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

This material is brought to you by eScholarship@UMMS. It has been accepted for inclusion in University of Massachusetts Medical School Faculty Publications by an authorized administrator of eScholarship@UMMS. For more information, please contact Lisa.Palmer@umassmed.edu.
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*

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 Landerinstitut 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.

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 activated by incorporation 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 (Apa-f1 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
p35. These cells are referred to as ‘undead’ cells. Consequently, expression of p35 in all ‘undead’ cells and concern has been raised about the involvement of Wg and Dpp in ‘genuine’ AiP [26,44,46] suggesting that other signaling pathways are also critical for AiP.

There are many other open questions in the field. For example, although it is well established that Dronc can stimulate JNK activity, the molecular mechanism of this interaction is not known. Furthermore, while JNK is best characterized for its ability to induce apoptosis [52], it is not always known how JNK induces proliferation [50,53]. For example, while in wing imaginal discs, JNK stimulates proliferation through activation of Yorkie, the downstream target of the Hippo growth control pathway, this does not appear to be a mechanism in eye imaginal discs [54,55], the preferred model of this study (see below). This question is also relevant for understanding of tumorigenesis, as for example death receptor signaling by Fas (CD95) can promote tumor growth through JNK-induced proliferation [56]. These considerations stress the necessity of a convenient genetic screening system to identify the genes and mechanisms involved in AiP.

Here, we present and test the feasibility of ‘undead’ and ‘genuine’ genetic models of AiP in eye imaginal discs. We identify additional components in the JNK pathway that mediate the activation of JNK by Dronc. We show that JNK activation occurs in dying cells as well as in neighboring surviving cells depending on the conditions used. We report the results of a pilot screen using the ‘undead’ AiP model that led to the identification of Spi/EGFR signaling as essential component for AiP. Finally, we demonstrate that Spi is at least partially required for regeneration in a ‘genuine’ AiP model of the eye disc.

Results

The ey->hid-p35 model

eyless (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-diRed [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 \textit{ark} genetically modify the AiP phenotype. Heterozygosity of \textit{dronc} and \textit{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 \textit{ark} also suppresses the AiP phenotype to a similar extend (Figure 2C). Therefore, these data demonstrate that the \textit{ey\-hid\-p35} model is sensitive to genetic alterations and extend previous findings that AiP not only requires \textit{dronc}, but also \textit{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 \textit{dcp-1\-drICE} double RNAi (Figure 2D). The RNAi stocks used are functional as \textit{dcp-1\-drICE} double RNAi suppresses \textit{hid} activity in a different apoptotic model, \textit{GMR-hid} (Suppl. Figure S2). In summary, the overgrowth of the \textit{ey\-hid\-p35} model is dependent on the apoptosome.
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 \( \text{ey-hid-p35} \) model. As expected, RNAi targeting \( \text{bsk} \), the JNK ortholog in \( \text{Drosophila} \), 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, \( \text{jun-related antigen (jra)} \) and the Fos ortholog \( \text{kayak (kay)} \), also suppressed the \( \text{ey-hid-p35} \) 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 (hep) and MKK4 (Figure 2F,G). The non-redundant functions of hep and MKK4 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 Traf0) as AiP suppressor (Figure 2F,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 Pvf/PVR, do not suppress AiP (Figure 2F,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 arn mutants or RNAi (Figure 2B,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-eiger, a known inducer of JNK activity causing a strong eye ablation phenotype (Figure 2H) [71,72]. Interestingly, while Traf2 knockdown effectively suppresses GMR-eiger as reported [73], Rho1 RNAi does not (Figure 2F,J). It is possible that Rho1 RNAi disrupts eye development by itself and that may be the reason for the failure to suppress GMR-eiger. However, Rho1 RNAi does not disrupt eye development (Figure 2K). These observations suggest that the role of Rho1 for JNK activation is independent of Eiger which is also consistent with the observation that Eiger knockdown does not suppress AiP (Figure 2F,G). Furthermore, these data raise the possibility that Traf2 serves as an integration point of both Eiger signaling and AiP for JNK activation. For these reasons, we place Rho1 upstream of Traf2 in the AiP pathway (Figure 2G), but there may also be other ways by which Rho1 controls JNK activation.

