmann et al., 1999; Qualmann and Kelly, 2000), and actin remodeling (Qualmann et al., 1999; Qualmann and Kelly, 2000; de Kreuk et al., 2011; Kostan et al., 2014) and cytokinesis (Takeda et al., 2013). Synd is thus poised to play a role in processes like furrow formation, which need orchestrated remodeling of both the membrane and the cytoskeleton (Bezanilla et al., 2015). Furrow elongation in syncytial Drosophila embryos is an excellent model system to study the role of proteins that drive its formation. Previous studies show that furrow formation involves membrane addition by trafficking and membrane extension by remodeling of the actin meshwork (Afshar et al., 2000; Stevenson et al., 2002; Cao et al., 2008; Crest et al., 2012; Figard et al., 2013; Holly et al., 2015; Rikhy et al., 2015). We have been able to conclusively demonstrate that Synd functions to promote furrow formation by organization and elongation of F-actin structures (Figure 8). We show that Synd is essential for recruitment and distribution of Pnut and Dia on the membrane (Figure 3). In turn, Pnut and Dia also affect Synd distribution on the membrane (Figure 4). RhogEF2/Dia and Anillin/Pnut have been previously shown to regulate F-actin architecture at cleavage and cellularization furrows (Afshar et al., 2000; Liu et al., 2012; Mavrakis et al., 2014), and loss of Synd in synd mutants therefore affects actin both directly and through its influence on Pnut and Dia localization. As with other actin-regulated processes, even though a linear pathway of association/regulation of these actin-remodeling proteins to the furrow membrane is unlikely, our data imply that Synd is a key component in the RhoGEF2-Dia-Anillin/Pnut pathway during actin-driven furrow elongation. Synd2 can bind and inhibit Rac1 via its SH3 domain, thus reducing Arp2/3 activity (de Kreuk et al., 2011), and may therefore be able to potentiate Dia
FIGURE 5: Aberrant furrow membrane phenotype and Pnut recruitment in rhogef2\textsuperscript{RNAi} embryos is reversed by Synd overexpression. (A–G) Pnut and rhogef2 mutant embryos have decreased metaphase furrow lengths, loose furrow membranes, and decreased x,y displacement, and rhogef2\textsuperscript{RNAi} phenotypes are reversed by Synd-GFP. Time-lapse orthogonal views (A) at 0, 3, 5, 6, and 7 min (corresponding to I, II, III, IV, and V) of furrow extension in Pnut\textsuperscript{RNAi}, rhogef2\textsuperscript{RNAi}, and Pnut\textsuperscript{P/+; synd}\textsuperscript{d} mutants expressing tGPH show a decrease compared with control and Synd-GFP; rhogef2\textsuperscript{RNAi} (B) (mean ± SEM) (n = 3; 5 furrows/embryo). Surface and orthogonal views of longest metaphase furrows in Pnut\textsuperscript{RNAi}, rhogef2\textsuperscript{RNAi}, and Pnut\textsuperscript{P/+; synd}\textsuperscript{d} compared with control and Synd-GFP; rhogef2\textsuperscript{RNAi} embryos in nuclear cycles 12 and 13 (C). Line scan-intensity profile across mutant furrow membranes shows a broader area (arrows) that is...
FIGURE 6: Rab5 early endosomes are depleted in synd and rhogef2RNAi embryos. (A) Dynamin (green) distribution is unaffected in synd mutant embryos. Dynamin levels are unaffected in syndDf embryos but have a punctate distribution in shRNA, shRNA, rhogef2RNAi, and Synd-GFP; rhogef2RNAi embryos (100%, n = 10) compared with wild type. (B) Synd is reduced from the furrow membrane in shRNA embryos (100%, n = 12). (C and D) Rab5 vesicle immunostaining and numbers/pseudocell are decreased in syndDf, shRNA, and rhogef2RNAi. Rab5 vesicle numbers are rescued in Synd-GFP; syndDf and not in Synd-GFP; rhogef2RNAi embryos (n = 3, n.s., not significant, *, p < 0.05, nonparametric Mann-Whitney U-test).
FIGURE 7: Synd overexpression reverses the actin organization and actin remodeling protein recruitment defects in rhogef2RNAi mutant embryos. (A–D) Dia, Anillin, and Pnut recruitment defects in rhogef2RNAi are reversed by Synd-GFP. Synd-GFP; rhogef2RNAi metaphase (DNA, blue) embryos show a reversion of Dia (magenta) (50%, n = 10 compared with 91%, n = 22 in rhogef2RNAi) (A), Pnut (green) and Anillin (magenta; 66%, n = 12 compared with 100%, n = 14 in rhogef2RNAi) (B) apical accumulation of actin (green) (50%, n = 10 compared with 100%, n = 16 in rhogef2RNAi) (C). F-actin
activity by increasing RhoA levels (Korobova and Svitkina, 2008). Such a mechanism can explain increased Dia function when Synd is overexpressed in RhoGEF2 knockdown embryos, which, along with recruitment of Pnut to the membrane, can help organize actin and elongate cleavage furrows (Figure 8).

