Genetic models of apoptosis-induced proliferation decipher activation of JNK and identify a requirement of EGFR signaling for tissue regenerative responses in Drosophila

Yun Fan
University of Massachusetts Medical School Worcester

Shiuan Wang
Baylor College of Medicine

Jacob Hernandez
MD Anderson Cancer Center

See next page for additional authors

Follow this and additional works at: http://escholarship.umassmed.edu/faculty_pubs

Part of the Cancer Biology Commons, Cell Biology Commons, Genetics Commons, and the Molecular Genetics Commons

Repository Citation
Fan, Yun; Wang, Shiuan; Hernandez, Jacob; Yenigun, Vildan Betul; Hertlein, Gillian; Fogarty, Caitlin E.; Lindblad, Jillian L.; and Bergmann, Andreas, "Genetic models of apoptosis-induced proliferation decipher activation of JNK and identify a requirement of EGFR signaling for tissue regenerative responses in Drosophila" (2014). University of Massachusetts Medical School Faculty Publications. 420.
http://escholarship.umassmed.edu/faculty_pubs/420
Genetic models of apoptosis-induced proliferation decipher activation of JNK and identify a requirement of EGFR signaling for tissue regenerative responses in Drosophila

Authors
Yun Fan, Shiuan Wang, Jacob Hernandez, Vildan Betul Yenigun, Gillian Hertlein, Caitlin E. Fogarty, Jillian L. Lindblad, and Andreas Bergmann

Creative Commons License
This work is licensed under a Creative Commons Attribution 4.0 License.

Rights and Permissions
© 2014 Fan et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

This article is available at eScholarship@UMMS: http://escholarship.umassmed.edu/faculty_pubs/420
Genetic Models of Apoptosis-Induced Proliferation Decipher Activation of JNK and Identify a Requirement of EGFR Signaling for Tissue Regenerative Responses in Drosophila

Yun Fan1*, Shiuan Wang2, Jacob Hernandez3, Vildan Betul Yenigun3, Gillian Hertlein4, Caitlin E. Fogarty1, Jillian L. Lindblad1, Andreas Bergmann1,2,3,4

1 University of Massachusetts Medical School, Department of Cancer Biology, Worcester, Massachusetts, United States of America, 2 Graduate Program in Developmental Biology, Baylor College of Medicine, Houston, Texas, United States of America, 3 MD Anderson Cancer Center, Department of Biochemistry & Molecular Biology, Houston, Texas, United States of America, 4 Länderinstitut für Bienenkunde, Humboldt Universität zu Berlin, Hohen Neuendorf, Germany

Abstract

Recent work in several model organisms has revealed that apoptotic cells are able to stimulate neighboring surviving cells to undergo additional proliferation, a phenomenon termed apoptosis-induced proliferation. This process depends critically on apoptotic caspases such as Dronc, the Caspase-9 ortholog in Drosophila, and may have important implications for tumorigenesis. While it is known that Dronc can induce the activity of Jun N-terminal kinase (JNK) for apoptosis-induced proliferation, the mechanistic details of this activation are largely unknown. It is also controversial if JNK activity occurs in dying or in surviving cells. Signaling molecules of the Wnt and BMP families have been implicated in apoptosis-induced proliferation, but it is unclear if they are the only ones. To address these questions, we have developed an efficient assay for screening and identification of genes that regulate or mediate apoptosis-induced proliferation. We have identified a subset of genes acting upstream of JNK activity including Rho1. We also demonstrate that JNK activation occurs both in apoptotic cells as well as in neighboring surviving cells. In a genetic screen, we identified signaling by the EGFR pathway as important for apoptosis-induced proliferation acting downstream of JNK signaling. These data underscore the importance of genetic screening and promise an improved understanding of the mechanisms of apoptosis-induced proliferation.


Editor: Norbert Perrimon, Harvard Medical School, Howard Hughes Medical Institute, United States of America

Received May 22, 2012; Accepted December 6, 2013; Published January 30, 2014

Copyright: © 2014 Fan et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Funding: This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under award number R01GM107789. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health. YF is supported by the Birmingham Fellowship, University of Birmingham, UK. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

* E-mail: yfan@bham.ac.uk (YF); andreas.bergmann@umassmed.edu (AB)

¤ Current address: School of Biosciences, University of Birmingham, Birmingham, United Kingdom.

Introduction

Apoptosis is the major form of programmed cell death. It is used during development and under stress conditions to remove excess, unwanted or damaged cells. Deregulated apoptosis can give rise to malignancies including cancer and neurodegeneration [1]. A central step for the execution of apoptosis is the activation of caspases, a family of cysteine- proteases that are ubiquitously expressed as inactive zymogens [2]. There are two different types of caspases. Initiator caspases are incorporated into multimeric complexes such as the apoptosome [3] in response to developmental signals, cellular stress and injury. The initiator caspase complex cleaves and activates effector caspases which then proteolytically process a large number of cellular proteins inducing the death of the cell.

Caspases are very well conserved in the animal kingdom. Of the seven caspases in Drosophila, only the initiator caspase Dronc and the two effector caspases DrICE and Dcp-1 have been implicated in apoptosis in imaginal discs [4–12]. Caspases are negatively regulated by inhibitor of apoptosis proteins (IAP) which directly bind to processed caspases and inhibit their activity [13]. Drosophila IAP1 (Diap1) binds to and inhibits Dronc, DrICE and Dcp-1 [14,15]. In cells committed to die, IAP-antagonists such as Reaper, Hid and Grim [16–18] promote ubiquitin-mediated degradation of Diap1, thus releasing Dronc, DrICE and Dcp-1 from Diap1 inhibition [19–23]. Dronc associates with the scaffolding protein Ark (Apafl related killer) to form the apoptosome which triggers activation of DrICE and Dcp-1.

