Necrosis-induced apoptosis promotes regeneration in *Drosophila*

wing imaginal discs

Jacob Klemm, Michael J. Stinchfield, Robin E. Harris

School of Life Sciences, Arizona State University, Tempe, AZ 85287-4501

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Corresponding Author Details:

Robin Harris,

Arizona State University

427 E Tyler Mall LSE 229

Attn: Dr. Rob Harris, LSE 333

Tempe

AZ 85287-4501

Robin.Harris@ASU.edu

(480)965 7543

Abstract

Regeneration is a complex process that requires a coordinated genetic response to tissue

loss. Signals from dying cells are crucial to this process and are best understood in the

context of regeneration following programmed cell death, like apoptosis. Conversely,

regeneration following unregulated forms of death such as necrosis have yet to be fully

explored. Here we have developed a novel method to investigate regeneration following

necrosis using the *Drosophila* wing imaginal disc. We show that necrosis stimulates

regeneration at levels comparable to that of apoptosis-mediated cell death, and activates

a similar response at the wound edge involving local JNK signaling. Unexpectedly

however, necrosis also results in significant apoptosis far from the site of ablation, which

we have termed necrosis-induced apoptosis (NiA). This apoptosis occurs independent of

changes at the wound edge and importantly does not rely on JNK signaling. Furthermore,

we find that blocking NiA inhibits blastema formation and subsequently limits

regeneration, suggesting that tissues damaged by necrosis activate programmed cell

death at a distance from the injury to promote regeneration.

Introduction

Apoptosis has a fundamental role in shaping organisms during development and in maintaining tissue homeostasis (Fuchs and Steller 2011; Suzanne and Steller 2013). This vital cellular process acts to counter infection, suppress tumor formation and promote recovery from damage (Fogarty and Bergmann 2017; Hacker 2018; Wong 2011). These events can occur because dying cells release signals that act on surrounding cells, leading to different cellular outcomes depending on the context and on the nature of the signal (Fogarty and Bergmann 2015; Fuchs and Steller 2015; Perez-Garijo and Steller 2015; Su 2015). Successful regeneration following injury can also depend on this apoptotic signaling, which has been shown to regulate various aspects of recovery including morphogenesis, inflammation and tissue regrowth (Bergmann and Steller 2010; Perez-Garijo and Steller 2015; Vriz et al. 2014). In many organisms, factors released from dying cells stimulate the proliferation of adjacent cells as a replacement mechanism (Chera et al. 2009; Li et al. 2010; Pellettieri et al. 2010; Su 2015; Tseng et al. 2007; Vriz et al. 2014). This specialized form of compensatory proliferation is known as apoptosis-induced proliferation (AiP) (Fogarty and Bergmann 2017), in which a number of mitogens, including WNTs, TGFβ, EGF and Hedgehog, are released from dying cells as part of this mechanism (Fogarty and Bergmann 2017; Fuchs and Steller 2015). Upstream factors that lead to their production, such as JNK signaling and the activation of caspases, have also been described (Fogarty and Bergmann 2017; Pinal et al. 2019). Conversely, apoptosis can also promote the death of surrounding cells, a process known as apoptosis-induced apoptosis (AiA), (Fogarty and Bergmann 2015; Perez-Garijo et al. 2013; Su 2015). This process also relies on JNK signaling and possibly represents a

mechanism to ensure the proper coordination of cell death (Perez-Garijo et al. 2013).

Signals from dying cells can also result in non-autonomous protection from cell death,

ensuring the preservation of neighboring cells after injury (Bilak et al. 2014). Thus, cell

death can strongly influence the behavior of surrounding cells and consequently regulate

the ability of a tissue to recover from damage.

Evidence that signals from apoptotic cells impact surrounding tissues first originated from

studies of the *Drosophila* wing imaginal disc, a larval epithelial tissue that forms the adult

wing (Huh et al. 2004; Perez-Garijo et al. 2004; Ryoo et al. 2004). The wing disc has been

extensively characterized as a model for growth and development, and for its significant

capacity to regenerate (Beira and Paro 2016; Hariharan and Serras 2017; Worley et al.

2012). Much of our understanding of imaginal disc regeneration has been through the

use of GAL4/UAS-based genetic ablation tools, in which tissue-specific apoptosis is

induced by a temperature change, permitting the study of regeneration *in situ* (Fox et al.

2020). However, these ablation tools rely on activating the apoptotic machinery to induce

damage, limiting our ability to explore other types of cell death. One such example is

necrosis, the rapid and disordered death of a cell characterized by the loss of membrane

integrity and release of cytoplasmic contents into the surrounding tissue (Fuchs and

Steller 2015). A number of factors released by cells undergoing necrosis have been

identified and characterized as signaling molecules that might influence the behavior of

surviving tissues, although their role in wound recovery and regeneration is not well

understood. In humans, necrosis can occur in all types of tissues and results from

environmental insults like burns or frostbite, microbial infection (Bonne and Kadri 2017;

Hakkarainen et al. 2014), and from common ischemic events such as heart attacks and

strokes (Konstantinidis et al. 2012; Radak et al. 2017; Yuan 2009). Various inherited and

congenital conditions can also lead to necrosis, including joint disorders and sickle cell

anemia (Masi et al. 2007; Milner et al. 1991). Thus, a better understanding of how a tissue

responds to damage could advance therapeutic methods to improve healing and

regeneration in a large number of human disease and injury contexts.

Here we have developed a method to induce necrotic cell death in the wing imaginal disc

and used it to characterize the genetic response to necrosis compared to apoptosis. Our

results show that wing discs can regenerate following necrosis but do so by inducing

extensive JNK-independent apoptosis at a distance from the site of injury. Importantly,

we demonstrate that this necrosis-induced apoptosis is required for proper blastema

formation and efficient regeneration.

Materials and Methods

***Drosophila* stocks and crosses**

Flies were cultured in conventional dextrose fly media at 25°C at 12 hr light-dark cycles.

