Cdc42 and Par proteins stabilize dynamic adherens junctions in the Drosophila neuroectoderm through regulation of apical endocytosis

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Introduction

Cadherin-based adherens junctions (AJs) are critical elements of intercellular adhesion between epithelial cells. In most epithelia, AJs are organized as an apical belt, the zonula adherens (ZA), which is a component of the apical junctional complex that segregates apical from basolateral membranes in these highly polarized cells. AJs are dynamic structures and, during cell rearrangement, have to rapidly disassemble and reform to maintain ZA continuity and epithelial integrity. Several mechanisms have been proposed to regulate AJ stability, but our understanding of how AJ integrity is maintained during dynamic morphogenetic movements in vivo remains limited (Gumbiner, 2000, 2005; Bryant and Stow, 2004; D’Souza-Schorey, 2005; Halbleib and Nelson, 2006).

The Drosophila melanogaster embryo assembles a ZA when the first epithelium forms (Tepass and Hartenstein, 1994; Müller and Wieschaus, 1996). The ZA is maintained in epithelia throughout morphogenesis, during which frequent changes in cell–cell contacts occur. One example is the ventral neuroectoderm, which is an epithelial layer that gives rise to neural and epidermal progenitor cells. About one third of the cells of the neuroectodermal epithelium ingress as individual cells and form neural progenitors (neuroblasts or neural stem cells), whereas the remaining cells retain epithelial character and differentiate into epidermis (Campos-Ortega and Hartenstein, 1997). Zygotic expression of Drosophila epithelial cadherin (DEcad), the major adhesion molecule at the ZA in the Drosophila embryo, is required to maintain AJs in the neuroectoderm, whereas maternal expression of DEcad is sufficient to maintain the ZA in other epithelia that do not undergo cell rearrangements, such as the dorsal ectoderm. Moreover, blocking neuroblast specification and, thus, neuroblast ingress ameliorates the requirement of zygotic DEcad expression to support the integrity of neuroectodermal AJs (Tepass et al., 1996; Uemura et al., 1996). These observations raise the question as to whether specific mechanisms are used to support AJ stability in the neuroectoderm.

Cell rearrangements require dynamic changes in cell–cell contacts to maintain tissue integrity. We investigated the function of Cdc42 in maintaining adherens junctions (AJs) and apical polarity in the Drosophila melanogaster neuroectodermal epithelium. About one third of cells exit the epithelium through ingestion and become neuroblasts. Cdc42-compromised embryos lost AJs in the neuroectoderm during neuroblast ingress. In contrast, when neuroblast formation was suppressed, AJs were maintained despite the loss of Cdc42 function. Loss of Cdc42 function caused an increase in the endocytotic uptake of apical proteins, including apical polarity factors such as Crumbs, which are required for AJ stability. In addition, Cdc42 has a second function in regulating endocytotic trafficking, as it is required for the progression of apical cargo from the early to the late endosome. The Par complex acts as an effector for Cdc42 in controlling the endocytosis of apical proteins. This study reveals functional interactions between apical polarity proteins and endocytosis that are critical for stabilizing dynamic basolateral AJs.
Studies in mammalian cell culture have pointed to the GTPases of the Rho family, Rho, Rac, and Cdc42, as one group of AJ regulators (Fukata and Kaibuchi, 2001; Van Aelst and Symons, 2002; Braga and Yap, 2005). Also, the analysis of Rho GTPases in Drosophila suggests that Rho1 is a critical regulator of AJ stability (Bloor and Kiehart, 2002; Fox et al., 2005) and that Cdc42 impacts on AJs through its role as a component of the Par complex that controls epithelial polarity, including ZA formation in early embryos (Hutterer et al., 2004; Macara, 2004). Cdc42 is a regulator of cell polarity in many systems, including yeast, the Caenorhabditis elegans zygote, Drosophila neuroblasts, and in migrating cells (Artavanis-Tsakonas et al., 1999). Expression of Cdc42 causes AJ defects in head development and dorsal closure. Also, cdc42 mutant embryos, which have a reduced maternal cdc42 contribution (Genova et al., 2000), display holes in the ventral epidermis and show compromised AJs in the neuroectoderm similar to da>Cdc42-DN embryos (Fig. 1, C, F, and L). The similarity between the defects observed in da>Cdc42-DN embryos and cdc42 mutant embryos suggests that Cdc42-DN specifically disrupts Cdc42 function in this system. As cdc42 mutants still have some maternal cdc42 contribution and the phenotypes of cdc42 mutants and da>Cdc42-DN embryos are similar, it is unlikely that Cdc42-DN expression completely removes Cdc42 function. We were not able to reproduce the observations reported by Hutterer et al. (2004), who showed that expression of Cdc42-DN with strong maternal drivers causes morphological defects before gastrulation or that expression of Cdc42-DN causes the loss of epithelial polarity throughout the embryo. Collectively, our findings suggest a significantly higher requirement for Cdc42 function to stabilize AJs in the neuroectoderm as compared with other regions of the ectoderm.