Developing organisms have the ability to compensate for massive apoptotic cell loss by inducing compensatory proliferation. For example, developing Drosophila imaginal discs can form a normal-sized and patterned organ even after more than 50% of their cells have been killed by X-ray treatment due to compensatory proliferation [24]. Surprisingly, work in Drosophila, and later in hydra, Xenopus, planarians, newt and mice, has revealed that apoptotic caspases may be the driving force for compensatory
Author Summary

Work in recent years has revealed that apoptotic caspases not only induce apoptosis, but also have non-apoptotic functions. One of these functions is apoptosis-induced proliferation, a relatively recently discovered phenomenon by which apoptotic cells induce proliferation of surviving neighboring cells. This phenomenon may have important implications for stem cell activity, tissue regeneration and tumorigenesis. Here, we describe the development of a genetic model of apoptosis-induced proliferation and the use of this model for convenient and unbiased genetic screening to identify genes involved in the process. We tested mutants of our RNAi transgenic lines targeting the core components of the apoptotic pathway and of JNK signaling, a known mediator of apoptosis-induced proliferation. These assays demonstrate the feasibility of the system for systematic genetic screening and identified several new genes upstream of JNK that are involved in apoptosis-induced proliferation. Finally, we tested the model in a pilot screen for chromosome arm 2L and identified spi, the EGF ligand in flies, as important for apoptosis-induced proliferation. We confirmed the involvement of EGF in a genuine apoptosis-induced regeneration system. These data underscore the importance of genetic screening and promise an improved understanding of the mechanisms of apoptosis-induced proliferation and regeneration.

proliferation in apoptotic tissue [12,25–35] (reviewed in [36–38]). Because this regenerative proliferation requires apoptotic caspases, it has been termed Apoptosis-induced Proliferation, henceforth referred to as AIP [38,39].

There are two commonly used experimental models that study AIP in larval imaginal discs, usually wing and eye discs in Drosophila. The first type of model takes advantage of the fact that another caspase inhibitor, the P35 protein from Baculovirus, specifically inhibits the effector caspases DrICE and Dcp-1, but not the initiator caspase inhibitor, the P35 protein from Baculovirus, specifically referred to as AiP [38,39]. It has been termed Apoptosis-induced Proliferation, henceforth referred to as AiP [38,39].

The ey→hid-p35 model

eyeless (ey) is a regulatory gene for eye development and is expressed during the growth phase of eye imaginal discs [57]. With the move of the morphogenetic furrow (MF) in 3rd instar larvae, ey expression ceases in and posterior to the MF [57]. Therefore, co-expression of hid and p35 during the growth phase of the eye disc using ey-Gal4 (referred to as ey→hid-p35) may provide a convenient model to induce AIP. Correspondingly, in eye imaginal discs, the anterior portion of the eye disc is overgrown compared to controls forming an expanded head capsule due to increased cell proliferation [29] (Figure 1A,B,C,D). Additional ocelli and bristles are observed (Figure 1D, arrow). The anterior overgrowth is at the expense of posterior tissue (Figure 1A,B) which specifies the retina. As a result, eyes are smaller than wild-type and often absent (Figure 1E,F). In eye discs, we use ELAV labeling which labels photoreceptor neurons, as a marker to assess the extent of anterior overgrowth and distortion of the eye disc (Figure 1B,G). We refer to these phenotypes as AIP phenotypes. The small eye tissue is likely due to the expansion of Wg expression anterior to the MF (Figure 1G,H) which is an inhibitor of MF progression [58]. We also observed anterior expansion of dpp-lacZ expression [29]. Finally, expression of the JNK marker puc-lacZ and TRE-dsRed [59] are strongly expanded anterior to the MF (Figure 1J; Suppl. Figure S1). Therefore, known markers of AIP are induced in the ey→hid-p35 model which therefore may represent a convenient AIP model for genetic screening.

The ey→hid-p35 model requires the apoptosome components dronc and ark, but is independent of effector caspases

To test the feasibility of the ey→hid-p35 model for genetic screening, we first examined if mutants and RNA interference
(RNAi) of caspases and ark genetically modify the AiP phenotype. Heterozygosity of dronc and dronc RNAi strongly suppressed the AiP phenotype (Figure 2A,B). Under these conditions, more than 95% of the flies display completely normal eye and head morphology. Heterozygosity of the apoptosome component ark also suppresses the AiP phenotype to a similar extent (Figure 2C). Therefore, these data demonstrate that the ey>hid-p35 model is sensitive to genetic alterations and extend previous findings that AiP not only requires dronc, but also ark, i.e. a functional apoptosome. 

Because this type of AiP is dependent on effector caspase inhibition by P35, it was inferred that it does not require effector caspases [25,27,28]. However, it was recently suggested that despite P35 inhibition, effector caspases may still be active at low levels in ‘undead’ cells [60]. This low level effector caspase activity may be insufficient to induce apoptosis, but sufficient to trigger non-apoptotic functions such as invasive behavior of ‘undead’ cells [60]. To test this possibility for AiP, we further reduced DrICE and Dcp-1 activity by double RNAi due to the redundancy of these two effector caspases [8]. However, in contrast to the invasive behavior of ‘undead’ cells [60], the AiP phenotype was not suppressed by dcp-1;drICE double RNAi (Figure 2D). The RNAi stocks used are functional as dcp-1;drICE double RNAi suppresses hid activity in a different apoptotic model, GMR-hid (Suppl. Figure S2). In summary, the overgrowth of the ey>hid-p35 model is dependent on the apoptosome.

Figure 1. The ey>hid-p35 model induces hyperplastic overgrowth and displays markers of apoptosis-induced proliferation. In this and the following figures, anterior is to the left. White dotted lines indicate the anterior portion of the eye imaginal discs. ELAV labels photoreceptor neurons and is used to mark the developing eye field posterior to the morphogenetic furrow (MF). (A,A’) An ey>p35 control eye disc labeled with PH3 as proliferation marker (red in A; grey in A’) and ELAV (green in A). (B,B’) An ey>hid-p35 experimental disc labeled with PH3 (red in B; grey in B’) and ELAV (green in B). Please note the increase in size of the region anterior to the MF at the expense of the posterior region (green). (C,D,E,F) Dorsal views of heads (C,D) and eyes (E,F) of ey>p35 control (C,E) and ey>hid-p35 experimental flies (D,F). Enlarged head cuticle with additional ocelli and bristles (arrows) is observed in ey>hid-p35 flies (D), while eyes are reduced in size (F). (G,G’,H,H’) Increased expansion of wg expression (wg-lacZ, red in G,H; grey in G’,H’) in ey>hid-p35 discs (H, arrow) compared to ey>p35 control discs (G). (I,J) In ey>p35 control discs, puc-lacZ expression (β-Gal; red in I, gray in J) as marker of Bsk/JNK activity is low anterior to the MF and induced posterior to the MF. (I’,J’) puc-lacZ expression (β-Gal; red in J, gray in J’) as marker of Bsk/JNK activity is strongly induced anterior to the MF in ey>hid-p35 eye discs (arrows). Note the reduction in the posterior eye field as visualized by ELAV labeling (green).

doi:10.1371/journal.pgen.1004131.g001
components Dronc and Ark, but independent of effector caspases.

