The adaptor protein Cindr regulates JNK activity to maintain epithelial sheet integrity

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A R T I C L E   I N F O

Article history:
Received 1 September 2015
Received in revised form 23 December 2015
Accepted 4 January 2016
Available online 7 January 2016

Keywords:
Cindr
Cd2ap
Cin85
JNK
Epithelial integrity

A B S T R A C T

Epithelia are essential barrier tissues that must be appropriately maintained for their correct function. To achieve this a plethora of protein interactions regulate epithelial cell number, structure and adhesion, and differentiation. Here we show that Cindr (the Drosophila Cin85 and Cd2ap ortholog) is required to maintain epithelial integrity. Reducing Cindr triggered cell delamination and movement. Most delaminating cells died. These behaviors were consistent with JNK activation previously associated with loss of epithelial integrity in response to ectopic oncogene activity. We confirmed a novel interaction between Cindr and Drosophila JNK (dJNK), which when perturbed caused inappropriate JNK signaling. Genetically reducing JNK signaling activity suppressed the effects of reducing Cindr. Furthermore, ectopic JNK signaling phenocopied loss of Cindr and was partially rescued by concomitant cindr over-expression. Thus, correct Cindr-dJNK stoichiometry is essential to maintain epithelial integrity and disturbing this balance may contribute to the pathogenesis of disease states, including cancer.

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1. Introduction

Multicellular organisms depend on epithelia for diverse functions including protection, compartmentalization of physiological systems, selective absorption, secretion and sensory reception. Given the importance of these functions, it is essential to better understand the mechanisms and molecules that, together, maintain the strength and integrity of epithelia. Diverse epithelia are assembled according to a similar plan: they typically consist of closely adherent polarized cells with simple shapes and at least one layer of cells closely associated with a basement membrane (Rodriguez-Boulan and Macara, 2014). Disrupting the internal organization of epithelial cells or their organization within the tissue can compromise the function of the epithelium. In addition the majority of fatal cancers are of epithelial origin (Weinberg, 2013). This is in part due to their exposure to carcinogens that can cause genetic mutations and because most epithelia retain mitotic potential to facilitate their rapid repair. If oncogenic mutations occur that deregulate proliferation, disrupt cell death and compromise cell polarity or adhesion, tumors and even metastases can occur (Halauoi and McCaffrey, 2015; Hanahan and Weinberg, 2011; Chaffer and Weinberg, 2011; Wogan et al., 2004; Martin-Belmonte and Perez-Moreno, 2012). A better understanding of how epithelia are maintained and regulated is therefore a priority.

Here we describe a role for the cytoplasmic Drosophila adaptor protein Cindr in maintaining the integrity of a pseudostratified epithelium, the fly wing. Cindr and its vertebrate orthologs Cd2ap and Cin85 contain multiple SH3 domains and several other protein interaction motifs that confer the ability to assemble multi-protein complexes that mediate diverse yet critical functions. Cindr and Cd2ap have previously been implicated in regulating the cytoskeleton and promoting stable cell adhesion via interactions with actin, the actin capping proteins (CPs), and GTPase activating proteins (GAPs) that target Arf6 and Cdc42 (Johnson et al., 2008, 2011, 2012; Faul et al., 2007; Bruck et al., 2006; Tang and Brieher, 2013; Zhao et al., 2013; Elbediwy et al., 2012; Yaddanapudi et al., 2011; Welsch et al., 2005; Mustonen et al., 2005; Lehtonen et al., 2002). Additionally an interaction between Cindr and Anillin at the cleavage furrow of mitotic cells is critical for cell proliferation (Haglund et al., 2010). In contrast the complexes assembled by Cin85 have mainly been implicated in regulating ubiquitination and endocytosis of receptor tyrosine kinases (RTK) (Dikic, 2002, 2006; Schlessinger, 2000; Jaffray, 2003). The adaptor protein Cindr regulates JNK activity to maintain epithelial sheet integrity

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as well as adhesion proteins of the slit diaphragm, a specialized junction of the vertebrate kidney (Tossidou et al., 2010). When, where and how Cindr, Cd2ap and Cin85 assemble appropriate protein complexes to accomplish these diverse functions remains a challenge. Genetically tractable Drosophila tissues serve as models to examine the nature and function of these complexes and address these challenges.

In exploring how Cindr maintains the integrity of the fly wing epithelium, we uncovered novel interactions with JNK (c-Jun N-terminal kinase) signaling. We found that reducing Cindr in the developing wing epithelium caused dramatic cell delamination: some cells migrated short distances and many cells died. These cell behaviors were mediated in part by ectopic JNK signaling that was triggered in cells with lower concentrations of Cindr. JNK signaling is a critical kinase cascade that responds to a variety of stimuli including DNA damage, environmental stress, wounding and Tumor Necrosis Factor-α (Adler et al., 1995; Rosette and Karin, 1996; Ramet et al., 2002; Igaki et al., 2002; Moreno et al., 2002). Appropriate responses to these stimuli include apoptosis, cell migration and even cell proliferation, effects that are mediated by expression of an array of genes targeted by transcription factors including c-Jun and c-Fos, which in turn are activated by JNK (Picco et al., 2013; Stonach, 2005; Rios-Barrera and Riesgo-Escovar, 2012).

