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The *Drosophila* EcR-Hippo component Taiman promotes epithelial cell fitness by control of the Dally-like glypican and Wg gradient

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Abstract

Rapidly dividing cells can eliminate slow growing neighbors through the apoptotic process of cell competition. This process ensures that only high fitness cells populate embryonic tissues and is proposed to underlie the ability of oncogene-transformed cells to progressively replace normal cells within a tissue. Patches of cells in the *Drosophila* wing disc overexpressing the oncogenic Taiman (Tai) transcriptional coactivator kill normal neighbors by secreting Spätzle ligands that trigger pro-apoptotic Toll signaling in receiving cells. However, extracellular signaling mechanisms responsible for elimination of slow growing cells by normal neighbors remain poorly defined. Here we show that slow growing cells with reduced Tai (Tai^{low}) are killed by normal neighbors through a mechanism involving competition for the Wingless (Wg/Wnt) ligand. Elevated Wg signaling significantly rescues elimination of Tai^{low} cells in multiple organs, suggesting that Tai may normally promote Wg activity. Examining distribution of Wg components reveals that Tai promotes extracellular spread of the Wg ligand from source cells across the wing disc, thus ensuring patterned expression of multiple Wg-regulated target genes. Tai controls Wg spread indirectly through the extracellular glypican Dally-like protein (Dlp), which binds Wg and promotes its extracellular diffusion and capture by receptors. Data indicate that Tai likely controls Dlp at two levels: transcription of *dlp* mRNA and Dlp intracellular trafficking. Overall, these data indicate that the Tai acts through Dlp to enable Wg transport and signaling, and that cell competition in the Tai^{low} model arises due to inequity in the ability of epithelial cells to sequester limiting amounts of the Wg growth factor.

eLife assessment

The authors study how cells with lower levels of the conserved steroid hormone signaling component Taiman (tai) are out-competed by neighboring wild-type cells with higher fitness in Drosophila imaginal discs. The findings are **useful** since they uncover an unexpected link between tai and Wingless signaling in cell competition. The evidence however is **incomplete**, since the tai loss-of-clone phenotype is based on one allele and the mechanism involved in cell competition through Dlp and Wg lacks adequate supporting data.

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Introduction

The development of an organism is a tightly controlled process, with multiple signaling pathways converging to achieve correct patterning, morphogenesis, and cell fates. As the earliest cells begin to populate tissues, it is advantageous that the fittest progenitors give rise to the entire organism. One example of this is in the formation of the epiblast—early embryonic cells go through a selection process, where more fit cells with higher amounts of pluripotency factors such as TEAD or Myc outcompete cells with a relatively lower dose of these factors[1,2]. This process of pruning unfit cells and selection of fitter cells for survival is known as "cell competition."

The phenomenon of cell competition was first described in the context of *Drosophila melanogaster* cells with defective ribosomal protein function, termed "*Minutes*", that could survive when surrounded by like cells but died in a heterotypic environment mixed with wildtype cells[3]. Cells that die in a heterotypic environment are called "losers," as they undergo apoptosis through mechanisms triggered by neighboring cells termed "winners". A variety of apoptotic mechanism have been proposed to underlie loser fate, including exposure to the pro-apoptotic cytokine Spätzle (Spz) produced by oncogene transformed 'winners'[4–6], non-autonomous induction of autophagy[7,8], loss of apicobasal polarity[9], and inequities in expression of the transmembrane factor Flower[10], the secreted protein SPARC[11], or the Ca^{+2} binding protein Azot[12]. Altering the dose of the dMyc oncogene has also been proposed to generate competitive differences by altering the ability of cells to compete for limiting amounts of the Dpp morphogen[13,14].

In previous work we found evidence that wing cells overexpressing the conserved coactivator and oncogene Taiman (Tai; human AIB/SRC3/NCOA3) kill neighboring cells by overproduction and secretion of Spz ligands, in particular Spz4[6], which is similar to a proposed mechanism by which excess Myc confers winner status[4]. Intriguingly, *Drosophila* cells with reduced Tai expression are viable, proliferate more slowly than normal cells, and generate small but properly patterned organs [15]. However, they have not been tested for their fitness status, and whether they become losers that resemble cells with reduced levels of the dMyc oncogene (i.e., Myc^{low} cells, as in [4,5]). Here we have used a homozygous viable allele of *tai* that behaves as a weak hypomorph to investigate the role of Tai in cell competition. We find that larval wing disc cells with reduced Tai (Tai^{low}) survive in a homotypic environment but are eliminated by neighboring wildtype cells in a heterotypic environment of clonal mosaics. A genetic screen to identify pathways involved in competitive elimination of Tai^{low} cells identifies alleles of the Wnt/Wg pathway inhibitor *Adenomatous polyposis coli* (*APC*) as suppressors of Tai^{low} elimination, suggesting that Tai^{low} elimination may be due to a deficit of Wg signaling. Examining the Tai-Wg link more closely reveals that Tai is required for formation of the Wg gradient in the larval wing

pouch and for patterned activation and repression of Wg target genes at different points along the Wg gradient. We trace this defect to a role for Tai in promoting levels and intracellular trafficking of the Dally-like protein (Dlp) glypican, which binds extracellular Wg and facilities its movement away from source cells. Evidence suggests that Tai is a key determinant of the effect of Dlp on Wg steady-state levels: excess Dlp triggers Wg accumulation in Tai-depleted cells, but triggers Wg loss in cells that also express Tai. Dlp accumulates intracellularly in Tai^{low} clones, confirming a link between Tai and Dlp trafficking. Given that cells lacking *Apc* are 'winners' in the wing pouch and adult intestine[16,17], we propose that Tai regulates competitive status though an underlying developmental role in promoting Dlp-dependent Wg capture and signaling. As a result, cells with reduced Tai are disadvantage with normal neighbors for capture of limiting amounts of Wg.

Results

Cells with reduced Tai are selectively killed in clonal mosaics

Combining the weak, viable hypomorph tai^{k15101} with a deletion (*Df ED678*) that completely removes the second copy of *tai* produces small but normally patterned adults with proportionally smaller organs[15]. Larval wing discs from these *taik15101/Df* animals contain background levels of apoptotic cells (**Fig. 1A-A',D**) suggesting that wing size reduction is the result of a proliferative deficit rather than surplus apoptosis. This hypothesis is consistent with our previous finding that Tai promotes cell division in the larval wing[15]. Generating boundaries between tai^{k15101} cells (tai^{k15101},*FRT40A*) and normal cells (*FRT40A*) using the Flp-FRT mosaic system results in significantly elevated cleaved Dcp-1 (cDCP-1) caspase within tai^{k15101} clones (**Fig. 1B-B", C-C", D**), indicative of apoptosis. This excess cDcp1 is especially evident in tai^{k15101} clones located in the wing pouch, a developing epithelium that is widely used to assess competitive status [4,18]. These data show that pouch cells with one hypomorphic *tai* allele (i.e., tai^{k15101}/*Df*) are viable when surrounded by like cells, but that cells with two copies of the tai^{k15101}hypomorph die when surrounded by tai^{wt}cells. These data indicate the existence of an extracellular competition mechanism that allows normal tai^{wt} cells to kill tai^{k15101}(hereafter tai^{low}) neighbors.

Elimination of tai^{low} cells requires Wg, Hippo, and canonical apoptosis pathways

A *mini-*w^{+}minigene present in the tai^{k15101} hypomorph generates red pigment that visually marks tai^{low} heterozygous or homozygous cells in the adult eye. As in the larval wing disc, tai^{k15101}/*Df* cells readily populate an adult eye composed of alike cells, but patches of tai^{low} cells form small clones when placed in competition with control ($white^{-}$;*FRT40A*) cells using an eye-specific Flpase transgene (*eyFLP*) (**Fig. 2A-B**). By comparison, cells carrying a *mini-*w^{+} marked *FRT40* chromosome occupy approximately 50% of the adult eye.

To identify genes and pathways involved in elimination of tai^{low}eye cells, a collection of mutant alleles of candidate competition factors (**Supplemental Table 1**) were screened for dominant rescue of tai^{low}small clone size in the adult eye (**Fig. 2C-H**). This approach yielded 'hits' in the pro-apoptotic Rpr-Hid-Grim (RHG) factors ($hid^{1}$and the *H99* deletion), the Hippo pathway kinase *warts* (wts^{1}), and the Wg pathway inhibitor *Adenomatous polyposis coli* ($Apc^{MI01007}$). Alleles affecting components of the Spz-Toll, IMD, or ecdysone pathways did not obviously modify tai^{low} clone size, nor did alleles of other candidate factors such as the transmembrane proteins *flower* and *Sas*, the transcription factors *p53* and *Xrp1*, the autophagy factor *Atg1*, and the secreted glycoprotein *Sparc* [8-11,19-22] (data not shown). These genetic data confirm separate elements of tai^{low} loser fate: rescue by $hid^{1}$and *H99* provide genetic evidence that elimination of tai^{low}cells requires the canonical RHG-Diap1-Caspase pathway (rev. in [23]), while rescue by wts^{1} is consistent with Tai protecting against the "loser" fate through Yorkie, which is bound by Tai and

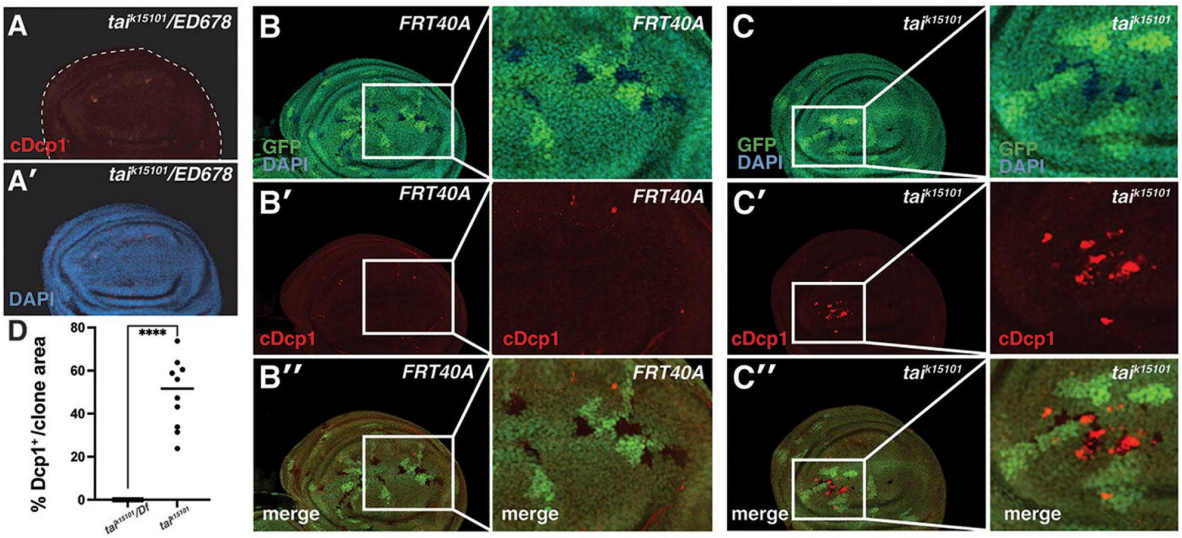

Figure 1.

tai^{low} cells survive in a homotypic environment but die in a heterotypic environment.

(A-A′) 3rd larval instar *tai*^{k15101}*/Df(2L)ED678* wing disc stained with anti-cleaved Dcp-1 (cDcp1; red) and nuclei (DAPI; blue). (**B-C**) *hsFlp* generated clones of control *FRT40A* (**B-B″**) or *tai*^{k15101}*,FRT40A* (**C-C″**) cells marked by the absence of GFP (green) and co-stained for cDcp-1 (red) and nuclei (DAPI; blue). Magnified insets are provided. **(D)** Quantification of cDcp-1 in *tai*^{k15101}*/Df(2L)ED678* heterotypic discs or *tai*^{k15101} clones calculated by percent Dcp1-positive area/total clone area (Student t-test, p <0.0001).

