A novel role for an APC2-Diaphanous complex in regulating actin organization in *Drosophila*

Rebecca L. Webb, Meng-Ning Zhou and Brooke M. McCartney*

The rearrangement of cytoskeletal elements is essential for many cellular processes. The tumor suppressor Adenomatous polyposis coli (APC) affects the function of microtubules and actin, but the mechanisms by which it does so are not well understood. Here we report that *Drosophila* syncytial embryos null for *Apc2* display defects in the formation and extension of pseudocleavage furrows, which are cortical actin structures important for mitotic fidelity in early embryos. Furthermore, we show that the formin Diaphanous (DIA) functions with APC2 in this process. Colocalization of APC2 and DIA peaks during furrow extension, and localization of APC2 to furrows is DIA-dependent. Furthermore, APC2 binds DIA directly through a region of APC2 not previously shown to interact with DIA-related formins. Consistent with these results, reduction of *dia* enhances actin defects in *Apc2* mutant embryos. Thus, an APC2-DIA complex appears crucial for actin furrow extension in the syncytial embryo. Interestingly, EB1, a microtubule +TIP and reported partner of vertebrate APC and DIA1, may not function with APC2 and DIA in furrow extension. Finally, whereas DIA-related formins are activated by Rho family GTPases, our data suggest that the APC2-DIA complex might be independent of RHOGEF2 and RHO1. Furthermore, although microtubules play a role in furrow extension, our analysis suggests that APC2 and DIA function in a novel complex that affects actin directly, rather than through an effect on microtubules.

**KEY WORDS:** Adenomatous polyposis coli (APC), Diaphanous, *Drosophila* syncytial development

**INTRODUCTION**

Orchestrated cytoskeletal rearrangements play fundamental roles in a diverse array of cellular and developmental processes, from cytokinesis and cell migration to cell shape changes that underlie morphogenesis. The Adenomatous polyposis coli (APC) family of tumor suppressors can influence microtubules, and has been suggested to regulate actin (reviewed by Nathke, 2004). In addition, APC proteins (see Fig. 1A,B) are essential negative regulators of Wnt signaling (reviewed by Logan and Nusse, 2004). Although it is clear that disruption of APC signaling plays a key role in the initiation of colon cancer, excessive Wnt signaling alone may not explain the role of APC in tumorigenesis (reviewed by Nathke, 2004).

APC proteins may affect both microtubules and actin in a variety of ways (reviewed by Nathke, 2004). The microtubule-associated functions of APC proteins have become clearer in recent years with the identification of a role for APC in kinetochore-microtubule interactions (Green and Kaplan, 2003), and as part of a ‘cortical template’ that directs microtubule network formation (Reilein and Nelson, 2005). Via its Armadillo repeats (Fig. 1A), APC can interact with Kinesin-associated protein 3 (KAP3) and appears to be transported along microtubules to the cortex via KIF3A/3B (Jimbo et al., 2002). The movement of APC along microtubules is enhanced in cell projections involved in migration (Mimori-Kiyosue et al., 2000; Nathke et al., 1996). In cultured cells, mammalian APC promotes microtubule stability (Kroboth et al., 2007), and in some contexts it promotes stability together with the formin DIA1 and the microtubule plus-end tracking protein (+TIP) EB1 (Wen et al., 2004). APC also affects microtubule dynamic instability independent of EB1 (Kita et al., 2006).

APC2 localizes with actin in multiple contexts in *Drosophila* embryos and epithelial cells (McCartney et al., 1999; Townsley and Bienz, 2000; Yu and Bienz, 1999). Such APC-actin interactions may influence Rho family GTPases, as APC has been shown to interact with the RacGEF ASEF and with IQGAP, an effector of RAC1 and CDC42 in cultured cells (Kawasaki et al., 2003; Kawasaki et al., 2000; Watanabe et al., 2004). Despite many reports of APC-cytoskeletal interactions, the specific mechanisms by which APC proteins affect the cytoskeleton are still poorly understood, particularly in coordinated cytoskeletal rearrangements.

The *Drosophila* syncytial blastoderm is a superb system in which to study dynamic coordinated actin and microtubule rearrangements. Early *Drosophila* embryogenesis is syncytial, with nuclear division occurring without cytokinesis (reviewed by Sullivan and Theurkauf, 1995). By interphase of nuclear cycle 10, most nuclei have migrated to the cortex to form the syncytial blastoderm. These nuclei undergo four rounds of roughly synchronous mitoses (cycles 10-13) before cellularization. During interphase, actin is organized into caps above each nucleus (see Fig. 1C,D) (reviewed by Schejter and Wieschaus, 1993). These caps ‘expand’ into diffuse rings at the periphery of each nucleus during prophase. Cortical actin becomes focused into tight rings surrounding each nucleus during prophase of cycles 11-13, and the actin extends into the embryo to form pseudocleavage furrows that surround each spindle (Fig. 1E,F). Reaching their maximum depth during metaphase, and quickly retracting during anaphase and telophase, these furrows serve as physical barriers between adjacent nuclei that prevent collisions. Such collisions might otherwise result in abnormal nuclei and nuclear loss from the cortex (reviewed by Sullivan and Theurkauf, 1995). As daughter nuclei reform during telophase, actin redistributes into caps. These cytoskeletal rearrangements continue through each cortical syncytial nuclear cycle.

