Notch-mediated repression of bantam miRNA contributes to boundary formation in the Drosophila wing

Isabelle Becam1,*, Neus Rafel1,*, Xin Hong2,3, Stephen M. Cohen2,3 and Marco Milán1,4,†

SUMMARY
Subdivision of proliferating tissues into adjacent compartments that do not mix plays a key role in animal development. The Actin cytoskeleton has recently been shown to mediate cell sorting at compartment boundaries, and reduced cell proliferation in boundary cells has been proposed as a way of stabilizing compartment boundaries. Cell interactions mediated by the receptor Notch have been implicated in the specification of compartment boundaries in veretebrates and in Drosophila, but the molecular effectors remain largely unidentified. Here, we present evidence that Notch mediates boundary formation in the Drosophila wing in part through repression of bantam miRNA. bantam induces cell proliferation and we have identified the Actin regulator Enabled as a new target of bantam. Increased levels of Enabled and reduced proliferation rates contribute to the maintenance of the dorsal-ventral affinity boundary. The activity of Notch also defines, through the homeobox-containing gene cut, a distinct population of boundary cells at the dorsal-ventral (DV) interface that helps to segregate boundary from non-boundary cells and contributes to the maintenance of the DV affinity boundary.

KEY WORDS: bantam, Enabled, Notch, Compartment, Drosophila

INTRODUCTION
The imaginal discs of Drosophila and the vertebrate central nervous system provide well-characterized experimental systems in which subdivision of the tissue into adjacent compartments depends on mechanisms that limit cell mixing in order to produce stable boundaries (Garcia-Bellido et al., 1973; Xu et al., 1999; Zeltsner et al., 2001). Activation of the Notch signaling pathway plays a major role in both developmental contexts (Cheng et al., 2004; Micchelli and Blair, 1999; Rauskolb et al., 1999), but the molecular effectors downstream of Notch and contributing to maintaining these affinity barriers remain so far largely unknown.

The Drosophila wing imaginal disc provides a suitable model system to identify these effectors. The wing primordium is subdivided into dorsal (D) and ventral (V) compartments by the restricted expression of the LIM-homeodomain protein Apterous in D cells (Blair et al., 1994; Diaz-Benjumea and Cohen, 1993). Cell interactions between D and V cells result in the activation of Notch along the dorsal-ventral (DV) boundary (Diaz-Benjumea and Cohen, 1995; de Celis et al., 1996; Doherty et al., 1996). Apterous induces expression of the Notch ligand Serrate in D cells and restricts expression of Delta, another Notch ligand, to V cells (Diaz-Benjumea and Cohen, 1995; Milán and Cohen, 2000). Dorsally expressed Serrate and ventrally expressed Delta activate Notch symmetrically in cells on both sides of the DV compartment boundary. Expression of the glycosyltransferase Fringe makes D Cells more sensitive to Delta and less sensitive to Serrate (Brückner et al., 2000; Moloney et al., 2000; Munro and Freeman, 2000), thus contributing to polarization of Notch activation towards the DV boundary. Notch activation induces expression of the secreted protein Wingless and the homeodomain transcription factor Cut in cells along the DV boundary (de Celis et al., 1996; Diaz-Benjumea and Cohen, 1995; Micchelli et al., 1997).

The establishment and maintenance of the DV affinity boundary evolves from early to late stages of wing development and relies on distinct molecular actors. Whereas restricted expression of the transmembrane proteins Capricious and Tartan in D cells contributes to the establishment of the DV affinity boundary (Milan et al., 2001a), Notch signaling plays a major role in its maintenance (Micchelli and Blair, 1999; Rauskolb et al., 1999). During late stages of wing development, Notch activity defines the so-called zone of non-proliferating cells (ZNC) (Herranz et al., 2008; O’Brochta and Bryant, 1985), which was proposed to decrease cell mixing at the DV boundary and to contribute to its maintenance. More recently, an actomyosin barrier has been shown to inhibit cell mixing at the DV boundary (Major and Irvine, 2005; Major and Irvine, 2006). Similar barriers have been reported in the embryonic ectoderm and at the interface between anterior and posterior compartments in the Drosophila wing, where they increase mechanical tension (Landsberg et al., 2010) and inhibit cell mixing (Monier et al., 2010). So far, the link between these actomyosin-based barriers and Notch signaling remains elusive and the contribution of reduced cell proliferation to the maintenance of the DV affinity barrier remains controversial (Blair, 1993).