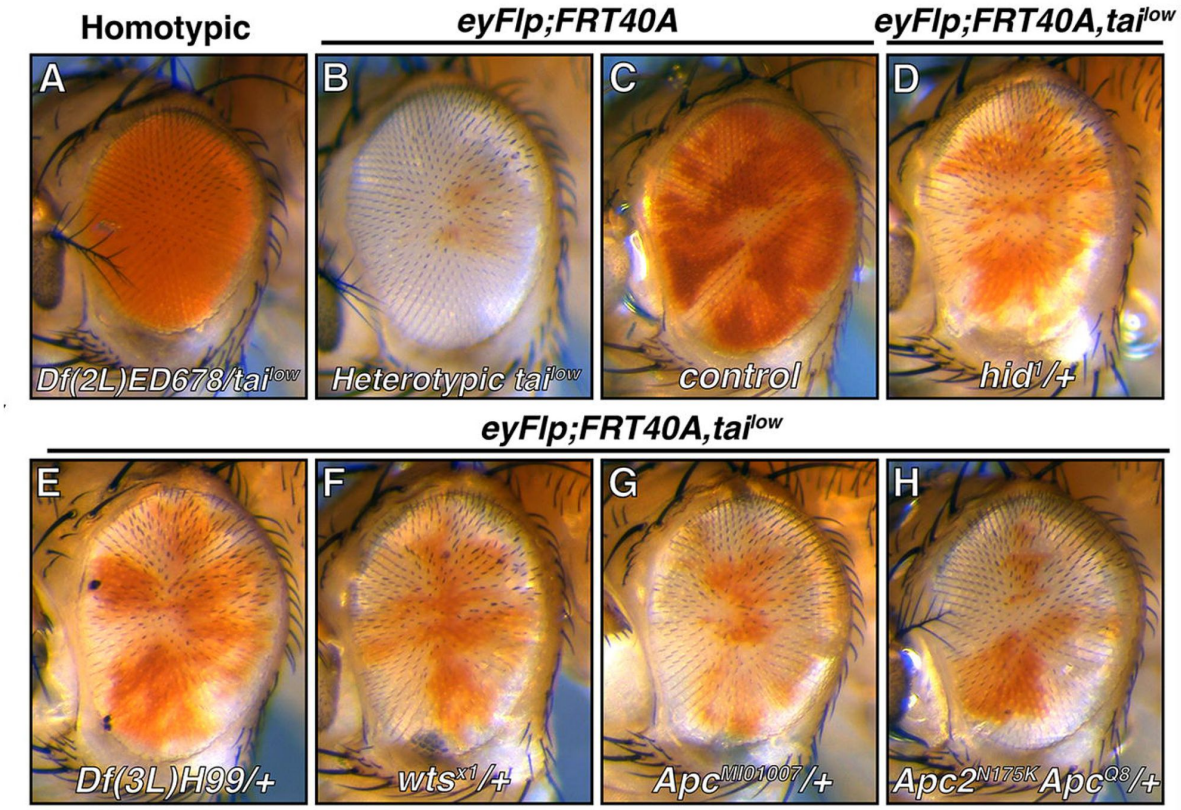

Figure 2.

Modification of *tai*^{low}clone survival in the adult eye.

Adult female eyes of the indicated genotypes: (**A**) *tai*^{k15101}*/Df(2L)ED678*; (**B-C**) *eyFLP* mosaic eyes with *w-;FRT40A* flipped over (**B**) *tai*^{k15101}*,FRT40A* or (**C**) *FRT40A,m-w*$^{+}$; (**D-H**) *eyFLP* mosaic eyes with *tai*^{k15101}*;FRT40A* flipped over *FRT40A,m-w*$^{+}$ in the background of (**D**) *hid*^{1}, (**E**) *Df(3L)H99*, (**F**) *wts*^{x1}, (**G**) *Apc*^{MI01007}, or (**H**) *Apc2*^{N175K}*,Apc*^{Q8}.

phosphorylated by Wts[15,24,25]. By contrast, *tai*^{low} rescue by *Apc* suggests an unexpected link between Tai competitive status and Wg signaling. A second *Apc* mutation (*Apc*^{Q8}) in combination with an inactivating allele in its paralog *Apc2* (*Apc2*^{N175A}) similarly increases survival of *tai*^{low} cells in the eye (**Fig. 2H**).

The larval wing pouch is bisected along the D-V (dorsoventral) midline by a stripe of Wg-expressing cells that generate mirror image gradients (dorsal and ventral) that guide wing growth and patterning[26]. Quantification of *tai*^{low} clone size within the larval wing pouch at 50hrs post induction (*hsFlp*) indicates that *RHG*, *wts*, or *Apc/Apc2* alleles recovered in the eye screen also increase the size of *tai*^{low} pouch cells (**Figure 3A-H**), with *H99* and the compound *Apc*^{Q8},*Apc2*^{N175A} allele having the largest effects. *H99* and *Apc* alleles also enhance recovery of 76hr old *tai*^{low} clones, which are normally eliminated by this time point (**Fig. S1**). Together, these data indicate that competitive elimination of *tai*^{low} cells requires RHG proteins and can be attenuated by derepressing the Wg or Hippo pathways.

Tai modulates transcription of Wg-regulated genes and formation of the Wg gradient

The extended survival of 76hr *tai*^{low} clones in *Apc* and *Apc,Apc2* heterozygous backgrounds imply a relatively strong link between Tai and Wg signaling. To test sensitivity of Wg pathway activity to Tai dosage, *UAS* transgenes were used to test whether *tai* overexpression or reduction affects transcription of two Wg target genes: *naked cuticle* (*nkd*), a mid-threshold target of the Wg gradient that is expressed in bands of cells on either side of the DV midline[27] (*nkd-lacZ*), and *wg* itself, which is repressed by an autoinhibition loop that refines *wg* transcription to a narrow stripe at the DV midline[28] (*wg-lacZ*). Tai overexpression (*en>tai*) expands *nkd-lacZ* expression into dorsal and ventral domains that correspond to distal tails of the Wg gradient and normally express low *nkd* (**Fig. 4A-A", B-B"**, see brackets, and **4D-E**). Tai depletion strongly retards *nkd-lacZ* in regions close to the DV midline that normally receive high Wg (**Fig. 4C-C", D-E**). Examining *wg* transcription with the *wg-lacZ* transgene shows that *tai* RNAi (*enGal4*) causes *wg-lacZ* to spread dorsally and ventrally away from the DV margin (**Fig. 5B-B'**, see arrow), while reciprocally elevating *tai* has little effect on *wg* transcription (**Fig. 5C-C'**). These data are consistent with Tai acting as a positive upstream regulator of Wg signaling in pouch cells, such that activation of *nkd* and autoinhibition of *wg* each fail when Tai is removed.

Failure to constrain *wg-lacZ* activity to DV margin cells in Tai-depleted discs (see **Fig. 5B'**) resembles the effect of mutations that block receipt of the Wg ligand[28]. Examination of the Wg gradient in pouch cells with reduced Tai in the posterior domain (*en>tai* RNAi) detects robust Wg in source cells but significant reduction in Wg spreading into the dorsal and ventral pouch (**Fig. 6A** vs. **6C**, arrows). This loss of the Wg gradient occurs despite expansion of the *wg* expression domain in Tai RNAi pouches (see **Fig. 5B-B'**). Overexpression of Tai produces gaps in the stripe of Wg protein in DV cells (**Fig. 6B**, arrows) that also does correlate with a loss of *wg* transcription (see **Figs. 5C-C'**), suggestive of a post-transcriptional effect of excess Tai on Wg stability, uptake, or trafficking in the DV regions. Quantification of anti-Wg staining intensity confirms that Tai RNAi blocks formation of the Wg gradient and indicates that Tai overexpression elevates Wg in regions further from the DV margin (**Figs. 6D-E**). Considered together, these data are consistent with a requirement for Tai in forming the Wg gradient by control of Wg protein extracellular diffusion and/or internalization and turnover.

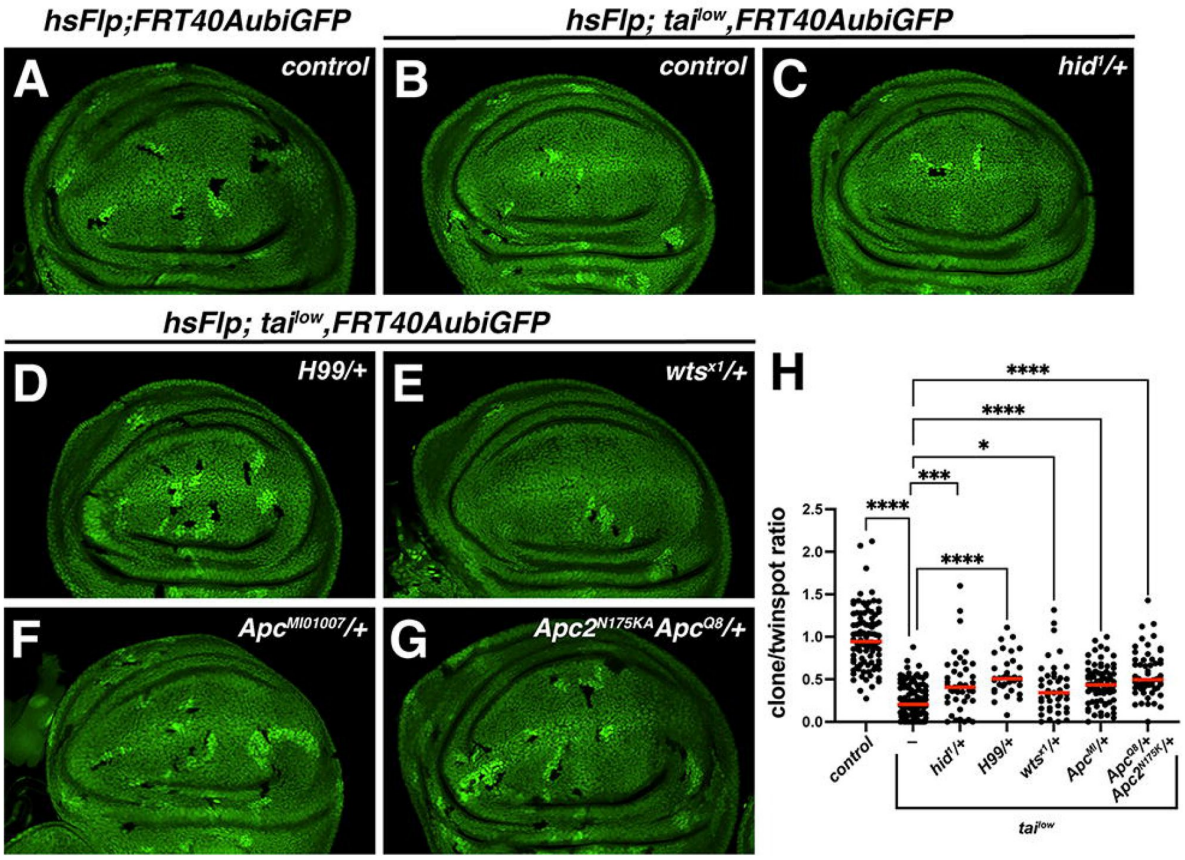

Figure 3.

Alleles from the eye screen also modify *tai^{low}* clone survival in L3 wing pouch

(**A-G**) Larval wing discs bearing *hsFlp/FRT*-generated 50hr-old *tai^{low}* clones (GFP-negative) either (**B**) alone, or in the background of the indicated alleles (**C-G**). Twinspots appear brighter due to two copies of *GFP*. **(H)** Quantification of *control*(*FRT40A*) or *tai^{low}* size ratio (area ratio of clone:twin-spot) alone (-) or in the indicated genetic backgrounds.. ****p <0.001, ***p= 0.0003, *p = 0.0157, *ns* = not significant (One-way ANOVA with Dunnett post hoc test).

