Planar cell polarity controls directional Notch signaling in the Drosophila leg

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SUMMARY
The generation of functional structures during development requires tight spatial regulation of signaling pathways. Thus, in Drosophila legs, in which Notch pathway activity is required to specify joints, only cells distal to ligand-producing cells are capable of responding. Here, we show that the asymmetric distribution of planar cell polarity (PCP) proteins correlates with this spatial restriction of Notch activation. Frizzled and Dishevelled are enriched at distal sides of each cell and hence localize at the interface with ligand-expressing cells in the non-responding cells. Elimination of PCP gene function in cells proximal to ligand-expressing cells is sufficient to alleviate the repression, resulting in ectopic Notch activity and ectopic joint formation. Mutations that compromise a direct interaction between Dishevelled and Notch reduce the efficacy of repression. Likewise, increased Rab5 levels or dominant-negative Deltex can suppress the ectopic joints. Together, these results suggest that PCP coordinates the spatial activity of the Notch pathway by regulating endocytic trafficking of the receptor.

KEY WORDS: Planar cell polarity, Notch, Dishevelled, Drosophila

INTRODUCTION
The development and physiology of all multicellular organisms requires cell communication through well-defined signaling pathways that each consist of distinct canonical components. Cross-talk between pathways is required for the relatively limited number of pathways to match the anatomical and functional complexity that cell signaling has to regulate. The mechanisms that enable the pathway cross-talk are thus of major importance for generation and maintenance of complex structures.

One highly conserved signaling pathway important for coordinating many developmental processes is mediated by Notch transmembrane receptors (Fiuza and Arias, 2007; Fortini, 2009). Besides Notch (N), core members of this pathway in Drosophila include two transmembrane ligands: Serrate (Ser; Jagged in vertebrates) and Delta (Dl). Upon ligand binding, N suffers two consecutive proteolytic cleavages and releases its cytoplasmic portion, which enters the nucleus and mediates a transcriptional response by binding to CSL transcription factors. Behind this apparent simplicity, a wide variety of biological functions and modes of action are made possible by context-dependent accessory mechanisms that help regulate the activation of N (Andersson et al., 2011; Bray, 2006). These include post-translational modifications, such as glycosylation and ubiquitylation, that affect endocytic sorting of both N and its ligands.

N activity is also modulated by key aspects of tissue organization, including planar cell polarity (PCP). PCP was first characterized in Drosophila epithelial cells, where it establishes a polarity axis in the tissue plane, orthogonal to the apical-basal axis (Goodrich and Strutt, 2011; Vladar et al., 2009). Its relevance is evident in the orientation of cell projections, such as hairs or microvilli, and it is also important in coordinating behavior in fields of cells, ensuring that they respond in a homogeneous directional fashion, including convergent extension in vertebrate embryos and ommatidial rotation in insect eyes. The latter is one example for which PCP and N are known to converge (Cooper and Bray, 1999; Fanto and Mlodzik, 1999; Tomlinson and Struhl, 1999).

The proteins of one of the main PCP pathways (the core, Fz or Stan system) associate in complexes at the cell membrane. They include the transmembrane proteins Van Gogh (Vang; also known as Strabismus, Stbm) (Taylor et al., 1998; Wolff and Rubin, 1998), Frizzled (Fz) (Vinson et al., 1989) and Flamingo (Fmi; also known as Strabismus, Stbm) (Taylor et al., 1998; Wolff and Rubin, 1998), Dishevelled (Dsh) (Klingensmith et al., 1994; Theisen et al., 1994) and Diego (Dgo) (Feiguin et al., 2001). In the wing epithelium, PCP protein complexes acquire an asymmetric proximal-distal localization (Strutt and Strutt, 2009). A Fz-Dsh complex localizes to the distal side of cells, together with Dgo, whereas a Stbm-Pk complex is localized to the proximal domain. These two complexes repel each other within the cell and both require Fmi and other proteins for their correct localization. Most of these core PCP proteins function in other planar polarized systems in Drosophila and in vertebrates, although the details of their localization or cellular actions might differ (Seifert and Mlodzik, 2007). Besides this role in PCP, a non-canonical Wnt pathway, Fz and Dsh are also required in canonical Wnt signaling, for which they trigger nuclear accumulation of β-catenin upon Wnt activation (MacDonald et al., 2009). Most mutations in Fz affect its role in both PCP and Wnt signaling (Povelones et al., 2005), whereas PCP-specific mutations of Dsh affect protein localization (Axelrod et al., 1998). In addition,
the interaction partners also influence the outcome as the association with Dgo produces a bias towards PCP to the detriment of Wnt (Wu et al., 2008).