The coincidence of neuroblast ingression and AJ breakdown in da>Cdc42-DN embryos suggests that the ingression process itself causes the higher Cdc42 requirement. The ingestion of epithelial cells requires dynamic AJs to maintain epithelial continuity. A majority of neuroectodermal cells undergo AJ disassembly and reformation as ~30% of cells of the neuroectodermal epithelium ingress (Fig. 1 I; Campos-Ortega and Hartenstein, 1997). In contrast, cell contacts remain constant in the dorsal ectoderm or the ventral midline cells during neurulation. To test for the possibility that the higher AJ turnover that results from neuroblast ingestion requires higher Cdc42 activity, we suppressed neuroblast specification, and thus ingestion, through the expression of a CA form of the Notch receptor (N extran; Lieber et al., 1993; Rebay et al., 1993; Struhl et al., 1993). Notch signaling specifies epidermal progenitor fate and prevents specification of neuroblasts in the Drosophila neuroectoderm (Campos-Ortega, 1993; Artavanis-Tsakonas et al., 1999). Expression of N extran in da>Cdc42-DN embryos effectively suppressed formation of ventral cuticle holes (Fig. 1, K and L) but not defects in head morphogenesis or dorsal closure (not depicted). Moreover, AJ integrity in the neuroectoderm of stage 11 embryos is dramatically improved in da>N extran da>Cdc42-DN embryos compared.

Results

Cdc42 is essential for maintaining AJs in the Drosophila neuroectoderm

To address the function of Rho GTPases in AJ formation and maintenance in vivo, we have expressed dominant-negative (DN) forms of Rho1, Rac1, and Cdc42 in the Drosophila embryo using the Gal4/upstream activation sequence (UAS) system and the ubiquitous driver line da-Gal4. We found that expression of Rho1-DN led to a rather general disruption of AJs, confirming the previous work of others (Bloor and Kiehart, 2002). Rac1-DN may also act through its effector Wiskott-Aldrich syndrome protein (Wasp) to control junction-associated actin (Otani et al., 2006) or may contribute to epithelial organization by regulating vesicle trafficking (for reviews see Cerione, 2004; Ridley 2006).

In this study, we address the function of Cdc42 in promoting the stability of dynamic AJs in the Drosophila neuroectoderm. Our findings suggest that Cdc42 acts through its effector, the Par complex, to modify apical endocytosis at two stages: Cdc42 prevents the endocytotic uptake of apical proteins from the plasma membrane, and it promotes the processing of apical proteins from the early to the late endosomal compartment.

AJ defects became apparent in da-Gal4 UAS-Cdc42-DN (da>Cdc42-DN) embryos at stage 9 and are most prominent at stage 11 when AJs are compromised in the entire ventral ectoderm, the neuroectoderm, excluding the ventral midline cells (Fig. 1, A, B, and G). About one third of the epithelial cells ingress from the neuroectoderm to become neuroblasts during stages 8–11 (Campos-Ortega and Hartenstein, 1997). At later stages of development of da>Cdc42-DN embryos, AJs are re-established in large areas of the ventral ectoderm, whereas cells in other ventral regions lose epithelial integrity and degenerate, causing the formation of holes in the ventral epidermis (Fig. 1 H). In contrast, AJs in the dorsal ectoderm and the ventral midline show only minor defects in da>Cdc42-DN embryos. Preparations of the cuticle of da>Cdc42-DN embryos show holes in the ventral cuticle that affect ~50% of the ventral region (Fig. 1, E and L). To quantify the strength of defects in the ventral epidermis, we counted the number of intact ventral abdominal denticle belts (Fig. 1 L). In contrast to wild-type embryos that display eight intact denticle belts, da>Cdc42-DN embryos have only four intact denticle belts on average. In addition, these embryos display defects in head development and dorsal closure.

Also, cdc42 mutant embryos, which have a reduced maternal cdc42 contribution (Genova et al., 2000), display holes in the ventral epidermis and show compromised AJs in the neuroectoderm similar to da>Cdc42-DN embryos (Fig. 1, C, F, and L). The similarity between the defects observed in da>Cdc42-DN embryos and cdc42 mutant embryos suggests that Cdc42-DN specifically disrupts Cdc42 function in this system. As cdc42 mutants still have some maternal cdc42 contribution and the phenotypes of cdc42 mutants and da>Cdc42-DN embryos are similar, it is unlikely that Cdc42-DN expression completely removes Cdc42 function. We were not able to reproduce the observations reported by Hutterer et al. (2004), who showed that expression of Cdc42-DN with strong maternal drivers causes morphological defects before gastrulation or that expression of Cdc42-DN causes the loss of epithelial polarity throughout the embryo. Collectively, our findings suggest a significantly higher requirement for Cdc42 function to stabilize AJs in the neuroectoderm as compared with other regions of the ectoderm.

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with da>Cdc42-DN animals (Fig. 1 J). To control for the possibility that the introduction of a second UAS construct could suppress the da>Cdc42-DN phenotype, we examined da>GFP da>Cdc42-DN embryos and found that they exhibit the same defects as da>Cdc42-DN embryos (Fig. 1 L). Together, our results suggest that the reformation of AJs that takes place as a result of neuroblast ingestion requires high levels of Cdc42 activity.