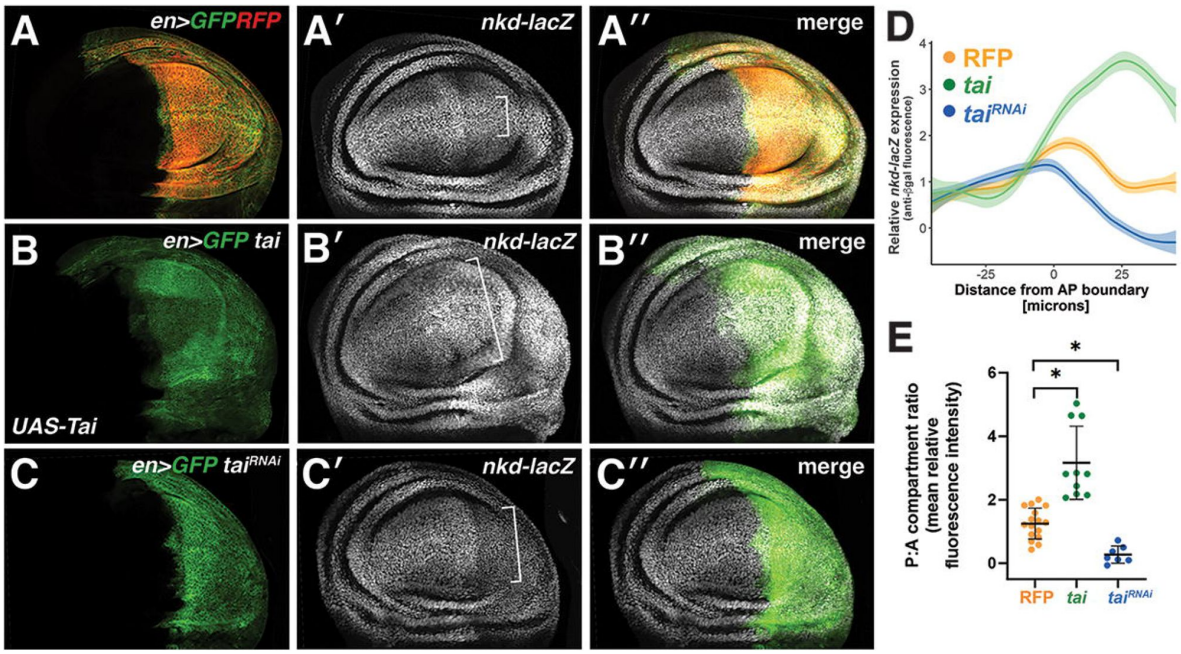

Figure 4.

tai promotes expression of the Wg pathway reporter *nkd-lacZ*.

(**A-C**) Expression of the *nkd-lacZ* reporter (greyscale) in (**A-A**″) *control* (*en>GFP,RFP*), (**B-B**″) Tai overexpressing (*en>tai,GFP*), or (**C-C**″) Tai-depleted larval wing discs. **(D)** Relative anti-ßGal fluorescence intensity on either side of the A-P boundary among pouch cells located just below the D/V boundary. **(E)** Mean relative fluorescence intensity plotted as a ratio of posterior to anterior intensity. *RFP* vs *tai* *p=0.0004; *RFP* vs tai^{RNAi} **p*<0.0001 (Unpaired student t-test with Welch's correction).

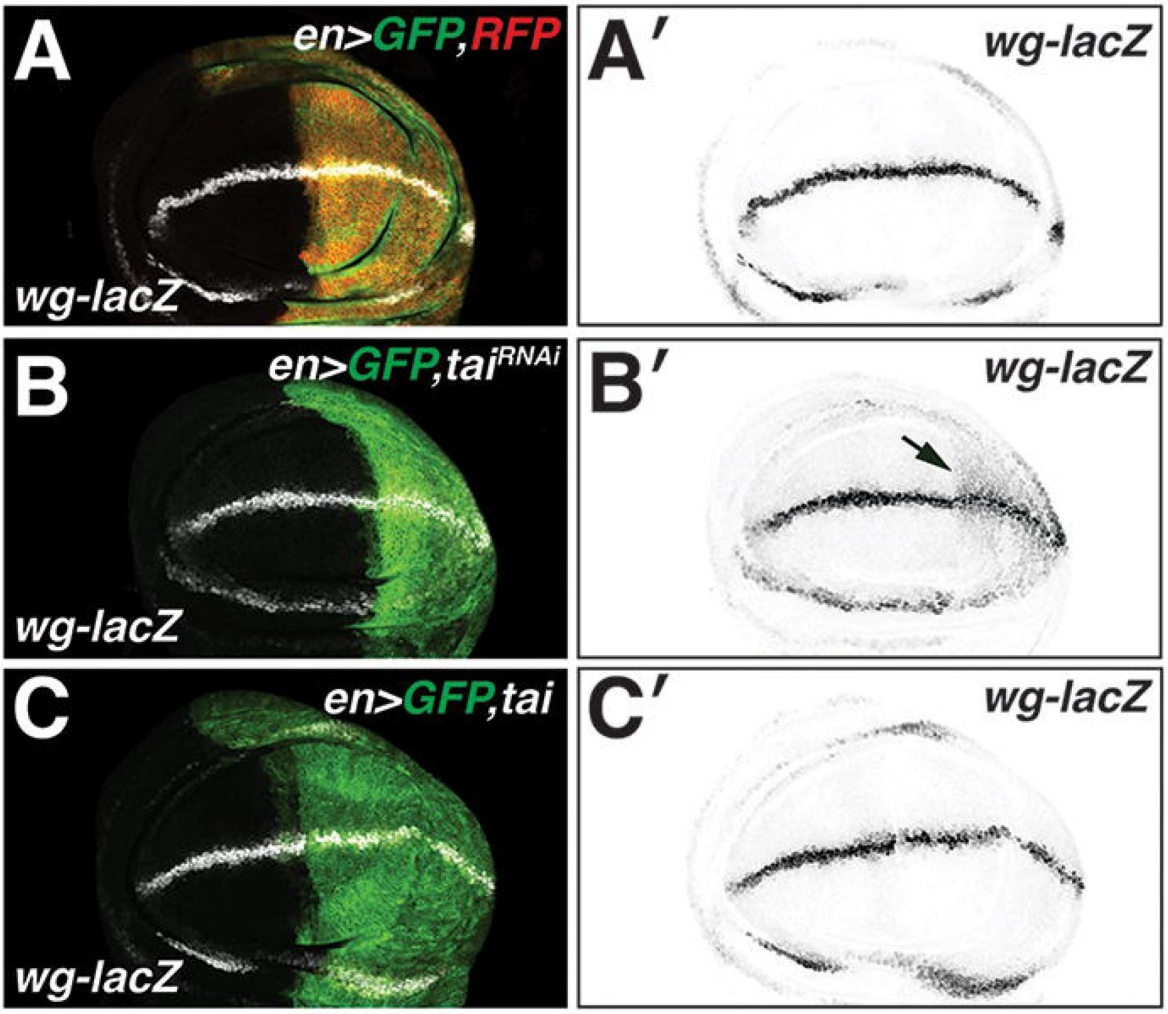

Figure 5.

Tai is required for the auto-inhibitory loop that refines *wg* transcription.

(A-C) Expression of the *wg-lacZ* reporter in *enGal4* larval wing discs as detected by anti-ßGal staining (white in **A-C**, black in **A'-C'**) in *control* RFP (**A**), Tai-depleted (**B**), or Tai overexpressing (**C**) discs. Arrow in **B'** indicates failure to refine *wg-lacZ* to the DV boundary in P-domains depleted of Tai.

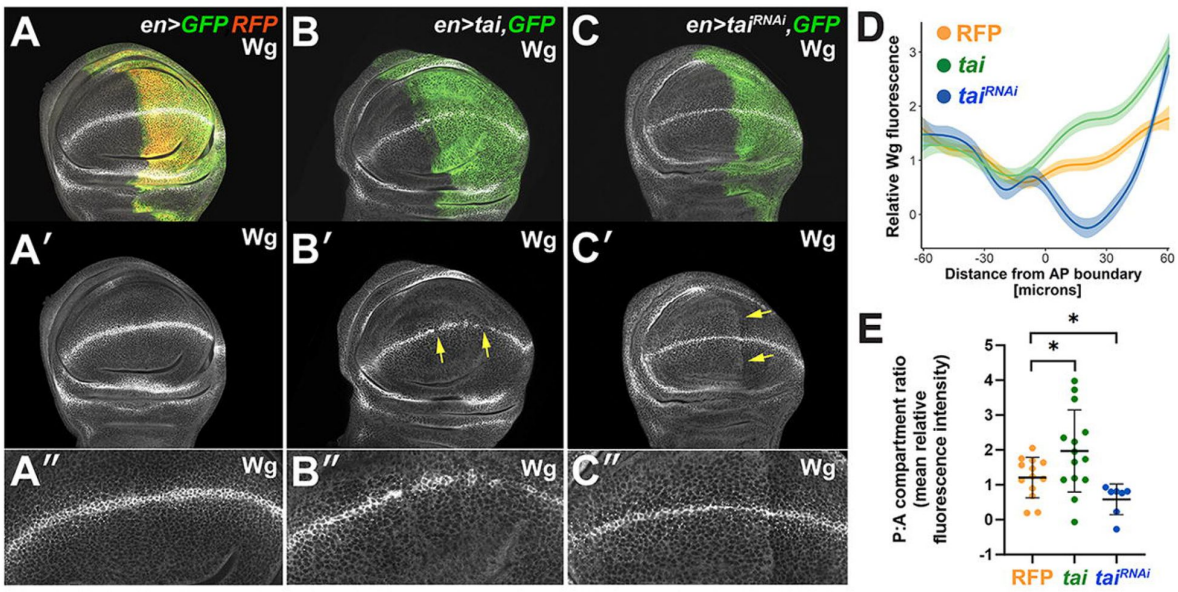

Figure 6

Tai is required for formation of the Wg gradient.

Wg protein (greyscale) in (**A-A**″) *control* (*en>GFP,RFP*), (**B-B**″) Tai overexpressing, or (**C-C**″) Tai-depleted larval wing discs. *enGal4* activity in the P-domain is marked by GFP. Arrows in **B**′ mark gaps in Wg DV stripe characteristic of Tai overexpression. Arrows in **C**′ mark the clear drop in total Wg on the DV flanks of P-domains depleted of Tai. **A**″**-C**″ provide higher magnification views of regions in **B**′**-C**′**. (D)** Relative Wg fluorescence intensity of pouch cells below D/V boundary (to avoid Wg source cells) plotted from anterior to posterior. **(E)** Mean Wg relative fluorescence intensity plotted as a ratio of posterior to anterior intensity. *RFP* vs *tai* *p=0.0443, *RFP* vs tai^{RNAi} *p<0.0156 (Unpaired student t-test with Welch's correction).

Tai is required for expression of Dally-like protein, a glypican required for Wg signaling

The GPI-anchored glypican Dally-like protein (Dlp) binds lipidated Wg and facilitates its extracellular diffusion and capture by Frizzled receptor[29–33]. Notably, homozygous loss of *Apc* produces competitive 'winners' by upregulating the secreted enzyme, Notum, which then cleaves Dlp and deprives normal neighbors of the ability to sequester or sense Wg[17]. Given that *Apc* heterozygosity rescues tai^{low} elimination, *tai* alleles were tested for modulation of Dlp levels in the larval pouch. Excess Tai significantly elevates Dlp protein among posterior cells (*en>tai*) and Tai depletion had the opposite effect of depleting Dlp (**Figs. 7A-C** and graphs in **7D-E**). Expression of the Dlp-related glypican Dally[34] also rises upon Tai overexpression but is insensitive to Tai depletion (*dally-lacZ*; **Figs. S2A-C**), other than shrinkage of the *dally-lacZ* pattern due to reduced Posterior (P)-domain size due to Tai loss (arrows **Figs. S2A'** vs. **S2C'**). These data indicate that Tai is rate-limiting for Dlp expression in the pouch and may be able to induce *dally* expression when overexpressed.