The relationship between JNK activity and the maintenance of epithelial integrity is complex. JNK drives cytoskeletal changes and migratory cell behaviors necessary to repair epithelial wounds (Rios-Barrera and Riesgo-Escovar, 2012; Repiso et al., 2011). Here we show that this JNK function contributes to the movement of cells that lack Cindr. In addition, JNK is an important antagonist of the APF, maintained at 25 °C unless otherwise noted. We assayed the effects of reducing JNK signaling activity modified cindrRNAi2-phenotypes. Again, only male larval progeny were dissected. UAS-sifp WT-HA-25 (Garlena et al., 2010, gift from Beth Stonach) was combined with UAS-cindrRNAi2.21 (Johnson et al., 2008) to generate stable fly lines and crossed to PGG to test whether ectopic Cindr could quash ectopic JNK activity. When PGG was used as the maternal parent, both male and female larval progeny were dissected.

To assay JNK activity we generated stable fly lines that carried ptc-GAL4, UAS-GFP and pucERT (puc-lacZ, BL-6762), hid-lacZ (Fan et al., 2010, gift from Andreas Bergman) or TRE-RFP-16 (Chatterjee and Bohmann, 2012, gift of Dirk Bohmann) and crossed these to UAS-cindrRNAi2.21 males. For better detection of TRE-RFP-16 expression, crosses were raised 29 °C. The ptc-GAL4, UAS-GFP; pucERT line was also used to test whether UAS-cindrPC1D+ suppressed UAS-sifp WT-HA-25-induced JNK activity. High expression of cindrRNAi2 was mainly pupal-lethal. To generate pupal cindrRNAi2 tissue for live cell imaging, we maintained cultures of UAS-cindrRNAi2 crossed to PGG at 18 °C until the progeny pupated. Male pupae were gathered at 0 h after pupariation formation (APF), maintained at 25 °C, and imaged 14 h later. Live imaging is described below.

2.2. Dissection, immunofluorescence and microscopy

Wandering third instar larvae were dissected in PBS and fixed in 4% formaldehyde using standard procedures. Progeny of crosses utilizing PGG or PGG were imaged within 24 h of dissection. For immunofluorescence, primary antibodies were rabbit anti-Cindr (1:300, Johnson et al., 2008), rat anti-Drosophila Ecdysone (1:50, DSHB DCA2), rabbit anti-cleaved caspase-3 (Cell Signaling Technology, #9661S), mouse anti-MMP1 (1:10, DSHB 3B8D12-S), mouse anti-Protein 40 (1:300, Johnson et al., 2008), rat anti-

2. Materials and methods

2.1. Drosophila genetics

All fly crosses were raised at 25 °C unless otherwise noted. We generated the fly lines UAS-GMA, UAS-Dcr-2; ptc-GAL4, UAS-GFP (X, II) and ptc-GAL4, UAS-GFP; UAS-GMA (II, III) with transgenic stocks obtained from the Bloomington Stock Center (BL-6874, BL-2017, BL-24646, BL-31774, BL-31776). We nicknamed these stocks GDGP and PGG respectively. The transgenic lines used to reduce Cindr are described in Johnson et al. (2008). UAS-cindrRNAi2.21+23 combines two identical RNAi transgenes that target nucleotides 1016 to 1518 (nucleotide positions relate to the longest, predominantly expressed cindr transcript). A second line, UAS-cindrRNAi3.73+81 combines two identical RNAi transgenes that target nucleotides 1664 to 2246. Both UAS-cindrRNAi2.21+23 and UAS-cindrRNAi3.73+81 reduce expression of long and intermediate Cindr isoforms (described in Johnson et al., 2008), but UAS-cindrRNAi2.21+23 is three times more effective than UAS-cindrRNAi3.73+81 in reducing cindr transcripts. We therefore used cindrRNAi2.21+23, abbreviated throughout the manuscript to UAS-cindrRNAi2, for most studies.

To assay the effects of reducing cindr, we crossed GDGP females to UAS-cindrRNAi2+23 males and dissected male third larval instar progeny, which had higher levels of Dcr-2 expression than females. Stable stocks carrying UAS-cindrRNAi2 and UAS-p35 (BL-5072) were generated and crossed to PGG to block cell death in the ptc-domain of the progeny. Stable stocks carrying UAS-cindrRNAi2 and UAS-bskD (BL-9311) or bsk E (BL-3088) or jra (Fanto et al., 2000, gift from Ursula Weber) were established and crossed to PGG to assess whether reducing JNK signaling activity modified cindrRNAi2-phenotypes. Again, only male larval progeny were dissected. UAS-sifp WT-HA-25 (Garlena et al., 2010, gift from Beth Stonach) was combined with UAS-cindrPC1D+ (Johnson et al., 2008) to generate stable fly lines and crossed to PGG to test whether ectopic Cindr could quash ectopic JNK activity. When PGG was used as the maternal parent, both male and female larval progeny were dissected.

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were driven with the used to determine statistically relevant differences in the size of type control and independently, three times. When assessing rescue of the disabling JNK signaling, the phenotypes of wings were ranked main integrity, the width of the entire wing blade. Students' relative area between the L3 and L4 longitudinal wing veins. For spanning the Imager as follows: the pixel intensity of a rectangle approximately disc, the relative pixel intensities were determined using NIH 2.3. Phenotypic analyses and statistics

This preparation was then directly imaged with confocal microscope described above.

The culture of pupae for live imaging is described above. Our live-imaging protocol was inspired by (Classen et al., 2008). At 14 h APF the pupal case was partially removed to reveal one wing and the pupa arranged on a microscope slide to display the exposed wing and stabilized with double-sided tape. Oxygen-permeable hydrocarbon oil was placed directly on to the pupa to cover the wing and prevent dehydration before cover-slipping. This preparation was then directly imaged with confocal microscopy.

All images were prepared for publication using Adobe Photoshop. Minimal adjustments were applied to the whole image and equal minimal adjustments applied to images of control and experimental tissue. Maximal Image Projection of confocal serial sections were generated using ZEN2009 software.