We previously showed that APC2 localizes with actin caps and pseudocleavage furrows during syncytial development, and that hypomorphic mutations in *Drosophila Apc2* result in nuclear loss without significant defects in actin or microtubule organization.
Development 136 (8) 1284

(Castrillon and Wasserman, 1994), and wild type (WT; approximation of the normal distribution. For each genotype were assessed. Statistics employed the binomial approximation of the microtubule +TIP EB1 and RH101 signaling.

MATERIALS AND METHODS

Fly stocks

The following were used: Apc2Δ11 (McCartney et al., 1999), Apc2Δ10 and Apc2Δ10 (McCartney et al., 2006), dia Δ FRT40A (Afshar et al., 2000; Castillion and Wasserman, 1994), diaΔCyO[Bloomington Stock Center (BSC)], diaΔCyKrGFP (Castillion and Wasserman, 1994), FRTG13 Rho1L3 (Hacker et al., 2003), FRTG13 RhoGEF2Δ962 (Hacker and Perrimon, 1998) and wild type (WT; Oregon-R-S, BSC). The Eb1-null allele (Eb1Δ11) is a deletion resulting from the imprecise excision of a local P-element (L. Lee, personal communication). FRT Eb1Δ11 was a gift from P. Kolodziej (Vanderbilt University, Nashville, TN, USA). Mutant embryos maternally diaΔ FRT40A, FRTG13 Eb1Δ11, FRTG13 Rho1Δ or FRTG13 RhoGEF2Δ962 were generated using FLP/FRT/DFS (Chou and Perrimon, 1996). During syncytial development, zygotic transcription is not significantly active. Genotypes referred to are maternal, and females were mated to WT males.

Immunolocalization and imaging

Embryo preparation

Embryos were collected for 2 hours (syncytial) or 6 hours (gastrulated) at 27°C, fixed and stained as described by McCartney et al. (McCartney et al., 1999), or were hand devitellinized. Antibodies and labels were as follows. Anti-β-tubulin (E7, 1:500, Developmental Studies Hybridoma Bank), anti-acetylated tubulin (1:350, Sigma), anti-APC2 [1:500 (McCartney et al., 1999)], anti-DIA [1:5000 (Afshar et al., 2000)] and anti-Anillin [1:1000 (Field and Alberts, 1995)]. Secondary antibodies were labeled with Alexa Fluor 488, 568 or 647 (1:1000, Invitrogen). Actin was detected using Alexa Fluor 488-phalloidin (1:500, Invitrogen). DNA was stained with DAPI (1:1000, Sigma) or propidium iodide (25 μg/ml, Invitrogen) for 30 minutes, followed by a 2-hour incubation with RNase A (10 mg/ml). Embryos were mounted in Aqua-Poly/Mount (Polysciences).

Image acquisition and analysis

Images were acquired with a spinning-disc confocal microscope (Solamere Technology Group) with a Yokogawa scanhead on a Zeiss Axiovert 200M using QED InVivo software. ImageJ and Adobe Photoshop were used for image analysis. z-stacks of 0.2 μm optical slices were taken from the apical surface to below the cortical nuclei/microtubules. To generate cross-sections from z-stacks, the x-y image stack was resliced in the x-z plane in ImageJ (Figs 2, 5, 7 and 8). Alternatively, cross-sectional single images of embryos were acquired (Fig. 4; see Fig. S4 in the supplementary material). Embryos were assigned to nuclear and cell cycle stage according to features of their DNA and microtubules.

Live imaging

Dechorionated embryos containing ZeusGFP, a microtubule marker (Morin et al., 2001), were mounted in halocarbon oil (700 series, Halocarbon Products) on PetriPERM dishes (Sigma). Images were acquired every 30 seconds.

Furrow depth analysis

The most apical actin section of the embryo was designated as the 0 μm position, and –0.8, –1.6, and –2.2 μm depths were also analyzed. This captured the entire furrow in the WT. Each slice was scored for complete and incomplete actin rings (i.e. those missing any portion of the ring) (see Fig. S1 in the supplementary material). Five embryos (~200 actin rings) for each genotype were assessed. Statistics employed the binomial approximation of the normal distribution.

Spindle dynamics

We measured the pole-to-pole distance of ten spindles in three embryos for each genotype, from metaphase through anaphase B. We measured the midbodies in telophase. Two iterations of adaptive deconvolution using AutoDeblur Gold CF software version X2.1.1 (Media Cybernetics) were performed on the images in Fig. 3D-E’ and Fig. S2K-N (see Fig. S2 in the supplementary material).

Colocalization

We examined the localization patterns of APC2 and DIA in multiple nuclear cycle 12 WT embryos throughout the cell cycle at approximately ~1.0 μm. Colocalization was defined as when pixel intensities 150 to 255 were detected in the same position in the APC2 image and the correlated DIA image using the ImageJ Colocalization plug-in (Fig. 4Ae-Fc).

Plasmid construction

N-terminal Glutathione S-transferase (GST) and Maltose-binding protein (MBP) fusions were generated by PCR, followed by subcloning of fragments encoding EB1 (amino acids 1-291), human APCΔBasic (167-2843), human APCΔBasic (2167-2674), human Apc2Δ10 (2673-2843) and Drosophila Apc2ΔBasic (2135-2412) into pGEX-4T1 (GE Healthcare); APC2N (1-490) into pGEX-4T3 (GE Healthcare); APC2Δ10 into PBX-EB1 (491-1067), DIA1 (1-506) and DIA3 (484-1091) into pLM1 (Pai et al., 1996); EB1 (1-291) and Chickadee (CHIC, Drosophila profilin; amino acids 1-126) into pMAL-c2x (NEB). His-DIAC484 (pQE80, 519-1091) was provided by H. Muller (Grosshans et al., 2005).