Examining Dlp dynamics further, we find that RNAi depleting the extracellular protein Pentagone, which promotes Dlp/Dally glypican internalization and turnover[34], produces little change in Dlp levels among Tai-depleted cells (**Fig. S3A-C**, see bracketed regions). RNA-seq analysis of Tai-expressing wing discs detects elevated *dlp* mRNA, indicating that Tai may control *dlp* mRNA abundance (**Fig. S4)**. Consistent with this hypothesis, EcR CUT&RUN analysis [35] in 3rd instar larval wing discs detects EcR binding peaks on the *broad* and *dlp* loci; *dlp* is flanked by two EcR peaks with another located in a *dlp* intron (**Fig. S4**). Orthogonal slices that traverse the Wg stripe of *en>tai* discs from control (anterior) to Tai overexpressing (posterior) regions confirm that Tai overexpression lowers Wg protein levels (**Fig. S5**). Notably, expression of a *dlp* transgene causes Wg accumulation on the DV flanks of Tai-depleted wing discs (**Fig. 7E-E'**), indicating that *tai* RNAi cells are similar to *wt* cells and retain Wg when provided extra Dlp[31]. However, expression of *dlp* together with *tai* (*en>tai,dlp*) has a reciprocal effect of enhancing Wg loss protein at the DV margin (**Fig 7F-F'**) and Wg build-up on the dorsal hinge (asterisk in **7G'**). Given that Tai expression with the same driver (*en>tai*) elevates Wg transcriptional output across the pouch (see **Figs. 4-5**), this loss of Wg may be due to enhanced trafficking and/or uptake. These data suggest that Tai status determines the effect of excess Dlp on Wg levels: Dlp depletes Wg levels across the pouch cells when excess Tai is present but retains Wg in Tai-depleted cells. A reciprocal test of a Dlp role in Tai overexpressing discs indicates that two different *dlp* RNAi lines do not rescue gaps in the Wg stripe that appear with Tai-overexpressing (arrows, **Fig. S6A-D**). These data indicate that Tai status determines the effect of excess Dlp on Wg, but that excess Tai may engage a different mechanism to modulate Wg protein in DV margin cells.

In the course of these analyses, we noted that wild type Tai or a version of the protein lacking PPxY motifs required to bind Yki [15] (Tai^{PPxA}) drive accumulation of Dlp protein across the pouch (*enGal4*) (**Fig. S7A-B**) including in the DV midline region where Dlp is normally excluded (e.g., see arrows in **Fig. 7A**). Under normal circumstances, Dally is expressed in this region (e.g., see **Fig. S2**) and promotes short range Wg signaling from source cells[36]. Consistent with this local dependence on Dally, Tai-depletion only in DV midline cells with a wing margin driver (*big bang (bbg)-Gal4*) has only a mild effect on distribution of Wg protein; however, providing exogenous Tai to these cells broadens the Wg-positive domain (**Fig. 8A-C**). Given that Tai does not elevate *wg* transcription (see **Fig. 5C**), this finding indicates that overexpressing Tai in DV midline cells is sufficient to enhance local spread of Wg protein and increase abundance of Wg-positive puncta (in **Fig. 8B'**) which have been shown to correspond to secretory vesicles[37]. Thus, expression of Tai in source cells enhances Wg secretion, while expression in the DV flanks can cooperate with excess Dlp to deplete Wg across the Posterior (P) -domain.

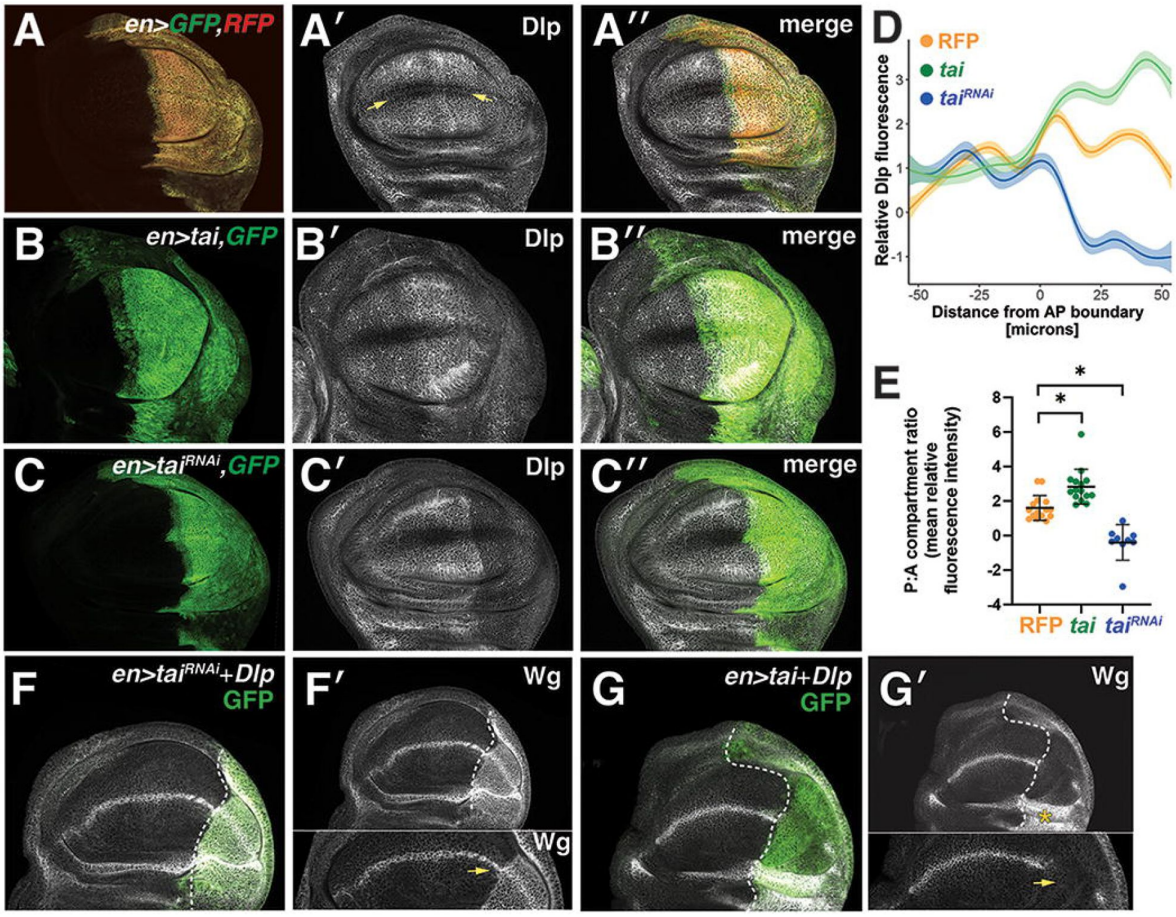

Figure 7

Tai controls Dally-like protein (Dlp) levels.

(A-C,F-G) Anti-Dlp staining (greyscale) in (**A-A**″) *control* (*en>GFP,RFP*), (**B-B**″) Tai overexpressing (*en>tai,GFP*), and (**C-C**″) Tai-depleted cells. Arrows in **A**′ mark Dlp exclusion from the DV boundary region. Overexpression of Dlp restores Wg in Tai-depleted cells (**F-F**′; see arrow in magnified view), but causes complete loss of the Wg DV stripe in Tai overexpressing disc regions (**G-G**′; see arrow in magnified view). **(D)** Relative Dlp fluorescence intensities of pouch regions below D/V boundary plotted from anterior to posterior. **(E)** Mean relative Dlp fluorescence intensity plotted as a ratio of posterior to anterior intensity. *RFP* vs *tai* **p*=0.0008, RFP vs tai^{RNAi} **p*=0.0002 (Unpaired student t-test with Welch's correction).

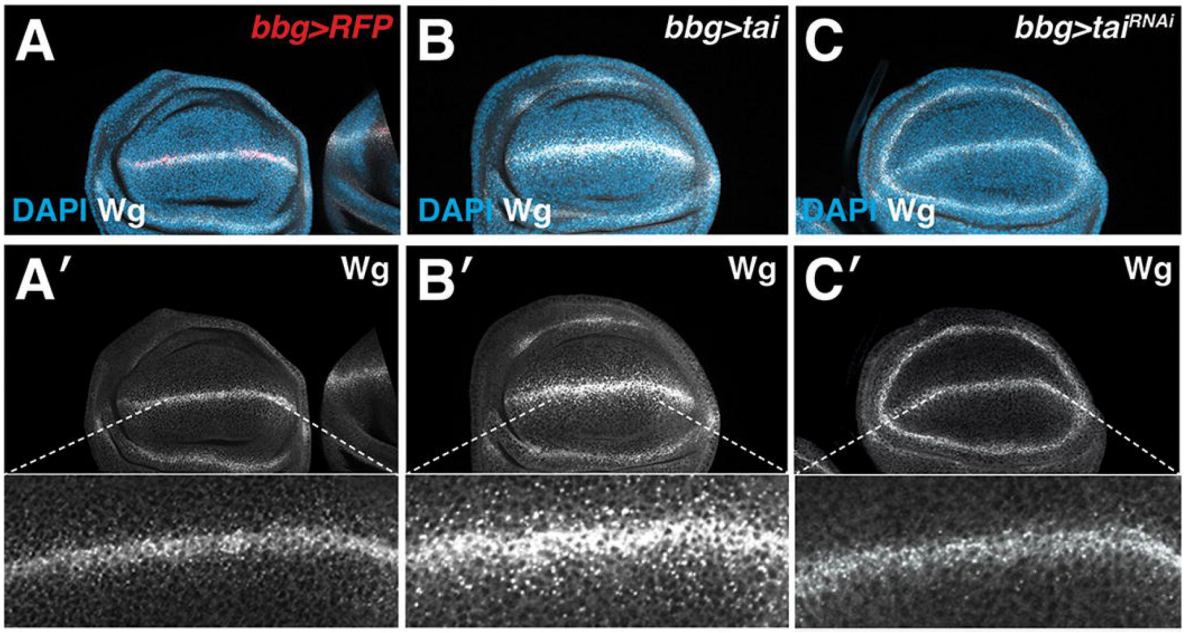

Figure 8

Tai expression at the D/V boundary enables excessive Wg spread.

(**A-C**) Anti-Wg signal (greyscale) in **(A-A′)** control (*bbg>RFP*), (**B-B′**) Tai-overexpressing (*bbg>tai*), or Tai-depleted (**C-C′**) discs co-stained for nuclei (DAPI; blue). Dotted lines denote magnified views of Wg in **A′-C′**.

Dlp protein is altered in *tai^{low}* clones

Relative to the lethal *tai* RNAi transgene (e.g., with *actin5c-Gal4*[38]), the viable *tai^{low}* allele is predicted to yield correspondingly weaker phenotypes. To improve recovery of comparatively rare *tai^{low}* pouch clones, *hsFlp* was applied in the *H99/+* background (see **Fig 3**). In this configuration, *tai^{low}* pouch clones contain elevated levels of Dlp relative to adjacent control cells (arrows, **Fig. 9A-A"**). This result suggests that *tai^{low}* could perturb Dlp intracellular traffic, either during secretion or internalization. To test this model, Dlp was reanalyzed in *tai^{low}*clones under conditions that do not permeabilize membranes; this approach detects only basal levels of Dlp on the surface of control and *tai^{low}* disc cells (**Fig. 9B-B"**). Indeed, closer inspection of *tai^{low}*hypomorphic clones in tangential slices indicates that Dlp is mislocalized to the cytoplasm (**Fig. 9C-D**). Given that removing Pent, which stimulates Dlp internalization[34], does not rescue Dlp loss in Tai RNAi cells, Tai may promote both *dlp* mRNA expression and Dlp protein secretion, and that the consequent decline in ability to compete for Wg with normal neighbors deprives *tai^{low}* cells of a signal necessary for growth and survival.

Discussion

Here we show that cells with a reduced dose of the Tai coactivator, which functions in the ecdysone and Hippo pathways[15,39], are killed by normal neighbors through a mechanism involving competition for the Wingless (Wg/Wnt) ligand. Elevated Wg signaling significantly rescues elimination of Tai^{low} cells in multiple organs, suggesting that Tai may normally promote Wg activity. Examining distribution of Wg components reveals that Tai promotes extracellular spread of the Wg ligand from source cells across the wing disc, thus ensuring patterned expression of multiple Wg-regulated target genes. Tai controls Wg spread indirectly through the extracellular glypican Dally-like protein (Dlp), which binds Wg and promotes its extracellular diffusion and capture by receptors. Data indicate that Tai likely controls Dlp at two levels: transcription of *dlp* mRNA and Dlp intracellular trafficking. Overall, these data indicate that the Tai acts through Dlp to enable Wg transport and signaling, and that cell competition in the Tai^{low} model arises due to inequity in the ability of epithelial cells to sequester limiting amounts of the Wg growth factor.