2.3. Phenotypic analyses and statistics

To determine puc-lacZ or hid-lacZ expression in larval wing discs, the relative pixel intensities were determined using NIH ImageJ as follows: the pixel intensity of a rectangle approximately spanning the ptc-domain at the dorsal-ventral boundary was determined and the pixel intensity of a neighboring equal-sized control sample (within the posterior domain of the wing disc) subtracted. The Students' T-test was used to determine statistically relevant differences in pixel intensity (β-Gal activity).

Adult wings were analyzed with NIH ImageJ to determine the relative area between the L3 and L4 longitudinal wing veins. For each wing, this area was normalized by division by the area of the entire wing blade. Students' T-tests and one-way ANOVAs were used to determine statistically relevant differences in the size of this domain.

To determine differences in mean apical area of cells anterior to the ptc expression domain, within the ptc domain and immediately posterior to the A/P adherens boundary in ptc > Dcr-2, GFP, cindrRNAi and ptc > Dcr-2, GFP, lacZ wing discs, 96 cells were randomly selected in each of these three zones from 4 different wing discs. Areas were calculated using NIH ImageJ. Students T-tests were used to determine statistically relevant differences in apical cell area.

To score the modification of ptc > Dcr-2, cindrRNAi by partially disabling JNK signaling, the phenotypes of wings were ranked independently, three times. When assessing rescue of the ptc domain integrity, the width of the ptc domain was compared to wild type control and cindrRNAi-expressing wings. Wings were scored as no modification (same width as ptc > Dcr-2, cindrRNAi), mild rescue (10–30% improvement in the width of the domain), moderate rescue (50–75% improvement in ptc-domain width) and strong rescue (100–75% the width of the ptc domain of ptc > Dcr-2, cindrRNAi wings). To assess modifications in the migratory behavior of cells, the amount cell displacement posterior to the A/P adherens boundary was assessed and wings scored as no modification (0–10% change in cell displacement), weak rescue (10–30% reduction in cell displacement), moderate rescue (30–80% reduction) and strong rescue (80–100% reduction in cell displacement). Statistical analyses were not performed on these analyses as the number of discs assessed (between 14 and 21 of each genotype) was deemed too low.

2.4. Co-immunoprecipitation analyses

Cindr-dJNK complexes were co-immunoprecipitated from CantonS embryos or embryos in which UAS-bskmyc (Rallis et al., 2010, gift from Julian Ng) or UAS-cindrPC (Johnson et al., 2008) were driven with the dauntherless-GAL4 driver line (BL-5460) using standard protocols. For this we utilized rabbit anti-Cindr (Johnson et al., 2008), rabbit anti-JNK (Santa Cruz Biotechnology, sc-571) or rabbit anti-JNK (Cell Signaling Technology, #9252), rabbit anti-pJNK (Promega Corporation, V793) or mouse anti-pJNK (Cell Signaling Technology #9255) and mouse anti-myc (Cell Signaling Technology, 9B11). Samples were analyzed using standard Western Blot analysis.

3. Results

3.1. Loss of Cindr compromised epithelial integrity

Reducing Cindr in the developing Drosophila wing revealed an important role for Cindr in the correct development and integrity of this epithelium. Specifically, we used the patched-GAL4 driver line (ptc-GAL4) to express short hairpin RNA interference (RNAi) transgenes that targeted cindr (UAS-cindrRNAi23 +23) (Johnson et al., 2008) in a central panel of the developing wing – the ptc expression domain (Fig. 1A). We abbreviate the genotype of these animals to ptc > cindrRNAi throughout this manuscript. For wild-type control wing tissue we expressed green fluorescent protein (GFP) or β-Galactosidase (β-Gal) (ptc > GFP and ptc > lacZ respectively). Reducing Cindr led to almost complete absence of the ptc domain from the adult wing (Fig. 1B–D), suggesting that reducing cindr in this tissue during wing development led to loss of the majority of these cells.

This mass reduction in tissue has not been reported in other Drosophila tissues requiring Cindr. For example, reducing Cindr in the pupal fly eye does not reduce final eye size. Instead Cindr is required for correct local cell movements that organize cells into stereotypical positions (Johnson et al., 2008, 2011, 2012). This function is mediated through interactions with actin regulatory proteins that bind Cindr, including the CPs that limit and stabilize actin polymerization and GAPS that inactivate Arf (Johnson et al., 2008, 2011). These interactions underscore a requirement for Cindr to keep actin polymerization in check during eye morphogenesis. In addition Cindr regulates adhesive junctions to promote maintenance of correctly arranged cells during eye patterning (Johnson et al., 2008, 2012). Given these observations, we wondered whether reducing cindr in the ptc-domain of the wing modified actin and adhesion to promote cell behaviors that compromised wing cell viability. We addressed this question by examining the behavior of cindrRNAi-expressing cells in larval and pupal wing epithelia.