Direct protein-protein interactions

Bound protein (10 μg) was incubated for 1 hour at 4°C with free protein (10 μg) in HKT buffer (Miles et al., 2005) or modified RIPA buffer (Wen et al., 2004) with 1 mM DTT. The amount of protein in the bead (B) lanes was four times that in the input and supernatant (S) lanes. Immunoblots probed with HRP-conjugated anti-MBP (1:10,000, NEB) or anti-DIA (1:10,000) were developed using the HRP SuperSignal West Pico Chemiluminescent Substrate Kit (Pierce).

Immunoprecipitation

WT 0-2 hour embryos (27°C) were lysed in 50 mM HEPES (pH 7.5), 115 mM KAc, 2.5 mM Mg(Ac)2, 0.5% Nonidet P40 substitute (Sigma), 0.5 mM EDTA, 0.5 mM EGTA, 1% Complete protease inhibitor cocktail (Roche), 1% Phosphatase inhibitor cocktail 2 (Sigma). Anti-Myc (DSHB) immunoprecipitations were at 1:40 and anti-APC2 (McCartney et al., 1999) at 1:50. Complexes were precipitated with Protein G-agarose (Zymed). Western blots probed for APC2 (1:1000) or DIA (1:5000) were developed as described above.

RESULTS

Complete loss of APC2 results in furrow extension defects

In our original study of APC2 function in the early embryo (McCartney et al., 2001), the alleles of Apc2 were not null; both Apc2Δ11 and Apc2Δ10 produce mutant proteins (McCartney et al., 1999; McCartney et al., 2006). Apc2Δ10 is a nonsense mutation that changes amino acid 383 to a stop (Fig. 1B). No truncated protein was detected in the same position in the APC2 image and the correlated DIA image using the ImageJ Colocalization plug-in (Fig. 4Ae-Fc).

To assess cytoskeletal defects in Drosophila Apc2 mutants, we examined actin and microtubules in fixed, stage-matched wild-type (WT) and mutant syncytial embryos. Metaphase Apc2Δ10 embryos exhibited incomplete actin rings that were occasionally associated with apparent spindle collisions (Fig. 2A, arrow and arrowhead). We also observed incomplete actin rings in Apc2Δ10 embryos (Fig. 2A, arrow). To determine whether these reflect defects in furrow extension, we examined stage-matched WT and mutant embryos in

DEVELOPMENT
cross-section. Although furrows initiated in some Apc2\textsuperscript{240} and Apc2\textsuperscript{210} embryos, they did not extend normally (Fig. 2B, arrows). By contrast, furrow extension in Apc2\textsuperscript{240} embryos appeared largely as in WT (Fig. 2B). To quantify actin defects, we assessed actin rings as viewed from the surface at four depths, using the presence of incomplete actin rings as a measure of furrow depth (see Fig. S1 in the supplementary material). This analysis clearly demonstrated a statistically significant increase in the percentage of incomplete actin rings as a measure of furrow depth (see Fig. S1 in the supplementary material). Finally, we analyzed WT and Apc2g10 mutants (Fig. 2C). Mutants appeared to have the same density and organization as in WT (Fig. 3D-F). Apc2g10 mutants exhibited defects in furrow assembly in the syncytial embryo and during cytokinesis (Afshar et al., 2000; Castrillon and Wasserman, 1994). Interestingly, mouse DIA1 (also known as DIAP1) is reported to function with diaphanous mutant embryos exhibit defects in furrow extension

To understand how loss of APC2 affects actin organization, we asked what other proteins function with APC2 in this process. Formins nucleate and elongate unbranched actin filaments (reviewed by Goode and Eck, 2007), and, consistent with this function, the Drosophila formin Diaphanous (DIA) influences actin furrow assembly in the syncytial embryo and during cytokinesis (Afshar et al., 2000; Castrillon and Wasserman, 1994). Interestingly, mouse DIA1 (also known as DIAP1) is reported to function with APC2 and Diaphanous organize actin

Anaphase microtubules are important in furrow formation in the subsequent cell cycle (Riggs et al., 2007). We examined Apc2 mutant microtubule organization and dynamics during cycle 12 anaphase. Spindles in Apc2 mutants did not exhibit morphological defects (see Fig. S2A-J in the supplementary material), and exhibited the same dynamic behavior as WT (Fig. 3C). Furthermore, non-kinetochore microtubules and astral microtubules in Apc2 mutants appeared to have the same density and organization as in WT (Fig. 3D-F); see Fig. S2K-L in the supplementary material), as did interphase microtubule arrays (see Fig. S2M,N in the supplementary material). Finally, we analyzed WT and Apc2\textsuperscript{240} astral microtubules in cycles 9 and 10 when asters are robust, and observed no significant differences in microtubule density, in the distribution of microtubules around the astral center, or in the average maximum length of microtubules (Fig. 3G-H; see Fig. S3 in the supplementary material). The lack of stabilized microtubules in the syncytial embryo, coupled with the lack of any discernable defects in Apc2 mutant microtubules, suggest that APC2 might affect furrow extension directly through actin.
APC to stabilize microtubules in migrating cultured cells (Wen et al., 2004). To further explore the role of DIA in pseudocleavage furrow formation, and assess the potential similarities with Apc2 mutants, we examined the dia-null (dia5) phenotype in more detail. In some cases, most actin remained in caps during metaphase in dia5 mutants (Fig. 2F,F'), as previously reported (Afshar et al., 2000), but more frequently actin was located in weak rings (Fig. 2G,G'), similar to those of Apc2 mutants (Fig. 2E,E'). Furrow extension was significantly impaired in all dia5 mutants (Fig. 2F,G). APC2 and DIA colocalize during furrow extension, and the localization of APC2 to furrows is DIA-dependent