A striking feature of flies mutant for core PCP members is that they have supernumerary joints in the tarsal region of the leg (Held et al., 1986). Normally composed of five segments (T1 to T5) separated by joints with a ball and socket structure, tarsal mutant for core PCP genes contain ectopic joints in segments T2, T3 and T4 and, less frequently, T1. Joints are determined at the end of larval development, when a stripe of Ser-expressing cells is specified within each segment and activates the receptor in distal cells triggering transcription of several N targets that control different aspects of joint differentiation (Bishop et al., 1999; de Celis et al., 1998; Rauskolb and Irvine, 1999). Ser appears to be the functional N-ligand in this process, as joints are absent in Ser mutants although other aspects of leg morphology appear normal, and in PCP mutant legs the ectopic joints correlate with ectopic Notch activity although the mechanism is unknown (Bishop et al., 1999).

The ectopic joint phenotype in PCP mutant flies implies that the PCP system has a role in regulating N signaling (Bishop et al., 1999). The likely scenario is that, when PCP is disrupted, N becomes activated in cells proximal to Ser-expressing cells, as well as those distal. How this regulation occurs is, however, unknown. In the eye, where the R3/R4 photoreceptor fate choice is crucial for ommatidial polarity, Fz activity in the presumptive R3 is essential for polarizing N activity (Cooper and Bray, 1999; Fanto and Rubin, 1993) with appropriate recombinant chromosomes. To induce the fmi192 phenotype, as the defect occurs with mutations affecting any core PCP genes. An \( \beta \)-N-terminally truncated Dsh mutant genomic fragment was introduced into the Ser-expressing cells. In prepupal legs of \( \text{dsh}^{-} \) mutants a PCP-specific reporter has previously been shown to respond to dsh- \( \beta \)-catenin, mouse anti-Fmi, mouse anti-Nicd, mouse anti-Necd and rat anti-E-cadherin were obtained from the Developmental Studies Hybridoma Bank (University of Iowa, USA). Actin cytoskeleton was labeled with Phalloidin-TRITC (Sigma, St Louis, MO, USA).

Samples were examined using a Leica DM RXA2 microscope and Leica TCS SP Confocal system (Leica Microsystems, Wetzelar, Germany). Images were processed and analyzed with Leica Confocal Software, ImageJ suite and Adobe Photoshop.

### MATERIALS AND METHODS

#### Fly stocks

The following mutant alleles were used, either homozygous or in mitotic clones: \( \text{pk}^{w1} \), \( \text{dsh}^{-} \), \( \text{dsh}^{-}/ \), \( \text{fmi}^{w} \), \( \text{fz}^{-} \), \( \text{Dro}^{k} \) (described in FlyBase, http://flybase.org). To monitor N activation we used the following reporter constructs: \( \text{UAS-GFP} \), \( \text{dsh-GFP} \), \( \text{dsh-} \) \( \beta \)-galactosidase (\( \text{dsh-1.5-lacZ} \)), \( \text{UAS-robo} \), \( \text{UAS-robo} \) in combination with \( \text{UAS-FZ} \) driven by \( \text{ap-Gal4} \), \( \text{UAS-dxmRZF} \) (described in FlyBase, http://flybase.org; our unpublished data).

#### Biochemistry

To map the domains of Dsh interacting with the intracellular domain of Notch (NIC), glutathione s-transferase (GST) pull-down experiments were performed as described (Djiane et al., 2005); by incubating GST-NIC fusion with \( \text{35S} \)-labeled Dsh fragments (primers are listed in supplementary material Tables S1, S2). Specific amino acids were mutated by site-directed mutagenesis using the QuikChange Site-Directed Mutagenesis Kit (Agilent Technologies, Santa Clara, CA, USA). The relative intensity of the bands was calculated using the gel analysis application of the ImageJ suite, by plotting the lane profile and calculating of the resulting peak areas. Two gels were analyzed for each pair of bands.

### RESULTS

#### The double joint planar cell polarity phenotype correlates with ectopic N activity

Mutations affecting core PCP genes result in supernumerary joints in the tarsal region, most commonly in tarsal segments 2-4 (Bishop et al., 1999; Held et al., 1986). Ectopic joints are located proximal to the normal joint and have reversed polarity (Fig. 1A,B). Such ectopic joints appear to be a bona fide PCP phenotype, as the defect occurs with mutations affecting any core PCP gene: phenotypes of \( \text{pk} \), \( \text{fz} \), \( \text{dsh} \), \( \text{Vang} \), \( \text{fmi} \) and \( \text{dgo} \) are consistent and differ from other mutant conditions affecting joint development (Held et al., 1986; Wolff and Rubin, 1998) (http://flybase.org; our unpublished data).