Reducing cindr using two independent RNAi transgenes disrupted the larval and pupal wing epithelia (Figs. 2, 3 and 51). UAS-cindrRNAi23 +23 (abbreviated to cindrRNAi) more effectively reduces cindr than UAS-cindrRNAi77 + 81 (cindrRNAi) (Johnson et al., 2008, 2012) and was therefore used for all further investigations. To enhance detection of the cell body, filopodia and apical zonula adherens (ZA) we expressed cytoplasmic and nuclear GFP as well as GMA (a GFP:moesin-actin-binding-domain fusion protein that interacts with actin filaments) in ptc-domain cells. Reduction of Cindr in the larval wing disc triggered mass displacement of cells from the ptc-domain (compare Fig. 2B–C with D–E). The ptc-domain abuts the anterior–posterior (A/P) boundary (Fig. 2A and B). In ptc > cindrRNAi wings we identified an A/P ‘adhersens boundary’ which we define here as that most-posterior column of cells with clearly defined ZAs marked by GMA accumulation (Fig. 2D and D’). The A/P adherens boundary likely coincides with the A/P compartment boundary defined by lineage analysis, gene expression and Myosin II-dependent cell bond tension (García-Bellido et al., 1973; Lawrence and Struhl, 1996; Landsberg et al., 2009), unless these features are disrupted by expression of cindrRNAi (not tested). Many cindrRNAi cells were observed posterior to the A/P adherens boundary (Fig. 2D’) and the width of the ‘intact’ ptc-
domain – taken as those columns of cells anterior to the A/P adherens boundary – was dramatically reduced (Fig. 2B′ and D′). The larval wing disc is a pseudostratified monolayer epithelium. Most displaced cindrRNAi2-cells lay within the lower half of the epithelium, having lost contact with the apical epithelial surface (compare Fig. 2C and E and Fig. 3B to E). Expression of cindrRNAi2 less effectively reduced cindr transcripts (Johnson et al., 2008) but also induced delamination of cells (Fig. S1E–F).

To understand the morphology of displaced cindrRNAi2-cells better, we examined the effect of reducing Cindr in cuboidal epithelial cells of the pupal wing. At 14 h after puparium formation (h APF), these cells are four to five times larger than cells of the larval wing epithelium. At 14 h APF the wing is rather like an oval water balloon: the single-layered cuboidal epithelium encloses a fluid-filled lumen. We peeled back the chitinous pupal-case to expose the dorsal surface of the wing for live-imaging (Fig. 2F). Using this strategy we observed GFP-labeled cells projecting dynamic extensions and confirmed that in ptc > GFP wings, cells remained in stable positions, shifted only by occasional cell division (Fig. 2G, data not shown). In contrast, reducing Cindr released small groups and individual cells from the epithelium (Fig. 2H–K). These cells delaminated into the underlying lumen and we expect were later swept away in the fluid hemolymph. Whilst delaminating, some cells adopted morphologies reminiscent of migrating mesenchymal cells (Fig. 2I). These observations support the hypothesis that in the absence of Cindr, epithelial cells delaminate and acquire migratory potential.

3.2. Features associated with cell delamination and migration accompanied loss of Cindr

The apical circumferences of many cindrRNAi2-cells still within the ‘intact’ ptc-domain (defined above) were mildly reduced (compare Fig. 3′P and G′, H-b and I-b, quantified in Fig. S3), indicating apical constriction which often portends cell delamination (Katoh and Fujita, 2012; Eisenhoffer and Rosenblatt, 2013). Consistent with this suggestion, we observed several small cindrRNAi2-cells distributed through the ptc domain (examples are colored green in Fig. 3I-c) as well as groups of cells arranged in rosettes (examples are colored pink in Fig. 3I-c) – we expect that a cell originally lay in the center of these rosettes, but had delaminated. These observations are consistent with those of delamination in other systems (for eg. Marinari et al. (2012) and Muliyil et al. 2011)) and described by T2 transition models (Fletcher et al., 2014). Interestingly, the apical circumferences of several rows of cells posterior to the A/P adherens boundary were enlarged (Fig. 3I-b, for quantification see Fig. S3) – the cause of this non-autonomous effect of reducing Cindr requires further investigation.

In each wing disc between one and five plump round cindrRNAi2-cells were observed still within the apical third of the epithelium, but well away from the ptc-domain (for example, Fig. 3C and D). We also frequently observed large cells at or near the A/P adherens boundary that were oval in shape (for eg. cell marked with arrow in Fig. 3I-d). These were located within the apical third of the epithelium and appeared to protrude into the posterior region across the A/P adherens boundary (Fig. 3I-a, compare to Fig. 3H-a). Enriched F-actin in most of these larger apical cells suggested reorganization of the actin cytoskeleton (Fig. 3I-d and I-e, compare to Fig. 3H-d and H-e). We conclude that in addition to basal delamination, some cindrRNAi2-cells were released apically into the posterior compartment. This would require crossing or eroding a Myosin cable that spans the length of the wing to separate anterior and posterior compartments (Landsberg et al., 2009). How this occurs is the subject of future investigation.

Ecadherin is not only detected at AJs but also along the length of the lateral membranes of wing epithelial cells, albeit at lower concentrations – Ecadherin outlines the basal circumference of these cells (Fig. 3J′). Reducing Cindr disrupted cell morphology so extensively that the honey-comb pattern of basal Ecadherin was...