Identification of JNK pathway components involved in AiP

It is unknown how the apoptosome induces JNK activity for AiP. To obtain further insight into this question, we tested components of the JNK pathway in a pilot RNAi screen for modification of the ey\(^{>hido-p35}\) model. As expected, RNAi targeting \(bsk\), the JNK ortholog in \(Drosophila\), completely suppresses the AiP phenotypes in more than 90% of the flies (Figure 2E,F,G). Downstream of JNK, RNAi knockdown of the components of the AP1 transcription factor, \(jun\)-related antigen \((\text{jra})\) and the Fos ortholog \(kayak\) \((\text{kay})\), also suppressed the \(ey^{>hido-p35}\) AiP phenotypes, although to a lesser extent (Figure 2F,G) suggesting that they are at least partially required for AiP.

To identify upstream components in the JNK pathway involved in AiP, we tested RNAi lines targeting all known components in the JNK pathway [52]. Interestingly, only a subset of them were found to suppress the AiP phenotypes (Figure 2F,G). This includes...
the JNKKK dTak1 and the JNKKs hemipterous (hpt) and M KK4 (Figure 2 F,G). The non-redundant functions of hpt and M KK4 for AiP is puzzling, but has been previously reported in different contexts [61,62]. Further upstream in the JNK signaling pathway, we only identified Traf2 (also known as Traf6) as AIP suppressor (Figure 2 F,G). Another regulator of JNK signaling, the small GTPase Rho1 [63–66], was also identified as AIP suppressor. In contrast, the two ligand/receptor systems known to activate JNK, Eiger/Wengen and Ptvl/PVR, do not suppress AIP (Figure 2 F,G).

The RNAi lines against these genes are functional as shown in Suppl. Figure S3 and in [67–69]. Theoretically, it is possible that the suppression of AIP by these RNAi transgenes is an indirect result of suppression of apoptosis, as observed in the case of dronc and arks mutants or RNAi (Figure 2 B,C; Suppl. Figure S4B). To exclude this possibility, we labeled ey->hid-p35 eye imaginal discs expressing these RNAi constructs with cleaved Caspase-3 (Cas3*) antibody, a marker of Dronc activity [70], and ELAV antibody to evaluate rescue of disc morphology. Despite the rescue of disc morphology, Cas3* labeling is not significantly suppressed by these RNAi constructs (Suppl. Figure S4C–H) suggesting that the suppression of the AIP phenotype by reducing JNK activity is not due to suppression of caspase activity.

Because Rho1 is the least well characterized regulatory component in the JNK pathway, we examined the effect of Rho1 knockdown on JNK activity in the AIP model. Loss of Rho1 suppresses puc-lacZ in ey->hid-p35 eye discs (Suppl. Figure S5A,B). Rho1 RNAi also suppresses the AIP marker Wg (Suppl. Figure S5C,D). These data show that Rho1 acts genetically upstream of JNK in the AIP model consistent with previous reports [63–66].

To further place Rho1 into the AIP pathway and to relate it to Traf2, we examined the ability of Rho1 and Traf2 to suppress GMR-GMR in a pseudo-dominant manner using FLP-out approach and analyzed puc-lacZ expression as JNK reporter. GFP was used to mark hid/p35-expressing clones. Using this approach, puc-lacZ was predominantly expressed in hid/p35 expressing cells (Figure 3A,B; arrows). However, we also noted a few examples where puc-lacZ was expressed in GFP+ tissue (Figure 3A,B; arrowheads). These observations suggest that JNK activation occurs largely in ‘undead’ cells, but also in neighboring, normal cells.

To address this question in a ‘genuine’ (p35-independent) AIP model, we repeated the experiments by Bergantinos et al. (2010) [43] in wing imaginal discs. These authors reported JNK activity in neighboring surviving cells only. We induced hid in a temporally and spatially controlled manner using ptc-Gal4 and tub-Gal80° (ptc->hid) by temperature shifts for various times. In control experiments, just expressing GFP in the ptc domain does not affect the puc-lacZ pattern (Figure 3C,C’). However, when hid expression was induced, depending on the conditions, different results were obtained regarding the location of JNK activity. In response to a short pulse (6 hours) of hid expression followed by a 6 hours recovery period (ts6hR0h), an elevation of puc-lacZ activity was detected in dying cells and neighboring, surviving cells (Figure 3E’, F’), i.e. in the ptc domain which had been exposed to hid 6 hours earlier, but have survived for unknown reasons. Similar results were observed in Figure 3E: the surviving cells inducing puc-lacZ are located in the GFP region, i.e. in the ptc domain (Figure 3E”, F”; arrowheads). Thus, it is not clear whether JNK activity in surviving cells is induced autonomously in response to hid expression, or by a signaling event from the dying Cas3*-positive cells. In any case, these data show that both in ‘undead’ and ‘genuine’ AIP models, JNK activity can be detected in ‘undead’/dying cells as well as in neighboring, surviving cells.

Identification of spi as AIP suppressor

A systematic mutagenesis screen for genes involved in AiP has not been performed to date due to absence of a convenient screening assay. However, the data presented in Figure 2 demonstrate that suppression of ey->hid-p35-induced AIP provides a convenient assay for genetic screening. Therefore, as proof of principle, we screened a total of 106 chromosomal deficiencies deleting segments on the left arm of chromosome 2 (2L) for modification of the AIP phenotype and identified four chromosomal segments as dominant AiP suppressors and seven deficiencies as dominant AiP enhancers (Table 1; Suppl. Table S1), validating the deficiency approach. Enhancers display an even stronger AiP phenotype with severely overgrown head cuticle and strong semi-lethality.