**Activation of JNK signaling in ‘undead’/dying cells and neighboring, surviving cells**

The lack of a requirement of Eiger/Wengen and Pvf/PVR in our AiP model (Figure 2F,G) may suggest that activation of JNK occurs in dying cells. However, conflicting data have been reported about the location of JNK activity in various AiP models. Initially, JNK signaling was observed in ‘undead’ cells [27]. In a p35-independent regeneration model, it was reported that JNK signaling occurs only in neighboring surviving cells [43]. More recently, JNK activity was reported to be both in dying and neighboring surviving cells [44]. While there are experimental differences between these studies, none of them used a mosaic approach to determine the location of JNK activation. Therefore, to clarify this issue, we re-examined both ‘undead’ and ‘genuine’ AiP models for location of JNK activity.

In a mosaic ‘undead’ model, we expressed hid and p35 in clones in eye and wing discs using a 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 is 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-Gal800 (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 (ts6hRh0), an elevation of puc-lacZ activity was detected in dying cells and neighboring, surviving cells (Figure 3E', F'), dying cells containing puc-lacZ are highlighted by arrows, while surviving cells are marked by arrowheads). This JNK activity was induced during the recovery period, because immediately after hid induction (ts6hRh0), no alteration of puc-lacZ expression was detected (Figure 3D'). However, when hid expression was induced for a long period (16 hours) followed by 6 hours recovery (ts16hRh0), puc-lacZ was strongly down-regulated in dying cells, likely as a result of apoptosis in these cells. Nevertheless, upregulation of puc-lacZ was detected in neighboring surviving cells (Figure 3F', arrowheads). This result is consistent with Bergantinos et al. (2010) [43]. However, the upregulation of puc-lacZ still occurred in GFP+ cells (Figure 3F'', 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'', E'''', 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 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)ED1303 (Table 1) and led to the identification of spi/caspa (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 A’, A”, B’, B”’). 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 (ptcTs). 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), Casp3* (death domain) and β-Gal (puc-lacZ, i.e. JNK activation). The ptc domain is shown as a white, dotted line. Note that the death domain does not completely overlap with the ptc-domain (see for example E’9, E’900 and F9, F900). (C–C”900) A control disc just expressing GFP under the experimental conditions to visualize the normal puc-lacZ pattern (β-Gal). (D–D”900) 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). (E–E”900) An experimental disc that was allowed to recover for 6 hours after a 6 hours pulse of hid expression (ts6hR6h). puc-lacZ expression is induced in many cells both inside (arrows) and outside (arrowheads) of the death domain (E9, E90). However, these cells are present in the ptc domain (GFP; E’9, E’90). An experimental disc that was allowed to recover for 6 hours after a pulse of hid expression for 16 hours (ts16hR6h). Although apoptosis is now strongly induced (F9), it is not detectable in the entire ptc domain (GFP; F’9). 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 (F’9, F”9). Genotypes: (A,B) hs-FLP/UAS-hid; UAS-p35/act–y’>GAL4 UAS-GFP; puc-lacZ/+; (C) ptc-Gal4 tub-Gal80ts/+; UAS-GFP/puc-lacZ. (D–F) UAS-hid/+; ptc-Gal4 tub-Gal80ts/+; UAS-GFP/puc-lacZ. doi:10.1371/journal.pgen.1004131.g003
the hypothesis that the EGFR pathway regulates AiP. Consistently, heterozygosity of Egfr suppresses the ey>hid-p35 phenotype in eye discs (compare Figure 4G−I with Figure 4A,B). We also found that Egfr RNAi suppresses an AiP model in wing imaginal discs (Suppl. Figure S6). Downstream of EGFR, mutant alleles of the Drosophila orthologs of Ras (Dras) and MAPK (rolled (rl)) act as dominant suppressors of ey>hid-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] [26,46].