Actin stabilization into continuous structures reversed the furrow length defect in synd mutant embryos. Jasp blocks actin turnover at the contractile ring (Murthy and Wadsworth, 2008) and affects cleavage furrow invagination while preserving furrow integrity (Cao et al., 2008), and hence showed fewer punctae in synd and rhogef2 mutant embryos. CytoD, on the other hand, allows actin polymerization (Goddette and Frieden, 1986; Franki et al., 1992), and as a result,

synd and rhogef2 mutant embryos treated with CytoD displayed more organized actin structures and elongated furrows (Figure 7E). This provides mechanistic insight into how Synd functions in regulating actin polymerization and may be further investigated through kinetic studies of actin polymerization.

Overexpression of Synd and not Pnut in the rhogef2RNAi-containing embryos partially reversed pseudocleavage furrow recruitment and morphology defects seen in rhogef2RNAi and increased the furrow length compared with wild type. Synd activity is thus needed at the pseudocleavage furrow for extension, and some as yet uncharacterized proteins play a role in furrow limitation. It is interesting to compare the functions of F-BAR domain proteins, Synd with Cip4 in furrow elongation and Dia recruitment. Cip4 antagonizes Dia function, and its overexpression has dia loss-of-function phenotypes like missing furrows (Yan et al., 2013). It is possible that opposing activities of F-BAR proteins Synd and Cip4 with respect to Dia are in a balance, and future experiments can test whether this function plays a role in limiting the growth of pseudocleavage furrows.

Because Synd’s SH3 domain interacts with Dynamin (Kumar et al., 2009a), and Dynamin has a role in endocytosis and furrow extension in syncytial divisions and cellularization (Sokac and Wieschaus, 2008a; Rikhy et al., 2015), it remained to be investigated whether Clathrin-dependent endocytosis defects in synd mutants also affect furrow elongation. We showed that synd mutant embryos have defects in cleavage furrow–tubule length and Rab5 vesicle numbers (Figure 6 and Supplemental Figure S4). Decrease in Rab5 vesicle numbers is also seen in rhogef2 mutant embryos. However, Synd-GFP overexpression in rhogef2 mutant embryos is able to reverse the furrow-extension defect without rescuing the Rab5 endocytic vesicle defect. Taken together, our data show that Synd has a role in endocytosis, but the reversal of furrow phenotypes in rhogef2 mutant embryos is due to the ability of Synd to recruit and organize actin and proteins of the actin-remodeling machinery such as Dia and Pnut.