To identify the genes in the deficiencies that dominantly cause the suppression of AIP, we tested available mutants and UAS-RNAi stocks against all genes that map to these deficiencies. This approach has been completed for Df(2L)ED1353 (Table 1) and led to the identification of spitz (spi) as a potential regulator of AiP (compare Figure 4C–F with Figure 4A,B). spi encodes the EGF ortholog in Drosophila [74]. Therefore, our deficiency screen raises
Figure 3. Location of Bsk/JNK signaling in ‘undead’ and ‘genuine’ AiP models. 

puc-lacZ was used as JNK activity marker. hid expressing areas are marked by GFP. Arrows indicate JNK activity in ‘undead’ dying cells, while arrowheads mark JNK activity in surviving cells. A double arrow in (C–F) marks the ptc domain. (A,B) Location of JNK signaling in ‘undead’ AiP models by mosaic analysis. Clones expressing hid and p35 were induced by FLP-out technology. In eye (A) and wing (B) imaginal discs, puc-lacZ expression is mostly induced in hid/p35-expressing clones (arrows in A9, A0, A90, B9, B0, B90). However, a few examples of puc-lacZ expression are noted in cells outside of hid/p35-expressing clones (arrowheads). (C–F) Location of JNK activity in a ‘genuine’ AiP model in wing imaginal discs. hid expression was under control of ptc-Gal4 and tub-Gal80ts (ptc-ts). hid expression was induced by a temperature shift (ts) to 30°C for the indicated amount of time during 3rd larval instar. After the indicated recovery period (R), discs were labeled for GFP (to visualize the ptc domain), Cas3* (the death domain) and b-Gal (puc-lacZ, i.e. JNK activation). The ptc domain is outlined by white, dotted lines. Note that the death domain does not completely overlap with the ptc domain (see for example E9, E90). A control disc just expressing GFP under the experimental conditions to visualize the normal puc-lacZ pattern (b-Gal). (D–F) An experimental disc that was dissected immediately after a 6 hours pulse of hid expression without recovery (ts6hR0h). While caspase activity has been induced (D9), the puc-lacZ pattern is mostly unaffected (D90). An experimental disc that was allowed to recover for 6 hours after a 6 hours pulse of hid expression (ts6hR6h). Although apoptosis is now strongly induced (F9), it is not detectable in the entire ptc domain (GFP; F900). Nevertheless, there is an increase of puc-lacZ expression in cells outside of the death domain (F9; arrowheads). However, these cells reside in the ptc expression domain (F9,F90). Genotypes: (A,B) hs-FLP/UAS-hid; UAS-p35/act-γ-Gal4 UAS-GFP; puc-lacZ/+; (C) ptc-Gal4 tub-Gal80+/+; UAS-GFP/puc-lacZ. (D–F) UAS-hid+/; ptc-Gal4 tub-Gal80+/+; UAS-GFP/puc-lacZ.

doi:10.1371/journal.pgen.1004131.g003
the hypothesis that the EGFR pathway regulates AiP. Consistently, heterozygosity of 

\(\text{Egfr}\) suppresses the \(\text{e}^+\text{hid}-\text{p35}\) phenotype in eye discs (compare Figure 4G–I with Figure 4A,B). We also found that 

\(\text{Egfr}\) RNAi suppresses an AiP model in wing imaginal discs (\(\text{hud}^+\text{hid}-\text{p35}\)) (Suppl. Figure S6). Downstream of EGFR, mutant alleles of the \(\text{Drosophila}\) orthologs of Ras (\(\text{Dra}\)) and MAPK (\(\text{rolled}\) (\(\text{rl}\))) act as dominant suppressors of \(\text{e}^+\text{hid}-\text{p35}\) (Figure 4I) suggesting that MAPK activity is required for AiP. These data imply that EGFR/Ras/MAPK signaling is essential for AiP in both eye and wing discs. These findings are exciting giving the controversy of the role of Wg and Dpp for AiP (see Introduction). Imply that EGFR activation occurs in cells adjacent to apoptotic, \(\text{JNK}\)–activating cells. This assumption is directly confirmed by the observation that \(\text{kek}-\text{lac}\) activity, a downstream marker of EGFR signaling, and \(\text{Cas3}\) labeling as apoptotic marker do not overlap (Figure 5F, arrows). In summary, these data imply that \(\text{spi}\) expression occurs downstream of \(\text{Bsk/JNK}\) activity and that EGFR signaling acts in signal-receiving, proliferating cells.

### Characterization of ‘genuine’ AiP in the eye imaginal disc: the \(\text{DE}^+\text{hid}\) model

Finally, we tested if genes identified in the ‘undead’ (P35-dependent) AiP model are also involved in ‘genuine’ (P35-independent) regeneration in the eye disc. To accomplish this we used a similar approach as previously described in wing discs ([42–44]). \(\text{hid}\) expression was spatially restricted to the dorsal half of the eye disc by \(\text{dorsal eye-Gal4} (\text{DE-Gal4})\) ([77]) and controlled by \(\text{Gal80}\) ([78]) by a transient temperature shift (ts) to 30°C for 12 hours (Figure 6E). We refer to this system as \(\text{DE}^+\text{hid}\). This model also induces \(\text{GFP}\) label to \(\text{hid}\)-expressing cells. Before and after the temperature shift, animals were incubated at 18°C (Figure 6E) to inhibit \(\text{Gal4}\) activity and therefore \(\text{hid}\) and \(\text{GFP}\) expression. Note that although \(\text{GFP}\) is expressed only during the 30°C pulse, it is a rather stable protein and can be detected in control discs 72 h later (Figure 6D).

In experimental discs immediately after the 30°C pulse (recovery 0 hours – \(\text{R0}\) h), a strong apoptotic response is detectable (Figure 6A) which causes tissue loss and disruption of the bilateral symmetry of the disc 24 hours later (\(\text{R24}\) h). In extreme cases, this treatment can result in ablation of the entire dorsal half (Figure 6B, asterisk), but usually some dorsal tissue remains. At that time, many cells are still \(\text{Cas3}\)–positive (Figure 6B), 72 hours after the temperature shift (\(\text{R72}\) h), the disc has fully recovered in shape and also has a normal photoreceptor pattern as judged by \(\text{ELAV}\) labeling (Figure 6C). \(\text{Cas3}\) activity is no longer detectable. The recovery is the result of increased proliferation in the dorsal half of the eye disc (compare Figure 6G to Figure 6P; quantified in Figure 6H). The reduction of the \(\text{GFP}\) signal in the dorsal part (Figure 6C,G) compared to the control disc (Figure 6D) suggests that most of the \(\text{GFP}\) cells have died and have been replaced by new, \(\text{GFP}^+\) cells.