One key conclusion from these data is the mechanism through which Tai^{high} cells kill normal neighbors (e.g., through Spz-Toll)[6] is distinct from the mechanism that eliminates Tai^{low} cells. The former mechanism is produced by triggering an innate immune pathway and may require priming by chronic microbial infection[18], while the latter derives from a developmental role in Dlp-mediated Wg diffusion and turnover (this study). These mechanisms may both occur in vivo, although in different contexts, with Tai^{high} overexpression mimicking oncogene activation in cancer, and Tai^{low} representing cells in developing tissues that receive weaker proliferative or survival signals than neighbors. In the developing wing disc, gradual scaling of the Wg gradient as the tissue grows ensures that adjacent cells experience only incremental changes in concentration of pro-growth morphogens[40]. Artificially steepening of a gradient, as occurs in *pent* mutant wing discs[21], or creating patches of cells deficient in morphogen capture (e.g., with *tai^{low}* or *tai^{RNAi}*) or signaling (e.g., as in Wg pathway mutants[17]) within an otherwise intact gradient each create sharp differences in morphogen activity. This model is supported by the finding that artificial boundaries between glypican expressing and non-expressing cells is sufficient to induce cell competition among *Drosophila* follicle stem cells[41]. Intriguingly, *dlp* follicle clones are 'winners' while *dally* clones are 'losers', which implies different roles for Wg in survival of pouch cells vs. follicle stem cells.

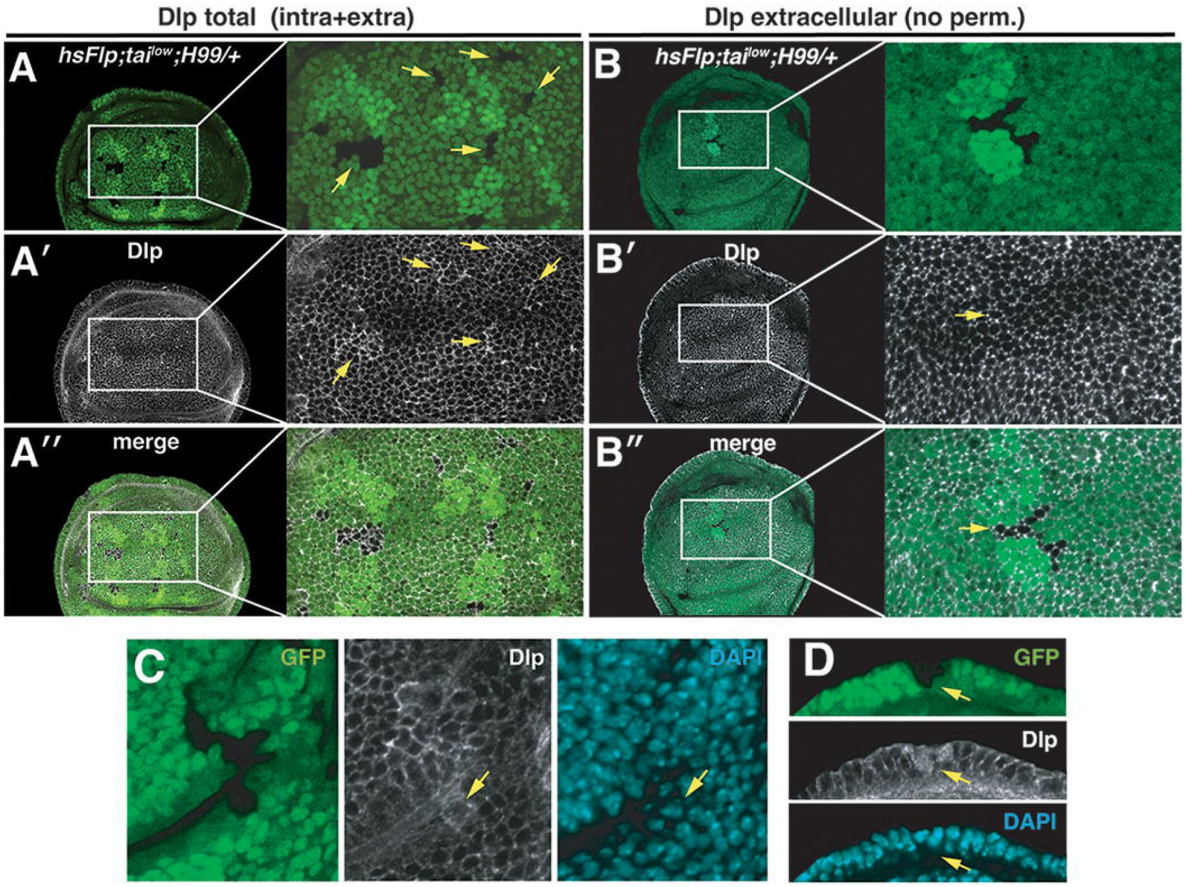

Figure 9

The *tai*^{low} hypomorph causes Dlp intracellular accumulation in pouch cells.

(**A-D**) *hsFlp* generated *tai*^{low} clones (GFP negative) in a *H99/+* background co-stained for Dlp (greyscale) and nuclei (DAPI; cyan). Discs in panels **A-A**″ and **C** were permeabilized to detect total Dlp (intracellular and extracellular), while discs in panel **B-B**″ were processed without permeabilization and only detect extracellular Dlp. Arrows in **C** and **D** denote *tai*^{low} cells in side-view with intracellular Dlp.

The finding that *tai* alleles perturb Dlp expression, retard the Wg gradient, and interact with *Apc* alleles in eye and wing epithelia seems to suggest that Tai gain and loss phenotypes in these tissues may be driven in part by changes in Wg signaling. It remains to be determined whether Tai acts broadly across multiple tissues and developmental stages to modulate Wg, or whether this role is limited to specific cell types. As Tai is a transcriptional coactivator it is likely to mediate its Wg regulatory effects through other factors that directly contact DNA. The identity of this factor(s) is unclear. One candidate is the ecdysone receptor EcR, which brings Tai into a transcriptional regulatory complex whose components are conserved across metazoans (i.e., ERα-NCOA3-p300) [42]. The role of EcR in innate immune transcription[43] is consistent with our finding that EcR is involved in intertissue invasion led by Tai^{high} cells[6]. However, the role of an EcR-Tai complex in death of Tai^{low} cells has not been examined. Ecdysone can promote (or 'gate') activity of both major morphogen gradients in the wing disc[44], and the presence of EcR CUT&RUN peaks in the *dlp* genomic region (see **Fig. S4**) seems to imply EcR may have some role in Dlp expression. EcR can also repress *wg* transcription in areas of the pouch[45], much as we have found that Tai represses *wg* transcription on either side the DV margin (see **Fig. 5B**). However further work is required to determine whether either of these roles requires an EcR-Tai complex. Mild rescue of tai^{low} elimination by a *wts* allele indicates that slight elevation of Yki activity can promote tai^{low}survival. However, the ability of the non-Yki binding form of Tai, Tai^{PPxA}, to efficiently induce Dlp accumulation in pouch cells is not consistent with a requirement for Tai to bind Yki during the competition process. Alternatively, Tai may modulate Wg signaling independent of interactions with EcR and Yki, perhaps through other transcription factors. Determining Tai-binding partners involved in regulation of the Wg pathway and establishing Tai transcriptional targets whose products modulate secretion and/or endocytosis of glypicans could yield broad insight into mechanisms that calibrate morphogen diffusion in development and disease.

Lead contact and resource availability

Requests for resources and reagents should be directed to and will be fulfilled by Lead Contact (kmoberg@emory.edu).

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Author Contributions

Conceived and designed the experiments: CKS, KHM. Performed the experiments: CKS. Analyzed the data: CKS, VCP, KHM. Authored the paper: CKS. Edited the manuscript: CKS, KHM. Funding and Acquisition: CKS, KHM.

Materials and Methods

Drosophila culture

Fly stocks were maintained under standard culture conditions at 25°C, 12 hr light:dark cycles in humidity-controlled incubators. Experiments used a mix of female and male animals. All crosses were maintained on standard molasses food supplemental with yeast. Unless specified, flies were mated and allowed to lay eggs for a period of 24-48 hours, and then dissected at wandering third instar. Lines used are referred to in **Key Resources Table** (BDSC stock numbers indicated).

Strategy for randomization and/or stratification

Animals of both sexes were used for experiments. A minimum of 10 total imaginal wing discs over three biological replicates were used in all experiments. Figures presented are representative images of each genotype.

Adult eye screen

Adult females were aged for three days to allow condensation of pigment granules then frozen at −20°C for >5 minutes before imaging with a Nikon SMZ800N microscope at 25X magnification (2.5X objective x 10X eyepiece) using a Leica MC170HD camera and a Nii-LED High intensity LED illuminator. Flies were submerged in 70% ethanol to eliminate glare. Multiple focal planes were imaged and merged in Photoshop to generate a final image.

Cell Competition Assays

Mated flies were allowed to lay for 24 hrs before flipping into a new vial. 48-50 hrs after egg lay (AEL), FLP recombinase was induced by heat-shocking of the larvae at 37°C for about one hour, except for in the generation of “Flp-out” clones where larvae were heat-shocked for 1.5 hrs. Third instar larvae were then dissected at 96 hrs AEL. Both male and female larvae were dissected. Clonal areas were measured using ImageJ, and only clones in the wing pouch were considered for analysis.

Immunofluorescence and microscopy

Immunofluorescence and microscopy were performed using standard methods. Briefly, wing discs were dissected in 1X phosphate-buffered saline (PBS), fixed for 20 minutes in 4% paraformaldehyde (PFA) at room temperature (RT), rinsed 5X in 1X PBS, and then permeabilized with 1X PBS and 0.3% Triton X-100 (0.3% PBST). For extracellular stain without permeabilization, the protocol was performed as in [46]. Discs were then blocked with 10% normal goat serum (NGS) and then incubated in diluted primary antibody containing 10% NGS and 1X PBS and 0.1% Triton X-100 (0.1% PBST). Samples incubated in primary antibody solution at 4°C overnight, washed 5X with 0.1% PBST, incubated with DAPI (1:500) for 5 minutes, washed 3X with 0.1% PBST, and then incubated for 1 hr at RT with secondary antibody solution diluted with 10% NGS and 0.1% PBST. Discs were then washed 5X times with 0.1% PBST and incubated in n-propyl gallate (NPG, 4% w/v in glycerol) overnight. Discs were mounted in NPG on glass coverslips and then imaged with a Nikon A1R confocal system using 20X and 40X objectives. Images were processed with Fiji, Photoshop, and Illustrator software. ImageJ was used for clonal area measurements. Refer to **Key Resources Table** for full list of antibodies, dilutions, and other reagents used.

Fluorescence intensity analysis

Fluorescence intensities were measured across equal regions of interest (ROIs) using Image J/Fiji. Briefly, the ROI was positioned such that it was: 1) centered over the AP boundary as defined by the *en>GFP* control channel, 2) below the DV line (approximately halfway between the DV boundary and the bottom of the pouch), and 3) extended approximately halfway into each compartment (anterior and posterior). Raw fluorescence intensity values were standardized such that the mean anterior fluorescence was equal to 1, and posterior fluorescence was relative to anterior. Analyses and fluorescence intensity plots were performed and created in R (R version 4.1.1 (2021-08-20)). Posterior: anterior mean fluorescence intensity ratios were plotted, and statistics performed using GraphPad Prism. Unpaired t-tests with Welch's corrections were performed.

Quantitation and Statistical Analyses

Unpaired Student's t-tests or one-way ANOVAs (GraphPad Prism) were used to analyze significance between datasets. Significance was considered to be $p<0.05$. Normal distributions were assumed.