The recipe for dextrose media contains 9.3 g agar, 32 g yeast, 61 g cornmeal, 129 g

dextrose, and 14 g tego in 1 L distilled water. Complete fly line details and RRIDs are

available in the Reagent Table. The lines used as ablation stocks are as follows: *hsflp;*

hsp65; R85E08-DBD, DVE>>Gal4 (DC^{NA}), *hsflp; lexAop-GluR1^{Lc}, hsp65; R85E08-DBD,*

DVE>Gal4/S-T (DC^{GluR1}), *hsflp; lexAOp-GluR1^{Lc}, hsp65/CyO; R85E08-DBD/TM6C, sb*

(DC^{GLuR1} *no Gal4*), *hsflp; lexAop-hep^{CA}, hsp65; R85E08-DBD, DVE>>Gal4/S-T*

(DC^{hepCA}), and *hsflp; lexaOp-rpr, hsp65/CyO, R85E08-DBD, DVE>>Gal4* ($DC^{rpr,}$ Harris et

al., 2020). The following stock was generated for this study: *UAS-miRHG; PCNA-GFP*.

The stock DR^{wnt} was used as a marker for early regeneration (Harris et al., 2016). The

following stocks were obtained from Bloomington Drosophila Stock Center: *UAS-y^{RNAi}*

(64527), *UAS-p35* (5073), *PCNA-GFP* (25749), *UAS-bsk^{RNAi}* (53310), *UAS-bsk^{DN}* (9311),

UAS-egr^{RNAi} (58993), *puc^{A251}* (11173), *hep^{r75}* (6761), *UAS-hepCA* (58981), *nos-*

PhiC31:int; su(Hw)attP5 (32231). *CyclinE-disc-GFP* was a gift from the Wei Du lab. *UAS-*

grnd^{RNAi} was a gift from the Bilder lab at UC Berkeley. *UAS-miRHG* and *UAS-nlsGFP;*

egr-Gal4 were gifts from the Hariharan lab at UC Berkeley. *UAS-GluR1^{Lc8}* (Liu et al. 2014)

was obtained from the Xie lab at Stowers Institute.

Generation of *lexAOp-hep^{CA}* and *lexAOp-GluR1^{LC}* flies

To generate *lexAop-hep^{CA}*, the coding region for *hep^{CA}* was cloned from *UAS-hep^{CA}* stock

and subcloned into the *lexAop-GFP* vector following excision of GFP, using XhoI and XbaI

sites. *LexAop-GluR1^{LC}* was generated by cloning out the *GluR1^{LC}* coding region from

UAS-GluR1^{Lc8} and subcloning it into the *lexAop-GFP* vector following excision of the GFP,

using XhoI and XbaI sites. The *lexAop-hep^{CA}* and *lexAop-GluR1^{LC}* constructs were

sequence verified and inserted into the Su(Hw)attP5 landing site via PhiC31 insertion.

Transgenic flies were generated by embryo injections performed by BestGene, Inc.

Ablation Experiments

DUAL Control experiments were performed essentially as described by Harris et al. 2020.

Experimental crosses were cultured at 25°C and density controlled at 50 larvae per vial.

Larvae were ablated at day 3.5 or 4.5 of development (84 and 108 hours after egg lay

(AEL), respectively) by placing vials in a 37°C water bath for 45 minutes followed by a

return to 25°C. The non-ablating version of DUAL Control (DC^{NA}) was used as a control

while *UAS-y^{RNAi}* was used as a control for RNAi experiments. Unless stated otherwise,

all wing disc images taken were from larvae ablated on day 3.5 that had recovered for 18

hours.

Regeneration Scoring and Wing Measurements

For each experiment two sets of larvae were heat shocked, one at day 3.5 and one at

day 4.5 of development, reflecting times of high and low regenerative capacity,

respectively. Larvae were left to pupariate into adults, whose wings were scored and

measured. The left wing of each adult fly was used for binning into categories for

regeneration scoring. For measurements wings were mounted in Permount solution and

photographed using a Zeiss Discovery.V8 microscope and measured using the Image J

software. Male and female adults were measured separately, to account for sex

differences in wing size, using a reproducible measuring protocol that excludes the

variable hinge region of the wing (details of measuring protocol available on request).

Statistics were performed using GraphPad Prism 9.0.

Immunohistochemistry

Unless otherwise noted, early L3 larvae were dissected 18 hours after the heat shock,

while regeneration was still ongoing. Larvae were dissected in PBS followed by a 20-

minute fix in 4% paraformaldehyde in PBS. After 3 washes in 0.1% PBST (Triton-X),

larvae were washed in 0.3% PBST and then blocked in 0.1% PBST with 5% NGS for 30

minutes. Primary staining was done overnight at 4°C, while secondary staining was done

for 4 hours at room temperature. The following primary antibodies were obtained from the

Developmental Studies Hybridoma Bank: mouse anti-Nubbin (1:25), mouse anti-Wg

(1:100), Mouse anti-Mmp1 C-terminus (1:100), Mouse anti-Mmp1 catalytic domain

(1:100), mouse anti-LacZ (1:100), and rat anti-DE-Cahdherin (1:100). Rabbit anti-Dcp1

(1:1000) was obtained from Cell Signaling Technologies, and chick anti-GFP (1:2000)

was obtained from Abcam. The secondary anti-Chick 488 antibody was obtained from

Abcam as well. Other secondary antibodies, anti-rabbit 647, anti-rat 647, and anti-mouse

555 were obtained from Invitrogen. All secondary fluorophore-conjugated antibodies were

used at 1:500. Images were obtained on a Zeiss AxioImager.M2 with ApoTome. For each

experiment at least 15 discs were analyzed prior to choosing a representative image.

Images were processed using Affinity Photo and Affinity Designer.