Cdc42-compromised neuroectodermal cells lose apical membrane-associated proteins

To further characterize the neuroectodermal defects in da>Cdc42-DN embryos, we examined additional molecular markers that highlight AJs and the apical and basolateral membrane of neuroectodermal cells. In addition to DEcad (Fig. 1), we found that the AJ markers Armadillo (Arm; Drosophila...
minor defects in the apical localization of these proteins were detected in the ventral midline cells or the dorsal ectoderm. Moreover, apical markers, similar to AJ proteins, showed a normal distribution in ventral epidermal cells that survive to later stages of development. In addition to the loss of apical and AJ proteins from the plasma membrane, we noticed that the apical transmembrane proteins Crb, Notch, Delta, and Cad87A but not the AJ proteins DEcad and Ed accumulated in prominent cytoplasmic puncta in da > Cdc42-DN embryos (Fig. 2 G; see following sections). These puncta were not confined to regions that had lost apical and AJ proteins from their plasma membrane and were seen throughout the ectoderm. Collectively, our findings suggest that reduction of Cdc42 activity causes a loss of apical polarity in the neuroectodermal epithelium as it undergoes dynamic changes in cell–cell contacts.

Cdc42 negatively regulates apical endocytosis

To determine whether not only polarity proteins but also other apical proteins are down-regulated, we examined Notch and its ligand Delta, which are also enriched in the marginal zone, and the cadherin Cad87A, which is a marker of the free apical surface (Fung et al., 2008). Again, we found that all three transmembrane proteins were strongly reduced or undetectable in neuroectodermal cells in da>Cdc42-DN embryos (Fig. 2, I–L; and not depicted). Finally, we determined that basolateral proteins, the transmembrane protein Neurotactin (Nrt), and the membrane-associated cytoplasmic adaptor protein Scribble (Scrib) showed a normal distribution in the neuroectoderm of da>Cdc42-DN embryos (Fig. 2, M–P). The general loss of apical and AJ proteins is confined to the neuroectoderm, and only minor defects in the apical localization of these proteins were detected in the ventral midline cells or the dorsal ectoderm. Moreover, apical markers, similar to AJ proteins, showed a normal distribution in ventral epidermal cells that survive to later stages of development. In addition to the loss of apical and AJ proteins from the plasma membrane, we noticed that the apical transmembrane proteins Crb, Notch, Delta, and Cad87A but not the AJ proteins DEcad and Ed accumulated in prominent cytoplasmic puncta in da>Cdc42-DN embryos (Fig. 2 G; see following sections). These puncta were not confined to regions that had lost apical and AJ proteins from their plasma membrane and were seen throughout the ectoderm. Collectively, our findings suggest that reduction of Cdc42 activity causes a loss of apical polarity in the neuroectodermal epithelium as it undergoes dynamic changes in cell–cell contacts.
expresses GFP-Cdc42 under Gal4/UAS control. Cdc42 antibodies and GFP-Cdc42, as detected with anti-GFP antibodies, showed identical distribution patterns (Fig. 3, A and D–F; and Fig. S1, available at http://www.jcb.org/cgi/content/full/jcb.200807020/DC1), with one exception (see following paragraph). Cdc42 is found in a punctate distribution throughout the cytoplasm of all ectodermal epithelial cells. Cdc42 appears enriched at the plasma membrane, in particular the AJ, where it is also found in small puncta rather than uniformly distributed as suggested by the examination of deconvolved confocal z stacks (see Materials and methods). Thus, Cdc42 colocalized with the apical membrane and the AJ but did not show any obvious apical enrichment.
though the number of FM4-64–labeled vesicles remained the same in mutant versus wild-type embryos, vesicles in da > Cdc42-DN embryos appeared significantly larger, accounting for the overall increase in labeling intensity. These findings suggest that loss of Cdc42 activity increases endocytosis in neuroectodermal cells.

To identify the compartment that accumulates apical proteins in da > Cdc42-DN embryos, we used several markers that highlight different stages in the endocytotic pathway. Double labeling of da > Cdc42-DN embryos with Crb and either Avlanche (Avl), a syntaxin associated with early endosome (Lu and Bilder, 2005), the early endosome marker Rab5 (Wucherpffennig et al., 2003), the recycling endosome marker Rab11 (Dollar et al., 2002; Pelissier et al., 2003), the multivesicular body/late endosome marker Rab7 (Entchev et al., 2000), or Hrs, which marks an early transitory stage between early and late endosomes (Lloyd et al., 2002; Kanwar and Fortini, 2008), showed that only Hrs colocalized with Crb (Fig. 5, A–J) and other apical transmembrane proteins (not depicted). Hrs labels a large number of cytoplasmic puncta. However, colocalization with Crb, Cdc42, and other apical proteins was only seen in approximately one large vesicle per cell in da > Cdc42-DN embryos. These double-labeling experiments were also performed in cdc42 mutant embryos with similar results (Fig. S2, available at http://www.jcb.org/cgi/content/full/jcb.200807020/DC1; and not depicted). Hrs-positive vesicles of similar size were not seen in wild-type control embryos, suggesting that loss of Cdc42 function changes the morphology of endosomes, enlarging them likely by blocking the processing of apical proteins from early to late endosomes. Previous work has found that Cdc42 is associated with the Golgi and implicated Cdc42 in the regulation of Cdc42 function.

We next examined the distribution of Cdc42 in da>Cdc42-DN, da>Cdc42-CA, and da>GFP-Cdc42 embryos using Cdc42 antibodies, thus detecting both the mutant isoforms and endogenous protein. As expected, Cdc42 was overabundant in all three cases. Cdc42-DN–expressing embryos showed mislocalization of Cdc42 at the apical and lateral plasma membrane, an apparent enrichment of apical Cdc42-positive vesicles, and a small number of larger vesicles that could be found anywhere along the apical basal axis (Fig. 3, G–I and K). Embryos expressing Cdc42-CA showed a relatively normal distribution of Cdc42 (Fig. S1), whereas embryos expressing GFP-Cdc42 also displayed normal Cdc42 distribution except for a low frequency of large Cdc42-positive puncta similar to those seen in Cdc42-DN–expressing embryos (Fig. S1). This latter observation raises the possibility that the GFP tag has a slight negative effect on Cdc42 function.