Key resources table

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Antibodies		
Mouse anti-β-Gal (1:100)	Promega	Z3781; RRID: AB_430877
Rabbit anti-Dcp1 (1:100)	Cell Signaling	9578; RRID: AB_2721060
Mouse anti-Wg (1:50)	DHSB	4D4; AB_528512
Mouse anti-Dlp (1:50)	DHSB	13G8; AB_528191
Goat anti-mouse-Cy3 (1:50)	Jackson ImmunoResearch	115-166-003; RRID: AB_2338683
Goat anti-mouse-Cy5 (1:50)	Jackson ImmunoResearch	115-175-146; RRID: AB_2338712
Goat anti-rabbit-Cy3 (1:50)	Jackson ImmunoResearch	111-165-003; RRID: AB_2338000
Goat anti-rabbit-Cy5 (1:50)	Jackson ImmunoResearch	111-175-144; RRID: AB_2338013
Chemicals, peptides, and recombinant proteins		
Triton X-100		
20% Paraformaldehyde	Electron Microscopy Sciences	15713
Trizol	Invitrogen	15596018
DAPI	Invitrogen	D1306
Normal goat serum (NGS)	Jackson ImmunoResearch	005-000-121
n-propyl gallate (NPG)	Sigma	P-3130
Experimental models: Organisms/strains		
D. melanogaster: tai^{k15101}	BDSC	93042
D. melanogaster: tai^{k15101}, FRT40A	This study	N/A
D. melanogaster: FRT40A	BDSC	5758
D. melanogaster: hsflp; FRT40A,ubiGFP	BDSC	Constructed from component stocks
D. melanogaster: eyflp; FRT40A,ubiGFP	BDSC	Constructed from component stocks
D. melanogaster: tai^{PPxA}, FRT40A	S. Verghese, Emory University	N/A
D. melanogaster: Df (3L) H99 (hid, reaper, grim)	BDSC	1576
D. melanogaster: Df (2L) ED678 (tai)	BDSC	8906
D. melanogaster: UAS-tai (III)	BDSC	6378

D. melanogaster: UAS-RFP (II)	BDSC	30556
D. melanogaster: UAS-RFP (III)	BDSC	31417
D. melanogaster: UAS-tai-IR	BDSC	28971
D. melanogaster: UAS-taiPPxA	Moberg lab stock	Zhang et al, 2015 *Dev Cell*
D. melanogaster: UAS-wg	BDSC	5918
D. melanogaster: UAS-wg-IR	BDSC	32994
D. melanogaster: UAS-dlp	BDSC	9160
D. melanogaster: UAS-dlp-IR	BDSC	34089
D. melanogaster: UAS-dlp-IR	BDSC	34091
D. melanogaster: UAS-yki-IR	VDRC	104523
D. melanogaster: UAS-magu-IR	BDSC	51169
D. melanogaster: nkd-lacZ	BDSC	25111
D. melanogaster: wg-lacZ	BDSC	11205
D. melanogaster: hid^{1}	BDSC	631
D. melanogaster: Toll^{rv18} (Toll-1)	BDSC	30913
D. melanogaster: Tollo^{1} (Toll-8)	BDSC	36549
D. melanogaster: crb^{8F105}	BDSC	7099
D. melanogaster: Oatp74D^{BG0653} (EcI)	BDSC	12430
D. melanogaster: sas^{15}	BDSC	2098
D. melanogaster: p53$^{11-1B-1}$	BDSC	6816
D. melanogaster: Atg1^{3}	BDSC	60732
D. melanogaster: scrib^{di14}	BDSC	29014
D. melanogaster: Apc^{MI01007}	BDSC	34138
D. melanogaster: Apc^{Q8}Apc^{N175K}	BDSC	7211
D. melanogaster: sd^{l2}	BDSC	9371
D. melanogaster: SPARC^{MI00329}	BDSC	30711
D. melanogaster: wts^{x1}	BDSC	44251
D. melanogaster: Df (3R) BSC491 (SPE)	BDSC	24995
D. melanogaster: PGRP-LB^{A}€	BDSC	55715

D. melanogaster: p53$^{11\text{-}1B\text{-}1}$	BDSC	6816
D. melanogaster: Xrp1^{KO}	E. Storkebaum, Donders Institute	N/A
D. melanogaster: spz^{4} Rel^{E20}	BDSC	55718
D. melanogaster: ilp8KO	P. Leopold, Institut Curie	Boone et al, 2016 *Nat Commun*
D. melanogaster: fweDB25	BDSC	51996
D. melanogaster: UAS-EcRLBD	Wardwell-Ozgo, J. Emory University	Wardwell-Ozgo et al, 2023, *bioRxiv*
D. melanogaster: UAS-EcRLBD-A483T	Wardwell-Ozgo, J. Emory University	Wardwell-Ozgo et al, 2023, *bioRxiv*
Software and algorithms		
ImageJ	Open source	https://imagej.net/software/fiji/
Prism	GraphPad	https://www.graphpad.com/
Photoshop	Adobe	https://www.adobe.com/products/photoshop.html
Illustrator	Adobe	https://www.adobe.com/products/illustrator.html
R Studio	Open source	https:/r-project.org

Supplemental Figure Legends

Figure S1. *H99* and *Apc* alleles allow *tai^{low}*cells to survive 76hrs after clonal induction. Wing discs bearing 76hr old (post-hs) pouch clones of **(A)** *FRT40A* cells or (**B-G**) *tai^{low}* cells in the indicated genetic backgrounds. Clones are GFP-negative and twinspots are bright green. (**H**) Clone:Twinspot area ratios (pixels) of the same genotypes as in **A-G.** Note significant rescue of *tai^{low}* survival by *H99* and *Apc* heterozygosity. ****p <0.001 ***p = 0.0007, ns = not significant (One-way ANOVA with Dunnett post hoc test).

Figure S2. *dally* does not respond to Tai depletion but can be induced by excess Tai. (**A-C**) Expression of the *dally-lacZ* reporter detected by anti-ßgal stain (greyscale) in (**A-A**") *control* (*en>GFP,RFP*), (**B-B**") Tai overexpressing (*en>tai,GFP*), or (**C-C**") Tai-depleted (*en>tai^{RNAi},GFP*) discs. Arrows in **A**' and **C**' indicate shrunken pattern of *dally-lacZ* expression in a Tai-depleted Posterior (P)-domain.

Figure S3. RNAi of Pent, which promotes Dlp internalization, does not fully restore Dlp in Tai-depleted disc regions. Anti-Dlp signal in (**A-A**") control (*en>GFP*), (**B-B**") Tai-depleted (*en>tai^{low}*) discs, or discs (**C-C**") co-depleted for Tai and Pent (*en>tai^{RNAi}+pent^{RNAi}*). Brackets denote P-domain with Dlp depletion with *tai* RNAi.

Figure S4. Evidence of *dlp* transcription regulated by Tai. Top (A): IGV traces of RNA-seq reads from *control* (green; *en>GFP*) and Tai-expressing (red; *en>tai*) larval wing discs laid over (**middle-B**) a genomic map of the *dlp* region. **Bottom (C)**: EcR-association peaks in the *dlp* region (published in [35]).

Figure S5. Excess Tai downregulates Wg levels within source cells at the DV margin. Wg signal (greyscale) in a Tai overexpressing disc (*en>tai,GFP*) imaged *en face* (**A-A**') and (**B-B**') tangential slices corresponding to **region 1** and **region 2 in** magnified view **(B-B**'). Panel **C** and associated **regions 1** and **1** show equivalent analysis in control (*en>GFP,RFP*) discs.

Figure S6. RNAi depletion of Dlp is not sufficient to block the Tai-induced gaps in the DV stripe of Wg. Wg signal (greyscale) in wing discs expressing either of two *dlp* RNAi constructs alone (#1 or #2 in **A-B**) or in combination with Tai overexpression (**C-D**). Arrows in **C'** and **D'** mark gaps in the Wg stripe.

Figure S7. Tai^{PPxA} is able to induce Dlp expression in the midline region. Dlp signal (greyscale) in (**A-A"**) *control* (*en>GFP,RFP*) or (**B-B"**) Tai^{PPxA} expressing (*en>tai^{PPxA},GFP*) discs. Yellow arrows in **A'** mark Dlp exclusion from cells in either side of the DV margin; arrow in **B'** points to excess Dlp filling this region.

Supplemental Table 1: A genetic screen reveals dominant modifiers of *tai^{low}* cell death. Heterozygous candidate alleles selected from various pathways were placed in the background of a mosaic *eyFlp; Tai^{low}* eye, and positive screen "hits" were determined based on increased recovery of Tai^{low} clones (orange). An allele of *hid*, as well as the *H99* deletion (*reaper, hid, grim*) enhanced recovery of Tai^{low} cells. Other suppressors included *wts^{x1}*, a loss of function allele of the core Hippo pathway kinase and an allele of *Adenomatous polyposis coli* (*Apc*), a key inhibitor of the conserved Wg/Wnt pathway. Refer to Key Resources Table for information about alleles used.

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46. Witte L, Linnemannstons K, Honemann-Capito M, Gross JC (2021) **Visualization and Quantitation of Wg trafficking in the Drosophila Wing Imaginal Epithelium** *Bio Protoc* **11** https://doi.org/10.21769/BioProtoc.4040

Editors

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Senior Editor
Claude Desplan
New York University, New York, United States of America

Reviewer #1 (Public Review):

Summary:

Schweibenz et al are investigating how cells with lower levels of Tai are out-competed by neighboring wild-type (WT) cells. They show that clones homozygous for a tai hypomorphic

mutation are disadvantaged and are killed by apoptosis. But tai-low clones are partially rescued when generated in a background that is heterozygous for mutations in apoptotic genes, in the Hippo pathway component warts, or for the Wg/Wnt pathway negative regulator Apc. They then follow up in the link between tai LOF and Wg. The story then shifts away from clones and into experiments that have Tai RNAi depletion or Tai over-expression in the posterior compartment of the wing disc, using the anterior compartment as a control. These non-clonal experiments show that depletion of Tai in the posterior compartment of wing discs results in less Wg in this compartment. This is shown to be due to a reduction in the glypican Dally-like protein (Dlp). The fact that long-range Wg is reduced in tai-depleted discs that also show a reduction in Dlp, suggests that Tai somehow positively promotes Wg distribution. There is some data in the supplementary materials suggesting that Tai promotes dlp mRNA expression but this was not compelling. In fact, the compelling data was that Dlp protein in tai mutant clones is not abundantly on the cell surface, but instead somehow retained in the mutant cell. The authors don't further examine Dlp protein in tai clones. The final figure (Figure 8) shows that there is less Wg at the DV margin in wing discs when tai is depleted from wg-producing cells. In sum, the authors have uncovered some interesting results, but the story has some unresolved issues that, if addressed, could boost its impact. Additionally, the preprint seems to have 2 stories, one about tai and cell competition and the other about tai and Wg distribution. It would be helpful to reorder the figures and improve the narrative so that these are better integrated with each other.

Strengths:

The authors are studying competition between tai-low clones and their fitter WT neighbors, and have uncovered an interesting connection to Wg.

Weaknesses:

(1) It would be good to know whether the authors can rescue tai-low clones by over-expression UAS-Dlp.

(2) The data about tai-promoting dlp (Figure S4) is not compelling as there are no biological replicates and no statistical analyses.

(3) The data on Wg distribution seems disjointed from the data about cell competition. The authors could refocus the paper to emphasize the cell competition story. The role of Dlp in Wg distribution is well established, so the authors could remove or condense these results. The story really could be Figsured 1, 2, 3 and 7 and keep the paper focused on cell competition. The authors could then discuss Dlp as needed for Wg signaling transduction, which is already established in the literature.

(4) The model of tai controlling dlp mRNA and Dlp protein distribution is confusing. In fact, the data for the former is weak, while the data for the latter is strong. I suggest that the authors focus on the altered Dlp protein distribution on tai-low clones. It would also be helpful to prove the Wg signaling is impeded in tai clones (see #5 below).

(5) I don't know if the Fz3-RFP reported for Wg signaling works in imaginal discs, but if it does then the authors could make clones in this background to prove that cell-autonomous Wg signaling is reduced in tai-low clones.

https://doi.org/10.7554/eLife.97803.1.sa2

Reviewer #2 (Public Review):

The authors investigate the properties of the transcriptional co-activator Taiman in regulating tissue growth. In previously published work they had shown that cells that

overexpress Tiaman in the pupal wing can cause the death of thoracic cells adjacent to the wing tip to die and thus allow the wing to invade the thorax. This was mediated by the secretion of Spz ligands. Here, they investigate the properties of cells that are homozygous for a hypomorphic allele of taiman (tai). They show that homozygous mutant clones are much smaller than their wild-type twin spots and that cells in the clones are dying by apoptosis which is inferred from elevated levels of anti-Dcp1 staining (Figure 1).

By generating clones during eye development, the authors screen for dominant modifiers that increase the representation of homozygous tai tissue in the adult eye (Figure 2). They find that reducing the levels of hid, the entire rpr/hid/grim locus and Apc (and/or Apc2) each increase the representation of tai clones. They then show that the survival of tissue to the adult stage correlates with the size of lones in the third-instar larval wing disc (Figure 3). The rest of the study derives from the modification of the phenotype by Apc and investigates the interaction between Wnt signaling and tai clone survival.