If APC2 and DIA function together during furrow extension, they should colocalize. At the time when furrows begin to extend late in prophase, both APC2 and DIA were detected in the furrow (see Fig. S4B1-4, arrow, in the supplementary material), but DIA appeared to temporally precede APC2 (compare Fig. 4Bc with 4Bb). As furrows reached their maximum depth in metaphase, APC2 and DIA displayed the most extensive colocalization (Fig. 4Cd,e,Dd,e). In some cases, DIA was enriched at the furrow tip, whereas actin and APC2 were uniformly distributed (Fig. 4G, arrow; see Fig. S4B4-E4 in the supplementary material) (Afshar et al., 2000), or DIA extended beyond the domains of actin and APC2 (see Fig. S4D4 in the supplementary material). By late anaphase and telophase when furrows have retracted, the colocalization of APC2 and DIA was reduced (Fig. 4Ed,e,Fd,e). At telophase, APC2 exited the furrow before DIA; APC2 was detected only at the poles (Fig. 4Fb), whereas DIA resided along the entire ring and in the remnant furrow (Fig. 4Fc; see Fig. S4F3 in the supplementary material). Taken together, these observations reveal that APC2 and DIA localize to actin structures throughout the cell cycle, but colocalize most extensively when furrows are extending and have extended. Furthermore, APC2 appears to arrive in the furrow after DIA and to leave the furrow before DIA.

The distinct temporal pattern of DIA and APC2 colocalization suggests that APC2 localization to the furrow could be DIA-dependent. In dia-null embryos, APC2 localized to actin caps during interphase and early prophase as in WT (Fig. 5A,B and data not shown). However, APC2 failed to localize with actin in the partial metaphase rings in dia5 mutants (Fig. 5Fb, arrows), and remained in the residual caps (data not shown). This trend continued through anaphase (Fig. 5Ha,b, arrows). By contrast, Anillin (Scraps – FlyBase) localized to all remaining cortical actin structures in dia5 mutants (Fig. 5Fc,He, arrows), suggesting that the loss of APC2 localization is a specific consequence of the loss of DIA. During telophase, APC2 was located at the poles of actin rings (Fig. 5Ja,b, arrows) and in reforming...
Fig. 3. Syncytial embryos do not contain acetylated microtubules and Apc2 mutants have no visible microtubule defects. (A-B') Staining for tubulin (A,B, red in merge) versus acetylated tubulin (A',B', green in merge) in gastrulated (A-A') and syncytial (B-B') Drosophila embryos. Unlike the acetylated microtubules in gastrulated embryos (A'), anaphase microtubules in syncytial embryos are not acetylated (B'). Overexposure (insets) reveals weak staining for acetylated microtubules at spindle poles (arrow) in syncytial embryos. (C) Pole-pole distance measurements in live cycle-12 embryos; n=30 for each. (D-E') Anaphase microtubules in WT (D,D') and Apc2g10/H11032 (E,E') cycle-12 embryos have similar densities and organization. (F,F') Schematics indicating the plane of section in D-E'. (G-H') Three-dimensional volume-rendered views of deconvolved cycle 9 anaphase asters reveals qualitatively similar astral microtubule organization in WT (G,G') and Apc2g10/H11032 (H,H') embryos. Arrows in G and H indicate the asters that are shown at high magnification in G' and H'. Scale bars: 10 μm.

actin caps (data not shown). The dependence of APC2 on DIA specifically when rings and furrows are prominent largely parallels the timing of colocalization between APC2 and DIA in WT embryos (Fig. 4), and supports the hypothesis that APC2 and DIA function together specifically during actin furrow extension.

We then asked whether the localization of DIA is dependent on APC2. Not only was DIA localized to Apc2^{20/10} actin rings as in WT (Fig. 5K,L), but DIA also was enriched at the tip of the furrow in defective Apc2^{20/10} furrows, also as in WT (Fig. 5K, L', arrows). This suggests that the basic association of DIA with actin and with the leading edge of the furrow occurs independently of APC2, and that the localization of DIA alone is insufficient for normal furrow extension.