Colocalization experiments revealed that the large Cdc42-positive puncta are the same puncta that accumulate apical membrane proteins in da>Cdc42-DN embryos (Fig. 3, J and K) and are therefore likely vesicular compartments in the biosynthetic or endosomal pathways. To determine whether these vesicles are biosynthetic or endosomal, we exposed live da>Cdc42-DN embryos to FM4-64, a dye that is taken up into cells through endocytosis and labels all endocytotic compartments. FM4-64 colocalized with Crb (Fig. 4, A and B). (C) FM4-64 labeling intensity was measured for individual confocal z stacks comprising ~16 neuroectodermal cells (mean ± SEM [error bars]). Cdc42-DN embryos showed a substantial increase in FM4-64 uptake, as the observed difference in mean pixel intensity relative to the wild-type control is highly significant (P < 0.001). The differences between Cdc42-DN and wild-type embryos are the result of different particle sizes (P < 0.001; C′), whereas the particle number labeled by FM4-64 remained the same (C″). Bars: (A and B) 10 μm; (A′ and B′) 5 μm.
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Figure 5. Apical proteins accumulate in an Hrs-positive endocytotic compartment in Cdc42-compromised embryos. (A and B) Wild-type (A and A') and Cdc42-DN (B and B') embryos labeled with Crb and the endosome marker Hrs. (C and D) Wild-type (C and C') and Cdc42-DN (D and D') embryos labeled for Crb and the early endosome marker Rab5. (E and F) Wild-type (E and E') and Cdc42-DN (F and F') embryos labeled for Crb and the early endosome marker Avl. (G and H) Wild-type (G and G') and Cdc42-DN (H and H') embryos labeled for Crb and the recycling endosome marker Rab11. (I and J) Embryos expressing the late endosome marker UAS-YFP-Rab7 under the control of da-Gal4 (I and I') and embryos expressing both UAS-Cdc42-DN and UAS-YFP-Rab7 under the control of da-Gal4 (J and J') labeled for Crb and GFP. (K and L) Wild-type (K and K') and Cdc42-DN (L and L') embryos labeled for Crb and the Golgi marker Lva. (M and N) Wild-type (M and M') and Cdc42-DN (N and N') embryos labeled for Crb and the ER marker KDEL. Bars: (A–N) 10 μm; (A'–N') 5 μm.

exocytosis in some mammalian cells (Kroschewski et al., 1999; Músch et al., 2001). We did not detect Cdc42 in association with the Golgi, nor did we detect any abnormal accumulation of the seven membrane proteins we examined (Crb, Notch, Delta, Cad87A, DEcad, Ed, and Nrt) in the secretory pathway using markers for the ER (KDEL [Lys-Asp-Glu-Leu]), the Golgi (Lava lamp [Lva]), or the recycling endosome (Rab11), which serves as an exocytotic conduit (Fig. 5, G, H, and K–N; Lock and Stow, 2005; Blankenship et al., 2007). Together, these findings suggest that Cdc42 regulates endocytosis but not exocytosis in Drosophila embryonic epithelia.

Cdc42-compromised embryos displayed abnormally large endosomes containing apical cargo in both the neuroectoderm (0.95 per cell; n = 42), which had lost apical polarity, and in the
dorsal ectoderm at a similar frequency (0.92 per cell; \( n = 56 \)).

GFP-Cdc42–expressing embryos, in comparison, contained 0.4 enlarged Cdc42-, Crb-, and Hrs-positive compartments per cell (Fig. S1). Moreover, similar, abnormally large endosomes were seen at other stages of development such as cellularization, when no defects in epithelial polarity were apparent. We conclude that loss of Cdc42 function leads to the accumulation of apical transmembrane proteins in an abnormally enlarged endosomal compartment. Thus, Cdc42 function is required not only for preventing catastrophic loss of apical proteins in the neuroectoderm but also for the processing of apical proteins through the endocytotic pathway in all epithelia we examined.

To further support the hypothesis that Cdc42 activity negatively regulates apical endocytosis, we asked whether a reduction in endocytosis can ameliorate the phenotype of \( \text{da}>\text{Cdc42-DN} \) embryos and reconstitute apical protein localization in neuroectodermal cells. We coexpressed Rab5-DN with Cdc42-DN. Rab5 is a Rab GTPase critical for early steps in endocytosis, mediating the fusion of endocytotic vesicles with the early endosome. \( \text{da}>\text{Rab5-DN} \) embryos are lethal and displayed a defective cuticle, but no ventral holes were observed (Fig. 6 G). Neuroectodermal cells of \( \text{da}>\text{Cdc42-DN} \, \text{da}>\text{Rab5-DN} \) embryos showed a substantial improvement of normal localization of apical proteins, including Crb and DEcad (Fig. 6, A–F). Corresponding to the normalization of apical polarity during neurogenesis, the terminal phenotype of \( \text{da}>\text{Cdc42-DN} \) is significantly ameliorated by coexpression of Rab5-DN (Fig. 6, G and H). Furthermore, we note that expression of Rab5-DN does not prevent the formation of abnormally enlarged endosomes that accumulate apical proteins in \( \text{da}>\text{Cdc42-DN} \) embryos (Fig. 6 F). This, together with the observation that enlarged apical endosomes are seen in tissues that have not lost apical polarity, again suggests that Cdc42 acts independently in two steps of the apical endocytotic pathway: as a negative regulator of apical endocytosis and as a positive regulator of early to late endosomal processing.