To further characterize the involvement of Spi/EGFR signaling for AiP, we took advantage of the spi01068 allele which is an enhancer trap insertion of lacZ into the spi gene (spi-lacZ) and can serve as a reporter for spi expression [25]. This analysis is complicated by the fact that this spi allele itself is a dominant suppressor of AiP; about 75% of the ey>hid-p35/spi01068 flies show a weak AiP phenotype, while 25% are not suppressed and still show a moderately strong AiP phenotype (Figure 4E,F,I). Consistently, in about 25% of ey>hid-p35 eye discs (n = 28), we observed a strong induction of β-Gal labeling compared to control discs (Figure 5A,B). This percentage corresponds to the number of heterozygous spi01068 flies which display a moderately strong AiP phenotype (Figure 4E,F,I). The remaining 75% of ey>hid-p35 eye discs heterozygous for spi01068 show a normalization of disc morphology as visualized by ELAV labeling and spi-lacZ expression (Figure 5C). In addition, we found that a target gene of the EGFR pathway, kekkon-1(kek) [76] is induced during AiP (Figure 5D,E,F).

To determine the position of Spi/EGFR signaling in the AiP pathway, we performed epistasis experiments between spi and bsk. Heterozygosity of spi+ dominantly suppresses the adult AiP phenotype of ey>hid-p35 (Figure 4C,D,I). This suppression can also be visualized by the normalization of the ELAV pattern in ey>hid-p35 eye imaginal discs (Figure 5G, compare to Figure 1J). However, despite the normalization of the ELAV pattern, puc-lacZ expression is not reduced in this genetic background (Figure 5G, G′) suggesting that spi acts genetically downstream of bsk. This is further confirmed by the reciprocal experiment in which bsk RNAi completely normalizes the spi-lacZ pattern in ey>hid-p35 background (Figure 3H). bsk RNAi also normalizes the kek-lacZ pattern in ey>hid-p35 background (Figure 5I). The observations suggest that Spi/EGFR signaling acts genetically downstream of bsk activity. Because Spi is a secreted signaling molecule, these findings may imply that EGFR activation occurs in cells adjacent to apoptotic, JNK-activating cells. This assumption is directly confirmed by the observation that kek-lacZ activity, a downstream marker of EGFR signaling, and Cas3* labeling as apoptotic marker do not overlap (Figure 5F, arrows). In summary, these data imply that spi expression occurs downstream of Bsk/JNK activity and that EGFR signaling acts in signal-receiving, proliferating cells.

Characterization of ‘genuine’ AiP in the eye imaginal disc: the DEts>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]. hid expression was spatially restricted to the dorsal half of the eye disc by dorsal eye-Gal4 (DE-Gal4) [77] and controlled by Gal80* [78] by a transient temperature shift (ts) to 30°C for 12 hours (Figure 6E). We refer to this system as DEts>hid. This model also induces GFP to label hid-expressing cells. Before and after the temperature shift, animals were incubated at 18°C (Figure 6E) to inhibit Gal4 activity and therefore hid and GFP expression. Note that although 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 – 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 (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 Cas3*-positive (Figure 6B). 72 hours after the temperature shift (R72 h), the disc has fully recovered in shape and also has a normal photoreceptor pattern as judged by ELAV labeling (Figure 6C). 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 6F; quantified in Figure 6H). The reduction of the GFP signal in the dorsal part (Figure 6C,G) compared to the control disc (Figure 6D) suggests that most of the GFP+ cells have died and have been replaced by new, 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 R72 h, only these cells still show strong 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 1. Deficiencies that modify the ey>hid-p35-induced AiP phenotype as suppressors or enhancers.