Reduction of dia enhances the actin defects in Apc2 mutant embryos

We predicted that if APC2 and DIA function together during furrow extension, a 50% reduction in the dose of dia in Apc2^{20/10} embryos would enhance the Apc2^{20/10} phenotype. We reduced the dose of dia using two different alleles: dia^{a}, a deletion and reported null allele (Afshar et al., 2000), and dia^{b7155}, a P-element insertion in the 5'UTR (Berkeley Drosophila Genome Project). Because both alleles similarly affected the Apc2 phenotype, we report the findings for dia^{b7155} (dia^{b}) only. Reduction of dia enhanced the Apc2^{20/10} phenotype in two ways. The first conspicuous difference between metaphase Apc2^{20/10}, dia^{a}/CyO and dia^{b}/CyO; Apc2^{20/10} (Fig. 6B-D) embryos was at the apical surface, where some actin remained cap-like in dia^{a}/CyO; Apc2^{20/10} embryos (Fig. 6D, arrow), reminiscent of dia^{a} mutants (Fig. 2F,G). This metaphase cap-like actin is a striking enhancement; cap-like actin was not observed in Apc2^{20/10} mutants or dia^{a} heterozygotes (Fig. 6B,C). Second, we evaluated how reduction of dia affects Apc2^{20/10} furrow extension. We did not score rings at 0 μm for dia^{a}/CyO; Apc2^{20/10} embryos because the cap-like actin obscured the actin rings. Surprisingly, dia^{a} heterozygotes exhibited furrow extension defects similar in magnitude to those of Apc2^{20/10} at –1.6 μm and at –2.2 μm (data not shown), suggesting that DIA is limiting for furrow extension. Therefore, we focused on –0.8 μm where both Apc2^{20/10} and dia^{a} heterozygotes exhibited only weak defects (Fig. 6E). A 50% reduction in the dose of maternal dia in Apc2^{20/10} resulted in a significant increase in incomplete rings (47%) (Fig. 6E), as compared with either Apc2^{20/10} or dia^{a}/CyO alone (5-10%; P<0.001) (Fig. 6E). Together, these data demonstrate a dose-dependent genetic interaction between Apc2 and dia, suggesting that APC2 and DIA function in a common pathway to promote furrow extension and the dissolution of actin caps.

APC2 directly binds DIA

Previous work demonstrated that a complex including mouse DIA1, APC and EB1 influences microtubule stability in cultured cells (Wen et al., 2004). There, the C-terminus of mouse DIA1 (FH1 and
FH2 domains) binds directly to the basic domain of APC and to the N-terminal domain of EB1, while the EB1-binding domain (EB1bd) of APC binds to the C-terminus of EB1. These pairwise interactions led Wen et al. (Wen et al., 2004) to propose the formation of a ternary complex. Unlike mouse APC, Drosophila APC2 contains neither the basic domain shown to interact with DIA, nor the EB1bd (Fig. 1B).

To determine whether APC2 interacts with DIA via other domains, we asked whether His or GST fusions of APC2 and DIA bind directly in vitro. The C-terminal half of DIA (His-DIAC519) directly bound the C-terminal half of APC2 (APC2C), but not GST alone, nor the N-terminal half of APC2 (APC2N) (Fig. 6F). His-DIAC519 also bound directly to the predicted binding partner Chickadee (Chic, Drosophila Profilin), to Drosophila EB1, and to the basic domain of APC (Fig. 6F). These data indicate that although both mouse APC and Drosophila APC2 can bind DIA proteins directly, the underlying molecular interactions are distinct; mouse APC interacts with DIA1 through its basic domain (Wen et al., 2004), whereas Drosophila APC2 interacts with DIA through its central repeat region that includes the 15 and 20 amino acid repeats and the SAMP repeats (Fig. 6H).

To determine whether APC2 and DIA form a complex in vivo, we immunoprecipitated APC2 from 0-2 hour WT embryos and probed the blots with an anti-DIA antibody. DIA co-immunoprecipitated with APC2 through its central repeat region that includes the 15 and 20 amino acid repeats and the SAMP repeats (Fig. 6H).

An APC2-DIA complex may function independently of EB1 in furrow extension

In mouse, EB1 is reported to function with DIA1 and APC1 to promote microtubule stability (Wen et al., 2004). We examined whether Drosophila EB1 plays a role in furrow extension, first by asking whether Eb1 mutants exhibit actin defects similar to those of Apc2 and dia mutants. In contrast to Apc2g10 or dia mutants, maternal Eb1B13 (null) embryos did not have incomplete actin rings (Fig. 7A,B) and exhibited partially extended furrows (Fig. 7C, arrows); the average percentage of incomplete actin rings was similar to that of WT at 0, –0.8 and –1.6 μm (data not shown). At –2.2 μm, ~40% of the rings were incomplete (data not shown), compared with 92% for Apc2g10 (Fig. 2C). Approximately 25% of Eb1B13 embryos had actin caps during metaphase, similar to dia5 mutants; however, unlike dia5 mutants, these caps were associated with, and might be the result of, severe spindle disruptions (data not shown).

Eb1 mutants also exhibited a wide array of spindle morphologies (Fig. 7A/H11032, B/H11032), as predicted from studies in cultured Drosophila S2 cells and in syncytial embryos injected with anti-EB1 antibodies (Rogers et al., 2002). This might account for the higher frequency of nuclear loss in Eb1 mutants as compared with Apc2 or dia mutants. Furthermore, ~75% of Eb1B13 embryos exhibited disordered ‘mats’ of actin associated with regions of significant nuclear loss (Fig. 7A, B, arrows). These actin organization defects were not observed in Apc2g10 or dia mutants.