Mammalian Rab5 has been associated with both apical and basolateral endocytosis in epithelial cells (Bucci et al., 1994). In \textit{Drosophila} epithelial cells, however, Rab5 appears to

Figure 6. Inhibition of apical endocytosis rescues defects in Cdc42-compromised embryos. (A–C) Wild-type embryo (A), Cdc42-DN embryo (B), and embryo expressing both Cdc42-DN and Rab5-DN (C) labeled for DEcad. (D–F) Wild-type (D), Cdc42-DN (E), and Cdc42-DN, Rab5-DN (F and F') embryos labeled for Crb. Arrows point to enlarged endosomes. (G) The extent of ventral cuticle defects was quantified by counting the number of intact abdominal denticle belts (mean ± SEM [error bars]). For Cdc42-DN, Rab5-DN embryos, the difference in the mean number of intact belts relative to Cdc42-DN embryos is statistically significant (\( P < 0.001 \)). (H) Ventral cuticle of Cdc42-DN, Rab5-DN embryo. M, ventral midline; VNE, ventral neuroectoderm; DE, dorsal ectoderm. Bars: (A–F) 20 μm; (F') 10 μm; (H) 100 μm.
have an essential function only in apical endocytosis, as Rab5-null epithelial cells accumulate apical markers such as Crb and Notch at the plasma membrane but not basolateral markers such as DEcad (Lu and Bilder, 2005). This would imply that the endocytosis of apical proteins, which is counteracted by Rab5-DN, is the primary effect of the loss of Cdc42 function and that the failure to maintain AJs is secondary to the loss of apical polarity regulators such as Crb (Fig. 2, F and G) or the Par proteins (see following section), which are known to control AJ assembly and stability (Tepass et al., 2001; Knust and Bossinger, 2002). To further test this model, we studied functional interactions between Cdc42 and Crb, DEcad, or Notch by reducing the gene copy of crb, shotgun (shg; the gene encoding DEcad), and Notch from two to one in a da>Cdc42-DN background. The interactions were evaluated and quantified by examining the degree to which the ventral cuticle was disrupted (Fig. 7). Removal of a single copy of crb, shg, or Notch in a wild-type background does not cause lethality or defects in the embryonic epidermis. We did not find interactions with Notch (Fig. 7, A and E), which is consistent with the fact that Cdc42-compromised embryos did not show a Notch-like phenotype (Genova et al., 2000). In contrast, loss of one copy of shg in da>Cdc42-DN embryos led to a significant enhancement of the da>Cdc42-DN phenotype, and the loss of a single copy of crb caused a dramatic enhancement of the da>Cdc42-DN phenotype.
of the da>Cdc42-DN phenotype (Fig. 7, A–D). Fig. 7 A compares the mean phenotypic strength of different genotypes. This representation underestimates the actual strength of the phenotypic enhancement, as only an estimated 50% of embryos evaluated for each genotype are double mutants, whereas the other 50% are da>Cdc42-DN embryos. Therefore, we also present our data by listing the number of embryos in each phenotypic class (Fig. 7, B–E; 0 = no ventral epidermis; 8 = normal ventral epidermis). The majority of da>Cdc42-DN, crb/+ embryos apparently lack abdominal denticle bands and in fact lack most of their ventral epidermis (Fig. 7 C). The strong interaction between Cdc42 and crb compared with the weak interaction between Cdc42 and shg is consistent with the model that the loss of Crb from the membrane is the key event in response to Cdc42 down-regulation that compromises the ability of the neuroectoderm to maintain AJs. Collectively, our findings suggest that Cdc42 negatively regulates the frequency of apical endocytosis to promote apical polarity and, as a consequence, the stability of AJs during cell rearrangement.

**The Par complex acts downstream of Cdc42 in regulating the apical endocytotic pathway**

Cdc42 can contribute to endocytosis through regulation of its downstream effector Wasp and actin polymerization (for reviews see Cerione, 2004; Ridley 2006). Also, a second Cdc42 effector, the Par complex, was recently implicated in the regulation of endocytosis in *C. elegans* and human HeLa cells (Balklava et al., 2007). This study suggested that Cdc42 and the Par proteins Par3, Par6, and aPKC are required to promote endocytosis. However, the function of Cdc42 and Par proteins in endocytosis in epithelial cells was not investigated. To address the question whether *Drosophila* Par proteins cooperate with Cdc42 in the regulation of endocytosis in neuroectodermal cells, we first examined the distribution of Bazooka (Baz; *Drosophila* Par3), Par6, and aPKC in da>Cdc42-DN embryos. We found that all three Par proteins are strongly depleted from the apical membrane of neuroectodermal cells and colocalized with Cdc42 at enlarged apical endosomes similar to apical transmembrane proteins such as Crb (Fig. 8, A–F). Normal apical localization but abnormal accumulation of Par proteins at apical endosomes was also observed in other ectodermal epithelial cells that displayed normal apical polarity in da>Cdc42-DN embryos. The loss of both the Crb and Par complexes, which can act redundantly in promoting epithelial polarity (Tanentzapf and Tepass, 2002), from the apical membrane explains the inability of neuroectodermal cells to maintain their AJs.