The authors then investigate interactions between tai and the wingless (wg) pathway. First, they show that increasing tai expression increases the expression of a wg reporter (nkd-lacZ) while reducing tai levels decreases its expression (Figure 4) indicating that wg signaling is likely reduced when tai levels are decreased. This finding is strengthened by examining wg-lacZ expression since the expression of this reporter is normally restricted to the D/V boundary in the wing disc by feedback inhibition via Wg signaling. Expression of the reporter is increased when tai expression is reduced and decreased when tai expression is increased (Figure 5).

The authors then look at Wg protein away from the DV boundary. They find increased levels when tai expression is increased and decreased levels when tai is decreased. They conclude that tai activity increased Wg protein in cells (Figure 6). They suggest that this could be the result of the regulation of expression of Dally-like protein (Dlp). Consistent with this idea, increasing tai expression increases Dlp levels, and decreasing tai decreases Dlp levels (Figure 7). They then show that increasing Dlp levels when tai is reduced increases Wg levels which presumably means that Dlp is epistatic to tai. Puzzlingly, increasing both tai and Dlp decreases Wg.

The authors then examine the effect of reducing Dlp in the cells that secrete Wg. They find that increasing tai results in the diffusion of Wg further from its source while reducing tai reduces its spread (Figure 8). They then show that in clones with reduced tai, there is increased cytoplasmic Dlp (Figure 9). They therefore propose that tai clones fail to survive because they do not secrete enough Dlp which results in reduced capture of the Wg for those cells and hence decreased Wg signaling.

Evaluation

While the authors present good evidence in support of most of their conclusions, there are alternative explanations in many cases that have not been excluded.

From the results in Figure 1 (and Figure 3), the authors conclude that "The data indicate the existence of an extracellular competition mechanism that allows normal tai[wt] cells to kill tai[k15101] neighbors" (line 127). However, the experiments have been done with a single allele, and these experiments do not exclude the possibility that there is another mutation on the same chromosome arm that is responsible for the observed phenotype. Since the authors have a UAS-tai stock, they could strengthen their results using a MARCM experiment where they could test whether the expression of UAS-tai rescues the elimination of tai mutant clones. Alternatively, they could use a second (independent) allele to demonstrate that the phenotype can be attributed to a reduction in tai activity.

By screening for dominant modifiers of a phenotype one would not expect to identify all interacting genes - only those that are haploinsufficient in this situation. The authors have

screened a total of 21 chromosomes for modification and have not really explained which alleles are nulls and which are hypomorphs. The nature of each of the alleles screened needs to be explained better. Also, the absence of a dominant modification does not necessarily exclude a function of that gene or pathway in the process. This is especially relevant for the Spz/Toll pathway which the authors have previously implicated in the ability of tai-overexpressing cells to kill wild-type cells. The most important discovery from this screen is the modification by the Apc alleles. This part of the paper would be strengthened by testing for modification by other components of the Wingless pathway. The authors show modification by Apc[MI01007] and the double mutant Apc[Q8] Apc2[N175A]. Without showing the Apc[Q8] and Apc2[N175A] alleles separately, it is hard to know if the effect of the double mutant is due to Apc, Apc2, ˋor the combination.

RNAi of tai seems to block the formation of the Wg gradient. If so, one might expect a reduction in wing size. Indeed, this could explain why the wings of tai/Df flies are smaller. The authors mention briefly that the posterior compartment size is reduced when tai-RNAi is expressed in that compartment. However, this observation merits more emphasis since it could explain why tai/Df flies are smaller (Are their wings smaller?).

In Figure 7, the authors show the effect of manipulating Tai levels alone or in combination with increasing Dlp levels. However, they do not include images of Wg protein distribution upon increasing Dlp levels alone.

In Figure 8, there is more Wg protein both at the DV boundary and spreading when tai is overexpressed in the source cells using bbg-Gal4. However, in an earlier experiment (Figure 5C) they show that the wg-lacZ reporter is downregulated at the DV boundary when tai is overexpressed using en-Gal4. They therefore conclude that wg is not transcriptionally upregulated but is, instead secreted at higher levels when tai is expressed in the source cells. Wg protein is reduced in the DV stripe with tai is overexpressed using the en-Gal4 driver (Figure 6B') and is increased at the same location when tai is overexpressed with the bbg-Gal4 driver. (Figure 8) I don't know how to reconcile these observations.

In Figure 9, the tai-low clones have elevated levels of Dlp. How can this be reconciled with the tai-RNAi knockdown shown in Figure 7C' where reducing tai levels causes a strong reduction in Dlp levels?

https://doi.org/10.7554/eLife.97803.1.sa1

Reviewer #3 (Public Review):

Summary:

In this study, Schweibenz et al., identify the transcriptional coactivator, Taiman (Tai), as a factor that determines the fitness level of epithelial cells by regulating Wingless (Wg), which is an important determinant of cellular fitness. Taiman determines cellular fitness level by regulating levels of cell-surface glypican Dally-like protein (Dlp), which regulates extracellular Wingless (Wg) distribution. Thus, by affecting levels of Wg via glypican regulation, Tai participates in determining cellular fitness, and cells with low Tai levels are eliminated as they are deprived of adequate Wg levels.

Strengths:

(1) The authors make a strong case for the effect of tai on Dlp and Wg levels in experiments where a relatively large group of cells have reduced tai levels.
(2) The claim that tai-low clones are competitively eliminated is supported by experiments that show cell death in them, and their elimination at different time points.
(3) The manuscript is well written.

Weaknesses:

(1) The study has relatively weak evidence for the mechanism of cell competition mediated by Dlp and Wg.

(2) More evidence is required to support the claim that dlp transcription or endocytosis is affected in tai clones.

Other comments:

(1) The authors put the study in the context of cell competition, and the first figure indeed is convincing in this regard. However, most of the rest of the study is not in the clonal context, and mainly relies on RNAi KD of tai in the posterior compartment, which is a relatively large group of cells. I understand why the authors chose a different approach to investigate the role of tai in cell competition. However because ubiquitous loss of tai results in smaller organs, it is important to determine to what extent reducing levels of tai in the entire posterior compartment compares with clonal elimination i.e. cell competition. This is important in order to determine to what extent the paradigm of Tai-mediated regulation of Dlp levels and by extension, Wg availability, can be extended as a general mechanism underlying competitive elimination of tai-low clones. If the authors want to make a case for mechanisms involved in the competitive elimination of tai clones, then they need to show that the KD of tai in the posterior compartment shows hallmarks of cell competition. Is there cell death along the A/P boundary? Or is the compartment smaller because those cells are growing slower? Are the levels of Myc/DIAP1, proteins required for fitness, affected in en>tai RNAi cells?

1. The authors do not have direct/strong evidence of changes in dlp mRNA levels or intracellular trafficking. To back these claims, the authors should look for dlp mRNA levels and provide more evidence for Dlp endocytosis like an antibody uptake assay or at the very least, a higher resolution image analysis showing a change in the number of intracellular Dlp positive punctae. Also, do the authors think that loss of tai increases Dlp endocytosis, making it less available on the cell surface for maintaining adequate extracellular Wg levels?

2. The data shown in the last figure is at odds with the model (I think) the authors are trying to establish: When cells have lower Tai levels, this reduces Dlp levels (S2) presumably either by reducing dlp transcription and/or increasing (?) Dlp endocytosis. This in turn reduces Wg (availability) in cells away from source cells (Figure 6). The reduced Wg availability makes them less fit, targeting them for competitive elimination. But in tai clones, I do not see any change in cell-surface Dlp (9B) (I would have expected them to be down based on the proposed model). The authors also see more total Dlp (9A) (which is at odds with S2 assuming data in S2 were done under permeabilizing conditions.).

As a side note, because Dlp is GPI-anchored, the authors should consider the possibility that the 'total' Dlp staining observed in 9A may not be actually total Dlp (and possibly mostly intracellular Dlp, since the permeabilizing membranes with detergent will cause some (most?) Dlp molecules to be lost, and how this might be affecting the interpretation of the data. I think one way to address this would be to process the permeabilized and non-permeabilized samples simultaneously and then image them at the same settings and compare what membrane staining in these two conditions looks like. If membrane staining in the permeabilized condition is decreased compared to non-permeabilized conditions, and the signal intensity of Dlp in permeabilized conditions remains high, then the authors will have evidence to support increased endocytosis in tai clones. Of course, these data will still need to be reconciled with what is shown in S2.

https://doi.org/10.7554/eLife.97803.1.sa0

Author response:

> ***eLife assessment***
>
> *"...The evidence however is incomplete, since the tai loss-of-clone phenotype is based on one allele and the mechanism involved in cell competition through Dlp and Wg lacks adequate supporting data."*

We agree with the need for a second allele and are adding supporting data from a new tai lof allele we have generated by Crispr.

We also agree that additional functional data would help demonstrate that differences in Dlp levels are required for the mechanism of Tai cell competition. Experiments are ongoing to test whether normalizing Dlp levels across clonal boundaries rescues elimination of Tai-low clones.

> ***Reviewer #1:***
>
> *Overall Statements:*
>
> *"There is some data in the supplementary materials suggesting that Tai promotes dlp mRNA expression, but this was not compelling."*

We are currently testing effects on Tai on dlp and dally transcription using qPCR and reporter transgenes. As noted below, the effects of Tai on Dlp trafficking are 'strong', so resolving effects on Dlp transcription will complement this localization data.

> *"The authors don't further examine Dlp protein in tai clones."*

As noted by the Reviewer, we do examine Dlp levels and localization in tai-low clones (see Figure 9), but these experiments are challenging due to their very small size and the hypomorphic nature of the tai allele (tai[k15101]) that was used. Experiments are in progress to examine the effect of our Crispr null allele of tai on Dlp levels and localization in wing clones.

> *"In sum, the authors have uncovered some interesting results, but the story has some unresolved issues that, if addressed, could boost its impact. Additionally, the preprint seems to have 2 stories, one about tai and cell competition and the other about tai and Wg distribution. It would be helpful to reorder the figures and improve the narrative so that these are better integrated with each other."*

We agree. The results of our modifier screen required that we first understand how Tai regulates the Wg pathway before could apply this to understanding the competitive mechanism. Thus, the paper is composed of three sections: 1. the screen, 2. the Tai-Dlp-Wg connection in the absence of competition, and 3. the contribution of Dlp-Wg to the tai[low] 'loser' phenotype. These sections use different techniques (e.g., clonal mosaics with genomic alleles, Gal4/UAS and RNAi to define the effect of Tai loss on Wg and Dlp). Ongoing experiments return to clonal mosaics to test whether elevating Dlp can rescue tai lof clones in the same manner as Apc/Apc2 alleles (see Figs. 2-3), which elevate Wg pathway activity.

> *Specifics:*

> *"It would be good to know whether the authors can rescue tai-low clones by over-expression UAS-Dlp."*

As noted above, experiments are ongoing to test whether normalizing Dlp levels across clonal boundaries rescues elimination of Tai-low clones.

> *"The data on Wg distribution seems disjointed from the data about cell competition. The authors could refocus the paper to emphasize the cell competition story. The role of Dlp in Wg distribution is well established, so the authors could remove or condense these results. The story really could be Figs 1, 2, 3 and 7 and keep the paper focused on cell competition. The authors could then discuss Dlp as needed for Wg signaling transduction, which is already established in the literature."*

We appreciate the suggestion to reorganize the figures to focus the first part of the story on competition, and then follow with the role of Tai in controlling Dlp. We will consider this approach pending the results of ongoing experiments.

> *"The model of tai controlling dlp mRNA and Dlp protein distribution is confusing. In fact, the data for the former is weak, while the data for the latter is strong. I suggest that the authors focus on the altered Dlp protein distribution on tai-low clones. It would also be helpful to prove the Wg signaling is impeded in tai clones (see #5 below)."*

We agree but are currently testing how dlp reporters and mRNA respond to Tai in order to rigorously test a Dlp transcriptional mechanism. To complement the 'strong' evidence that Tai regulates Dlp distribution, we are testing Dlp in clones of our Tai Crispr null. Since submission, we have also assessed the effect of blocking the endocytic factor shibire/dynamin in Dlp distribution in Tai deficient cells to complement the data on Pentagone that is already in the paper (see Fig. S3).