Interestingly, a group of apoptotic cells appears to migrate out of the dorsal half into the center of the disc (Figure 6B, arrow). At \(\text{R72}\) h, only these cells still show strong \(\text{GFP}\)-labeling (Figure 6C, arrow). This ‘escape’ response of these ‘genuine’ apoptotic cells is reminiscent of the invasive behavior of ‘undead’ cells in wing discs which move out of the

<table>
<thead>
<tr>
<th>Suppressors of (\text{e}^+\text{hid}-\text{p35})-induced Overgrowth</th>
<th>Chromosomal Location</th>
<th>Enhancers of (\text{e}^+\text{hid}-\text{p35})-induced Overgrowth</th>
<th>Chromosomal Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>(\text{Df}(2L)\text{C }1, \text{Df}(2L)\text{ED}136)</td>
<td>22F4–23A2</td>
<td>(\text{Df}(2L)\text{ED}123)</td>
<td>22D1–22D3</td>
</tr>
<tr>
<td>(\text{Df}(2L)\text{LED}206, \text{Df}(2L)\text{US}17)</td>
<td>23C4–21C5</td>
<td>(\text{Df}(2L)\text{BSC}6)</td>
<td>26D3–26E1</td>
</tr>
<tr>
<td>(\text{Df}(2L)\text{Exel}7014, \text{Df}(2L)\text{BSC}28)</td>
<td>23C4–21C5</td>
<td>(\text{Df}(2L)\text{BSC}6)</td>
<td>26D3–26E1</td>
</tr>
<tr>
<td>(\text{Df}(2L)\text{BSC}31)</td>
<td>23E5–23F3</td>
<td>(\text{Df}(2L)\text{ED}508)</td>
<td>28C1–28C4</td>
</tr>
<tr>
<td>(\text{Df}(2L)\text{WTI}137)</td>
<td>?</td>
<td>(\text{Df}(2L)\text{Exel}7048)</td>
<td>31E3–31F4</td>
</tr>
<tr>
<td>(\text{Df}(2L)\text{ED}1303, \text{Df}(2L)\text{ED}1272)</td>
<td>37F2–38A2</td>
<td>(\text{Df}(2L)\text{ED}10)</td>
<td>35C1–35D1</td>
</tr>
<tr>
<td>(\text{Df}(2L)\text{Exel}7080)</td>
<td>38F5–39A2</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The indicated chromosomal location is the smallest overlap of overlapping deficiencies. \(\text{Df}(2L)\text{WTI}137\) is marked with a ‘?’ because other overlapping deficiencies do not suppress AiP (see Suppl. Table S1) indicating that the \(\text{Df}(2L)\text{WTI}137\) chromosome carries a suppressor mutation independent of the deficiency.

DOI:10.1371/journal.pgen.1004131.e001

---

**Table 1.** Deficiencies that modify the \(\text{ey}^+\text{hid}-\text{p35}\)-induced AiP phenotype as suppressors or enhancers.
The hyperplastic phenotype of ey>hid-p35 flies can be grouped in three categories, severe, moderate and weak. Flies were scored as severe when the head cuticle was strongly overgrown without discernible patterning and eyes were absent or strongly reduced in size. A moderate phenotype was scored when the head cuticle was overgrown, but recognizably patterned with duplicated ocelli and bristles. A weak phenotype was scored when size of head cuticle and eyes was almost normal with very few ectopic ocelli or bristles occasionally observed. (A-H) Representative pictures of ey>hid-p35 fly head cuticles scored in different categories. Completely suppressed ey>hid-p35 phenotype (wild-type-like head cuticles) by spi or Egfr heterozygotes are not shown here. Arrows indicate ectopic ocelli or bristles. (A,B) About 50% of ey>hid-p35 flies show severe hyperplastic overgrowth of the head cuticle (A), while the remaining 50% display a moderate phenotype (B). (C-H) Heterozygosity of spi1, spi1068 and Egfr2 almost completely eliminated the severe overgrowth phenotype of ey>hid-p35 flies and largely extends the population of flies with a weak phenotype. (I) Summary of the suppression of the ey>hid-p35 overgrowth phenotype in spi, egfr, dfrs and rolled (rt) heterozygous condition. Pink indicates severe, orange indicates moderate and green indicates weak phenotypes. Mutant alleles are indicated.

doi:10.1371/journal.pgen.1004131g004

Discussion

Apoptosis-induced proliferation (AIP) appears to be a mechanism by which developing organisms replace dying cells under stress conditions and initiate regenerative responses [reviewed by [37,45]]. In this paper, we described two AIP models in the developing Drosophila eye. The ‘undead’ ey>hid-p35 model generates a hyperplastic overgrowth phenotype. To date this is the only known phenotype that provides a robust and convenient assay for genetic screening and identification of novel regulators of
Figure 5. Epistasis analysis of \( \text{spi} \) and \( \text{bsk} \). Arrowheads indicate the morphogenetic furrow (MF) which separates the anterior (left) from the posterior eye tissue visualized by ELAV labeling. (A) \( \text{spi-lacZ} \) pattern (\( \beta\)-Gal; red in A; gray in A') in \( \text{ey}\rightarrow\text{p35} \) control discs. Note there is little expression anterior to the MF. (B,C) Because the \( \text{spi-lacZ} \) allele (\( \text{spi}^{01068} \)) is a suppressor of \( \text{ey}\rightarrow\text{hid-p35} \) adult overgrowth phenotype (Figure 4I), there is variation in the \( \beta\)-Gal pattern. About 25% of the eye discs show strong induction of \( \text{spi-lacZ} \) in the anterior portion of the eye disc (B, B'; arrows) with a strong reduction of the eye field (ELAV). The remaining 75% of the eye discs show a suppressed, largely normal \( \beta\)-Gal and ELAV pattern in \( \text{ey}\rightarrow\text{hid-p35} \) larvae (C, C'). This ratio corresponds to the suppression of the adult overgrowth phenotype (Figure 4I). (D,E) Strong induction of \( \text{kek-lacZ} \) (\( \beta\)-Gal; red in D, E; gray in D', E') in \( \text{ey}\rightarrow\text{hid-p35} \) eye discs (E; arrows) compared to \( \text{ey}\rightarrow\text{p35} \) control discs (D). (F,F') \( \text{kek-lacZ} \) (\( \beta\)-Gal; red in F, gray in F') is preferentially induced in patches of tissue adjacent to areas with high levels of active caspases (arrows, Cas3* in green). (G,G') Heterozygosity of \( \text{spi} \) normalizes the eye field (ELAV, green), but does not suppress ectopic \( \text{puc-lacZ} \) expression (\( \beta\)-Gal; red in G, gray in G') in \( \text{ey}\rightarrow\text{hid-p35} \) eye discs (arrows, compare to Figure 1J). Dotted white lines outline the region anterior to the MF. (H,H') Expression of \( \text{bskRNAi} \) in \( \text{ey}\rightarrow\text{hid-p35} \) discs normalizes the eye field (ELAV, green) and suppresses ectopic \( \text{spi-lacZ} \) expression (\( \beta\)-Gal; red in H, gray in H'). This pattern was observed in all experimental discs (n = 30). (I,I') Expression of \( \text{bskRNAi} \) in \( \text{ey}\rightarrow\text{hid-p35} \) discs normalizes the eye field (ELAV, green) and suppresses ectopic \( \text{kek-lacZ} \) expression (\( \beta\)-Gal; red in I, gray in I'; compare to E). The analysis in G, H and I strongly suggests that \( \text{spi} \) acts genetically downstream of \( \text{bsk} \).