<table>
<thead>
<tr>
<th>Suppressors of ey&gt;hid-p35-induced Overgrowth</th>
<th>Chromosomal Location</th>
<th>Enhancers of ey&gt;hid-p35-induced Overgrowth</th>
<th>Chromosomal Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>Df(2L)C144, Df(2L)ED136</td>
<td>22F4-23A2</td>
<td>Df(2L)ED123</td>
<td>22D1-22D3</td>
</tr>
<tr>
<td>Df(2L)ED206, Df(2L)US17</td>
<td>23C4-23C5</td>
<td>Df(2L)BSC6</td>
<td>26D3-26E1</td>
</tr>
<tr>
<td>Df(2L)Exel7014, Df(2L)BSC28</td>
<td>23C3-23C5</td>
<td>Df(2L)BSC6</td>
<td>26D3-26E1</td>
</tr>
<tr>
<td>Df(2L)BSC31</td>
<td>23E5-23F3</td>
<td>Df(2L)ED508</td>
<td>28C1-28C4</td>
</tr>
<tr>
<td>Df(2L)TW137</td>
<td>?</td>
<td>Df(2L)ED611</td>
<td>29B2-29C3</td>
</tr>
<tr>
<td>Df(2L)ED1303, Df(2L)ED1272</td>
<td>37F2-38A2</td>
<td>Df(2L)Exel7048</td>
<td>31E3-31F4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Df(2L)ED1050</td>
<td>35C1-35D1</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Df(2L)Exel7080</td>
<td>38F5-39A2</td>
</tr>
</tbody>
</table>

The indicated chromosomal location is the smallest overlap of overlapping deficiencies. Df(2L)TW137 is marked with a "?" because other overlapping deficiencies do not suppress AiP (see Suppl. Table S1) indicating that the Df(2L)TW137 chromosome carries a suppressor mutation independent of the deficiency.

doi:10.1371/journal.pgen.1004131.t001

Genetic Models of Apoptosis-Induced Proliferation
moderate phenotype (B). (C–H) Heterozygosity of overgrowth of the head cuticle (A), while the remaining 50% display a bristles. (A,B) About 50% of heterozygotes are not shown here. Arrows indicate ectopic ocelli or head cuticles scored in different categories. Completely suppressed occasionally observed. (A–H) Representative pictures of eyes was almost normal with very few ectopic ocelli or bristles three categories, severe, moderate and weak. Flies were scored as Hid-p35

Second, we determined if bsk is genetically required for tissue regeneration in the DE”>hid model. We used the photoreceptor pattern (ELAV) as a marker to reveal disc outline and thus assess the degree of regeneration. Control discs (DE”>hid) at R72 h had completely regenerated (Figure 7A; n = 50). However, if bsk was inactivated by RNAi during the apoptosis-inducing phase (Figure 6E), about 35% (9 of 25 discs) of the discs show incomplete regeneration (Figure 7B). The incomplete regeneration after bsk RNAi is weak, presumably because the 12 h down-regulation of bsk during the temperature shift is not sufficient to completely remove Bsk activity. It is also possible that Bsk is resynthesized quickly during the recovery period. Nevertheless, the incomplete regeneration after bsk RNAi suggests that Bsk is at least partially required for tissue regeneration after DE”>hid-induced tissue loss.

Next, we examined whether Egr/EGFR signaling is activated in the DE”>hid model. spi-lacZ expression is induced in the ablated GFP-expressing dorsal domain of the disc compared to controls (Figure 7F,F’,G,G’). kck-lacZ as EGR signaling marker is also strongly induced in the dorsal domain compared to controls (Figure 7H,H’,L,L’; arrow).