> *"I don't know if the Fz3-RFP reported for Wg signaling works in imaginal discs, but if it does then the authors could make clones in this background to prove that cell-autonomous Wg signaling is reduced in tai-low clones."*

We thank the reviewer for this suggestion, which we are now testing.

> ***Reviewer #2***
>
> *Overall Comments:*
>
> *"While the authors present good evidence in support of most of their conclusions, there are alternative explanations in many cases that have not been excluded."*

We appreciate this point and are conducting experiments for a revised submission that will help test alternative mechanisms and clarify our conclusions.

> *Specifics:*
>
> *"However, the experiments have been done with a single allele, and these experiments do not exclude the possibility that there is another mutation on the same chromosome arm that is responsible for the observed phenotype. Since the authors have a UAS-tai stock, they could strengthen their results using a MARCM experiment where they could test whether the expression of UAS-tai rescues the elimination of tai mutant clones. Alternatively, they could use a second (independent) allele to demonstrate that the phenotype can be attributed to a reduction in tai activity."*

As noted above, we agree with the need for a second allele and are adding supporting data from a new tai lof allele we have generated by Crispr.

The tai[k15101] allele acts as a tai hypomorph and has been shown to produce weaker phenotypes than the 61G1 strong lof in a number of papers (Bai et al, 2000; König et al, 2011, Luo et al, 2019, and Zhang et al, 2015). We agree that rescue of tai[k1501] with a UAS-Tai transgene would help rule out effects of second site mutations. We are currently pursuing the reviewer's second suggestion of phenocopy with a different allele, our new tai Crispr lof.

> *"The authors have screened a total of 21 chromosomes for modification and have not really explained which alleles are nulls and which are hypomorphs. The nature of each of the alleles screened needs to be explained better."*

We will update the text to better reflect what type of alleles were chosen. In most cases we preferred amorphs or null alleles over hypomorphs, however when the amorph option was not available, we used hypomorphs.

> *"Also, the absence of a dominant modification does not necessarily exclude a function of that gene or pathway in the process. This is especially relevant for the Spz/Toll pathway which the authors have previously implicated in the ability of tai-overexpressing cells to kill wild-type cells."*

We thank the reviewer for this completely accurate point. The dominant screen does not rule out effects of other pathways such as Spz/Toll. Indeed, we were surprised by the lack of dominant effects by Spz/Toll alleles on tai[low] competition given our prior work. The reciprocally clear dominant effect of Apc/Apc2 led us to consider that Wg signaling plays a role in this phenomenon, which then became the starting point of this study.

> *"The most important discovery from this screen is the modification by the Apc alleles. This part of the paper would be strengthened by testing for modification by other components of the Wingless pathway. The authors show modification by Apc[MI01007] and the double mutant Apc[Q8] Apc2[N175A]. Without showing the Apc[Q8] and Apc2[N175A] alleles separately, it is hard to know if the effect of the double mutant is due to Apc, Apc2, `or the combination."*

We agree that testing for modification with other components of the Wg pathway would be helpful to strengthen the connection between Tai low clonal elimination and Wg pathway biology. We also agree that separating Apc [Q8] and Apc2 [N175A] would be a good idea to check if both Apc proteins are equally important for rescuing Tai low cell death, and future experiments for the lab could investigate this distinction.

> *"RNAi of tai seems to block the formation of the Wg gradient. If so, one might expect a reduction in wing size. Indeed, this could explain why the wings of tai/Df flies are smaller. The authors mention briefly that the posterior compartment size is reduced when tai-RNAi is expressed in that compartment. However, this observation merits more emphasis since it could explain why tai/Df flies are smaller (Are their wings smaller?)."*

We agree that this is an exciting possibility. Growth effects of Tai linked to interactions with Yorkie and EcR could be due to a distinct role in promoting Wg activity. Alternatively, Tai may cooperate with Yorkie or EcR to control Wg pathway. These are exciting possibilities that we are pursuing in future work

With regard to the "small size" effect of reducing Tai, we have previously shown that RNAi of Tai using engrailed-Gal4 causes the posterior compartment to shrink (Zhang et al. 2015,

Figure 1C-F, H). In this paper, we also showed that tai[k15101]/Df animals are proportionally smaller than wildtype animals and quantified this by measuring 2D wing size (Zhang et al. 2015, Figure 1A and 1B)

> *"In Figure 7, the authors show the effect of manipulating Tai levels alone or in combination with increasing Dlp levels. However, they do not include images of Wg protein distribution upon increasing Dlp levels alone."*

We thank the reviewer for this reminder and have already generated these control images to include in a revised submission paper.

> *"In Figure 8, there is more Wg protein both at the DV boundary and spreading when tai is overexpressed in the source cells using bbg-Gal4. However, in an earlier experiment (Figure 5C) they show that the wg-lacZ reporter is downregulated at the DV boundary when tai is overexpressed using en-Gal4. They therefore conclude that wg is not transcriptionally upregulated but is, instead secreted at higher levels when tai is expressed in the source cells. Wg protein is reduced in the DV stripe with tai is overexpressed using the en-Gal4 driver (Figure 6B') and is increased at the same location when tai is overexpressed with the bbg-Gal4 driver. (Figure 8) I don't know how to reconcile these observations."*

We thank the reviewer for pressing us to develop an overall model explaining our results and how we envision Tai regulating Dlp and Wg. We are preparing a graphic abstract that illustrates this model and will be included in our revision.

Briefly, we favor a model in which Tai controls the rate of Wg spread via Dlp, without a significant effect on wg transcription. For example, the induction of Dlp across the 'engrailed' domain of en>Tai discs (Fig 7B-B") allows Wg to spread rapidly across the flanks and moderately depletes it from the DV margin (Fig 6B-B") as noted by the reviewer. Adding a UAS-Dlp transgene in the en>Tai background dramatically accelerates Wg spread and causes it to be depleted from the DV margin and build up at the far end of the gradient adjacent to the dorsal and ventral hinge. Significantly blocking endocytosis of Wg in en>Tai discs with a dominant negative shibire transgene also causes Wg to build up in the same location (new data to be added in a revision) consistent with enhanced spreading. The difference in the bbg-Gal4 experiment is that Tai is only overexpressed in DV margin cells, which constrains and concentrates Wg within this restricted domain; we are in the process of testing whether this effect on Wg is blocked by RNAi of Dlp in bbg>Tai discs.

> *"In Figure 9, the tai-low clones have elevated levels of Dlp. How can this be reconciled with the tai-RNAi knockdown shown in Figure 7C' where reducing tai levels causes a strong reduction in Dlp levels?"*

We apologize for not explaining this data well enough. First, the tai[k15101] allele is a weak, viable hypomorph (as shown in our Zhang et al, 2015 paper) whereas the Tai RNAi line is lethal with most drivers (including en-Gal4) and thus a stronger lof. Second, Tai RNAi lower Dlp levels (Fig 7C) while tai[k15101] causes Dlp to accumulate intracellularly (see Fig. 9A-C). These data indicate that reduced Tai leads to a defect in Dlp intracellular trafficking while its loss reduces Dlp overall levels; these data can be explained by a single role for Tai in Dlp traffic to or from the cell membrane, or two roles, one in trafficking and one Dlp expression. As noted, we are investigating both possibilities using dlp reporter lines and our new tai null Crispr allele.

> ***Reviewer #3:***
>
> *Overall Weaknesses:*

> *"The study has relatively weak evidence for the mechanism of cell competition mediated by Dlp and Wg."*

The screen and middle section of the paper provide genetic evidence that elevating Wg pathway activity rescues Tai[low} loser cells and that Tai controls levels/localization of Dlp and distribution of Wg in the developing wing disc. Our current work is focused on linking these two finding together in Tai "loser" clones.

> *"More evidence is required to support the claim that dlp transcription or endocytosis is affected in tai clones."*

As noted above, we are testing whether normalizing Dlp levels across clonal boundaries rescues tai[low] loser clones and assessing effects of Tai on dlp transcription and Dlp trafficking.

> *Specifics:*
>
> *"Most of the rest of the study is not in the clonal context, and mainly relies on RNAi KD of tai in the posterior compartment, which is a relatively large group of cells. I understand why the authors chose a different approach to investigate the role of tai in cell competition. However because ubiquitous loss of tai results in smaller organs, it is important to determine to what extent reducing levels of tai in the entire posterior compartment compares with clonal elimination i.e. cell competition. This is important in order to determine to what extent the paradigm of Tai-mediated regulation of Dlp levels and by extension, Wg availability, can be extended as a general mechanism underlying competitive elimination of tai-low clones. If the authors want to make a case for mechanisms involved in the competitive elimination of tai clones, then they need to show that the KD of tai in the posterior compartment shows hallmarks of cell competition. Is there cell death along the A/P boundary? Or is the compartment smaller because those cells are growing slower?"*

Based on data that cell competition does not occur over compartment boundaries (e.g., see review by L.A. Johnston, Science, 2009), we chose not to use UAS-Gal4 to assess competition, but rather to investigate underlying biology occurring between Tai, Wg, and Dlp.

> *"Are the levels of Myc/DIAP1, proteins required for fitness, affected in en>tai RNAi cells?"*

This is, of course, an interesting question given that Myc is a well-studied competition factor and is proposed to be downstream of the Tai-interacting protein Yki. We are not currently focused on Myc, but plan to test its role in the Tai-Dlp-Wg pathway in future work.

> *"The authors do not have direct/strong evidence of changes in dlp mRNA levels or intracellular trafficking. To back these claims, the authors should look for dlp mRNA levels and provide more evidence for Dlp endocytosis like an antibody uptake assay or at the very least, a higher resolution image analysis showing a change in the number of intracellular Dlp positive punctae. Also, do the authors think that loss of tai increases Dlp endocytosis, making it less available on the cell surface for maintaining adequate extracellular Wg levels?"*

As noted above, have added experiments using a dominant-negative shibire/dynamin allele to test whether Tai controls Dlp endocytosis. These data will be added to a revised manuscript. We have also gathered reagents to test effects of Tai gain/loss on Dlp secretion.

> *"The data shown in the last figure is at odds with the model (I think) the authors are trying to establish: When cells have lower Tai levels, this reduces Dlp levels (S2) presumably either by reducing dlp transcription and/or increasing (?) Dlp endocytosis. This in turn reduces Wg (availability) in cells away from source cells (Figure 6). The reduced Wg availability makes them less fit, targeting them for competitive elimination. But in tai clones, I do not see any change in cell-surface Dlp (9B) (I would have expected them to be down based on the proposed model). The authors also see more total Dlp (9A) (which is at odds with S2 assuming data in S2 were done under permeabilizing conditions.)."*

As noted above (under Rev #2 comments), we apologize for not explaining this data well enough. First, the tai[k15101] allele is a weak, viable hypomorph (as shown in our Zhang et al, 2015 paper) whereas the Tai RNAi line is lethal with most drivers (including en-Gal4) and thus a stronger lof. Second, Tai RNAi lower Dlp levels (Fig 7C) while tai[k15101] causes Dlp to accumulate intracellularly (see Fig. 9A-C). These data indicate that reduced Tai leads to a defect in Dlp intracellular trafficking while its loss reduces Dlp overall levels; these data can be explained by a single role for Tai in Dlp traffic to or from the cell membrane, or two roles, one in trafficking and one Dlp expression. We are investigating both possibilities using dlp reporter lines and our new tai null Crispr allele.

> *"As a side note, because Dlp is GPI-anchored, the authors should consider the possibility that the 'total' Dlp staining observed in 9A may not be actually total Dlp (and possibly mostly intracellular Dlp, since the permeabilizing membranes with detergent will cause some (most?) Dlp molecules to be lost, and how this might be affecting the interpretation of the data. I think one way to address this would be to process the permeabilized and non-permeabilized samples simultaneously and then image them at the same settings and compare what membrane staining in these two conditions looks like. If membrane staining in the permeabilized condition is decreased compared to non-permeabilized conditions, and the signal intensity of Dlp in permeabilized conditions remains high, then the authors will have evidence to support increased endocytosis in tai clones. Of course, these data will still need to be reconciled with what is shown in S2.*

We thank the reviewer for this excellent suggestion and are generating mosaic discs to test the proposed approach of synchronous analysis of total vs. intracellular Dlp.

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