Propidium Iodide staining and TUNEL Assay

Propidium iodide (PI) staining was achieved by incubating freshly dissected wing imaginal discs in Schneider's Media with 15µM PI for 10 minutes, followed by several washes in PBS and immediately mounting and imaging. Samples were imaged on a Zeiss AxioImager.M2 with ApoTome. The TUNEL assay was performed with the ApopTag Red *In Situ* Apoptosis Detection Kit (Millipore, S7165). Dissected larvae were fixed in 4% paraformaldehyde, followed by a 10-minute wash in 75µL equilibration buffer. Discs were then submerged in 55µL working strength TdT enzyme for 3 hours at 37°C. The reaction was stopped by adding 1mL stop/wash buffer and incubating for 10 minutes at room temperature, followed by 3 washes in PBS. Primary staining was done by incubating 65µL of the anti-digoxygenin rhodamine overnight at room temperature.

Quantification and Statistical Analysis

Adult wing measurements were gathered using the ImageJ software. GraphPad Prism 9.0 was used for statistical analysis and graphical representation. Graphs depict the mean of each treatment, while error bars indicate the 95% confidence interval. All experiments were repeated twice. The n for each experiment is indicated in the figure legends and Method Details. A One-Factor ANOVA was used to determine statistical significance, while a Tukey's multiple comparisons test was chosen for post-hoc testing.

Data and Reagent Availability

Strains and plasmids are available upon request, and details of stocks and reagents used in this study are available in the Reagent Table. The authors affirm that all data

necessary for confirming the conclusions of the article are present within the article,

figures, and tables.

Results

A genetic method to induce necrotic injury in the wing imaginal disc

To study the response to necrosis we developed a method to induce damage in the larval

wing disc by adapting a system we previously established to study regeneration called

DUAL Control (Harris et al. 2020). This system utilizes a split version of the bacterial

LexA/lexAOp transcriptional regulator to transiently express a pro-apoptotic gene in the

distal wing tissue under the control of the *spalt* (*salm*) enhancer following a short heat

shock (Figure 1A). This apoptosis stimulates regeneration over the subsequent ~24 to 48

hr, which can be quantitatively assessed by examining the degree to which the distal tip

of the wing is present in the adult fly (Harris et al. 2020). We previously used *lexAOp-*

driven *reaper* (*rpr*) to induce cell death (Harris et al. 2020), and have since established

another apoptosis-promoting transgene, *lexAOp-hep^{CA}*, a constitutive form of the JNK

kinase *hemipterous* (Adachi-Yamada et al. 1999). To study necrosis, we used the GluR1

protein, a murine glutamate receptor that regulates Ca^{2+} ion entry into a cell (Kohda et al.

2000). A characterized allele of this ion channel (*GluR1^{LC}*) confers constitutive activity,

leading to Ca^{2+} influx, osmotic swelling and catastrophic death of the cell (Kohda et al.

2000; Yang et al. 2013). We generated *lexAOp-GluR1^{LC}* and used it to build a version of

DUAL Control that expresses *GluR1^{LC}* in the developing wing disc (Figure 1A).

To test our ability to induce damage using this system, we heat shocked larvae bearing

DUAL Control expressing *GluRl^{LC}* alongside discs ablated by *rpr* or *hep^{CA}* (hereafter

DC^{GluRl}, *DC^{rpr}* and *DC^{hepCA}*), using the pouch marker *nubbin* (*nub*) and the cell adhesion

marker *DE-cadherin* (*DE-cad*) to evaluate disc integrity (Figure 1B). Ablation with *DC^{GluRl}*

leads to a loss of tissue in the *salm* domain, shown by an absence of both markers (Figure

1C), which is comparable to the loss of tissue resulting from ablation by DC^{rpr} (Figure 1D)

and DC^{hepCA} (Figure 1E). We next examined the degree to which wing discs can

regenerate following DC^{GluR1} ablation compared to DC^{rpr} and DC^{hepCA}. Regeneration was

assayed by appearance of the adult wing, scored for the presence of the distal wing tip

(Figure 1F and 1G) and measurement of the total wing area (Figure 1H). Ablation by DC^{rpr}

and DC^{hepCA} in early L3 (84 hr after egg deposition, AED) leads to significant regeneration,

illustrated by both wing scoring and area (Figure 1G and 1H). Ablation by DC^{GluRI} results

in comparable levels of ablation and regeneration (Figure 1G and 1H). The ability of discs

to regenerate is known to decline with developmental maturity from early to late L3 (Harris

et al. 2016; Harris et al. 2020). Ablation by each method in late L3 (108 hr AED) results

in a similar loss of distal wing tissue (Figure 1G and H). Together, these data show that

DC^{GluRI} can ablate the wing disc and induce regeneration comparable to apoptosis-based

methods.

To characterize how DC^{GluRI} induces damage we examined ablated discs for different cell

death markers. The loss of tissue in DC^{GluRI} coincides with strong propidium iodide (PI)

staining (Figure 2A, arrowhead), which labels cells with compromised membranes such

as those undergoing necrosis (Wlodkowic et al. 2011). Conversely, PI staining of DC^{hepCA}

ablated discs shows only weak and sporadic PI (Figure 2B). As activated caspases are a

hallmark of apoptosis rather than necrosis, we also stained ablated discs for the cleaved

caspase DCP1. As expected, ablation with DC^{rpr} or DC^{hepCA} yields a strong DCP1 signal

concentrated within the *salm* domain (Figures 2E and 2F). Sporadic caspase-positive

cells are seen outside of the ablation domain in all discs, likely as a result of the stress of

heat shock used to activate ablation (Figure 2C). Surprisingly, discs ablated with DC^{GluRI}

also have significant levels of DCP1 (Figure 2D). However, most of this staining is

observed in the lateral wing pouch at a distance from the ablated tissue (Figure 2D,

arrowheads). These DCP1 positive cells are clearly separable from the dying cells in the

salm domain. They are also not a result of dying cells moving away from the site of injury,

as a *lexAop-GFP* transgene that labels ablated cells fails to mark the caspase positive

cells outside of the *salm* domain (Figures 2G and 2H, arrowheads). This is in contrast to

DC^{hepCA} discs in which GFP and DCP1 almost entirely overlap (Figure 2I and 2J). Thus,

the observed apoptosis does not occur in cells killed by *GluRI* but is instead induced in

neighboring cells.