We next studied embryos in which da>Cdc42-DN is combined with baz, Par6, or aPKC mutations. Mutations in all three Par genes strongly enhance the ventral cuticle defects in da>DN-Cdc42 embryos, suggesting that Cdc42 and Par proteins cooperate in supporting apical polarity of neuroectodermal cells (Fig. 8 G). baz, Par6, and aPKC have strong maternal contributions of expression, and loss of maternal and zygotic expression for all three genes leads to strong epithelial defects at early stages of development, preventing a meaningful analysis of neurulation-stage embryos (Müller and Wieschaus, 1996; Wodarz et al., 2000; Petronczki and Knoblich, 2001; Rolls et al., 2003). Zygotic mutants for *aPKC* are not embryonic lethal and die at larval stages. par6 zygotic mutants are embryonic lethal but do not show defects in the ventral cuticle or loss of apical polarity in neuroectodermal cells. However, these embryos display enlarged endosomes that accumulate apical cargo (Fig. 8 I). Finally, baz zygotic mutants show prominent cuticle defects, including ventral holes similar to da>Cdc42-DN embryos. Also, large portions of the neuroectoderm of baz mutants show loss of apical polarity, and an accumulation of apical proteins in enlarged endosomes is seen in these embryos.

![Figure 8](image_url)

**Figure 8.** Cdc42 interacts with the Par complex to regulate apical endocytosis. (A and B) Wild-type [A] and Cdc42-DN [B] embryos labeled for Baz and Cdc42. (C and D) Wild-type [C] and Cdc42-DN [D] embryos labeled for Par6 and Cdc42. (E and F) Wild-type [E] and Cdc42-DN [F] embryos labeled for aPKC and Cdc42. (G) Cdc42-DN ventral defects are enhanced by the loss of zygotic aPKC, baz, or par6. The extent of ventral cuticle defects was quantified by counting the number of intact abdominal denticle belts [mean ± SEM [error bars]]. For all double-mutant combinations, the difference in the mean number of intact belts relative to Cdc42-DN embryos is statistically significant (P < 0.001). (H and I) baz mutant embryos (H and H') and par6 mutant embryos (I and I') labeled for Crb and Cdc42. Bars: [A–F, H', and I'] 5 μm; [H and I] 10 μm.
Our findings support a model (Fig. 10) posing that Cdc42 regulates two distinct steps of endocytosis in *Drosophila* epithelial cells. Cdc42 function slows the removal of apical proteins from the plasma membrane by decreasing endocytotic uptake, and it accelerates the processing of apical cargo from the early to the late endosome. Previous work has suggested that Cdc42 might promote endocytosis through its effector Wasp and the regulation of actin polymerization (for review see Ridley, 2006). However, our observations that (a) embryos with compromised Par complex function show similar endocytotic defects as embryos with reduced Cdc42 function and that (b) endocytotic defects in embryos with compromised Cdc42 function can be rescued by the expression of an active form of aPKC indicate that the Par complex acts as an effector of Cdc42 to regulate endocytosis in the *Drosophila* ectodermal epithelium. The targets of aPKC in the endocytotic pathway are unknown at present, and we cannot rule out that they include actin regulators.

We propose that aPKC has at least two distinct phosphorylation targets that regulate the apical endocytotic pathway. One of the two targets of aPKC is likely to control the uptake of apical proteins similar to *da > Cdc42-DN* embryos (Fig. 8 H). Together, these data suggest that the Par complex cooperates with Cdc42 in regulation of the apical endocytotic pathway. The fact that apical polarity seems intact but early to late endosomal processing is compromised in zygotic par6 mutant embryos provides further evidence that apical endocytosis and the processing of apical cargo through the endocytotic pathway may require distinct regulatory inputs from the Cdc42–Par complex and that the latter is more sensitive to the reduction in Cdc42–Par complex function.

To test whether the Par complex acts downstream and, thus, most likely as an effector complex of Cdc42 in the regulation of endocytosis, we coexpressed a CA form of aPKC (aPKC<sup>CAAXWT</sup>, Sotillos et al., 2004) and Cdc42-DN. Expression of aPKC<sup>CAAXWT</sup> strongly suppresses the phenotype of *da > Cdc42-DN* embryos; localization of apical proteins, including Crb and DEcad (Fig. 9, A–F), is partially restored, and ventral cuticle defects are ameliorated (Fig. 9, G and H). Moreover, the formation of enlarged endosomes containing an abnormal accumulation of apical cargo is completely abolished (Fig. 9 F and not depicted). We conclude that aPKC acts downstream of Cdc42 in the regulation of apical endocytosis.
study identifies Cdc42 and Par proteins as positive regulators of oocytes and coelomocytes as well as human HeLa cells. This did not detect colocalization of Cdc42 or apical proteins in either to stabilize apical proteins by promoting recycling. However, we of clathrin-independent cargo. Cdc42 and Par proteins might act endocytotic uptake of clathrin-dependent cargo or the recycling 

endosome (EE) to the multivesicular body/late endosome (MVB/LE). Apical and basolateral (including AJ) proteins follow distinct endocytotic routes. 