The implication of this phenotype is that PCP controls the directionality of cell signaling mediated by the N pathway, the main agent in joint determination (Bishop et al., 1999; de Celis et al., 1998; Rauskolb and Irvine, 1999). To ascertain whether this interpretation is correct, we have analyzed expression of three reporters of N activation in different viable mutants of core PCP genes. Reporter expression is fully established by 2-6 hours after puparium formation (APF) when the leg disc starts to evert. The best characterized direct N targets are the \( \text{E(spl)} \) genes. An \( \text{E(spl)1.5-lacZ} \) reporter has previously been shown to respond to N in the leg (Cooper et al., 2000; de Celis Ibeas and Bray, 2003), where it is expressed in a stripe distal to, and partially overlapping, the Ser-expressing cells. In prepupal legs of \( \text{dsh}^{-} \), a PCP-specific
Fig. 1. N is ectopically activated in Drosophila PCP mutants. (A, B) Wild-type leg with normal joints (A) and pkple1 leg with ectopic joints with inverted polarity (B). In these and subsequent panels arrowheads indicate normal joints terminating tarsal segments 2, 3 and 4, and the corresponding domains of expression. (C, D) E(spl)mB1.5-lacZ expression (X-gal, blue) in wild-type prepupal leg (C) and dsh1 mutant (D) with ectopic stripes. (E, F) bib-lacZ expression (green) in a single row of cells (anti-β-catennin, purple, cell contours) at the segment boundary in wild type (E) is duplicated in a pkple1 (F). (G, H) disco-lacZ (green) is expressed in a wider domain in wild type (G); normal and duplicated domains merge in a single broad territory in pkple1 (H). (I, I') bib-lacZ (green) is expressed distally adjacent to Ser (I, purple; I', gray). (J, J') In pkple1 the ectopic stripe (green) appears proximally adjacent to Ser (J, purple; J', gray); a sub-apical confocal section is shown to capture the nuclear β-galactosidase. (K, K') Large fz122 clone marked by absence of GFP (green); expression of Ser (K, purple; K', gray) is not altered.

allele, an ectopic domain appeared, confirming that disruptions in core PCP gene activity result in ectopic N activity (Fig. 1C,D). Equivalent ectopic domains of E(spl)mB1.5-lacZ were seen with alleles affecting other core PCP genes (see below).

Similar results were obtained with a lac-Z insertion into big brain (bib-lacZ), expression of which is also regulated by N (de Celis et al., 1998; Pueyo and Couso, 2011). bib-lacZ is expressed in a narrow band one or two cells wide just distal to the domain of Ser expression (Fig. 1E,I). In prepupal legs of pkple1, a strong hypomorphic allele of pk (Gubb et al., 1999), there was an ectopic bib-lacZ stripe proximal to the Ser-expressing cells (Fig. 1F,J). In addition, the levels of bib-lacZ were sometimes reduced or discontinuous (see below). A further marker of leg joints (although not a known direct target of N) is disco-lacZ (Bishop et al., 1999), an insertion into disconnected, which is expressed in a broader domain spanning three or four cell diameters (Fig. 1G). In a pkple1 mutant, the disco-lacZ domain was duplicated and, owing to its larger territory, the ectopic domain merged with the endogenous one from the preceding segment, resulting in a continuous domain of expression in most of the tarsal region (Fig. 1H).

Despite the evidence for ectopic N activity, there was no change in expression of the Ser ligand in pkple1 legs or in mitotic clones of fz122 (a strong fz hypomorph; Fig. 11-K) or of DI present at later stages (Bishop et al., 1999). Neither was there a clear alteration in the expression profile of the N receptor itself (supplementary material Fig. S1). Therefore, the extra stripes of N activation are a general feature of mutations affecting PCP but are unlikely to be the result of a simple change in the expression of N or its ligands.

Cell-autonomous effects of PCP alleles suggest a requirement in the signal-receiving cell

In order to know whether the mechanism of action of PCP on N is direct or indirect, or whether it is likely to act in ligand-sending or signal-receiving cells, we analyzed defects caused by clones of mutant cells. If the effects are direct in signal-receiving cells, activation of N targets should only be detected autonomously within mutant cells in clones located proximal to the site of ligand expression. Conversely, if PCP regulation affects the ligand, some non-autonomous defects would be seen. It is important to note that not all mutant alleles would be useful for this analysis, because several of them show a directional domineering non-autonomy owing to reorganization in PCP over neighboring cells. Therefore, we used only alleles reported to show autonomous polarization phenotypes: pkple1, fmi192, dsh1 and fz122 (Chae et al., 1999; Jones et al., 1996; Lee and Adler, 2002; Strutt and Strutt, 2007).