In addition to promoting apoptosis, caspases can perform other cellular functions in

imaginal discs unrelated to cell death (Su 2020). To examine whether the detected

caspase activity is related to cell death we also performed a TUNEL assay, which reveals

strong staining in the caspase positive cells found outside of the *salm* domain in DC^{GluRI}

discs (Figure 2K, arrowheads). This is consistent with *GluRI*-induced caspase activity

leading to cell death, as in DC^{rpr} and DC^{hepCA} ablated discs (Figure 2L and data not

shown). We also observed a separate weaker TUNEL signal in *GluRI* expressing cells

within the *salm* domain indicative of DNA fragmentation (Figure 2K, open arrowhead),

which has previously been described in necrotic cells (Grasl-Kraupp et al. 1995).

Together, these results demonstrate that ablation with DC^{GluR1} leads to tissue loss and

stimulates regeneration, but also unexpectedly activates widespread apoptosis in the

surrounding cells at a distance from the injury.

Tissue loss via DC^{GluRl} ablation occurs independent of caspase activity

To understand if the non-autonomous apoptosis observed in DC^{GluRl} discs contributes to

tissue loss, or alternatively is a consequence of it, we used the baculoviral caspase

inhibitor P35 to block apoptosis in the entire pouch (Hay et al. 1994). DUAL Control

permits the expression of UAS-driven transgenes in the wing pouch independent of

ablation under the control of a flip-out GAL4 (*DVE>>GAL4*), which is initiated by the same

heat shock that triggers ablation and persists throughout the subsequent regeneration

period (Figure 1A', (Harris et al. 2020). To test P35 in the DUAL Control system, we first

blocked apoptosis in *rpr* ablated discs using *UAS-p35* ($DC^{rpr}>>p35$). These discs have an

intact pouch epithelium, shown by *nub* and *DE-cad* staining (Figure 3A), and lack TUNEL

staining (Figure S1A). DCP1 is still detected in $DC^{rpr}>>p35$ discs although the intense

punctate staining is replaced by a diffuse cytoplasmic signal (Figures 3C and 3D), which

has been reported previously when caspase activity is inhibited by P35 (Perez-Garijo et

al. 2013). Conversely, P35 is unable to prevent tissue loss resulting from *GluRl*

expression, indicated by the absence of *nub* and *DE-cadherin* in the pouch (Figure 3B)

and presence PI staining in the *salm* domain (Figure 3G). The appearance of the DCP1

staining in $DC^{GluRl}>>p35$ discs is also diffuse (Figures 3E and 3F) similar to that of

$DC^{rpr}>>p35$, while TUNEL staining in the lateral pouch is now absent (Figure 3H),

indicating that the apoptosis in these regions is being blocked. However, the weak TUNEL

signal within the cells of the *salm* domain is still observed (Figure 3H, open arrowhead).

These data suggest that inhibition of caspase activity cannot block cell death or tissue

loss caused by GluRI within the *salm* domain.

In agreement with the observed disc phenotypes, blocking apoptosis with P35 in *rpr*

ablated discs results in full sized adult wings, shown by scoring and wing area

measurements of both early and late L3 ablated organisms (Figures 3I, 3K, 3K' and 3M).

By contrast, blocking apoptosis in *GluRI* ablated discs does not prevent tissue loss, as

adult wings that develop from DC^{GluRI}>>*p35* discs have comparable phenotypes to discs

ablated in the absence of P35 (Figures 3J, 3L, 3L' and 3M). Together these observations

suggest that GluRI can kill cells independent of caspase activity, and that the apoptotic

cells seen at a distance from the wound are a consequence of this tissue loss rather than

being required for it. Thus, we refer to DC^{GluRI}-induced tissue loss as necrotic ablation,

and the non-autonomous caspase-positive cell death in the surrounding tissue as

necrosis-induced apoptosis (NiA).

In our adult wing assays we noted a distinct category of wings from DC^{GluRI}>>*p35* animals

that are poorly patterned and have increased blistering and folding (Figure S1B and S1C).

This phenotype also occurs in DC^{hepCA}>>*p35* discs (Figure S1C). Blocking caspase

activity with P35 in cells undergoing apoptosis can produce undead cells that continue to

express mitogenic genes like *wg* and *dpp* downstream of JNK signaling, leading to

tumorous overgrowth of the surrounding tissue (Martin et al. 2009; Perez-Garijo et al.

2004; Ryoo et al. 2004). Indeed, DC^{hepCA}>>*p35* have significant ectopic *wg* expression in

the ablation domain overlapping the diffuse DCP1 compared to ablation in the absence

of P35 (Figure S1D and S1E). We hypothesized that blocking apoptosis in $DC^{GluRI}>>p35$

ablated discs might result in undead cells, which is responsible for the overgrown and

poorly patterned adult wing phenotype. However, *wg* expression appears mostly

unchanged in the pouch cells surrounding the wound in $DC^{GluRI}>>p35$ discs (Figure S1F),

as does *Dpp* shown by a *Dpp-lacZ* reporter (data not shown). These data suggest that

undead NiA cells do not activate the same genetic pathways as undead cells generated

by directly activating apoptosis in the presence of P35. However, our experiments do not

rule out other mitogens being produced that might lead to the observed overgrowth

phenotype of $DC^{GluRI}>>p35$ wings.

NiA and wound edge apoptosis originate separately

To investigate the origin and timing of the NiA seen in DC^{GluRI} discs we performed a time

course of ablation and regeneration (Figure 4). In order to observe the formation of the

wound we took advantage of the DR^{WNT} transgene, a damage-specific fluorescent

reporter of WNT expression, which is activated upon ablation and represents one of the

earliest signaling events in disc regeneration (Figure 4A-4F)(Harris et al. 2016). DR^{WNT}

expression starts to become apparent at the wound edge 6 hr post-ablation with GluRI

(Figure 4B), while most apoptotic cells in this region become obvious at around 12 hr

(Figure 4C, arrowhead). NiA populations are still not observed at this timepoint, but only

occur at 18 hr post ablation subsequent to the appearance of wound edge apoptosis and

DR^{WNT} activity (Figure 4D, arrowheads). The NiA persists as regeneration proceeds

(Figure 4E), and by 48 hr, when DR^{WNT} expression is diminished, the DCP1-positive

cellular debris appears to be pushed dorsally and ventrally as a result of pouch growth

(Figure 4F). At this time point the pouch is fully restored, indicated by *nub* expression

(Figure 4G). Interestingly, DR^{WNT} activity is never observed beyond the wound edge, and

does not occur in NiA cells. Thus, the time course shows that formation of NiA is not only

spatially distinct from the wound edge apoptosis and damage associated signaling shown

by DR^{WNT}, but is also temporally separated from it. These observations suggest that these

two populations might arise from different mechanisms.