Our analysis of membrane architecture and pseudocleavage furrow length in rhogef2, pnut, and synd mutants found that shorter furrows in each of these mutants were also loose/unstable and had slow lateral movement during the nuclear cycle (Figures 2 and 5 and Supplemental Figure S3). Septins brace the plasma membrane against aberrant cell-shape deformation and are able to tubulate phosphatidylinositol-4,5-bisphosphate liposome membranes when treated with a brain extract (Tanaka-Takiguchi et al., 2015). It is probable that Septin-mediated membrane tubulation activity and cell-shape effects are dependent on the presence of F-BAR proteins like Synd. Sept7 mutants in Xenopus show unstable and undulating membranes during gastrulation (Kim et al., 2010). This substantiates Synd’s role in maintenance of membrane integrity and shape by affecting actin organization and Pnut recruitment.

Overall mutant and epistatic analyses presented here find a significant role for the F-BAR domain protein Synd in mediating pseudocleavage furrow extension. Our study favors a model in which Synd, along with Anillin and RhoGEF2, provide a platform for
recruitment of Dia and Pnut to allow persistent and stable growth of assembly at large.

MATERIALS AND METHODS

Drosophila strains and genetics

Flies were raised on standard cornmeal agar at 25°C. Embryos from Canton S flies were used in control experiments. Homozygous escape adults from the transposon-tagged mutant synd1/dFRTG13/TM6B, Tb1 (V. Kumar, IISER, Bhopal, India [Kumar et al., 2009a]) or adults in with trans-allelic combination of synd1/dFRTG13/TM6B [3BI-SC43] [BL-7413] were used to generate synd mutant embryos. These embryos showed a loss of Synd immunostaining and high percentage of embryonic lethality by hatch assay (Figure 1). The synd mutant phenotype was rescued using Synd-GFP (T. Takeda and D. Glover, University of Cambridge, UK [Takeda et al., 2013]). syndRNAi (BDSC stock) was crossed to nanos-Gal4 and embryos laid by females of the genotype syndRNAi/nanos-Gal4 showed a lower embryonic lethality than the mutant (Figure 1).

For immunohistochemistry, the following stocks were used: w1; Dia; FRT40A/CyO [BL-9138], y1; w1; rhofgfr2A; 1 FRTG13/CyO [BL-9122], and pnutGFP; FRTG13/SM6a-TM6B, Tb1 (M. Mavrakis, Fresno Institute, Paris). Females carrying the mutant and heat-shock FLP were crossed to respective FRT ovoD males -ovoD FRT40A/CyO [BL-2121] or ovoD FRTG13/CyO to generate germ-line clones by heat-shocking third instar larvae, pupae, and adult flies for 1 h each at 37.5°C. The transheterozygous animals scraOD250/scrA[BL-4403, 4286] gave anillin (scrap) mutant embryos. shiG2 (R.R.) mutants were transferred to a restrictive temperature (32°C) for 5 min before fixation. Gap43-Venus (Mavrakis et al., 2009) with H2A-RFP [BL-25377] was used to show pseudocleavage furrow morphology changes across nuclear cycle 13. Metaphase furrow lengths in nuclear cycles 12 and 13 were measured by a tGPH; nanos-Gal4 recombinant line [BL-8163, 4937]. RNAi lines for rhofgfr2 [BL-34643], dia [BL-33424], and pnut (VDRC, Austria) were used. Ub-Synd-GFP/+; synd1/dFrtD was used to measure furrow and protein dynamics and Ub-Synd-GFP was combined with rhofgfr2RNAi to test rescue. UASP-mCherry::Pnut (T. Lecuit, IBDM, France [Guillot and Lecuit, 2013]) was used to overexpress Pnut in the background of rhofgfr2RNAi.