Model of the Cdc42–Par complex function in the regulation of the apical endocytotic pathway. Our data suggest that Cdc42 and the Par complex cooperate to regulate two distinct steps in the endocytosis of apical membrane components. The Cdc42–Par complex inhibits endocytosis from the plasma membrane and also promotes progression from the early endosome (EE) to the multivesicular body/late endosome (MVB/LE). Apical and basolateral (including AJ) proteins follow distinct endocytotic routes. 

Cdc42/Par

Figure 10. Model of the Cdc42–Par complex function in the regulation of the apical endocytotic pathway. Our data suggest that Cdc42 and the Par complex cooperate to regulate two distinct steps in the endocytosis of apical membrane proteins or their effective recycling back to the apical membrane. Apical proteins did not accumulate in the Rab11-positive recycling endosome in Cdc42-compromised embryos, suggesting that the Cdc42–Par complex could regulate entry into the recycling pathway but not the progression through this pathway back to the apical membrane. The suppression of Cdc42-DN–induced loss of apical proteins by the coexpression of Rab5-DN is consistent with both an endocytic or recycling defect given that this experiment does not allow us to determine whether the Cdc42–Par complex acts upstream or downstream of Rab5. However, the simplest explanation for the substantial increase in uptake of the endocytotic tracer FM4-64 in Cdc42-compromised neuroectodermal cells would be an increase in the frequency of endocytosis. A second aPKC target is likely associated with the Hrs-positive endosome, which marks the transition from early endosome to multivesicular body formation. Attractive candidates would be the ESCRT (endosomal sorting complex required for transport) complexes that regulate multivesicular body formation. Defects in the function of these complexes can also lead to abnormally enlarged endosomal compartments (Hurley, 2008). It is remarkable that loss of Cdc42 and Par complex function causes the appearance of a single (on average), enlarged endosomal compartment per cell containing apical cargo.

Recently, the first evidence was published for the involvement of the Par complex in the regulation of endocytosis. Balklava et al. (2007) showed that the Par complex, similar to Cdc42, is required for effective endocytosis in C. elegans oocytes and coelomocytes as well as human HeLa cells. This study identifies Cdc42 and Par proteins as positive regulators of endocytotic uptake of clathrin-dependent cargo or the recycling of clathrin-independent cargo. Cdc42 and Par proteins might act to stabilize apical proteins by promoting recycling. However, we did not detect colocalization of Cdc42 or apical proteins in either wild-type or da>Cdc42-DN embryos with the Rab11-positive apical recycling endosome, suggesting that the Cdc42–Par complex regulates surface uptake directly. This is also consistent with the reconstitution of apical proteins at the plasma membrane in da>Cdc42-DN da>Rab5-DN embryos. In addition to previous work, we show that the expression of an active form of aPKC suppressed the defects seen in da>Cdc42-DN embryos, suggesting that the Par complex acts downstream and, thus, likely as an effector complex of Cdc42 in endocytosis similar to other aspects of cell polarization.

Cdc42 has been implicated as either a positive or negative regulator in several aspects of vesicle trafficking in both the biosynthetic or endocytotic/recycling pathways (Kroshewski et al., 1999; Garrett et al., 2000; Cohen et al., 2001; Müsch et al., 2001; Wu et al., 2003; Schmidt et al., 2006; Wells et al., 2006; for review see Cerione, 2004), and Cdc42 can contribute to clathrin- and dynamin-dependent and -independent endocytotic pathways (Sabharanjak et al., 2002; Balklava et al., 2007; Mayor and Pagano, 2007). This diversity of Cdc42 requirements in vesicle trafficking suggests that its function is highly cell type and/or context dependent. Our work further extends the notion that Cdc42 has context-dependent functions, as we demonstrate that the highly dynamic AJs of the Drosophila neuroectoderm are susceptible to reduced Cdc42 activity, whereas AJs in morphogenetically “silent” regions of epithelia do not critically depend on normal levels of Cdc42 function. The rescue of neuroectodermal AJs in Cdc42-compromised embryos upon blocking neuroblast specification and ingestion suggests that the essential role of Cdc42 in stabilizing AJs is not a general property of the neuroectoderm but a direct consequence of the breakdown and reformation of AJs upon neuroblast ingestion. It remains to be seen whether Cdc42 becomes activated in response to cell rearrangement in the neuroectoderm or whether GTP-Cdc42 levels are uniform throughout the ectoderm, and an essential requirement for active Cdc42 only develops in response to cell rearrangement.

Cdc42 was reported to localize to the Golgi complex in mammalian cells, which is consistent with its function in Golgi to ER and Golgi to basolateral surface vesicle trafficking (for reviews see Cerione, 2004; Ridley, 2006). We did not find colocalization of Cdc42 as detected by Cdc42 antibodies or GFP-Cdc42 with Golgi markers or markers that label other components of the biosynthetic pathway in Drosophila embryonic epithelial cells. Moreover, Cdc42-compromised embryos did not accumulate apical or basolateral membrane proteins in the biosynthetic pathway, which is in contrast, for example, to embryos that lack exocyst function (Blankenship et al., 2007). Thus, we did not find any evidence for a function of Cdc42 in secretion in the Drosophila ectoderm. However, a minor defect in exocytosis such as a change in the kinetics of vesicle release from the Golgi (Müsch et al., 2001) may have been below our detection threshold. Alternatively, a role of Cdc42 in exocytosis may have not been detected because we did not study embryos that completely lacked Cdc42 function.