doi:10.1371/journal.pgen.1004131.g005

Figure 6. Characterization of ‘genuine’ AIP in the eye imaginal disc: the \( \text{DEts}\rightarrow\text{hid} \) model. \( \text{hid} \) expression was under control of \( \text{dorsal eye-} \)\text{-}(\( \text{DE-})\text{Gal4} \) and \( \text{tub}\text{-}\text{Gal80ts} \) (\( \text{DEts}\rightarrow\text{hid} \)). A temperature shift (ts) to 30°C for 12 h during 2nd larval stage induced \( \text{hid} \) expression (E). After the indicated recovery period (R), discs were labeled for GFP (to visualize the \( \text{DE} \) expression domain), Cas3* (the death domain) and ELAV (to outline the shape of the disc). (A–C) \( \text{DEts}\rightarrow\text{hid} \) experimental discs. \( \text{hid} \) expression induces a strong apoptotic response (A) causing strong tissue loss after 24 h recovery in some discs (panel B; R24 h, asterisk). After 72 h recovery (R72 h), the disc has fully recovered and has a normal photoreceptor pattern as judged by ELAV labeling (C). Please note the strong reduction of GFP intensity which suggests that most of the \( \text{GFP}^+ \) cells have been replaced by new \( \text{GFP}^- \) cells. Arrows highlight a patch of cells that are moving to the center of the disc. (D) A control disc 72 h after \( \text{DEts}\)-induced GFP expression. Please note that GFP is a very stable protein that can still be detected 72 h after synthesis. (E) The protocol of the \( \text{DEts}\rightarrow\text{hid} \)-induced tissue ablation followed by recovery periods. (F,F',F'',G,G',G'') PH3-labeling of control (\( \text{DEts}\rightarrow\text{GFP} \), F,F') and experimental discs (\( \text{DEts}\rightarrow\text{hid} \), G,G'). GFP marks the outline of the \( \text{DE} \) domain (F', G'). (H) Quantification of the number of PH3-positive cells in dorsal and ventral compartments of control (F) and experimental discs (G). n = 40 for each genotype.

doi:10.1371/journal.pgen.1004131.g006
AiP. In contrast, we have not identified a similar robust and convenient phenotype that would allow direct screening for genes involved in 'genuine' (p35-independent) AiP and regeneration. Nevertheless, we developed the \textit{DEts}\textit{hid} model to verify genes identified in the 'undead' screen as being involved in 'genuine' AiP and regeneration.

Although the use of p35 to keep dying cells in an 'undead' condition may be considered as unphysiological and artificial, to date all genes identified under p35-expressing conditions such as JNK, Wg and Spi, were also found to be involved in AiP in p35-independent models [42,43] (this study). Furthermore, cancer cells may resemble 'undead' cells. They often initiate, but cannot execute the apoptotic program due to genetic loss or inactivation of effector caspases or other apoptotic components [81–84]. Such 'undead' cancer cells may contribute to tumor growth. Therefore, our p35-expressing AiP model could provide insights into new regulators of AiP as well as how impaired apoptosis may promote tumor growth.

Apoptotic caspases play a critical role for AiP. In \textit{Drosophila}, the initiator caspase Dronc is required for activation of JNK activity which triggers AiP. However, it is unknown how Dronc activates JNK for AiP. Using RNAi, a specific subset of components in the JNK pathway were identified as required for AiP. The most upstream genes in the JNK pathway are Rho1 and Traf2. Traf2 appears to be an integration point for Eiger- and AiP-induced JNK activation, the latter one being mediated through Rho1 (Figure 2G). However, it is unknown how Dronc triggers Rho1 activation. It is unlikely that Dronc proteolytically cleaves Rho1 for two reasons. First, Rho1 does not contain a putative Dronc cleavage site [40,85]. Second, a proteolytic cleavage is likely to destroy Rho1; however, our genetic analysis implies that Rho1 function is required for AiP (Figure 2, Suppl. Figure S5). Therefore, it remains unknown how Dronc triggers Rho1 and thus JNK activation.

Interestingly, extracellular signaling pathways (Eiger/Wengen and Pvf/PVR) known to activate JNK [52] did not score as
suppressors of AiP, suggesting that Drone may autonomously activate JNK activity. This is also consistent with our observation that JNK activity occurs largely in hid- and p35-expressing clones (Figure 3). Nevertheless, it is also possible that a third extracellular signal is generated by 'undead' cells in a Drone-dependent manner that triggers JNK activity in an autocrine and/or paracrine manner. The observation that in both 'undead' and 'genuine' AiP models JNK activity is also detectable in neighboring surviving cells (Figure 3) may support such a mechanism. Further work is necessary to reveal the exact mode of JNK activation by 'undead' dying cells.

In the 'genuine' (p35-independent) AiP model (ptc>>hid), JNK activity is detectable in both dying and surviving cells. However, the surviving cells with increased JNK activity are also present in the ptc domain (Figure 3E,F) which was exposed to hid expression during the temperature shift. JNK activity is also restricted to the death domain in the DE>>hid model (Suppl. Figure S7). Therefore, it is unclear whether a signaling mechanism from dying cells induces JNK activity in surviving cells, or whether the previous hid induction accounts for the JNK activity in surviving cells. It is also unclear how these cells survive. Even after a 16 h pulse of hid induction causing a strong apoptotic response in a large fraction of cells in the ptc domain, some cells survive (Figure 3F). They may receive survival signals from cells outside of the ptc domain, but that needs to be determined. These are interesting questions to be addressed in the future.