Here, we identify two molecular effectors that mediate the role of Notch in maintaining the DV affinity boundary. We show that Notch exerts this activity in part through repression of bantam micro-RNA (miRNA) at the DV interface. bantam miRNA regulates G1-S transition (Brennecke et al., 2003; Herranz et al., 2008) and we have identified the Actin regulator Enabled (Ena) as a new target of bantam. We present evidence that increased levels of Ena and reduced proliferation rates contribute to the maintenance of the DV affinity boundary. Finally, we demonstrate...
that the activity of Notch also defines, through Cut, a distinct population of boundary cells at the DV interface and helps to segregate boundary from non-boundary cells. Our data indicate that this later subdivision contributes to the maintenance of a stable DV affinity barrier.

MATERIALS AND METHODS

Drosophila strains
trn-lacZ (Milan et al., 2001a); ap<sup>da</sup> (Milan and Cohen, 1999); msh<sup>lacZ</sup> (Müller and Nusslein-Volhard, 1987); UAS-<i>N</i>dsRNAi (Presente et al., 2004); UAS-dMyc (Johnston et al., 1999); bantam<sup>ΔP</sup>, bantam-sensor-GFP and UAS-bantam-GFP (Brennecke et al., 2003); sqh-GFP (Royou et al., 2002); UAS-FP4-mito (Gates et al., 2007); UAS-<i>en</i>RNAi (ID number: 43056 and 106484), UAS-cut-RNAi (ID number: 4138) and UAS-dicer-RNAi (ID number: 11429) are from Vienna Drosophila RNAi Center; other stocks are described in FlyBase.

Genetic mosaics and temperature shifts

The following <i>Drosophila</i> genotypes were used to generate loss-of-function clones by the FLP/FRT system (Xu and Rubin, 1993): hs-FLP; M(3L) ubi-GFP FRT80B/ban<sup>ΔP</sup> FRT80B FRT19/FRT19 GFP; hs-Flp cut<sup>145</sup> FRT18 / FRT18 arm-lacZ; hs-Flp.

Heat-shock was induced 3, 4 or 5 days after egg laying and late third instar wing discs were dissected. Notch<sup>h</sup> larvae were raised at 29°C for 48 hours and wing discs were subsequently dissected and labeled.

Immunohistochemistry

Antibodies used were: mouse anti-Cut (2B10), mouse anti-Wg (4D4), rat anti-BrdU (3G8) and mouse anti-Ena (5G2) (all from Developmental Studies Hybridization Bank); rabbit anti-GFP (Upstate); rabbit anti-β-Gal (Cappel); guinea-pig anti-Sens (Nolo et al., 2000); and rat anti-Ci (Mozny and Holmgren, 1995). F-Actin was labeled with Alexa Fluor 488- or Alexa Fluor 564-conjugated phallolidin (Molecular Probes) as described by Major and Irvine (Major and Irvine, 2005). BrdU staining and in situ hybridization were performed as described previously (Milan et al., 1996). A Digoxigenin-RNA Labeling Kit (Roche) was used to synthesize a probe of enabled.

3’UTR constructs

The ena-3’UTR was amplified by PCR from the SD08336 (Berkeley Drosophila Genome Project) plasmid with the following primers: Ena Sensor-Fwd: 5’-ATCGGCGATCATAATGCTGTCACG-3’; Ena Sensor-Rev: 5’-CCGCTCGATCTTAAATTTAGCAGTCGATGCTCTGGCG-3’; digested with Xhol/Eagl and cloned into the control sensor plasmid (P-Casper-tub-GFP) via the Xhol/NorI site. In order to prepare the ena-3’UTR with the mutated or deleted bantam site, the following reverse primers were used, respectively: Ena Sensor-Rev Mut: 5’-CCGCTCGATCTTAAATTTAGCAGTCGATGCTCTGGCG-3’; Ena Sensor-Rev Del: 5’-CCGCTCGATCTTAAATTTAGCAGTCGATGCTCTGGCG-3’; AATGTTGGTG-3’.