NiA is independent of JNK signaling

The DR^{WNT} reporter used in the time course is directly activated by JNK signaling (Harris

et al. 2016). Since DR^{WNT} expression is restricted to the wound edge, and JNK signaling

is a key pathway that regulates both apoptosis and proliferation in response to damage

(Pinal et al. 2019), we next evaluated JNK signaling in DC^{GluRI} ablated discs. Using a

reporter for AP-1 activity (*AP-1-GFP* (Chatterjee and Bohmann 2012) we found that JNK

signaling is present only in wound edge cells and not in cells undergoing NiA (Figure 5A),

consistent with the DR^{WNT} reporter expression. Examination of the JNK target genes *puc,*

wg and *Mmp1* supports these results (Figures 5B, 5C and 5D), suggesting that necrotic

ablation leads to JNK upregulation and low levels of apoptosis at the wound edge, but

induces NiA at a distance without activating JNK.

To test whether NiA does indeed occur independent of JNK, we investigated how altering

different elements of the JNK pathway might influence either the wound edge or NiA

populations in DC^{GluRI} ablated discs. Knockdown of the JNK kinase *hep* using RNAi

reduces the expression of the JNK target *Mmp1* but does not strongly alter apoptosis at

the wound edge (Figure 5E). Importantly, NiA cells are still observed in the absence of

hep (Figure 5E). This result is confirmed using a *hep* hemizygous mutant (*hep^{r75}/Y*),

although the level of apoptosis across the whole disc is somewhat reduced when using

this allele (Figure S2A). The expression of a dominant negative form of the JNK *basket*

(*UAS-bsk^{DN}*) strongly suppresses *Mmp1* expression (Figure 5F), and unlike the loss of

hep, *bsk^{DN}* also reduces apoptosis at the wound edge (Figure 5F), suggesting that this

cell death is dependent on *bsk*. The population of NiA cells is also unaffected in this

background (Figure 5F), supporting the idea that NiA formation does not depend on JNK

signaling. RNAi knockdown of *bsk* also confirms these results (Figure S2B). Since the

loss of *bsk*, but not *hep*, seems to influence wound edge apoptosis, we also targeted an

alternative JNK kinase, *Mkk4*, for knockdown in *DC^{GluRI}* ablated discs. Unlike *hep*,

reduction of *Mkk4* levels reduces both the apoptosis and *Mmp1* expression at the wound

edge, but again has no influence on the appearance of NiA (Figure 5G). We also reduced

expression of the TNF receptor *grindlewald* (*grnd*) and TNF ligand *egr* using RNAi.

Neither manipulation affected the apoptosis or JNK activity at the wound edge or the

appearance of the cells undergoing NiA outside the ablated domain (Figure S2C and

S2D). Moreover, a reporter for *egr* expression (*egr-GAL4, UAS-GFP*) shows no

upregulation of *egr* at the wound edge or in cells undergoing NiA (Figure S2E and S2F).

Overall, these data suggest that necrotic ablation induces low levels of apoptosis and

JNK signaling at the wound edge, which occurs downstream of the JNK receptor and is

dependent on both *Mkk4* and *bsk*, while also generating NiA at a distance via a JNK-

independent signal.

As NiA does not appear to require JNK, we sought to investigate factors upstream of the

observed activated caspase DCP1 that might be required for the production of NiA

following necrotic ablation. We used an RNAi targeting the dIAP1 inhibitor *rpr*, which

activates cell death immediately upstream of initiator caspases. Knockdown of *rpr* leads

to a moderate reduction in apoptosis at the wound edge, but importantly also reduces NiA

formation (Figure S2G). When a miRNA targeting *rpr* and the two additional dIAP1

inhibitors *hid* and *grim* was used (*UAS-miRHG*), NiA formation was eliminated (Figure

5H), as was the cell death normally observed at the wound edge, indicating that more

than one of these genes are required for both wound edge apoptosis and NiA. Importantly,

DC^{GluRl}-induced tissue loss still clearly occurs even in the absence of NiA (Figure S2H),

while JNK signaling shown by *Mmp1* expression is still observed (Figure 5H). Thus,

necrotic ablation leads to apoptosis at the wound edge and NiA in the surrounding pouch,

and although they both rely on the same downstream factors to ultimately cause cell

death, each appears to be induced by a different activating signal.

NiA is required for blastema formation and promotes regeneration

To understand the potential contribution of NiA to regeneration we examined how the

appearance of NiA coincides with blastema formation following necrotic ablation. We

used a reporter for *E2F* (*PCNA-GFP*) and *Cyclin E* (*cycE-GFP*) to examine changes in

proliferation that occur following ablation and during regeneration (Smith-Bolton et al.

2009). These markers show that proliferation induced by necrotic ablation does not

significantly increase in the wing pouch until around 24 hr, after the formation of NiA at

18 hr (Figure 6A, 6B, S3A, and S3B). To test whether NiA has a role in blastema formation

we sought to eliminate this apoptosis following DC^{GluRl} ablation. As NiA is unaffected by

blocking JNK signaling, and P35 allows dying cells to persist in the disc which could

complicate our analysis, we used *UAS-miRHG* to prevent the formation of NiA. The lack

of NiA in the pouch following necrotic ablation results in a loss of *PCNA-GFP* upregulation

that is normally seen at 24 hr (Figure 6C), suggesting that NiA is required for blastema

formation. Importantly, JNK signaling at the wound edge is still observed following *miRHG*

expression, indicated by the presence of *Mmp1* (Figure 6C), demonstrating that blastema

formation following necrotic ablation is not dependent solely on JNK activity from the

wound, but also requires NiA.