![Image](77x506 to 509x735)
Fig. 2. Reducing Cindr in the ptc-expression compromised epithelial integrity. (A) Whole wing disc dissected from a third instar larva expressing GFP in the ptc expression domain, which abuts the A/P adherens boundary. The white box represents the region of the larval wing pouch presented in panels B, D and throughout this manuscript. (B–C) In the wing pouch of control ptc > Dcr-2, GFP, lacZ larval wing discs, GFP is localized through the nucleus and cytoplasm and accumulates at the ZA (B’), also marked by Ecadherin localization (B’’). GFP expression ends abruptly at the A/P adherens boundary. Blue brackets mark approximate width of the ptc domain. A green line marks the A/P adherens boundary in B’’ and B’’’. Cindr is ubiquitously expressed (red, B’’’) and apically enriched at AJs (Ecadherin, C and C’). The position of this orthogonal section is indicated on panel B (arrow). (D–E) Many cells expressing cindrRNAi2 as well as Dcr-2 and GFP are displaced across the A/P adherens boundary into the posterior compartment. The A/P adherens boundary is marked by a white line in D, green line in D’–D’’’, and arrow in E. The approximate width of the ‘intact’ ptc domain (anterior to the A/P adherens boundary) is indicated with a blue bracket (D’). Most cells that cross the A/P adherens boundary (D’) have delaminated from the epithelium. Displaced cells are quickly replaced to maintain a confluent epithelium (D’’). Cindr is efficiently reduced in a graded manner across the ptc domain (D’’’). Delaminated and displaced cindrRNAi2-cells are clearly observed in orthogonal sections (E and E’, position indicated on D). Inset provides a higher magnification image of a cell emerging basally from the epithelium (arrow-head; dotted line indicates base of the epithelium). (F) The pupal case is partially removed for imaging of small regions of the dorsal pupal wing epithelium. Pink box represents region imaged. (G) Expression of GFP in the ptc domain enabled live imaging of the larger cuboidal cells of the pupal wing. GFP is enriched in cell nuclei (n) and some cells project filopodia across the A/P adherens boundary (arrowhead). (H–K) Live-imaging of ptc > Dcr-2, GFP/cindrRNAi2 wings captured single and groups of cells emerging from and basal to the epithelium (H, I). Delaminated cells entered the underlying haemolymph-filled lumen. Migratory cell morphologies were occasionally observed (I). Basally delaminating cells are easily observed in orthogonal sections (J–K).
destroyed (Fig. 3K). In fact, little Ecadherin was detected in most of the mass of basal cindrRNAi2-cells but in contrast, actin was enriched (Fig. 3K′, compare to Fig. 3J′). As discussed below, many of these cells died. Consequent collapse of the actin cytoskeleton may have accounted for the bright phalloidin and GMA puncta observed (white arrow in Fig. 3K′). However, in several large round cindrRNAi2-cells located in the posterior compartment we detected a modest increase in peripheral F-actin (Fig. 3K′′, inset). Peripheral Ecadherin was also observed in these cells (Fig. 3K′, inset). We hypothesize that increased F-actin powered migration of these cells and peripheral Ecadherin mediated their transient attachment to neighboring cells. A similar mechanism drives collective migration of the border cells within the Drosophila ovary (Cai et al., 2014; Niewiadomska et al., 1999; Fulga and Rorth, 2002). Consistent with active remodeling of the cytoskeleton, Profilin (Chickadee in Drosophila, Chic) was enhanced within cindrRNAi2-cells (Fig. 5A–B) and an antibody to matrixmetalloprotease 1 (MMP1) provided a snapshot of increased MMP production and release that would degrade extracellular matrix proteins and make way for migratory cells (Fig. 5C–D). These features often accompany transformation of epithelial cells to mesenchymal fates (Lim and Thiery, 2012; Parisi and Vidal, 2011; Baum et al., 2008), but we detected only occasional expression of the mesenchymal marker Twist in migrating cindrRNAi2-cells (Fig. S5A–B and data not shown). Taken together, these data suggest that reducing Cindr enables delaminating cells to actively migrate from the ptc expression domain. However, cells could also be passively dispersed into the posterior compartment after delamination.

3.3. Most cindrRNAi2-cells that escaped the ptc-domain died

The majority of delaminated cindrRNAi2-expressing cells were small or fragmented, consistent with cell collapse and fragmentation during apoptosis or anoikis. Terminal deoxynucleotidyl transferase (TdT)-mediated dUTP nick end labeling (TUNEL) confirmed wide-scale cell death (Fig. 4B, compare to Fig. 4A). We also detected significant activation of Caspase-3 (Fig. 4D, compare to 4C) and Dcp-1 (data not shown), caspases that mediate apoptosis. The vast majority of delaminating larval wing cells died within
a short distance from the intact ptc-domain. This raised the concern that large round or oblong cells described above as migrating were rather simply displaced by the mass of basal dying cells. We also questioned whether delamination was triggered by cell death or was an active process independent of cell death. To address these questions we co-expressed \textit{p35} in \textit{cindrRNAi2}-cells to repress apoptosis (Hay et al., 1994). This strategy generated a broad, twisting panel of \textit{cindrRNAi2}-cells (Fig. S5B and D, compare to S5A).

Numerous individual cells were still observed migrating from the ptc-domain (Figs. S5B and D). These data confirmed that apoptosis was not essential for the release of \textit{cindrRNAi2}-cells from the epithelium. However we cannot discount that at least some \textit{cindrRNAi2}-cells are passively dispersed consequent to severe morphological disruption of these wing discs.

The behaviors of \textit{cindrRNAi2}-cells were remarkably similar to those described as oncogenic-like cell invasion in several models that similarly utilized the \textit{Drosophila} larval wing. In these models the activity of Csk, Src, Rho1, Abl, Ret, Ras, Cpa or Sin3a were modified (Vidal et al., 2006; Singh et al., 2010; Vidal et al., 2010; Das et al., 2012; Rudrapatna et al., 2013; Dar et al., 2012; Cordero et al., 2010; Fernandez et al., 2014; Speck et al., 2003; Neisch et al., 2010). In each case, JNK signaling mediated cell migration and death. To test whether JNK was employed to trigger the death of \textit{cindrRNAi2}-cells, we partially impeded JNK activity by reducing \textit{Drosophila} JNK (encoded by \textit{bsk} but referred to hereafter as dJNK) or \textit{Jun} (\textit{jra} or \textit{dJun}) function. JNK is the final kinase in a cascade that activates transcription factors including \textit{Jun}. Reducing dJNK or dJun reduced Caspase-3 activation in \textit{cindrRNAi2}-cells (Fig. 4E and F, compare to 4D). This implied that JNK activity contributed to the death of delaminated \textit{cindrRNAi2}-cells. Below we describe other behaviors of \textit{cindrRNAi2}-cells mediated by JNK.