Immunohistochemistry

Embryos were collected for 3 h at 25°C (and at 28°C for RNAi experiments) on 3% sucrose agar plates; washed and dechorionated in 100% bleach for 1 min; fixed in 1:1:4% paraformaldehyde in phosphate-buffered saline (PBS):heptane for 15 min; hand/methanol devitellinized; permeabilized with 0.3% Triton-X in PBS (PBST); blocked in 2% bovine serum albumin (Sigma-Aldrich) in PBST; and immunostained with primary antibodies: Synd (rat, 1:150 [V. Kumar]), Dia (rabbit, 1:1000 [S. Wasserman, University of California, San Diego]), Pnut (mouse, 1:5 [DSHB-49H4]), Anillin (rabbit, 1:1000 [C. Field, Harvard, and Julie Brill, The Hospital for Sick Children, Toronto, Canada]), Rab5 (rabbit, 1:200 [Abcam]). RhoGEF2 antibody (rabbit, 1:500 [J. Grosshans]) staining was done after heat-fixation followed by 1:1:heptane:methanol devitellinization. Fluorescently coupled secondary antibodies (Alexa Fluor 488, 568, and 633; 1:1000; Life Technologies, Bangalore, India) were used. DNA was labeled with Hoechst 33342 (10 mg/ml; 1:1000; Life Technologies) and F-actin was labeled with Alexa Fluor 488/568 phalloidin (1:100; Life Technologies). The embryos were mounted in SlowFade Gold (Life Technologies). These samples were imaged using a Plan-Apochromat 40x/1.3 NA oil-immersion objective on a confocal laser scanning microscope (LSM 710, Zeiss, Bangalore, India). z-Stacks were acquired on sequentially scanned images with a spacing of 1.08 μm between slices. n values indicate number of syncytial cycle 12 or 13 embryos screened. Embryos defective for a phenotype were calculated as a percentage of n. For quantitative analysis of Rab5-positive vesicles and Amph furrow tubules, images were acquired using a Plan-Apochromat 63x/1.3 NA oil-immersion objective on a confocal laser scanning microscope (LSM 710, Zeiss) with pinhole set at 1 AU for best signal/noise.

Zeiss LSM 800 with Airyscan (0.15 μm slice thickness) was used to acquire and process high-resolution images of Hoechst and phalloidin-stained embryos.

Drug treatment with actin-binding drugs

Dechorionated embryos were added to a solution of 1:1::(R)-(-):Limonene (Sigma):heptane to which the drug dissolved in DMSO was added to achieve the desired final concentration (200 nM Jasp, 50 μM/100 μM CytoD, 10 μM LatA, or DMSO without drug in case of control) and incubated with shaking for 5 min (adapted from Rand et al., 2010; Schulman et al., 2013). The solution was then replaced with fresh heptane and subsequently fixed, hand devitellinized, and immunostained as described in the protocol described above.

Live-embryo time-lapse imaging

Embryos were collected for 1 h, dechorionated, and mounted in a LabTek chamber with PBS (Mavrakis et al., 2008) and imaged in four dimensions (every 30 s with 0.48/0.18 μm thickness) using a Zeiss Plan-Apochromat 40x/1.4 NA oil-immersion objective on a Zeiss LSM 780 inverted confocal microscope. Staging of embryos during the cell cycle was done by corroborating the presence of the nuclear envelope and its breakdown with metaphase furrow length. Because some tGPH is in the cytoplasm, these events are easy to distinguish in the live movies to accurately stage the embryos.

Image processing

Images were processed with ImageJ (National Institutes of Health) and compiled with Adobe Photoshop CS5. Immunostains are shown from single optical planes for sagittal (x,z) or surface views (x,y). A Gaussian smoothing filter with a radius of one pixel was used to reduce noise. Processed Images of F-actin and DNA obtained from Airyscan were imported into Imaris8.1 software (Bitplane, Hyderabad, India), and snapshots of single z-slices (Slice), 3D surface rendering (Surface), and MIP were represented.

FRAP

For FRAP (Mavrakis et al., 2008), three prebleach scans and 30 bleach iterations (0.03 s each) were taken on living Synd-GFP and tGPH embryos in ~2.5 μm2 regions on the apical and FT membrane. Recovery of fluorescence intensity was recorded until a steady state was reached. The data were background corrected and normalized to the prebleach intensity and transformed on a 0-1 scale. The individual postbleach intensities were fit with a one-phase exponential association equation (Y = Ymax (1− e−Kb t) + c) using GraphPad. Non-linear regression was used obtain the Ymax or mobile fraction for Synd-GFP (R2 = 0.83 ± 0.1 SD and 0.83 ± 0.03 SD for apical and FT membranes, respectively). The immobile fraction (1-mobile fraction)
was calculated and plotted as scatter plots using GraphPad for apical and FT membranes.