To further test the model that EB1 plays a role with the APC2-DIA complex during furrow extension, we reduced the dose of Eb1 in Apc2g10 embryos. We predicted that if Eb1 functions with

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**Fig. 4. APC2 and DIA proteins colocalize together and with actin in WT embryos.**

(Aa-Fe) APC2 (Ab-Fb) and DIA (Ac-Fc) colocalize with actin (Aa-Fa) throughout the cell cycle in WT cycle-12 Drosophila embryos. Colocalization of APC2 and DIA (yellow in Ad-Fd and white in Ae-Fe) is not uniform throughout the cell cycle, but peaks during prometaphase (Cd, Ce) and metaphase (Dd, De). (G) Metaphase; in cross-section APC2 (green) and DIA (red) colocalize with actin (blue) as the furrows extend. DIA is enriched at the furrow tip (arrow). Scale bars: 10 μm.
Fig. 5. DIA is required for normal APC2 localization, but APC2 is not required for DIA localization. (Aa-Jc) Stage-matched cycle-12 WT (A,C,E,G,I) and dia^5 (B,D,F,H,J) Drosophila embryos showing the localization of actin (Aa-Ja), APC2 (Ab-Jb) and Anillin (Ac-Jc). APC2 (Fb,Hb, arrow) fails to localize to actin rings (Fa,Ha, arrow) during metaphase and anaphase in dia^5 mutant embryos, whereas Anillin continues to colocalize with actin (Fc,Hc, arrow). During telophase, APC2 localizes to remnant actin rings and reforming caps in dia^5 embryos (Ja,Jb, arrow). (K,L) In WT (K) and Apc2^210 (L) cycle-12 metaphase embryos, DIA localizes to actin rings. (K',L') In cross-section (at the yellow lines in K,L), DIA (green) is enriched at the furrow tips in Apc2^210 embryos (L', arrow) as in WT (K', arrow). Scale bars: 10 μm.

APC2-DIA, reduction of Eb1, like the reduction of dia (Fig. 6A-E), would result in the presence of cap-like actin during metaphase, and in a more severe furrow extension defect. Unlike dia^5/Cyo; Apc2^210 embryos (Fig. 6D), apical actin appeared WT in Eb1^813/Cyo; Apc2^210 (Fig. 7G) embryos. Furthermore, there was no significant increase in the percentage of incomplete actin rings (Fig. 7H).

Finally, we asked whether Drosophila EB1 forms a complex with APC2 and DIA in vitro. Although APC2 lacks the defined Eb1^1st (Fig. 1B), it might bind EB1 through a novel domain. As predicted, EB1 bound directly to DIA\(^{948}\) and human APC2\(^{146}\) (Fig. 7I). However, neither APC2\(^{25}\) nor APC2\(^{25}\) interacted with EB1 (Fig. 7I). APC2\(^{25}\) and APC2\(^{25}\) did bind to the known partners KAP3 and Armadillo, respectively (data not shown). Thus, differences in syncytial actin phenotypes and the lack of a genetic interaction with Ap2, coupled with the lack of direct binding to APC2, suggest that an APC2-DIA complex might function independently of EB1 in furrow extension.

**Rho1 and RhoGEF2 mutant phenotypes are distinct from those of Apc2 and dia**

Our data support a model in which an APC2-DIA complex functions in the development of actin furrows during cortical syncytial mitoses. Because RHO activates DIA-related formins (DRFs) (reviewed by Goode and Eck, 2007), we predicted that APC2-DIA functions downstream of RHO. To test this hypothesis, we examined the actin phenotypes of embryos maternally mutant for a hypomorphic allele of Rho1 [Rho1^123 (Padash Barmchi et al., 2005)] and a null allele of RhoGEF2 [RhoGEF2^94291] (Hacker and Perrimon, 1998). The syncytial actin defects associated with these two mutants were similar (Fig. 8D,E), but those of RhoGEF2 were more severe, consistent with the fact that RhoGEF2^94291 is a null. If DIA is a direct downstream effector of RHO1 signaling during syncytial actin rearrangements, we predicted that the RhoGEF2 and Rho1 mutant phenotypes would include the Apc2 and dia mutant phenotypes. Contrary to expectation, the actin defects in RhoGEF2 and Rho1 mutants were distinct from those of Apc2 and dia. Rho1 (Fig. 8D) and RhoGEF2 (Fig. 8E) mutant rings exhibited areas of decreased actin (arrows) and areas of excessive actin accumulation (arrowheads) that appeared gauzy (Fig. 8D, inset) and sometimes included protruding actin ‘bulbs’ (Fig. 8E, inset). We did not observe such actin defects in WT, Apc2 or dia mutants (Fig. 8A-C, insets). In addition, we never observed actin remaining in apical caps during metaphase in Rho1 or RhoGEF2 mutants (data not shown) as we saw in dia^5 and dia^CyO; Apc2^210 mutants (Fig. 2F,G; Fig. 6D). Finally, although the actin furrows in RhoGEF2 and Rho1 mutants are not WT, they do not have the extension defects exhibited by Apc2 and dia mutants (Fig. 8F). Similar to the surface views, RhoGEF2 and Rho1 mutant furrows in cross-section often appeared thickened (Fig. 8F, arrows), consistent with areas of excessive actin accumulation. Furthermore, both DIA and APC2 localized to actin in RhoGEF2 mutants (Fig. 8G-G\*), suggesting that the actin associations of DIA and APC2 are not disrupted when RHO1 signaling is disrupted. The distinct mutant phenotypes of RhoGEF2 and Rho1 mutants suggest that APC2 and DIA are not in a simple linear pathway downstream of RhoGEF2 and RHO1.