Generation of a bantam sponge

The bantam sponge sequence [CGGGCCGCAATACGACCTTCTTTTGAATCAGCTTCTTTTGTACTCATCTAGA] contains ten binding sites that are complementary to the mature bantam sequence and has a central bulge to prevent direct mRNA cleavage. The DNA sequence was synthesized by Mr Gene (www.mrgene.com), cloned (NorI/XbaI) and digested with a dsRed coding sequence into a pUAST vector. Transgenic flies were generated using P element-based random integration. The pairing between bantam and sponge sequences is shown in Fig. 2F.

Quantification of the smoothness of the DV affinity boundary

We quantified the degree of smoothness of a given DV boundary by measuring an index which was calculated as the ratio between the smoothest length of a given DV boundary and the real measurement. An index value close to one meant that the DV boundary was smooth. Both lengths were measured using ImageJ software and along the entire membrane interface of DV boundary cells located in the wing pouch. In fixed wing discs, membrane interfaces corresponding to DV boundary cells were identified by the expression of <i>ap-lacZ</i> or msh-lacZ in D cells. Measurements were performed on one confocal section corresponding to a basolateral plane of the wing pouch. Images were captured using a 40× objective on a Leica SP5 confocal microscope.

RESULTS

In <i>Drosophila</i> tissues, local regulation of actomyosin contractibility induces cell bond tension at compartment boundaries (Landsberg et al., 2010) and plays a role in cell...
Fig. 2. Notch-mediated downregulation of bantam activity contributes to dorsal-ventral (DV) boundary formation. (A, A’) Wild-type (A) and vg(BE)-Gal4, UAS-NdsRNA (A’) late third instar Drosophila wing discs labeled to visualize expression of a bantam-GFP-sensor (green), and Cut (A) or Wg (A’) protein (red). White arrowheads in A’ point to the dorsal-ventral compartment boundary. (B-D) Wild-type (B), sdGal4, UAS-bantam (C, C’) and vg(BE)-Gal4, UAS-bantam (D) wing discs labeled to visualize the DV boundary by expression of apterous-lacZ (ap-lacZ, antibody to β-Gal; B-C’) or msh-lacZ (antibody to β-Gal, D) in dorsal cells (green or white), the anterior-posterior boundary by Ci protein expression in anterior cells (B, C’; red or white) and activity of Notch by Wg protein expression (C, D; red or white). (E-E’) vg(BE)-Gal4, UAS-NdsRNA (E), vg(BE)-Gal4, UAS-NdsRNA, bantamΔ1/4 (E’) and vg(BE)-Gal4, UAS-NdsRNA, UAS-bantamponge (E’) late third instar wing discs labeled to visualize expression of msh-lacZ (antibody to β-Gal, white). (F) Cartoon depicting the pairing between the sequences of bantam and bantamponge. (G) Histogram plotting the smoothness index (see Materials and methods for details) of the DV compartment boundary in late third instar wing discs of different genotypes. Error bars indicate s.d. This index was significantly reduced in bantam-sd>bantam (P<10⁻⁸ and vg(BE)>bantam: P<10⁻⁶) or NdsRNA (P<10⁻⁵) expressing wing discs when compared with wild-type controls. Reducing the levels of bantam activity partially rescued the reduction in the smoothness index caused by NdsRNA expression (in all cases, P<10⁻³). Average smoothness index values: wild type=0.91±0.027 (n=15); sd>bantam=0.78±0.069 (n=38); vg(BE)>bantam=0.82±0.048 (n=21); vg>NdsRNA=0.86±0.037 (n=26); vg>NdsRNA, bantamΔ1/4=0.92±0.03 (n=16); vg>NdsRNA>dcr-1=0.91±0.034 (n=15); vg>NdsRNA>bantamponge=0.91±0.027 (n=16). (H) Scheme depicting the role of Notch-mediated downregulation of bantam activity in the maintenance of the DV affinity boundary. a, anterior; d, dorsal; p, posterior; v, ventral.