**Image analysis and quantification**

Intensity density on membrane regions from confocal images of Synd and Amph was computed using ImageJ. After background subtraction, the ratio of Synd:Amph was plotted as a box plot using GraphPad. A nonparametric Mann-Whitney U-test was performed to test for significance between means. Intensity of Synd-GFP (in apical, lateral, and FT membrane regions) was similarly measured from images in metaphase of cycles 11, 12, and 13 and plotted as a scatter plot using GraphPad. The mean intensity values were compared for significance using one-way analysis of variance (ANOVA), Tukey's multiple-comparison test. For furrow length, freehand lines along the lateral membrane to FT from orthogonal views at desired time points of time-lapse movies were measured, and the mean ± SEM of the furrow length was plotted using GraphPad. Lateral furrow broadness was represented as intensity peaks on a line across the SEM of the furrow length was plotted using GraphPad. Lateral membrane movement of metaphase furrows in the Z plane was measured, and the mean ± SEM of the furrow length was plotted using GraphPad. Lateral furrow broadness was represented as intensity peaks on a line across furrows in orthogonal views using the Plot profile analysis tool of ImageJ. For numbers of Rab5-positive vesicles, the ImageJ plug-in 3D-Objects Counter was used. Only objects in the volume of the pseudocell and below 250 nm diameter were counted. The absolute number was normalized to the number of pseudocells in the pseudocell and below 250 nm diameter were counted. The absolute number was normalized to the number of pseudocells in the pseudocell and below 250 nm diameter were counted. The absolute number was normalized to the number of pseudocells in the region of interest (ROI) and plotted for 3 embryos/genotype using ImageJ. For quantification of furrow-tubule length, images of fixed Amph-stained embryos in prometaphase during cycle 13 were used; freehand lines were drawn along the tubules, and their length was measured using ImageJ and their number was counted. The length and number (per furrow) were plotted for a minimum of five embryos/genotype using GraphPad.

**Kymograph analysis**

Lateral membrane movement of metaphase furrows in the x,y plane was plotted using the Multiple Kymograph plug-in of ImageJ on single-plane time-series movies of tGPH::GFP-labeled embryos. Lines were drawn to generate tracks across four metaphase 13 furrows. The displacement was quantified by selecting the initial to final points of furrow movement using the line tool and, subsequently, the macro "read velocities from tsp" to obtain displacement/velocities. The displacement was plotted using GraphPad. An unpaired t test (two-tailed) with Welch's correction was used to test significance between means, and an F-test was used to compare significant difference in variances.

**ACKNOWLEDGMENTS**

This study was motivated by K. S. Krishnan, and we dedicate this study to him. We thank Manos Movrikis, Vimlesh Kumar, Thomas Pucadyil, Aurnab Ghose, Girish Ratnaparkhi, L. S. Shashidhara, Anuradha Ratnaparkhi, Girish Deshpande, and R.R. lab members for critical comments throughout this work. A.S. thanks Sharmik Banerjee for discussions and critical reading of the manuscript. Ramya Balaji, Prachi Richa, and Vishnu Saraswathy helped with preliminary characterization of synd mutants. We thank Vimlesh Kumar, Steve Wasserman, Hugo Bellen, Tetsuya Takeda, Manos Movrikis, Thomas Lecuit, Christine Field, and Julie Brill for reagents. We thank the Bloomington Stock Center for fly stocks. We thank the IISER, Pune, Drosophila imaging and facility imaging for help with fly maintenance and microscopy. The LSM 800 Airyscan microscope for high-resolution imaging was kindly shared by Zeiss, India. A.S. thanks the Council of Scientific and Industrial Research for a graduate fellowship. R.R. thanks the Department of Biotechnology and IISER, Pune, for funding this work.

**REFERENCES**