We first examined effects on the E(spl)mB1.5-CD2 reporter [containing the same regulatory element as E(spl)mB1.5-lacZ], a direct target of N pathway. In clones of fz122, expression of E(spl)mB1.5-CD2 is de-repressed autonomously within the mutant cells (Fig. 2A). Furthermore, in several examples the mutant cells were juxtaposed with putative ligand-producing cells that were wild type. These results argue that the effect of fz122 on the N pathway is autonomous and is most likely to occur in the signal-receiving cells. E(spl)mB1.5-CD2 is also autonomously de-repressed in dsh1 mutant clones (not shown).

The behavior of disco-lacZ in pkple1 and fmi192 clones was identical to that of E(spl)mB1.5-CD2. In both genotypes, disco-lacZ was de-repressed in a completely autonomous manner (Fig. 2B,C). Again, expression of lacZ in cells at clone edges suggested a requirement for polarization in the signal-receiving cell rather than on the ligand.

The effects of mutations on bib-lacZ were, however, slightly different. In all three of the mutants tested (dsh1, pkple1, fmi192) de-repression of the reporter was detected only in mutant cells and not in adjacent wild-type cells (Fig. 2D,E; supplementary material Fig. S2). However, unlike E(spl)mB1.5-CD2 and disco-lacZ, ectopic activation of bib-lacZ was variable in intensity (weak to similar to endogenous bib-lacZ) and in extent. In some clones, only a few cells showed ectopic expression whereas in others it filled the whole width of the mutant clone. Nevertheless, the fact that bib-lacZ can be de-repressed at the clone boundaries is consistent with
adjacent to the mutant cells, which argues against an effect of PCP
on Ser or on a second signaling pathway. These results were
replicated in earlier stages (third instar larval discs) and in smaller
clones (supplementary material Fig. S3).

Asymmetric distribution of core PCP proteins in the
developing leg
Core PCP proteins adopt a polarized distribution in Drosophila
pupal wing cells, which are arranged in a regular hexagonal lattice
(between 20 and 24 hours APF). Dsh and Fz become localized to
the distal edge of each cell, Pk and Vang to the proximal edge
(Strutt and Strutt, 2009). Some degree of polarization is also
evident in prepupal stages (Aigouy et al., 2010; Strutt et al., 2011).
Cells in the prepupal leg epithelium are mostly irregular in shape
and size, unlike the wing, making it difficult to detect clear
organization in cell morphology or protein distribution. To
investigate whether there was any asymmetry in core PCP protein
distribution, we generated patches of cells expressing Fz::GFP,
Vang::GFP and Dsh::GFP and examined protein distributions at
clone borders, as was done previously in the wing to investigate
protein asymmetries (Axelrod et al., 2001; Strutt et al., 2002; Strutt,
2001). Fz::GFP and Dsh::GFP levels were higher at the distal side
of cells compared with proximal (Fig. 3A,B). Conversely,
Vang::GFP levels were highest on the proximal sides of each cell
(Fig. 3C). Some differences in Fmi localization were also evident:
the protein was more enriched at proximal-distal boundaries than
at dorsal-ventral (Fig. 3D), a characteristic that was most obvious
in the tarsus-preptarsus boundary where cells have a more regular
morphology (Fig. 3D').

Cells receiving the N signal also exhibited distinct morphology.
Detection of β-catenin, localized to sub-apical adherens junctions,
revealed that the bib-lacZ-expressing cells were roughly
quadrangular. Their distal edges formed a straight line, probably
marking the boundary between adjacent tarsal segments (Fig. 3E).
These features were also observed in the ectopic domain of bib-
lacZ in the PCP mutants (Fig. 3F). In addition, the intensity of bib-
lacZ expression was correlated with cell morphology, both in the
normal and ectopic domains of expression. This suggests that high
levels of N activation result in ordered alignment of the leg
epithelial cells.