sorting (Major and Irvine, 2005; Major and Irvine, 2006; Monier et al., 2010). During the establishment of the DV affinity boundary, filamentous Actin (F-Actin) accumulates at the adherens junction of boundary cells to form a long Actin cable (Major and Irvine, 2005; Major and Irvine, 2006) (Fig. 1A) and no major enrichment of F-Actin, Ena and Sqh is found at the DV interface (Major and Irvine, 2005) (Fig. 1B,B’). However, Ena protein levels were generally increased in those cells close to the DV boundary (Fig. 1B’ and see below). Maintenance of the DV affinity boundary during the late stages of development relies on Notch activity (Micchelli and Blair, 1999; Rauskolb et al., 1999). At these stages of development, two distinct cell populations are distinguished at the DV boundary: boundary cells expressing the transcription factor Senseless (Fig. 1C). F-Actin and Sqh are enriched at the interface between boundary and non-boundary cells in two parallel stripes, whereas Ena is enriched in cells expressing Senseless (Major and Irvine, 2005; Major and Irvine, 2006) (Fig. 1C’,C”). In this study, we aim to characterize those molecular effectors downstream of Notch that contribute to the generation of these actomyosin cables and to the maintenance of the DV affinity barrier.
GFP was barely detectable when a dsRNA form of Notch (N\textsubscript{D\textsubscript{RNA}}) was expressed in boundary cells with the vgr\textsubscript{(BE)}-Gal4 driver (Fig. 2A'), indicating that Notch represses bantam activity in these cells (see also, Herranz et al., 2008). Because increased levels of GFP were already observed at the DV boundary of mid-third instar wing discs (see below), we questioned whether reduced bantam activity participates, downstream of Notch, in the maintenance of the DV affinity boundary during the mid- and late stages of wing development. To address this issue, we expressed bantam in the whole wing pouch, including DV boundary cells, using the scalloped\textsubscript{D\textsubscript{Gal4}} (sd\textsubscript{Gal4}) driver. We then analyzed the impact on the DV affinity boundary, visualized with the apterous-lacZ or msh-lacZ [msh (Dr – FlyBase) is a target gene of Ap] (Milan et al., 2001b) reporters to label D cells. We focused our attention on late third instar wing discs and quantified the degree of smoothness of the resulting DV interfaces by calculating the ratio of the putative smoothest length of a given DV boundary and the true measurement (see Materials and methods). As shown in Fig. 2C,C' and quantified in 2G, the DV affinity boundary was greatly disturbed and, interestingly, the anterior-posterior (AP) compartment boundary, visualized with antibodies against Cubitus Interruptus (Ci) to label the A compartment, was straight and smooth (Fig. 2C', compare with 2B). These observations indicate that the phenotype observed is specific to the DV boundary and not due to a general disorganization of the wing disc. Ectopic expression of bantam at the DV boundary, using the vgr\textsubscript{(BE)}-Gal4 driver, also disrupted the DV affinity boundary (Fig. 2D,G). Similar defects were observed in mid-third instar wing discs (data not shown). Note that in all cases Notch signaling, monitored by the expression of the Notch-regulated gene wingless (wg), was not compromised (Fig. 2C,D). These results indicate that ectopic expression of bantam in boundary cells compromises the maintenance of the affinity boundary without altering the Notch activity levels. As bantam activity is downregulated at the DV boundary by Notch signaling, we then hypothesized that Notch maintains the DV affinity boundary in part by downregulating bantam activity. Wing discs expressing N\textsubscript{D\textsubscript{RNA}} with the vgr\textsubscript{(BE)}-Gal4 driver showed defects in the DV affinity boundary (Fig. 2E, see quantification in 2G). These defects were largely rescued by halving the doses of bantam (Fig. 2E,G), by expressing a dsRNA form of Dicer-1 (Dcr-1\textsubscript{D\textsubscript{RNA}}) (data not shown; Fig. 2G), which is involved in the biogenesis of most miRNAs (Lee et al., 2003), or by expressing a bantam sponge (Fig. 2E,G), which contains ten binding sites that are complementary to the mature bantam sequence (Fig. 2F) and reduces bantam activity by sequestration (data not shown) (Loya et al., 2009). These results indicate that Notch controls the maintenance of the DV affinity boundary in part by repressing bantam activity (Fig. 2H).