**DISCUSSION**

**Cytoskeletal functions of APC2**

APC family proteins have many well-documented effects on the microtubule cytoskeleton, whereas APC functions with actin are much less well understood. The Drosophila syncytial embryo is an excellent in vivo system in which to study the role of APC2 and its partners in organizing the cytoskeleton. We previously demonstrated...
that *Drosophila* APC2 localizes to actin in syncytial embryos, and suggested a role for APC2 in tethering cortical microtubules to actin (McCartney et al., 2001).

Here we report the cytoskeletal consequences of eliminating all APC2 in the syncytial embryo. *Apc2*-null mutants exhibit incomplete actin rings and a failure of actin furrow extension (Fig. 2). *Apc2*ΔS mutants exhibit more nuclear loss than do null mutants (McCartney et al., 2006), but have weaker actin defects (Fig. 2), suggesting that the *APC2*ΔS protein might interfere with a tethering process for which APC2 is not essential. The presence of actin furrow defects in embryos that are mutant for multiple alleles of *Apc2*, including a null (Fig. 2), strongly suggests that APC2 functions in the normal organization of actin furrows.

### An APC2-Diaphanous complex

We demonstrate a novel role for an APC2-DIA complex in the organization of the actin cytoskeleton. Formins such as DIA are best known for their ability to nucleate unbranched actin filaments and accelerate filament elongation (reviewed by Goode and Eck, 2007). *Drosophila* DIA functions in actin-based furrow assembly during cellularization and conventional cytokinesis (Afshar et al., 2000; Castrillon and Wasserman, 1994; Padash Barmchi et al., 2005). *dia* mutant syncytial embryos have defects in the initiation and elongation of actin furrows, consistent with DIA subcellular localization and known roles for formins (Figs 2 and 4) (Afshar et al., 2000). We show that APC2 and DIA colocalize together and with actin specifically at times when furrows are elongating (Fig. 4). The fact that APC2 and DIA bind directly in vitro (Fig. 6), but their colocalization is cell cycle-dependent, suggests that the interaction is regulated in vivo.

The simplest model for the function of an APC2-DIA complex in actin furrow formation is that DIA-dependent nucleation and elongation of unbranched actin filaments is essential for furrow extension, and that APC2 promotes DIA activity (Fig. 9A). The fact that the *dia*-null phenotype is more severe than that of *Apc2* (Fig. 2), coupled with the enhancement of the *Apc2*-null phenotype by a reduction of *dia* (Fig. 6), support the model that APC2 is not essential for, but might enhance, DIA activity. The dependence of APC2 on DIA for localization (Fig. 5) indicates that DIA may directly affect the regulation of its own activity.

One mechanism regulating the activity of formins has been extensively studied. DIA-related formins (DRFs) are autoinhibited through the binding of the N-terminal DIA inhibitory domain (DID) to the C-terminal DIA autoregulatory domain (DAD) (Fig. 6H). Binding of the GTPase-binding domain (GBD) by RHO-GTP relieves the autoinhibition and activates DRFs, which function as dimers (reviewed by Goode and Eck, 2007). Although RHO1 and RHOGEF2 have been reported to act upstream of DIA during *Drosophila* cellularization and embryonic morphogenesis (Grosshans et al., 2005; Homem and Peifer, 2008), other reports suggest that they are in a parallel pathway during these times (Mulini et al., 2008; Padash Barmchi et al., 2005). The distinct actin defects in *Rho1* and *Rhogef2* mutants as compared with *Apc2* and *dia* mutants (Fig. 8) suggest that RHO1 is not the GTPase that directly activates DIA during furrow formation in the syncytial embryo. However, because *Rho1*-null embryos cannot be generated genetically, it is possible that there is a role for RHO1 in activating DIA independent of RHOGEF2. In addition, although we cannot rule out the activity of other GEFs and GTPases, these observations, along with those of formins in other systems (reviewed by Higgs, 2005), suggest the existence of alternative mechanisms for DRF activation.

Here we show that APC2 and DIA can bind directly to each other. Thus, APC2 could directly affect the function of DIA, perhaps by stabilizing the open conformation required for optimal DIA activity.
Alternatively, APC2 could enhance the activity of DIA by binding to and recruiting other DIA-activating factors to the complex (Fig. 9A). Once DIA is activated it might dissociate from this complex, resulting in two pools of DIA. This notion is supported by our observation that DIA, but not APC2, is enriched at the furrow tip (Fig. 4G; see Fig. S4 in the supplementary material). We propose that in the absence of APC2, the efficiency of DIA activation is reduced, resulting in a decrease in the amount of unbranched actin filaments and a consequent production of shallow furrows (Fig. 9A). Consistent with this model for APC2 function, APC proteins are thought to play a scaffolding role in the Wnt regulatory ‘destruction complex’ (reviewed by Kennell and Cadigan, 2008). Furthermore, vertebrate APC binds ASEF and IQGAP, activators of RAC and RAC/CDC42, respectively, through its N-terminal Armadillo repeats (Kawasaki et al., 2000; Watanabe et al., 2004). Thus, APC2 may promote the association of DIA with GEFs and GTPases, or with other proteins that promote the open conformation or otherwise enhance DIA activity.