We have tested signaling pathways known to be involved in growth control for modification of the ey>>hid-p35 model. One example is the Hippo/Warts/Yorkie pathway [96,87]. However, neither mutants of this pathway nor transcriptional reporters (ex-lacZ) scored positive in the ey>>hid-p35 model (data not shown). Therefore, at least in the eye disc, not every pathway involved in growth control is also involved in AiP. These observations stress the necessity to perform unbiased genetic screens aimed at identifying the genes and mechanisms involved in AiP.

Therefore, we performed a pilot screen for modifiers of the ey>>hid-p35 AiP model using deficiencies of chromosome arm 2L. We identified four deficiencies as suppressors and three as enhancers (Table 1). Identification of AiP enhancers implies that there is also negative regulation of AiP. In one case we identified spi, encoding the Drosophila EGF ortholog, as a suppressor of AiP suggesting an involvement of EGFR signaling for AiP. This is further confirmed by the strong transcriptional induction of spi and an EGFR target gene, kekkon, in our AiP model. We also found that EGFR signaling is involved in an 'undead' AiP model in the wing and – more importantly – in the 'genuine' DE>>hid regeneration model in the eye. The latter finding is crucial as it demonstrates that genes identified in the 'undead' screen may be relevant players for 'genuine' regeneration in response to apoptotic tissue loss. An involvement of EGFR and MAPK for regeneration is not unprecedented. It was previously shown that EGF is one of a few signals that stimulate hepatocyte proliferation during liver regeneration in mammals [88,89]. In the Hydra regeneration model, apoptosis-induced proliferation depends on MAPK activation [90]. Therefore, these findings and considerations validate our screening approach using the 'undead' AiP model.

Identification of Spi/EGFR signaling as suppressor of AiP was unexpected because EGFR signaling negatively regulates the apoptotic activity of hid [91,92]. Thus, by reducing EGFR activity, hid has increased apoptotic activity which is expected to induce even more AiP. Therefore, the AiP phenotype should be enhanced by heterozygosity of EGFR pathway components. However, the identification of spi, Egr, Dros and n as suppressor of AiP suggests that EGFR signaling is also required for AiP. One possibility to explain these two opposing functions of EGFR (negative regulation of hid and positive requirement for AiP) may be the exclusive appearance of Cas3-positive areas and areas with EGFR activity (Figure 3F). Accordingly, while the Spi signal is generated in Cas3-positive, apoptotic areas, it signals to neighboring Cas3-negative, surviving areas to inactivate Hid and promote proliferation.

The identification of Spi/EGFR signaling may help to resolve a controversy about the signaling pathways involved in AiP. The exact roles of Wg and Dpp for AiP are unclear [26,44,46] and signaling by the EGFR pathway may contribute to the proliferative response in AiP.

Recently, a genetic screen has been reported aimed at identification and characterization of genes required for compensatory growth [93]. These authors induced apoptosis conditionally using a temperature-sensitive cell lethal mutant (sec3). Under normal conditions, the ablated tissue is replaced by new tissue due to compensatory proliferation. The authors then screened for mutants that fail to renew the lost tissue [93]. This was done in a clonal screen for chromosome arm 2L, the same chromosome arm we screened in the deficiency screen in our model. However, the genes identified in the sec3 screen [93] do not map to the deficiencies that we have identified in our analysis (Table 1). Because it is unknown if sec3-induced compensatory proliferation requires caspase activity in apoptotic cells [93], it is not clear if this is a model of apoptosis-induced proliferation.

In summary, we have developed and tested the feasibility of the ey>>hid-p35 model for genetic screening. We are confident that this model will close gaps in our understanding of AiP regulation under p35-expressing conditions and in p35-independent regeneration. Finally, it will have implications for the understanding of tumorigenesis by 'undead' as well as 'genuine' apoptotic tumor cells [94].

Materials and Methods

Fly stocks and genetics

The following mutants and transgenic stocks were used: drone [99], ak [100], spi [101], Egfr [102], ra [103,104], n [105], ey-Gal4; ptc-Gal4; DE-Gal4; tub-Gal80 [106]; UAS-p35; UAS-hid; UAS-GFP; wg-lacZ; puc-lacZ; kek1-lacZ; spi-lacZ; spi-TM6B, y; TRi-Gal80; GMN-Gal4; GMR-Gal4 UAS-egr; UAS-based RNAi stocks of the following genes were obtained from various stock centers (VDRC, Bloomington and NIG) and were tested for suppression of AiP: drone, dap-1, dhhCE, bsk, egr, usn, PVR, dTraf1, dTraf2, Rho1, min, slpr, Taka1, dMekk1, dMekk4, Jma, bai, spi, Egfr. The exact genotype of ey>>hid-p35 is UAS-hid; ey-Gal4 UAS-p33/5/CyO,tub-Gal80. Expression of tub-Gal80 in this stock suppresses the semi-lethality associated with ey-induced expression of hid and p35.

Mosaic analysis

Larvae of the following genotype were heat shocked for 15 min at 37°C, raised at room temperature for 48 h before they were analyzed at the late 3rd instar larval stage. Genotype: hs-FLP/UAS-hid; UAS-p33/pct>y/+; UAS-GFP; puc-lacZ/+.

Tissue ablation using ptc>>hid and DE>>hid

Larvae of genotype UAS-hid/+; ptc-Gal4 tub-Gal80/+; UAS-GFP/+ (Figure 3) and UAS-hid/+; UAS-GFP/+; DE-Gal4 tub-Gal80/+ (Figure 6) were raised at 18°C. hid expression was induced by temporal temperature shift to 30°C for the indicated amount of time (Figure 3) or for 12 hours (Figure 6E). After the indicated recovery periods at 18°C, discs were dissected and analyzed as indicated in the panels.
PH3 labelling and statistics in DEα>hid model

Two rounds of experiments (ts12hR24h, at least 20 discs were analyzed each round) were done for both DEα>GFP (control) and DEα>hid. Increase of PH3-positive cells in dorsal eye disc portions of DEα>hid animals are consistently observed. PH3-positive cell numbers were counted in dorsal (GFP) and ventral eye disc portions in selected discs. Size of the dorsal (GFP) and ventral eye disc portions were measured through the “histogram” function in Adobe Photoshop CS. To compare the density of PH3+ cells in each disc portion, number of PH3+ cells were divided by size (in pixels) of the corresponding tissue which is used to calculate the number of cells in 100,000 pixels (density). Such normalized density of PH3+ cells in various portions of eye discs (mean ± SD) were used for the statistical chart. PH3+ cell numbers in 100,000 pixels is on average 88 in DEα>hid dorsal eye discs compared to 62 in the control dorsal discs. Their statistical significance was evaluated through a two-tailed, unpaired Student’s t-tests (P<0.04). In contrast, the number of PH3+ cells are comparable in ventral disc portions of each genotype suggesting that increased proliferation mostly occurred in the dorsal part of the disc (at least at the time point of R24 h).