A role of the zone of non-proliferating cells in DV boundary formation

bantam regulates G1-S transition in wing disc cells and reduced bantam activity at the DV boundary mediates the formation of the zone of non-proliferating cells (ZNC) (Brennecke et al., 2003; Herranz et al., 2008), which is characterized by its failure to incorporate BrdU (Fig. 3A). The ZNC can be observed in mid- and late third instar wing primordia (Fig. 3A; data not shown). Interestingly, reduced cell proliferation has been proposed to decrease cell mixing at the DV boundary and to contribute to its maintenance (O’Brochta and Bryant, 1985). Consistent with this proposal, reduced Notch activity or ectopic expression of bantam induced boundary cell proliferation (Fig. 3A',A") and the DV affinity boundary was compromised (Fig. 3F). We then tested

Notch-mediated repression of bantam contributes to DV boundary formation

Notch activity at the DV boundary induces a reduction in the activity levels of bantam miRNA (Herranz et al., 2008). Thus, a bantam-sensor that expresses GFP under the control of a ubiquitously active tubulin promoter and having two perfect bantam target sites in its 3'UTR shows increased levels of GFP at the DV boundary of wild-type wing discs (Fig. 2A) (Brennecke et al., 2003). This increase in
whether induction of cell proliferation by other means was also able to cause defects in the DV affinity boundary. For this purpose, we expressed either the G1-S and G2-M rate-limiting factors Cyclin E and String (Cdc25) in boundary cells (Edgar and O’Farrell, 1989; Knoblich et al., 1994) or the proto-oncogene Cyclin E and String (Cdc25) in boundary cells (Edgar and O’Farrell, 1989; Knoblich et al., 1994) or the proto-oncogene

**enabled is a target of bantam**

**enabled is a target of bantam that is required to maintain the DV affinity boundary**

In mid-third instar stages, the protein levels of Ena were increased at the DV boundary and this increase correlated with low bantam activity, visualized with the bantam sensor (Fig. 4A). Interestingly, the 3’UTR of ena contains a binding site for bantam (Stark et al., 2003), suggesting that bantam is responsible for keeping Ena protein levels low in wing blade cells. Consistent with this proposal, over-expression of bantam led to a reduction in Ena levels (Fig. 4C) and clones of cells mutant for bantam showed increased levels of Ena (Fig. 4E). An ena 3’UTR sensor transgene consisting of the ena 3’UTR cloned into the tubulin-promoter-EGFP reporter plasmid recapitulated the expression pattern of Ena protein (Fig. 4F). This sensor was subject to regulation by bantam as over-expression of bantam in the D compartment reduced expression of the ena 3’UTR sensor (Fig. 4G) and expression of a bantam-sponge induced an increase in GFP levels (Fig. 4H). By contrast, two transgenes carrying the ena 3’UTR lacking the bantam site or bearing a mutated bantam site (see Materials and methods for details) showed uniform expression of GFP (Fig. 4I,K) and expression of GFP was largely unaffected upon over-expression of bantam (Fig. 4J,L). These results indicate that ena is a direct target of bantam in wing disc cells.