Direct interaction of N and Dsh
Drok (Rok – FlyBase) is one of the main mediators of the
cytoskeletal response to PCP: it is important for restricting wing
hair generation and for ommatidial rotation (Winter et al., 2001).
We tested whether Drok had any effect on the bib-lacZ and
E(spl)mβ1.5-CD2 reporters. Although Drok mutant clones showed
defects in ommatidial rotation and in tissue morphology (data not
shown), none resulted in ectopic expression of the bib-lacZ or
E(spl)mβ1.5-CD2 reporters (Fig. 4A,B). Therefore, this function of
the core PCP pathway does not seem to be mediated by the actin
cytoskeleton.

Previous studies have shown a physical interaction between Dsh
and N, which contributes to inhibition of N signaling in the wing
margin (Axelrod et al., 1996; Munoz-Descalzo et al., 2010). We
questioned whether a similar mechanism operates in joint
regulation. Overexpression of Dsh driven by ap-Gal4 in T4 and
proximal T5 had two clear effects (Fig. 4C,D). First, there was a
disruption of PCP that has already described for Dsh
overexpression in the wing (Axelrod et al., 1998). Second,
formation of the joint between these tarsi was repressed, as would
be expected if Dsh were capable of repressing N. A possible caveat
to this interpretation is that Dsh overexpression could produce

Fig. 2. Proximal de-repression of N in Drosophila PCP mutants is
cell autonomous. In all panels, mutant clones are revealed by absence
of GFP (green); ectopic expression of reporters (purple; single channel
on the right) is indicated by arrowheads. (A) Mutant fz22 clone; ectopic
expression of E(spl)mβ1.5-CD2 coincides with clone border despite
presence of adjacent wild-type (ligand-expressing) cells. (B) Mutant
fmi192 clones; autonomous expression of disco-lacZ in cells adjacent to
wild-type GFP-positive cells. (C) Mutant clones of pksple1; several ectopic
domains of disco-lacZ occur autonomously within the mutant clones.
(D) Large clone of cells mutant for dsh1; some ectopic expression of bib-
lacZ appears in tarsal segment 3, but not in segment 2. (E) Elongated
clonal cells mutant for pksple1; ectopic activation of bib-lacZ that can
occupy the full width of the clone. Occasional downregulation of the
normal stripe of bib-lacZ is also detected (arrows).

a requirement for PCP in signal-receiving cells, rather than through
effects on Ser. We note also that in some fmi and pk clones
the endogenous domain of bib-lacZ is weakened within the clone (Fig.
2E). This observation also correlates with the fact that in whole
legs mutant for core PCP genes, normal bib-lacZ expression can be
weakened compared with the ectopic expression (Fig. 1F; supplementary
material Fig. S2).

Both the variability of bib-lacZ de-repression within clones and
the weakening of endogenous expression in mutant cells might
reflect a difference in the threshold of N activity required for bib-
lacZ activation compared with disco-lacZ and E(spl)mβ1.5-CD2
(see Discussion). Nevertheless, N reporters were de-repressed
autonomously in all the core PCP mutant genotypes when mutant
cells were located proximal to the Ser domain. No ectopic
expression of the reporters was observed in wild-type tissue
adjacent to the mutant cells, which argues against an effect of PCP

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patterning defects causing a secondary effect on joints. However, the effects of expressing Dsh in clones do not support this possibility. For example, a large dorsal clone of Dsh-expressing cells produced autonomous expression of bib-lacZ (Fig. 4E,E'). Although this clone contained two small putative axis duplications (ectopic leg tips in the form of circular domains of bib-lacZ) expression in tarsi 2 and 5; Fig. 4C', arrowhead), segmentation appeared to correlate with cell size, shape and alignment both in normal and ectopic domains.

To test functional relevance of the direct interaction of Dsh and N in leg segmentation, we set out to find a mutant form of Dsh that had reduced ability to interact physically with N. To map the interacting regions we used glutathione-s-transferase (GST) pull-down experiments. From a set of deletions spanning different regions of Dsh, only constructs with an intact DIX domain were successfully retained by the intracellular portion of N (GST-NIC; Fig. 5A,B). Deletion of the N-terminal region of this DIX domain was sufficient to abolish this interaction (compare constructs Dsh5 and Dsh6). Unfortunately, as the DIX domain is also required for Axin recruitment (Julius et al., 2000; Kishida et al., 1999), these deletions also prevented Axin binding (Fig. 5B). It was therefore important to identify mutations that would affect binding of NIC but not Axin. We first tested effects of mutations in residues that are conserved between Dsh and the mammalian Dvl proteins. Of the three mutations tested, only V43E (present in mut1 and mut4) abolished interaction with NIC and this also affected Axin binding (Fig. 5C-E; data not shown).