Cdc42 localizes to a population of small puncta throughout the cytoplasm and plasma membrane–associated puncta that are enriched at the level of AJs. Expression of Cdc42-DN causes a relocation of Cdc42; a more uniform labeling is
observed along the lateral membrane, AJs, and marginal zone. In the cytoplasm, Cdc42 remains distributed in small puncta, which, however, now appear enriched in the apical cytoplasm, and Cdc42 is seen associated with an abnormally enlarged Hrs-positive (but Rab11, Rab5, Avl, and Rab7 negative) endosomal compartment. The N17 DN mutations of Rh and Ras GTPases are believed to have a higher affinity for guanine nucleotide exchange factors (GEFs) than the normal protein but remain GDP bound and thus inactive, suggesting that DN proteins such as Cdc42-DN act by binding and sequestering GEFs (Feig, 1999). A GEF that activates Cdc42 at the apical membrane or along the apical endocytotic pathway remains to be identified.

Several findings are consistent with the model that endocytic regulation of apical proteins rather than endocytosis of AJ proteins is the immediate result of the Cdc42–Par complex function: (a) the fact that reduced Rab5 function rescues the loss of apical polarity observed in da>Cdc42-DN embryos, although Rab5 is essential for endocytosis of apical proteins but not AJ proteins in Drosophila epithelial cells (Lu and Bilder, 2005); (b) the tight association of Cdc42 effectors Par6 and aPKC with the apical membrane (Wodarz et al., 2000; Petronczki and Knoblich, 2001); and (c) the strong genetic interaction between Cdc42-DN and crb compared with the weak interactions between Cdc42-DN and shg. Thus, the loss of AJs in the neuroectoderm is presumably a secondary consequence of the loss of apical polarity proteins in Cdc42-compromised embryos. This model is also consistent with the observation that apical (e.g., Crb) and basolateral (e.g., DEcad or Ed) membrane protein follow different endocytotic routes. Despite the loss of DEcad and Ed from the membrane, these proteins are not detected in the abnormally enlarged Hrs-positive endosomes that accumulate apical proteins. Apical/tight junction proteins and basolateral/AJ proteins also take distinct endocytotic routes. Despite the loss of AJs, most likely also through endocytosis.

Independent regulatory mechanisms for apical and basolateral AJs may provide a low maternal contribution of Cdc42 as previously described (Genova et al., 2000).
Embryos were gradually chilled to 10°C on apple agar and dechorionated in ice-cold 50% bleach for 4 min. Embryos were washed with ice-cold water and incubated in 5 μg/ml FM4-64–FX (Invitrogen) in 0.9% NaCl over a phase tube for 10 min at 4°C. Embryos were then fixed in 6% paraformaldehyde in PEMS buffer over a phase tube for 10 min at 4°C and dehydrinated by hand. A shortened immunohistochemical protocol was followed to avoid excessive washing of the FM4-64 dye. Fixed embryos were then given three washes of 10 min each in PBT (1.3 M NaCl, 0.07 M NaH2PO4, 0.03 M Na2HPO4, and 0.3% Triton X-100), a 30-min incubation in PBT plus 2% normal goat serum and 2% BSA (PBTB), and 1 h in primary antibody. Embryos were then given three washes of 10 min each in PBTB and mounted in Vectashield.

Image acquisition, processing, and statistical analysis

Fixed embryos were imaged with a confocal microscope (LSM 510; Carl Zeiss, Inc.) with Plan Apochromat 63× NA 1.4 and Plan Neofluor 40× NA 1.3 objectives at room temperature using LSM 510 software (Carl Zeiss, Inc.). Confocal z stacks were deconvolved with Volocity software (PerkinElmer). All images are deconvolved confocal stacks unless otherwise indicated. Fluorescence intensity measurements were taken using ImageJ software (National Institutes of Health) from deconvolved confocal stacks. Mean fluorescence intensity, mean particle size, and number of events were first processed by conversion to 8-bit grayscale and automatic thresholding. Mean fluorescence intensity, mean particle size, and number of particles were measured for each n confocal stacks [each generated from a different embryo and pooled from at least four independent experiments], and the data are represented as the mean ± SEM. For ventral cuticle defects, intact denticle belts were counted per embryo for n embryos, and the data are represented as mean ± SEM. For the counting of enlarged endosomes, Cdc42- and Crb-positive compartments were counted per cell and the data are represented as the mean ± SEM. For the counting of enlarged endosomes, Cdc42- and Crb-positive compartments were counted per cell and the data are represented as the mean ± SEM. For ventral cuticle defects, intact denticle belts were counted per embryo for n embryos, and the data are represented as mean ± SEM. For the counting of enlarged endosomes, Cdc42- and Crb-positive compartments were counted per cell and the data are represented as the mean ± SEM. For ventral cuticle defects, intact denticle belts were counted per embryo for n embryos, and the data are represented as mean ± SEM. For the counting of enlarged endosomes, Cdc42- and Crb-positive compartments were counted per cell and the data are represented as the mean ± SEM. For ventral cuticle defects, intact denticle belts were counted per embryo for n embryos, and the data are represented as mean ± SEM. For the counting of enlarged endosomes, Cdc42- and Crb-positive compartments were counted per cell and the data are represented as the mean ± SEM.
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