Immunohistochemistry

Imaginal discs were dissected from late 3rd instar larvae and stained using standard protocols. Antibodies to the following primary antigens were used: PH3 (Upstate), anti-cleaved Caspase-3 (Cell Signaling), β-GAL (Promega), ELAV and Wg (DHSB). Secondary antibodies were donkey Fab fragments from Jackson ImmunoResearch. Images were taken with either a Zeiss AxioImager or a confocal microscope.

Supporting Information

Figure S1 The JNK activity marker TRE-dsRed is induced in ‘undead’ ey>hid-p35 cells. Shown are (A) wild-type (wt), (B) ey>p35 and (C) ey>hid-p35 eye imaginal discs labeled for dsRed (JNK marker, red in A–C; grey in A–C') and ELAV (photoreceptor neurons, green in A–C; grey in A–C'). Only ey>hid-p35 discs induce TRE-dsRed expression (C, C'; arrow) and disrupt the ELAV pattern (C').

(TIF)

Figure S2 The UAS-dep-RNAi and UAS-drICE-RNAi stocks are functional. Combined expression of UAS-dep-RNAi and UAS-drICE-RNAi stocks suppresses both TUNEL-positive apoptosis (A,B) and eye-ablation of GMR-hid (C,D) suggesting that these stocks contain functional RNAi transgenes targeting dep-1 and drICE.

(TIF)

Figure S3 Several UAS-RNAi transgenes of the JNK pathway suppress GMR-eey. (A) The unmodified GMR-Gal4 UAS-eiger (GMR>eiger) eye ablation phenotype. (B-H) RNAi transgenes targeting the genes indicated above the panels suppress the eye ablation phenotype induced by GMR-Gal4 UAS-eiger (GMR>eiger) suggesting that they are functional.

(TIF)

Figure S4 Inactivation of JNK pathway genes in ey>hid-p35 eye discs does not affect caspase activity. (A) A ey>hid-p35 disc labeled for Cas3* and ELAV. (B) dronc RNAi suppresses Cas3* and normalizes the ELAV pattern in ey>hid-p35 discs. (C-H) RNAi transgenes targeting the indicated JNK pathway components normalize the ELAV pattern, but fail to suppress Cas3* activity in ey>hid-p35 discs suggesting that they suppress AiP downstream of caspase activation.

(TIF)

Figure S5 Rho1 acts upstream of JNK in the ‘undead’ AiP model. (A,A',C,C') ey>hid-p35 discs are characterized by strong puc-lacZ (A,A') and avg (C,C') expression as well as disrupted photoreceptor pattern (ELAV). (B,B',D,D') RNAi targeting Rho1 suppresses puc-lacZ (B,B') and avg (D,D') expression as well as normalizes the ELAV pattern in ey>hid-p35 discs. Caspase activity is not affected suggesting that Rho1 acts downstream of Drone and upstream of JNK.

(TIF)

Figure S6 Egr is required for AiP in a wing model. (A) A control wing disc expressing UAS-Gal4 under nubbin (nub)-Gal4 (nub>p35) control shows normal Wg expression (A') and little to no Cas3* labeling (A'). (B) An experimental AiP disc expressing hid and p35 under nub control (nub>hid-p35) displays strong overgrowth with abnormal Wg pattern (B') and strong Cas3* labeling (B'). Together with (D), these data suggests that nub>hid-p35 is a suitable ‘undead’ AiP model. (C) A nub-Gal4 UAS-p35 (nub>p35) control disc. puc-lacZ expression is detectable at low level. (D) Coexpression of hid and p35 induces strong JNK activity (puc-lacZ) in the enlarged nub domain. (E) RNAi targeting Egr suppresses the overrepresentation of the nub domain, but leaves puc-lacZ intact. This result suggests that EGRF signaling is required for AiP in the wing disc and acts downstream of JNK. (F,G) Control disc expressing Egr RNAi in the nub domain without hid, in the presence (F) or absence (G) of p35. The size of the nub domain is not significantly altered by Egr RNAi compared to (C).

(TIF)

Figure S7 Induction of the JNK activity marker TRE-dsRed in DEα>hid eye imaginal discs. (A–D) hid and GFP expression were temporally induced for 12 h by temperature shift to 30°C during early third instar larval stage as indicated in Figure 6E. dsRed expression (red in A–D; grey in A–D'; see arrows) was monitored at 0 h (A), 6 h (B), 12 h (C) and 24 h (D) recovery after the temperature shift. GFP (green in A–D; grey in A–D') marks the DE domain. Blue is DAPI labeling to outline the discs. dsRed labeling is weakly detectable at R0 h, peaks at 6 h after recovery and fades off at R12 h. At R24 h, it is barely visible. (E) A DEα>GFP control disc at 6 h recovery after the temperature shift, labeled for dsRed (red in E, grey in E'). JNK activity is not induced. GFP expression in (E') is strong. Blue in (E) is DAPI labeling to outline the discs.

(TIF)

Table S1 Chromosomal deficiencies tested in the AiP screen on 2L. Listed are the names of the deficiencies, the extent of the chromosomal deletions and the score in the AiP screen. Green marks suppressors and yellow marks enhancers. Deficiencies marked with * could not be scored, because they caused lethality in the ey>hid-p35 background.

(PDF)

Acknowledgments

We are grateful to our colleagues who have shared their knowledge and reagents, especially Konrad Basler, Dirk Bohmann, Joe Duffy, Michael Galko, Georg Halder, Masayuki Miura, Hyung Don Ryoo, the Bloomington Stock Center in Indiana, and the Developmental Studies Hybridoma Bank in Iowa.

Author Contributions

Conceived and designed the experiments: YF AB. Performed the experiments: YF SW JH VBY GH JLL CEF. Analyzed the data: YF SW AB. Contributed reagents/materials/analysis tools: YF AB. Wrote the paper: AB YF.
References