Finally, we examined how blocking NiA might influence the discs capacity to regenerate.

Evaluating adult wings that develop from $DC^{GluRl}>>miRHG$ discs shows they have a

reduced ability to regenerate compared to control discs (Figure 6E and 6F). This result is

significant, as blocking apoptosis with *miRHG* would normally be expected to improve

regeneration, as it does in DC^{rpr} ablated discs (Figure 6D and 6F). Together, these results

show that NiA is required for the formation of a blastema to promote regeneration in

response to necrosis.

Discussion

Necrosis induces apoptosis at a distance in the wing imaginal disc

Necrotic ablation induces apoptosis in cells in two regions of the injured disc: at the wound

edge and more extensively in the surrounding pouch. These two populations of dying

cells are likely induced by separate mechanisms and contribute differently to regeneration

(Figure 7). The wound edge apoptosis coincides with JNK activity and is likely dependent

on it, as interference with *bsk* strongly limits the caspase observed at the wound. The

factors that can activate JNK signaling, and those downstream that regulate whether cells

subsequently proliferate or undergo apoptosis, are complex and context dependent (La

Marca and Richardson 2020; Pinal et al. 2019). However, our experiments show that

pathway activation following necrotic ablation occurs downstream of the receptor *grnd*

and relies on the JNK kinase *Mkk4* more than *hep*. There are a number of signals that

can induce JNK activity in this way, including loss of polarity, mechanical inputs and the

release of immediate stress signals such as reactive oxygen species (ROS)(La Marca

and Richardson 2020). ROS has been shown to upregulate both JNK and P38, another

factor that regulates proliferation and apoptosis, via Ask1/AKT (Santabarbara-Ruiz et al.

2019; Santabarbara-Ruiz et al. 2015), while ROS is known to be an important regulator

of regeneration in the wing disc (Brock et al. 2017; Khan et al. 2017; Santabarbara-Ruiz

et al. 2019; Santabarbara-Ruiz et al. 2015). Thus, it is possible that the JNK signaling and

associated apoptosis at the wound edge induced by necrotic ablation is mediated via this

pathway. It is likely that this JNK activity contributes to recovery following necrosis, as it

does in apoptosis-induced regeneration. However, our observation that blocking NiA

limits regeneration, despite wound edge JNK being unaffected, suggests that

regeneration does not solely depend on it.

The signals that lead to the NiA at a distance from the necrotic injury are less clear,

however. A related phenomenon to the one we have observed, in which cells undergoing

programmed cell death induce additional non-autonomous apoptosis, has been

described in the wing imaginal disc and the mouse hair follicle (Perez-Garijo et al. 2013).

However, in both contexts these events are induced by apoptotic cell death rather than

necrosis, and are mediated by JNK signaling, unlike the formation of NiA. In a parallel

observation to that of apoptotic cells communicating with surrounding tissues, studies

have shown that cells undergoing necrosis might also release factors that regulate the

behavior of neighboring cells. These factors are collectively known as damage associated

molecular patterns or DAMPs (Gong et al. 2020; Roh and Sohn 2018). Such signals often

consist of endogenous intracellular molecules like cytoskeletal components, DNA, RNA,

histones and metabolites, which are passively released and inappropriately exposed to

the extracellular environment. DAMPs are detected by immune cells that in turn activate

immune pathways to mount a stress response, known as sterile inflammation (Gong et

al. 2020). Beyond these initial inflammatory responses, DAMPs are also important for

orchestrating the subsequent steps in tissue repair and regeneration (Venereau et al.

2015). In *Drosophila*, the actin-binding protein α-actinin has been shown to act as a

DAMP when purified and injected into adult flies, inducing a humoral immune response

in the form of cytokine signal activation specifically in the fat body (Gordon et al. 2018;

Srinivasan et al. 2016). Similarly, apoptotic-deficient *Drosophila* constitutively activate

immune signaling in the larval fat body due to the presence of circulating DAMPs in the

hemolymph (Ming et al. 2014). Recently it was shown that imaginal disc damage leads to

the upregulation of circulating metabolites produced by the fat body, which are necessary

for proper disc repair (Kashio and Miura 2020), highlighting the importance of this

interorgan communication in the context of regeneration. Thus, one possibility is that

necrotic cells release DAMP signals to induce pro-regenerative NiA in the disc via an

immune response involving the fat body. The role of hemocytes, an essential population

of immune cells, in the regeneration of damaged imaginal discs has also been explored

following physical and apoptotic damage (Fogarty et al. 2016; Katsuyama and Paro 2013;

Pastor-Pareja et al. 2008), and in the context of sterile inflammation that occurs following

necrosis (Shaukat et al. 2015). Considering the vital roles hemocytes play in these

processes it is possible they also mediate immune or other signals to induce NiA

formation. Alternatively, DAMPs are also known to have stimulatory effects on non-

immune cells (Chen and Nunez 2010; Gong et al. 2020), and thus could be sensed

directly by the immediately surrounding pouch tissues to induce NiA. Going forward it will

be important to identify the both the identity of the signal and the physiological mechanism

by which necrosis leads to non-autonomous cell death in the wing disc.

NiA is necessary for blastema formation and subsequent regeneration

Our data show that blocking apoptosis following necrosis restricts blastema formation and

limits regeneration, strongly suggesting that NiA is a vital part of the recovery process.