3.4. \textit{Cindr} and \textit{dJNK} (bsk) reside in complexes

Notably, \textit{Cindr} and \textit{dJNK} were identified as interactors in two independent proteome-wide yeast two-hybrid (Y2H) screens that utilized either Gal4- or LexA-based Y2H strategies (Giot et al., 2003; Stanyon et al., 2004). These findings suggested that a direct
Fig. 5. Cindr and dJNK were identified in endogenous complexes and regulated JNK signaling activity. (A) Co-immunoprecipitations of dJNK (left panel) and Cindr (right hand panels) from wild type Canton S embryos confirmed that both proteins resided in a protein complex. Blots were probed with antibodies to Cindr (left), JNK (middle) and phosphorylated JNK (right). (B–C) Mild reduction of cindr (C) in the ptc-domain activated the puc-lacZ transcriptional reporter (red arrow), a target of Jun/Fos transcription factors that are activated by dJNK. Little puc-lacZ expression was detected in the wing pouch of control wing discs (B). Endogenous JNK activity drives puc-lacZ expression in the dorsal region of the wing disc (black arrows) and a strip of cells in the overlying peripodial membrane (blue arrow). (D) Quantification of puc-lacZ expression (detection of β-Gal activity). Significantly more enzymatic activity was detected in ptc>cindrRNAi2 wing pouches (p < 0.00001, n = 21) in comparison to ptc>GFP wing pouches (n = 20). To correct for background enzymatic activity, pixel intensity of a sample in just posterior to the A/P adherens boundary was subtracted from an equivalently-sized neighboring sample in the ptc-domain. Tissue posterior to the A/P adherens boundary of many ptc>GFP wings had a mildly higher pixel intensity tissue within the ptc-domain resulting in a negative relative intensity for this genotype. AU, arbitrary units. (E–F) Reduction of cindr (F) activated hid-lacZ transcription (red arrow). Some background hid-lacZ expression was detected in control ptc>GFP wings (E, red arrow). (G) Quantification of hid-lacZ expression. Significantly more enzymatic activity was detected in ptc>cindrRNAi2 (p < 0.00001, n = 27) than ptc>GFP (n = 16) wing pouches. Error bars represent standard deviation. AU, arbitrary units.
Fig. 6. JNK signaling mediated the migratory behavior of cindrRNAi2-expressing cells. In all left-hand panels, maximum projections of confocal sections that encompassed the ZAs (green, referred to as apical) are overlaid onto maximum projections of all confocal sections gathered below the ZA zone (red, sub-ZA). Orthogonal projections (right-hand panels) are of the same wings presented en face. (A–B) Expression of lacZ in the ptc-domain disturbed neither cell nor tissue morphology. The A/P adherens boundary is illustrated with a white line and apical and sub-ZA projections provided separately. In orthologous projections of this same wing disc, we observe a minor 'bulge' in the GFP-labeled tissue (green arrow, B). A straight dotted white line marks the apical limit of the A/P adherens boundary in B. (C–D) Reducing cindr triggered cell movement. In orthogonal projections we observed a mass of delaminated and migrating cells (D). Green arrow marks a cell that migrated further into the posterior compartment. A blue bracket indicates the depth of the wing pouch. (E–J) Compromising JNK activity in jra (E–F) or bsk heterozygotes (G–H), or wings co-expressing bskDN (I–J) mildly reduced cell delamination and migration. Green arrows mark the cell furthest from the A/P adherens boundary in F, H, J. Depth of the tissue (blue brackets) was increased in comparison to the ptc>Dcr-2, GFP, cindrRNAi2 disc. (K–L) Repressing JNK activity via puc expression in cindrRNAi2-cells largely repressed cell delamination and migration. Occasional cells were observed beyond the A/P adherens boundary (green arrow in L).
link between JNK signaling and Cindr may have crucial functions in epithelia. We confirmed that Cindr and dJNK resided in complexes in vivo using multiple approaches. We co-immunoprecipitated endogenous Cindr and dJNK from wild type Drosophila embryos (Fig. 5A). Complexes of ectopically expressed Cindr and dJNK were also identified in vivo (Fig. 5G and data not shown). Further, we identified activated, phosphorylated dJNK ([pJNK]) amongst the Cindr co-immunoprecipitate (Fig. 5A). Hence at least some dJNK is activated when complexed with Cindr. This led us to question whether Cindr interacts with dJNK to modify the activity of JNK signaling.