To determine if spi is genetically required in the DE”>hid regeneration assay, we inactivated it by RNAi during the 30°C temperature shift, following the protocol in Figure 6E. In a control experiment, because spi is required for photoreceptor differentiation posterior to the morphogenetic furrow [79,80], we tested if a 12 h spi RNAi treatment followed by 72 h recovery (R72 h) affects normal photoreceptor differentiation. However, eye discs treated in this way have a normal ELAV pattern (Figure 7C,C’; n = 20). After this control experiment, we tested for a genetic requirement of spi for regeneration of lost tissue due to hid expression. Strikingly, the regeneration response as judged by ELAV labeling was partially impaired when spi was inactivated by RNAi during hid induction (Figure 7D,D’; arrow). All experimental discs (n = 30) showed incomplete regeneration. The regeneration is only weakly affected, likely because spi is inactivated by RNAi only during the 30°C pulse during hid expression (Figure 6E) and is likely restored soon after reducing the temperature to 18°C. Nevertheless, in a heterozygous spi condition, the discs also incompletely regenerated after DE”>hid treatment (Figure 7F,F’; N = 20). In summary, because spi RNAi and spi heterozygosity cause a partial failure to regenerate, these data imply a requirement of spi for regeneration in the ‘genuine’ DE”>hid AiP model. Furthermore, these data support the notion that genetic screening using the simpler ‘undead’ AiP model can lead to identification of genes that may also have important roles for regeneration in ‘genuine’ AiP.

### 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 'undeath' domain [60]. What makes these cells move is unknown, but an interesting avenue for further research in the future.

**Requirement of bsk and spi for regeneration in the ‘genuine’ AiP model DE”>hid**

Because JNK activity is essential for ‘undead’ AiP (Figure 2E), we examined a requirement of bsk in the ‘genuine’ (P35-independent) DE”>hid model. First, we examined if JNK activity is induced in the DE”>hid model. Consistent with the ‘genuine’ AiP models in the wing [42–44], this was indeed observed. TRE-dsRed as marker of JNK activity [59] peaked at 6 h after recovery (R6 h) and is still detectable at R12 h (Suppl. Figure S7B,C). It is mostly gone after 24 h recovery (Suppl. Figure S7D). TRE-dsRed is confined to the GFP area, i.e. in the death domain (Suppl. Figure S7B,C).

Figure 4. Suppression of ey>hid-p35 by spi and Egrf inactivation. 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 Egrf 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, spi1066 and Egrf2 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, egrf, 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.1004131.g004
Figure 5. Epistasis analysis of spi and bsk. Arrowheads indicate the morphogenetic furrow (MF) which separates the anterior (left) from the posterior eye tissue visualized by ELAV labeling. (A) spi-lacZ pattern (β-Gal; red in A; gray in A’) in ey->p35 control discs. Note there is little expression anterior to the MF. (B,C) Because the spi-lacZ allele (spi<sup>100</sup>) is a suppressor of ey->hid-p35 adult overgrowth phenotype (Figure 4I), there is variation in the β-Gal pattern. About 25% of the eye discs show strong induction of 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 β-Gal and ELAV pattern in ey->hid-p35 larvae (C,C’). This ratio corresponds to the suppression of the adult overgrowth phenotype (Figure 4I). (D,E) Strong induction of kek-lacZ (β-Gal; red in D,E; gray in D’,E’) in ey->hid-p35 eye discs (E; arrows) compared to ey->p35 control discs (D). (F,F’) kek-lacZ (β-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 spi normalizes the eye field (ELAV, green), but does not suppress ectopic puc-lacZ expression (β-Gal; red in G, gray in G’) in ey->hid-p35 eye discs (arrows, compare to Figure 1J). Dotted white lines outline the region anterior to the MF. (H) Expression of bskRNAi in ey->hid-p35 discs normalizes the eye field (ELAV, green) and suppresses ectopic kek-lacZ expression (β-Gal; red in I, gray in I’; compare to E). The analysis in G, H and I strongly suggests that spi acts genetically downstream of bsk.