In mid-third instar wing discs, no distinct accumulation of Actin or Myosin II was observed at the DV interface (Fig. 1B,B’), suggesting that increased levels of Ena protein might be required only in subsequent stages. Consistent with this proposal, we noted that the distinct accumulation of F-Actin observed at the DV boundary of late third instar wing discs (Fig. 1C-C’) was not observed upon overexpression of bantam (Fig. 4D) or upon expression of a dsRNA form of ena (ena siRNA) (Fig. 5E, compare with Fig. 1C-C’). In the latter case, the resulting boundary showed
an irregular shape (Fig. 5A,F). Similar defects were observed upon expression of FP4-MITO (Fig. 5B,F), a fusion protein known to deplete Ena from its normal subcellular location, by sequestering it on mitochondria and neutralizing its function (Goh et al., 2002). The anterior-posterior compartment boundary was not affected upon expression of enaRNAi transgene or the fusion protein FP4-MITO (Fig. 5C,D), consistent with the previous observation that overexpression of bantam mRNA levels were reduced in Cut-expressing cells (Fig. 6A,B), and when a dsRNA form of cut (cutdsRNA) was expressed in dorsal cells (Fig. 6C), the reduction in Ena protein levels took place only in ventral cells expressing Cut (Fig. 6F, compare with 6D). These results indicate that Cut is required to reduce Ena levels at the DV boundary. This regulation appears to be transcriptional as ena mRNA levels were reduced in Cut-expressing cells (Fig. 6A') and this reduction was not observed in cut mutant wing discs (Fig. 6B'). Interestingly, the distinct localization of F-Actin and Sqh at the interface of boundary and non-boundary cells was disturbed in mature cut mutant or cut-depleted wing discs (compare Fig. 6H-J with Fig. 1C'). Moreover, ectopic expression of Cut was able to induce an ectopic actin cable at the interface of Cut-expressing and non-expressing cells (Fig. 6K). The early actin cable observed in early wing discs was not affected in a mutant condition for cut (Fig. 6G), consistent with the fact that cut is expressed only in boundary cells of mature wing discs (Buceta et al., 2007; Micchelli et al., 1997). These results indicate that Cut reduces the levels of Ena in boundary cells and suggest that this reduction contributes to the establishment of the two actomyosin cables observed at the interface of boundary and non-boundary cells in late wing discs. We next addressed whether the enrichment in F-actin and Sqh observed in late third instar wing discs at the interface of boundary and non-boundary cells reflects a process of cell sorting between these two types of cells. We noted that this interface was rather smooth (Fig. 6A), and thus analyzed the topological location of clones of wild-type cells with respect to the interface between boundary and non-boundary cells (Fig. 7C). Clones were induced at different stages of larval development and visualized in late third instar discs, and boundary cells were marked by the expression of Cut or Wingless. Most of the clones located close to the boundary and induced in second instar stages violated the interface between boundary and non-boundary cells and respected the dorsal-ventral lineage restriction boundary. A larger percentage of clones induced at later stages of development respected the interface between boundary and non-boundary cells (Fig. 7A, see quantification in 7C). The role of Cut in inducing this cell sorting was then tested. When clones were mutant for cut, the frequency of clones induced in second instar or at later stages and respecting the interface between boundary and non-boundary cells was largely increased (Fig. 7B, see quantification in 7C). Thus, cells mutant for cut tended to be excluded from the Cut-expressing domain. These results indicate that Cut activity contributes to sorting boundary from adjacent non-boundary cells and that this differential cell sorting is probably reflected by the presence of the two actomyosin cables observed at late stages of wing development (Fig. 1C'). It is worth noting that this is not a strict lineage restriction boundary as Cut expression requires the continuous activity of Notch to be induced (Micchelli et al., 1997).

Finally, we analyzed the role of Cut and this later subdivision to the stability of the DV compartment boundary. Depletion of Cut induced an irregular DV affinity boundary at late stages of wing development (Fig. 7D,F, see quantification in 7F). Even though Cut is required for the maintenance of the Notch signaling center (Buceta et al., 2007; Micchelli et al., 1997), the defects at the DV affinity boundary caused by cut depletion were observed before Notch signaling was compromised (Fig. 7D). These results indicate that Cut contributes to the role of Notch in maintaining the DV affinity probably by defining the later subdivision of boundary and non-boundary cells.
DISCUSSION

Here, we have identified two downstream effectors of Notch involved in the maintenance of the DV compartment boundary: bantam miRNA and the homeodomain-containing transcription factor Cut. The identification of these molecular actors provides new insights, at the molecular level, of boundary formation in animal development.

Cell divisions lead to cell rearrangements that may challenge straight and sharp compartment boundaries (Monier et al., 2010). The DV boundary of mid- and late third instar wing primordia is characterized by a reduced rate of cell proliferation which defines the zone of non-proliferating cells (ZNC). The contribution of the ZNC to the maintenance of the DV affinity boundary was proposed many years ago (O’Brochta and Bryant, 1985) but this notion was subsequently questioned (Blair, 1993). Here, we provide evidence that the ZNC does indeed play a role in boundary formation. bantam miRNA positively modulates the activity of the E2F transcription factor and drives G1-S transition in Drosophila tissues (Herranz et al., 2008). Notch-mediated downregulation of bantam miRNA defines the ZNC (Brennecke et al., 2003; Herranz et al., 2008) and contributes to maintain a stable DV affinity boundary (Fig. 8A).