3.5. Cindr regulates dJNK signaling

To address the role of Cindr–dJNK complexes in vivo we assayed the response of JNK signaling in cells in which Cindr was only mildly reduced. Our intention was to avoid extensive cell delamination and death observed when we severely reduced Cindr because such disruption could independently trigger stress or wound-healing responses that activate JNK. Thus reducing Cindr below the threshold required for mass cell delamination and migration enabled us to isolate the direct effects of perturbing Cindr–dJNK complexes. To achieve this, we drove cindrRNAi2 in the absence of Dcr-2 (Figs. 5 and Fig. S7), an approach that modestly reduced Cindr (Johnson et al., 2008). In these wing discs we detected activity of three independent transcriptional reporters that are targets of JNK signaling; puckered-lacZ (puc-lacZ, Fig. 5B–D, Fig. 5A–B, (Adachi-Yamada, 2002)), head involution defective-lacZ (hid-lacZ, Fig. 5E–G, (Fan et al., 2010)) and TRE-red (Fig. 5C–E (Chatterjee and Bohmann, 2012)). In a fourth assay we examined accumulation of Chic, also a transcriptional target of JNK signaling (Jasper et al., 2001). Higher levels of Profilin (Chic) accumulated in many basal cindrRNAi2–cells (Fig. 5A–B, note that Dcr-2 was co-expressed in these wing discs). Because Profilin facilitates actin polymerization, increased Chic could be indicative of activation of the cytoskeleton to drive cell migration. In contrast, expression of hid-lacZ (also a proxy for expression of pro-apoptotic hid) suggested that the apoptotic machinery had been engaged. Taken together, these data confirmed that wild-type levels of Cindr are required to quash JNK signaling in the developing wing epithelium. We propose that when complexed with Cindr, activated dJNK is repressed.

3.6. JNK activity mediates cindrRNAi2 phenotypes in wing epithelia

Earlier, we discussed that JNK activity mediated the death of cindrRNAi2–cells (Fig. 4D–F). To confirm that JNK also mediated the movement of cindrRNAi2–expressing cells, we employed several strategies to simultaneously dampen JNK activity (Fig. 6). First, we expressed cindrRNAi2 in the ptc-domain of wings heterozygous for dJNK (bsk) or one of its transcription factor targets djun (jra) (Fig. 6E–H). Second, we expressed a dominant negative dJNK isoform (bskDN) together with cindrRNAi2–transgenes (Fig. 6L–J). We observed insignificant improvements to the integrity and width of the ‘intact’ ptc-domain in these wings, when compared to ptc > cindrRNAi2–wings (compare Fig. 6C to E, G and I). These data are quantified in Fig. S8A. In contrast, cell migration was curbed (compare Fig. 6C to 6E′, G′ and I′, and Fig. 6D to F, H and J). Specifically, when JNK signaling was impeded, we observed a reduction in the number of cindrRNAi2–cells that lay in the posterior compartment and the distance that cells moved beyond the A/P adherens boundary in 86%, 81% and 63% of wing discs heterozygous for dJNK (n = 14), djun (n = 15) or expressing bskDN (n = 21), respectively (Fig. S8B). These data suggest that modest reduction in JNK signaling did not affect delamination of cindrRNAi2–cells, but rather reduced the ability of these cells to disperse. This modification of cell behavior, compounded with a decrease in cell death, likely accounted for an increase in the thickness of the epithelium (compare Fig. 6F, H and J to C), especially obvious in wings co-expressing bskDN with cindrRNAi2 (Fig. 6J).

To more severely impede JNK activity, we co-expressed puckered (puc), which deactivates dJNK (Martin-Blanco et al., 1998), with cindrRNAi2–transgenes. This strategy dramatically rescued the integrity of the ptc-domain in 100% of the wing discs dissected (n = 18, compare Fig. 6K and L to C and D). Little cell delamination and movement were observed, suggesting that directly inactivating dJNK completely removed the requirement for Cindr in this tissue. In support of this hypothesis, expression of puc completely restored the tissue between the L3 and L4 veins of the adult wing, which was lost when cindr expression was reduced throughout wing development (compare Fig. 7C to B). Expression of puc in otherwise wild-type cells of the ptc domain had no effect on cell morphology or behavior (data not shown) or the relative size of the L3–L4 intervein area (Fig. 7D).

3.7. A balance of Cindr and JNK activity maintained epithelial integrity

When taken together, our data suggests that activated dJNK is repressed when complexed with Cindr. This mechanism could limit JNK signaling in tissues rich in Cindr, including the wing (Fig. 2B), unless concentrations of activated dJNK outpaced that of Cindr. To test this hypothesis, we elevated the expression of the dJNK kinase kinase slipper (slpr) in the ptc domain (Stronach and Perrimon, 2002). This effectively triggered JNK-signaling (assessed by puck-lacZ expression, Fig. 8B compare to A). The uneven spread of puck-lacZ expression in these wing discs correlated with movement of cells beyond the A/P adherens boundary (Fig. 8G, compare to F) in 81% of ptc > slpr, GFP, puck-lacZ wing discs (n = 16), which phenocopied cell displacement in ptc > cindrRNAi2 wing discs. Next we introduced ectopic Cindr into cells expressing slpr (Fig. 8C and H). This modestly reduced JNK activity (measured by the intensity of puck-lacZ, see Section 2, Fig. 8C and E) and reduced slpr–induced cell migration (Fig. 8H). Indeed cell delamination and movement was not observed in 68% of ptc > slpr, cindr, puck-lacZ wing discs (n = 24). We propose that in these wing epithelia ectopic Cindr partially corrected Cindr:dJNKcRNAi2–stoichiometry to reduce JNK signaling.

4. Conclusions

Our finding that Cindr represses JNK activity to preserve epithelial integrity brings to light a role for this adaptor protein family that is likely of great importance in oncogenesis. Indeed the behavior of cindrRNAi2–cells is akin to several established models of oncogenic-like cell migration that similarly utilize the Drosophila larval wing (Vidal et al., 2006; Singh et al., 2010; Vidal et al., 2010; Das et al., 2012; Rudrapatna et al., 2013; Dar et al., 2012; Cordero et al., 2010; Fernandez et al., 2014; Speck et al., 2003; Neisch et al., 2010). In these models, JNK activity mediated the migratory behavior of cells. Our data indicate that Cindr functions in a complex with Drosophila JNK to repress JNK signaling. Hence in the fly wing epithelium, Cindr functions as a tumor suppressor to repress oncogenic activity. The vertebrate orthologs Cd2ap and Cin85 have not yet been ascribed tumor suppressor activity, though their altered expression in a range of cancers has been reported (Bogler et al., 2000; Nam et al., 2007; Wakasaki et al., 2010; Ma et al., 2011; Mayevska et al., 2006) and genomics efforts have detected missense mutations in a small number of tumors, predominantly carcinomas (http://cancer.sanger.ac.uk/cosmic). Hence the role and regulation of Cd2ap/Cin85 in these cancers requires further study.
investigation. Cindr and its orthologs may well also modulate JNK signaling in other contexts. For example, Cindr may regulate JNK to facilitate efficient healing of wounds and the appropriate morphogenesis of embryonic tissues.