Role of EB1 in an APC2-DIA complex

EB1 regulates microtubule function in many organisms including *Drosophila*, in which its disruption affects spindle positioning and dynamics in the early embryo (Rogers et al., 2002). Mouse EB1 can bind both DIA1 and APC1 and the binary interactions identified have suggested a ternary complex (reviewed by Kennell and Cadigan, 2008). Furthermore, vertebrate APC binds ASEF and IQGAP, activators of RAC and RAC/CDC42, respectively, through its N-terminal Armadillo repeats (Kawasaki et al., 2000; Watanabe et al., 2004). Thus, APC2 may promote the association of DIA with GEFs and GTPases, or with other proteins that promote the open conformation or otherwise enhance DIA activity.

![Fig. 7. EB1 may function independently of APC2-DIA. (A-B) Apical views of actin (A, A', B, B') and microtubules (A', A', A', B, B') in cycle-12 metaphase *Eb1B13* embryos. Arrows in A and B indicate actin mats; yellow lines indicate plane of sections in C. (C) Partial furrow extension (arrows) in *Eb1B13* embryos in cross-section. *Eb1B13* mutants exhibit a wide array of spindle morphologies, including apparently normal spindles (A') and severely disrupted spindles (B'). (D-G) Actin in cycle-12 metaphase embryos of the indicated genotypes. (H) Quantification of furrow extension shows that there is no significant effect of reduction of Eb1 on the *Apc2P314* phenotype. (I) Free MBP-EB1 binds directly to DIA(4–484) and human APCEB1bd (positive control), but to neither *Drosophila* APC2 fragment in HKT buffer. B, bead; S, supernatant.

Building a furrow

Unlike conventional cytokinesis that uses actomyosin-based contraction to drive membrane invagination, Myosin II function is dispensable for pseudocleavage furrow formation (Royou et al., 2004). Many proteins are known to affect the dynamic organization of syncytial actin (Fig. 9B). Centrosomin, a core centrosome component, Sponge, a putative unconventional RacGEF, and Scrambled, a novel protein, all have roles in normal cap formation (Postner et al., 1992; Stevenson et al., 2001; Vaizel-Ohayon and Schejter, 1999). Cap formation and expansion require the Arp2/3 complex.
Interestingly, we have shown that in the absence of elongation of unbranched filaments necessary for furrow extension. Delivered to this site, APC2-DIA might promote the nucleation and furrow extension (Fig. 9B) (Riggs et al., 2007). Once actin has been recycling endosome to move membrane and actin to the site of pathway, which utilizes microtubule-based transport from the \( NUF \) (Arfophilin)-RAB11-DAH (Dystrophin) et al., 2006). Stabilize actin filaments, as it does in the furrow extension (Mermall and Miller, 1995), where it might The Myosin VI protein Jaguar appears to play a specific role in (Fig. 9B), but rather regulate the overall balance of actin activity. The best-understood mechanism for pseudocleavage furrow extension is the NUF (Arfophilin)-RAB11-DAH (Dystrophin) complex and its activator SCAR (Stevenson et al., 2002; Zallen et al., 2002). Well-known actin regulators such as RHO1, RHOGEF2 and Abelson (Abl tyrosine kinase) (Grevenbroed et al., 2003; Grosshans et al., 2005; Padash Barmchi et al., 2005; Postner et al., 1992; Sullivan et al., 1993) may not affect furrow extension directly (Fig. 9B), but rather regulate the overall balance of actin activity. We thank C. Ettensohn, T. Harris, J. Hildebrand, J. Minden, M. Peifer and members of the lab for insightful comments; C. Fried, T. Jarvela and K. Vasilev for constructs; J. Crowley for deconvolution expertise; C. Flynn for the MatLab program; and U. Hacker, C. Homem, D. Fox, M. Peifer, the Bloomington Stock Center and other members of the fly community for sharing reagents. This work was supported by Research Grant 5-FY05-34 from the March of Dimes Birth Defects Foundation and NIH R01 GM073891-01A2 to B.M. Deposited in PMC for release after 12 months.

Supplementary material
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Fig. 8. Rho1 and RhoGEF2 mutants. (A-F) Cycle-12 metaphase Drosophila embryos. Rho1(D) and RhoGEF2(E) mutants display areas of decreased actin (D,E, arrows), as well as areas of excessive accumulation of actin associated with rings (D,E, insets, arrowheads), which are not observed in WT (A), APC2\(^{2310}\) (B) or dia\(^2\) (C) embryos. (F) Cross-sections stained for actin show defective thickened furrows in Rho1 and RhoGEF2 embryos (arrows). (G-G') APC2 (G') and DIA (G') localize to cortical actin (G) in a RhoGEF2\(^{2310}\) mutant cycle-12 anaphase embryo. Scale bars: 10 μm.

Fig. 9. Model for Drosophila APC2-DIA function. (A) We propose that APC2 promotes the activity of DIA by facilitating the interaction between DIA and an activator. This interaction enhances the efficiency of actin nucleation in the pseudocleavage furrow. In the absence of APC2, DIA and its activator interact less efficiently, resulting in defective furrow extension. (B) Many proteins affect syncytial actin rearrangements (see Discussion).

mutant embryos reduced for dia, some actin remains cap-like (Figs 2 and 6). This intriguing observation suggests that there is a relationship between the dissolution of caps and the formation of furrows, and that these distinct pools of branched and unbranched actin might be in a balance. The APC2-DIA complex has emerged as a key factor affecting actin organization in the early embryo, and further study will reveal how the many regulatory pathways converge to influence dynamic changes in actin organization.

References