Induction of proliferation in boundary cells by the ectopic expression of bantam, the cell cycle regulators Cyclin E and String, or the proto-oncogene dMyc, which is known to drive G1-S transition (Johnston et al., 1999), compromises the formation of a smooth DV affinity boundary. A similar reduction in proliferation rates is observed at the rhombomere boundaries in the developing hindbrain (Guthrie et al., 1991), suggesting that reduced rate of cell proliferation might often be used in compartment boundary formation.

Notch-mediated downregulation of bantam activity is not only required to define the ZNC but also to establish the actomyosin cables observed at the interface between boundary and non-boundary cells. We have identified Ena, a regulator of Actin elongation, as a direct target of bantam that is involved in DV boundary formation. The multiple roles of bantam in promoting G1-S transition and tissue growth, blocking apoptosis (Brennecke et al., 2003; Herranz et al., 2008) and regulating Actin dynamics unveil a new molecular connection between these three processes that might have relevance in growth control and tumorigenesis.

Intriguingly, bantam miRNA has no major role in the maintenance of the anterior-posterior compartment boundary of the developing wing and this boundary is not affected upon depletion of Ena protein levels. Thus, different regulators of actin cytoskeleton and direct cell sorting in...
Fig. 7. A late role of Cut in sorting boundary from non-boundary cells. (A, B) Clones of wild-type (A) or cut145 mutant (B) cells induced in early second (L2) or early third (eL3) larval stages, dissected in late third instar, marked by the absence of GFP (green) and labeled to visualize expression of Cut or Wingless protein (red). (C) Histogram plotting the percentage of wild-type and cut145 mutant clones induced at different stages and respecting (black bars) or violating (gray bars) the Cut-expressing domain, and diagram depicting the behavior of clones respecting (R) or violating (V) the Cut domain (red). Only those clones at the dorsal-ventral compartment boundary were taken into consideration. Percentage of clones respecting/violating the Cut-expressing domain: wild type (L2)=2.7/97.3 (n=37); wild type (eL3)=22.95/77.05 (n=61); cut145 (L2)=43.61/56.4 (n=39); cut145 (eL3)=51.1/48.9 (n=45). (D, E) Late third instar cut6 mutant (D) and sdGal4, UAS-cut145 (E) Drosophila wing discs labeled to visualize expression of ap-lacZ (D, E; antibody to β-Gal, white) and Wingless protein (D, white). (F) Histogram plotting the smoothness index (see Materials and methods for details) of the dorsal-ventral compartment boundary in late third instar wing discs of different genotypes. Error bars indicate s.d. This index was significantly reduced upon expression of a cut145 transgene or in cut6 mutant wing discs when compared with wild-type control wing discs (sd<cut145; P<10^{-4} and cut6, P<10^{-8}). Average smoothness index values: wild type=0.91±0.03 (n=15); sd<cut145=0.85±0.02 (n=8); cut6=0.82±0.02 (n=13).

diverse developmental contexts. Whether reduced levels of bantam miRNA and increased levels of Ena protein are required to maintain differential cell sorting in the embryonic ectoderm or other imaginal tissues remains to be elucidated.

Cut is a late target of Notch that is expressed in boundary cells and is required to induce a stable Notch signaling center (Buceta et al., 2007; Micchelli et al., 1997). Here, we demonstrate that Cut activity has also a specific function in reducing Ena mRNA and protein levels in boundary cells (Fig. 8B). Although depletion of Cut compromises the formation of the actomyosin cables at the interface of boundary and non-boundary cells and the maintenance of a stable DV affinity boundary, cell lineage and clonal analysis of wild-type and cut mutant cells reveal that Cut plays a major role in sorting boundary from non-boundary cells. Our finding that the Notch signaling pathway defines, through Cut, a distinct population of boundary cells at the DV interface reinforces the mechanistic similarities in the maintenance of compartment boundaries within the vertebrate hindbrain and the Drosophila wing (Cheng et al., 2004). In both developmental contexts, Notch defines a distinct population of boundary cells and contributes to segregating boundary from non-boundary cells. Although Cut mediates the role of Notch in the Drosophila wing, the molecular effectors mediating the role of vertebrate Notch in boundary formation remain uncharacterized. Our data indicate that the later subdivision into boundary and non-boundary cells contributes to the maintenance of a stable DV affinity barrier in the mature wing primordium.

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Compartment boundary formation

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