doi:10.1371/journal.pgen.1004131.g005

Figure 6. Characterization of ‘genuine’ AIP in the eye imaginal disc: the DE<sup>ts</sup>-hid model. hid expression was under control of dorsal eye-(DE-)Gal4 and tub-Gal80<sup>ts</sup> (DE<sup>ts</sup>-hid). A temperature shift (ts) to 30°C for 12 h during 2<sup>nd</sup> larval stage induced hid expression (E). After the indicated recovery period (R), discs were labeled for GFP (to visualize the DE expression domain), Cas3* (the death domain) and ELAV (to outline the shape of the disc). (A–C) DE<sup>ts</sup>-hid experimental discs. 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 GFP<sup>+</sup> cells have been replaced by new GFP<sup>−</sup> cells. Arrows highlight a patch of cells that are moving to the center of the disc. (D) A control disc 72 h after DE<sup>ts</sup>-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 DE<sup>ts</sup>-hid-induced tissue ablation followed by recovery periods. (F,F’,F”G,G, G’) PH3-labeling of control (DE<sup>ts</sup>-GFP; F,F’) and experimental discs (DE<sup>ts</sup>-hid, G,G’). GFP marks the outline of the 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 \textit{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 DEts>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 [86,87]. 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 stressed 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 the necessity to perform unbiased genetic screens aimed at identifying the genes and mechanisms involved in AiP.

Materials and Methods
Fly stocks and genetics
The following mutants and transgenic stocks were used: drone129; eyTS108; ptc-Gal4, eyTS108; EgfrF2; ra1AC40; n59a, ey-Gal4; ptc-Gal4; DE-Gal4; tub-Gal80f/+; UAS-p35; UAS-hid; UAS-GFP, wg-lacZ; pac-lacZ; khh-lacZ; spi-lacZ = spi102a; TRE-d-Rot; GMR-hid; GMR-Gal4 UAS-erg. 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, ptc-Gal4 tub-Gal80f/+; UAS-p35; UAS-hid; UAS-GFP, wg-lacZ; pac-lacZ; khh-lacZ; spi-lacZ = spi102a; TRE-d-Rot; GMR-hid; GMR-Gal4 UAS-erg.

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-p35/uac>y->Gal4 UAS-GFP; pac-lacZ+/.

Tissue ablation using ptc129>hid and DEts>hid
Larvae of genotype UAS-hid+/; ptc-Gal4 tub-Gal80f/+; UAS-GFP/+ (Figure 3) and UAS-hid+/; UAS-GFP+/; DE-Gal4 tub-Gal80f/+ (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 DEts->hid model

Two rounds of experiments (is12hR24h, at least 20 discs were analyzed each round) were done for both DEts->GFP (control) and DEts->hid. Increase of PH3-positive cells in dorsal eye disc portions of DEts->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 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 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–G; 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-dp-1RNAi and UAS-dICE-RNAi stocks are functional. Combined expression of UAS-dp-1RNAi and UAS-dICE-RNAi stocks suppresses both TUNEL-positive apoptosis (A,B) and eye-ablation of GMR->lacZ (C,D), suggesting that the stocks contain functional RNAi transgenes targeting dp-1 and dICE. (TIF)

Figure S3 Several UAS-RNAi transgenes of the JNK pathway suppress GMR-eGFP. (A) The unmodified GMR-Gal4 UAS-eGFP (GMR>eGFP) eye ablation phenotype. (B-H) RNAi transgenes targeting the genes indicated above the panels suppress the eye ablation phenotype induced by GMR-Gal4 UAS-eGFP (GMR>eGFP) 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 ApI 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 pac-lacZ (A,A’) and ugc (C,C’) expression as well as disrupted photoreceptor pattern (ELAV). (B,B’,D,D’) RNAi targeting Rho1 suppresses pac-lacZ (B,B’) and ugc (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 Egfr is required for AiP in a wing model. (A) A control wing disc expressing UAS-p35 under nanbim (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. pac-lacZ expression is detectable at low level. (D) Coexpression of hid and p35 induces strong JNK activity (pac-lacZ) in the enlarged nub domain. (E) RNAi targeting Egfr suppresses the overrepresentation of the nub domain, but leaves pac-lacZ intact. This result suggests that EGFR signaling is required for AiP in the wing disc and acts downstream of JNK. (F,G) Control disc expressing Egfr 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 Egfr RNAi compared to (C). (TIF)

Figure S7 Induction of the JNK activity marker TRE-dsRed in DEts->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 DEts->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