Substitution of two adjacent hydrophilic residues that are specific to Drosophila Dsh, K46V+Q47A, showed some specificity for NIC. Quantitative analysis of the band intensities revealed that this mutation (mut6) reduced binding to NIC by 95%, but interaction with Axin was reduced by only 65%. This mutation was therefore a candidate to test relevance for N regulation.

To investigate whether the mut6 form of Dsh was compromised for N regulation in the leg, we introduced the K46V+Q47A mutation into a dsh genomic rescue construct that had been used previously (Axelrod, 2001). Multiple insertions of the mutant protein were tested for their ability to rescue dsh' and dsh'26 mutant phenotypes. The former only affects PCP function; the latter is a null allele affecting both PCP and Wnt signaling. All three constructs could rescue the embryonic lethality of dsh'26, so they can function in the canonical Wnt pathway. As expected, the PCP ectopic leg joint phenotype was rescued by the wild-type dsh construct but not by dsh' (Fig. 6A). Importantly, the mut6 constructs showed a reduced ability to rescue the ectopic leg joint phenotype (Fig. 6A,B), although the proximal-distal and dorsal-ventral patterns were wild type, including the distal tip, which is the part of the leg most sensitive to alterations in Wnt signaling (Galindo et al., 2002). In addition, when combined with dsh'26, the resulting adult flies had largely wild-type wings and both leg bristles and wing hairs...
exhibited normal planar polarization (Fig. 6B-E). Expression levels of the GFP-tagged Dsh proteins produced by mut6 were similar to those from the wild-type dsh construct (Fig. 6B,C). These results, therefore, are consistent with the hypothesis that a direct interaction between Dsh and N is important for suppressing N activity in the domain proximal to Ser stripe. However, we cannot rule out the alternative possibility that the inability of mut6 to rescue leg joints reflects a difference in the threshold levels of Dsh activity required for this process compared with others.

The antagonistic effect of Dsh on N signaling has been described previously in the wing, where N is also important for patterning sensory organs at the wing margin. However, although overexpression of known N repressors such as Numb (Nb) and Hairless (H) (Frise et al., 1996; Nagel et al., 2005) produced nicks in the wing margin and repression of the Notch-target Cut (supplementary material Fig. S4), ectopic Dsh was sufficient neither to produce nicks in the adult wing nor to repress Cut at larval stages (supplementary material Fig. S4). Although the

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interpretation of these results might be confounded by the fact that overexpression of Dsh at the margin can also lead to expression of N ligands and to N activation, possibly explaining the ectopic bristles observed in the wing blade (supplementary material Fig. S4), the effects of overexpression of N are nevertheless relatively minor compared with the overexpression of Nb and H. The results suggest, therefore, that the ability of Dsh to suppress N is restricted to certain contexts, making it less likely that it antagonizes the cleaved, active form of N (Niced).

To investigate further whether Dsh could antagonize Niced, we assayed the effects on an N-responsive reporter (NRE-luciferase) of co-expressing Dsh and Niced in transient transfection assays. Expression of Niced alone resulted in strong induction of NRE-luciferase that was little altered by co-expression with Dsh (supplementary material Fig. S4). Therefore, although Dsh binds to the intracellular domain of N, it does not inhibit Ntrans-activation function, suggesting that it is likely to regulate the receptor prior to cleavage.

**Role of endocytic regulators**

It has been suggested that Dsh influences endocytic trafficking of proteins including N (Chen et al., 2003; Munoz-Descalzo et al., 2010; Yu et al., 2007). One model therefore is that recruitment of Dsh to the distal edge of the cells would result in downregulation of N by endocytosis. To investigate this, we tested the consequences of expressing several different endocytic regulators in the T4 segment with ap-Gal4 (Fig. 4C) to determine their effect on the ectopic joint present in dsh1 mutants.