How this type of cell death might promote proliferation is still unclear, however. Apoptosis-

induced proliferation (AiP) is a well-established phenomenon, in which dying cells release

mitogens, such as *wg* and *dpp*, downstream of JNK signaling to stimulate localized

proliferation (Fogarty and Bergmann 2017; Perez-Garijo and Steller 2015). These

mitogens act via a feed forward mechanism that involves the release of ROS, recruitment

of hemocytes and induction of further JNK signaling to promote repair (Fogarty and

Bergmann 2017; Fogarty et al. 2016). By contrast, we have shown that cells undergoing

NiA do not detectably express *wg* or *dpp*, even in an undead state, and do not activate

JNK signaling. Although we have not ruled out other characterized mitogens being

involved, these findings suggest that NiA may not promote proliferation via the

established AiP mechanism. An important consideration is whether cells undergoing NiA

release specific signals to direct tissue regrowth, as seen with AiP, or if the tissue loss

resulting from necrosis and NiA is instead sensed more generally at the level of the whole

disc, stimulating coordinated regrowth in addition to localized proliferation (Hariharan

2015). The identification of signals produced by NiA cells and a better understanding of

proliferation rates across a recovering disc will help to reveal the contribution of these

different mechanisms to necrosis-induced regeneration.

Tissue necrosis is associated with many types of traumatic injury and diseases in

humans, including ischemic injuries, infections and cancer. Using model systems, like the

one we have developed here, to understand how necrotic cells impact neighboring

healthy tissues, and how these tissues enact mechanisms to effectively recover, may help

to identify therapeutic interventions that promote healing in tissues which otherwise

struggle to recover from necrosis, such as those of humans.

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Competing interests

No competing interests declared.

Figure 1

Figure Legends

Figure 1. *Drosophila* wing imaginal discs regenerate comparably following

ablation with DC^{rpr}, DC^{hepCA} and DC^{GluR1}.

(**A-A'**) A schematic of the DUAL Control genetic ablation system, based on a split LexA

transcriptional activator which can form a complete transcriptional activator

(yellow/purple protein) using complementary leucine zipper domains following a heat

shock, inducing *lexAOp*-driven ablation in the *salm* domain (green area of disc) (**A**), with

the *DVE>>Gal4* driver used to drive *UAS*-based transgenes in the wing pouch

independent of ablation (red area of disc) (**A'**). *salm*: *spalt* enhancer, *DBD: DNA Binding*

Domain, *dve*: *defective proventriculus* enhancer.

(**B-E**) Wing discs stained for the Nubbin pouch marker (Nub, red) and DE-cadherin (DE-

cad, gray) in an unablated control (**B**) and following ablation with DC^{GluR1} (**C**), DC^{rpr} (**D**),

and DC^{hepCA} (**E**). DAPI, blue. Arrowheads in (**C-E**) indicate loss of Nub pouch marker.

(**F**) Adult wing ablation phenotypes following DUAL Control ablation (see also Harris et

al., 2020).

(**G**) Regeneration scoring of adult wings from early L3 discs ablated by DC^{rpr} (n = 62),

DC^{hepCA} (n = 66), and DC^{GluR1} (n = 68), and late L3 discs ablated by DC^{rpr} (n = 62),

DC^{hepCA} (n = 69), and DC^{GluR1} (n = 83).

(**H**) Mean pixel area of adult wings from early L3 ablated wings in an unablated control

(NA, n = 19), DC^{rpr} (n = 22), DC^{hepCA} (n = 12), and DC^{GluR1} (n = 17). ns, not significant.

Data analyzed using one-factor ANOVA and Tukey's multiple comparisons test.

Figure 2

Figure 2: Ablation with *DC^GluR1^* generates significant apoptosis at a distance.

(**A-B**) Propidium iodide (PI) staining (yellow) of *DC^GluR1^* (**A**) and *DC^hepCA^* (**B**) ablated wing discs, arrowhead in (A) indicates PI-stained dying cells in the *salm* domain of the pouch. Non-specific PI staining of tracheal tubes is observed in both samples. DAPI, blue.

(**C-F**) Caspase staining (DCP1, gray) of wing imaginal discs in a control unablated heat shocked disc (**C**), and following ablation with *DC^GluR1^* (**D**), *DC^rpr^* (**E**), and *DC^hepCA^* (**F**). DAPI, blue. Arrowheads in (D) indicate non-autonomous caspase outside of the ablation domain.

(**G-J**) Wing imaginal discs bearing the *lexAOp-GFP; UAS-RFP* reporter and ablated with *DC^GluR1^* (**G-H**) or *DC^hepCA^* (**I-J**). GFP (green) labels the *salm* ablation domain, RFP (red) labels the surrounding unablated pouch, and DCP1 (gray) labels apoptotic cells, DAPI, blue. (**G**) Discs ablated with *DC^GluR1^* shows DCP1-positive cells outside of the ablation domain (arrowheads), red line indicates transverse section shown in (H). (**H**) A transverse section through the pouch of the disc in (G) confirms that these lateral DCP1-positive cells are not labeled with GFP. (**I**) Ablation by *DC^hepCA^* shows almost complete overlap between the GFP and DCP1 signals, red line indicates transverse section shown in (J). (**J**) A transverse section of the disc in (I) confirming significant overlap of GFP and DCP1. PM: peripodial membrane, DP: disc proper.

(**K-L**) TUNEL-labeling (red) of wing discs ablated with *DC^GluR1^* (**K**) and *DC^rpr^* (**L**). Solid arrowheads indicate strong TUNEL staining in both panels, open arrowhead in (K) indicates weak TUNEL staining present in the *salm* domain.

Figure 3

Figure 3. Inhibition of caspase activity fails to prevent ablation in DC^{GluR1} discs.

(**A-B**) Wing discs stained for Nub (red), DE-cad (gray), and DAPI (blue) following ablation with $DC^{rpr}>>p35$ (**A**) and $DC^{GluR1}>>p35$ (**B**). Loss of tissue by *GluRI* ablation in the presence of P35 is indicated by the arrowhead in (B).

(**C-F**) DCP1 staining (gray) in wing discs ablated with DC^{rpr} (**C**), $DC^{rpr}>>p35$ (**D**), DC^{GluR1} (**E**), $DC^{GluR1}>>p35$ (**F**). The arrowheads indicate strong DCP1 staining in the ablated *salm* domain in (C) and non-autonomous apoptosis in (E), while the open arrowheads in (D) and (F) indicate the diffuse, cytoplasmic DCP1 staining in these populations that occurs in the presence of P35.