We found the stoichiometry of Cindr-dJNK complexes to be crucial: even mild reduction of Cindr was sufficient to trigger some expression of JNK signaling targets. When Cindr was more severely reduced, JNK signaling was sufficient enough to drive cells to constrict, delaminate, migrate and die. Occasionally, cindrRNAi2 cells were also observed traveling through the apical third of the wing epithelium. These phenotypes were remarkably well rescued in the presence of ectopic Puc, the dJNK phosphatase. This was surprising as Cindr (and its orthologs) has the capacity to assemble diverse protein complexes, yet our data suggested that Cindr-dJNK complexes dominate in the larval wing, where these are required to maintain the epithelium in a state of equilibrium appropriate for its correct development. Cindr’s repression of dJNK is modeled in Fig. 9. We predict that we have uncovered a conserved mechanism that fine-tunes JNK activity and warrants investigation in other systems.

Given that Cindr limits JNK activity, two immediate questions come to mind. First, when cell migration is triggered in oncogenic-like Drosophila models, during wound healing, or during morphogenetic movements in the embryo, how is Cindr’s repressive hold on JNK alleviated? We anticipate that a variety of strategies could be employed during these events. These include elevation of the concentration of activated JNK to disrupt Cindr-dJNK stoichiometry or direct modification of Cindr to disrupt its interaction with dJNK. Ectopic Rho1 activity, for example, which drives cell migration (Speck et al., 2003; Neisch et al., 2010), might elevate the concentration of activated dJNK to bypass the inhibitory effect of Cindr. Mammalian orthologs of Cindr appear to be targets of Src (Kirsch et al., 1999) and, in the fly wing, ectopic Src activity also drives cell movement (Vidal et al., 2006). We hypothesize that ectopic Src phosphorylates Cindr to modify the integrity or function of Cindr-dJNK complexes, triggering JNK activity. Expression of cindr may also be repressed to facilitate JNK activity. However, it turns out that the ortholog Cd2ap is a transcriptional target of Jun/Fos complexes when activated by Epidermal Growth Factor Receptor signaling in vitro (Lu et al., 2009). If cindr expression is also activated as a consequence of JNK signaling, this would provide a route for negative feedback that further fine-tunes JNK.

Second, our data raises the intriguing question: what mechanism is employed by Cindr to repress dJNK? We anticipate that...
Fig. 8. Correct Cindr-dJNK stoichiometry was required to maintain epithelial integrity. (A) Wild type JNK activity (puc-lacZ-expression) was observed in ptc > GFP, GFP, puc-lacZ wing discs. (B) In ptc > slpr, GFP, GFP, puc-lacZ tissue JNK was activated through the ptc-domain which was disrupted, indicating extensive cell migration. (C) Co-expression of cindr reduced slpr-induced JNK activity. (D) Ectopic JNK activity was not detected in ptc > slpr, cindr, GFP, puc-lacZ wings. (E) Quantification of puc-lacZ expression in ptc > slpr, GFP, GFP, puc-LacZ (n = 20) and ptc > slpr, cindr, GFP, puc-LacZ wing discs (n = 21) confirmed that ectopic Cindr suppressed slpr-induced JNK activity (* significant at the 5% level, p = 0.0017). Error bars represent standard deviation. AU, arbitrary units. (F–H) Expression of slpr triggered cell delamination and displacement (G) that was suppressed when cindr was co-expressed with slpr (H). Note that GMA was not expressed in these wing discs and the adherens junctions are hence not visible. Expression of two GFP transgenes (F) and cindr (not shown) did not disrupt wing epithelia.
Cindr could sequester dJNK from its target effectors or directly repress dJNK activity. For this latter possibility, we expect that effector proteins that mediate dJNK dephosphorylation or degradation could be recruited to Cindr-dJNK complexes. This suggestion highlights the important contributions that adaptor proteins play in assembling protein complexes that are crucial for the development, maintenance and function of epithelium. Indeed, our data illustrates that perturbing Cindr-dJNK complexes undermines tissue integrity, underscoring the importance of these proteins in developing and adult epitelium.

Acknowledgments

We thank numerous colleagues for donations of fly lines used in this study (listed in Experimental Procedures). In addition many stocks were obtained from the Bloomington Drosophila Stock Center (NIH P40OD018537). We thank Michael Weir, Stephen Devoto and Ross Cagan and his research team for constructive discussion and Laura Grabel and Michael Weir for feedback on this manuscript. Mark Hellerman provided invaluable technical support. This work was supported by Project Grants awarded to RIJ by the National Institute of Health (NIH P40OD018537). We thank Michael Weir, Stephen Devoto and Ross Cagan and his research team for constructive discussion and Laura Grabel and Michael Weir for feedback on this manuscript. Mark Hellerman provided invaluable technical support. This work was supported by Project Grants awarded to RIJ by the National Institute of Health (NIH P40OD018537).

Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.ydbio.2016.01.003.

References