First, we tested consequences of expressing three different Rab GTPases, Rab5, Rab7 and Rab11, which regulate vesicle trafficking to early endosome, late endosome and recycling endosome compartments, respectively (Stenmark, 2009). In previous studies, overexpression of Rab5-GFP and Rab7-GFP were able to suppress the ectopic N activation seen in lethal giant discs [lgd; l(2)gd1 – FlyBase] mutants (Jaekel and Klein, 2006). Overexpression of Rab5 in a wild-type background had no effect (Fig. 7A,C), but in a dsh1 mutant background it was able to modify the ectopic joint phenotype in 80% of the legs examined, resulting in a partial suppression (Fig. 7B,D). By contrast, neither Rab11 nor Rab7 had any effect in this assay (data not shown), suggesting that the defect is linked to transit to early endosomes. The implication is that dsh1 leads to a defect in endocytic transport of N from the plasma membrane, preventing its activation by Ser, and that this can be compensated for by increasing the levels of Rab5. To test this hypothesis, we examined whether overexpression of Dsh::myc, which resulted in lack of joints and downregulation of bib-lacZ (Fig. 4C-E), had any impact on N protein distribution. In ap-Gal4, UAS-dsh-myc legs there was reduced N at the apical membrane and a large fraction of N colocalized with Dsh in intracellular puncta (Fig. 8A). Many of the N-containing puncta appeared to correspond to early endosomes based on their colocalization with Rab5 (Fig. 8B). Furthermore, N depletion from the cell surface and accumulation in puncta was evident using antibodies against either the extracellular or the intracellular portion of N (Fig. 8C,D). This implies that a significant fraction of the endocytosed N is uncleaved and, therefore, that the Dsh-mediated change in localization occurs independently of ligand binding or γ-secretase cleavage.

Rab5 has also been found to inhibit the ectopic N signaling caused by increased levels of the Delta (Dx) E3 ubiquitin ligase (Hori et al., 2004; Matsuno et al., 2002). The effect of Dx is complex, as it can result in ligand-independent activation or in downregulation of N signaling, depending on the context (Mukherjee et al., 2005; Wilkin et al., 2008; Yamada et al., 2011). Both modes of regulation require Rab5-mediated endocytosis of N to early endosomes. To test whether the dsh1 phenotype in T4 could be modified by expression of Dx and derivatives, we assayed full-length Dx and mutations affecting some of its functional domains (Matsuno et al., 2002): proline-rich region (DxPro), ring-H2 domain (DxProRZ) and N-binding region (DxNBS).

Expression of Dx and DxPro phenocopied the defects caused by PCP mutations (Fig. 7E), arguing that N activity at these ectopic sites might involve modifications to its trafficking, and neither was able to modify the dsh1 phenotype (Fig. 7F). DxProRZ had no effect in wild type or in dsh1 (not shown). By contrast, expression of DxNBS resulted in a striking phenotype of joint fusion (Fig. 7G,H) in both wild type and dsh1, resembling consequences of dx null alleles in certain conditions of altered N activity (Gorman and Girton, 1992). DxNBS thus appears to have a dominant-negative effect, blocking the endogenous T4-T5 joint as well as the ectopic joint in dsh1. This contrasts with the wing, in which DxNBS exhibits little residual activity (Matsuno et al., 2002) and suggests that the Dx context-dependent effects (Wilkin et al., 2008) are likely to rely on other factors that could be titrated by DxNBS.

Our results reveal that two endocytic regulators, Rab5 and Dx, can alter N activation at the site of ectopic joint formation, although there are mechanistic differences between them. Overexpression of Rab5 had no effect on wild-type tarsus but could rescue the mutant phenotype of dsh1. This suggests that ectopic N activity in PCP mutants is associated with a change in N trafficking that can be...
suppressed by Rab5. By contrast, overexpression of Dx induced ectopic joints even in the wild-type background arguing that it is sufficient to overcome repression of N mediated by PCP.

**DISCUSSION**

Spatially coordinated regulation of signaling pathways is essential to generate correct anatomical and functional structures, as exemplified by the *Drosophila* leg, in which activity of the N pathway is required to specify leg joints (Bishop et al., 1999; de Celis et al., 1998; Rauskolb and Irvine, 1999). In this case, only cells distal to the stripe of Ser expression appear to be capable of responding to the ligand. Here, we show that activity of the core PCP pathway is required in those cells proximal to the domain of Ser expression to prevent them from responding to this N ligand. This regulation correlates with the asymmetric distribution of the core PCP proteins, as we show that Fz and Dsh are enriched at the distal side of each cell, which in the non-responding cells faces the neighboring Ser-expressing cells. Conversely, in those cells distal to Ser, Fz and Dsh are depleted from the proximal side, leaving N free to interact with its ligand to promote joint formation. It appears that elimination of core PCP gene function in cells proximal to the Ser-expressing cells is sufficient to alleviate the repression resulting in ectopic N activity and ectopic joint formation. Such regulation of the membrane availability of Notch could equally affect Dl-mediated activation, although Ser appears to be the major ligand responsible in the joints (Bishop et al., 1999). Other factors are likely to influence proximal repression of N because ectopic joints are also observed in alterations of the EGFR pathway (Galindo et al., 2005) and mutants of *defective proventriculus* (Shirai et al., 2007).

We note also that the domains of N activation (both normal and ectopic) extend beyond the cells at the interface with Ser. We have not sought to investigate this additional level of regulation here, but our results indicate that it is unlikely to be due to a secondary signal emanating from the Ser-interfacing cells because the loss of function clones show complete autonomy, without any ‘shadow’ of activation adjacent to the clone. An alternative possibility is that the cells make more extensive contacts, as has been seen in other tissues (Cohen et al., 2010; De Joussineau et al., 2003; Demontis and Dahnmann, 2007).

PCP regulation of N has been observed in other developmental processes, most notably in photoreceptor fate choice in the *Drosophila* eye (Cooper and Bray, 1999; del Alamo and Mlodzik, 2006; Fanto and Mlodzik, 1999; Strutt et al., 2002). There, much of the regulation is via effects on levels and activity of the ligand. However, we detected no change in the pattern of N or Ser expression in PCP mutants. Instead, our evidence suggests that regulation involves direct interaction between Dsh and N and that this interaction has consequences on the endocytic trafficking of N, resulting in its inactivation. The interaction requires the amino-terminal portion of the Dsh DIX domain, which is also required for Axin binding in the canonical Wnt pathway (Julius et al., 2000; Kishida et al., 1999), making it difficult to dissect its role in the PCP-mediated N inhibition. Nevertheless, we were able to generate one mutation that reduced interactions with N with minor consequences on Axin binding. Rescue experiments with this mutant form of Dsh indicated that it was less effective in PCP function in the leg joints compared with others (e.g. polarity of leg bristles). These results support the model that a direct interaction between Dsh and N is relevant in the context of joint determination. However, we cannot fully rule out the possibility that the mutation has more generalized effects on Dsh, if the joints are particularly sensitive to the levels of Dsh activity.

Several studies indicate that endocytic sorting of N is involved in its regulation, with either positive or negative effects depending on the particular context (Fortini and Bilder, 2009; Furthauer and Gonzalez-Gaitan, 2009). Our findings suggest that regulation of N by PCP in the leg is mediated by interaction with Dsh, and probably involves the control of N endocytic trafficking. This suggests a model whereby the interaction between Dsh and N results in increased endocytosis of the N receptor, so reducing its capability to interact with ligands on neighboring cell. Removal of Fz or Dsh compromises this endocytic trafficking, allowing N to be activated. The interaction between Dsh and N is thus only likely to be relevant under circumstances in which there is a strong localization of Dsh co-incident with an interface between N and ligand-expressing cells.

Previous studies have also suggested a role for Dsh in regulating N and on promoting its endocytosis (Axelrod et al., 1996; Munoz-Descalzo et al., 2010). In both instances, these effects were linked to Wg signaling, rather than to the core PCP pathway as here. Nevertheless several aspects are consistent with our results, most notably the direct binding between Dsh and N. Additionally it has been argued that Dsh specifically antagonizes Dx-mediated effects of N (Ramain et al., 2001), which is compatible with their complementary effects on joint formation. However, it is also evident that the ability of Dsh to inhibit N depends on the developmental context. For example, whereas overexpression of Dsh in the leg is sufficient to inhibit N activation at presumptive joints, overexpression of Dsh at the wing margin is not sufficient for its repression.
to repress N signaling: there are no nicks and cut expression is not inhibited. Interestingly, differences in Dx behavior are also evident in these two contexts. At the wing margin (Matsuno et al., 2002), Dx^{PRE} acts as a dominant-negative form of Dx, whereas Dx^{NBS} is inactive. By contrast, in the leg joints Dx^{PRE} behaves as wild-type Dx, whereas Dx^{NBS} is a dominant negative. We postulate, therefore, that the subcellular localization of Dsh and the availability of Dx are important for determining the regulation of N trafficking at joints. The autonomous effect of core PCP mutants was clear when we used the E(spl)mB1.5-CD2 N reporter and disco-lacZ. However, the consequences on bib-lacZ were more complex. Although larger clones of mutant cells always exhibited autonomous ectopic expression, similar to E(spl)mB1.5-CD2, some narrow clones exhibited no ectopic expression. We suggest that this might be due to bib-lacZ having a higher threshold of response, so it would need stronger N activation. The domain of bib-lacZ is narrower than that of the other known reporters, in agreement with this model. Furthermore, we found some cases in which there was a reduction of the normal bib-lacZ expression in the mutant cells, in addition to ectopic expression. This suggests that PCP-mediated distal localization of Dsh would be required not only for inhibition of N in proximal cells, but also for efficient activation of N in distal ones.

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