(**G**) PI staining (yellow) of a $DC^{GluR1}>>p35$ ablated wing disc. Non-specific PI staining of the tracheal tube is observed. DAPI, blue.

(**H**) TUNEL-labelling (red) of a $DC^{GluR1}>>p35$ ablated wing disc. The open arrowhead indicates weak TUNEL staining in the *salm* domain, while the lateral TUNEL staining is no longer observed in the presence of P35.

(**I-J**) Regeneration scoring of adult wings from early and late L3 discs ablated by DC^{rpr} (**I**) or DC^{GluR1} (**J**) in the presence and absence of P35. Number of wings scored: early and late L3 DC^{rpr} (n = 74, n = 87), early and late L3 $DC^{rpr}>>p35$ (n = 110, n = 125), early and late L3 DC^{GluRI} (n = 100, n = 38), early and late L3 $DC^{GluRI}>>p35$ (n = 101, n = 27).

(**K-L'**) Adult wing phenotypes following ablation with DC^{rpr} (**K**) or $DC^{rpr}>>p35$ (**K'**), and DC^{GluR1} (**L**) and $DC^{GluR1}>>p35$ (**L'**). Arrowheads indicate an incomplete L5 vein, which is a consequence of *p35* expression on vein development, reported previously (Perez-Garijo et al. 2004).

739   (**M**) The mean area of adult wings from discs ablated with DC^{rpr} (n = 31), $DC^{rpr}>>p35$ (n

740   = 19), DC^{GluR1} (n = 10), and $DC^{GluR1}>>p35$ (n = 15), ns, not significant, *** p = 0.0002,

741   data analyzed by one-factor ANOVA and Tukey's multiple comparisons test.

Figure 4

Figure 4. Necrosis-induced apoptosis (NiA) forms after wound edge signaling occurs.

(**A-F**) A time course of regeneration for wing discs bearing a fluorescent reporter of a damage-responsive WNT enhancer (DR^{WNT}, green, (Harris et al. 2016) ablated with DC^{GluR1} and stained for DCP1 (gray) at (**A**) 0 hr, (**B**) 6 hr, (**C**) 12 hr, (**D**) 18 hr, (**E**) 24 hr, (**F**) 48 hr after heat shock. Arrowhead in (C) indicates wound edge apoptosis at 6 hr coinciding with the appearance of DR^{WNT} expression, arrowheads in (D) indicates NiA at 18 hr.

(**G**) A wing imaginal disc at 48 hr of recovery following ablation with DC^{GluR1}. The pouch marker Nub (red) and DAPI staining (blue) show continuity of the pouch is restored (arrowhead).

Figure 5

Figure 5. Necrosis-induced apoptosis (NiA) acts independently of the JNK pathway.

(**A-B**) Wing discs ablated with DC^{GluR1} and bearing the *AP-1-GFP* (green) (**A**) and *puc^{A251}* (red) (**B**) reporters of JNK pathway activity and stained for DCP1 (gray), DAPI, blue. These reporters show strong overlap with the wound edge apoptosis, but not with the NiA cells. As in other panels, the dashed line outlines the ablated *salm* domain, indicated by the appearance of cells labelled by DAPI.

(**C-D**) Wing imaginal discs ablated with DC^{GluR1} and stained for the JNK targets Wg (red) (**C**) and Mmp1 (red) (**D**). DCP1, gray; DAPI, blue. Arrowhead in (C) indicates ectopic Wg at the wound edge.

(**E**) A wing imaginal disc ablated with $DC^{GluR1}>>hep^{RNAi}$ stained for DCP1 (gray) and Mmp1 (red), DAPI, blue. Both the wound edge apoptosis and NiA cells remain unaffected following knockdown of *hep*.

(**F**) A wing imaginal disc ablated with $DC^{GluR1}>>bsk^{DN}$ stained for DCP1 (gray) and Mmp1 (red), DAPI, blue. Wound edge apoptosis is largely absent, while NiA cells remain unaffected.

(**G**) A wing imaginal disc ablated with $DC^{GluR1}>>Mkk4^{RNAi}$ stained for DCP1 (gray) and Mmp1 (red), DAPI, blue. Wound edge apoptosis is strongly reduced, while NiA cells remain unaffected.

(**H**) A wing imaginal disc ablated with $DC^{GluR1}>>miRHG$ stained for DCP1 (gray) and Mmp1 (red), DAPI, blue. Both the wound edge apoptosis and NiA (open arrowheads) are eliminated following knockdown of *rpr, hid,* and *grim* with *miRHG*.

Figure 6

Figure 6. Blocking NiA cell activity impairs regeneration.

(**A-B**) Wing discs bearing an *E2F* transcriptional reporter (*PCNA-GFP,* green) ablated with DC^{GluR1} and stained for Mmp1 (red) and DCP1 (gray) at 18 hr (**A**) and 24 hr (**B**) of recovery. DAPI, blue. Arrowhead in (B) shows the regeneration blastema that is only present after 24 hr of recovery.

(**C**) Wing disc bearing *PCNA-GFP* (green) ablated with A DC^{GluR1}>>*miRHG* and stained for Mmp1 (red) and DCP1 (gray), DAPI, blue. The open arrowhead indicates a reduced proliferation upon *miRHG* expression. JNK signaling, indicated by Mmp1 staining, is still present in these discs.

(**D-E**) Regeneration scoring of adult wings from early and late L3 discs ablated with DC^{rpr} (**D**) or DC^{GluR1} (**E**) in the presence and absence of *miRHG*. Number of wings scored: early and late L3 DC^{rpr} (n = 62, n = 63), early and late L3 DC^{rpr}>>*miRHG* (n = 137, n = 88), early and late L3 DC^{GluRl} (n = 91, n = 53), early and late L3 DC^{GluRr}>>*miRHG* (n = 138, n = 47). While *miRHG* leads to more full and nicked wings following DC^{rpr} ablation, the opposite is seen following DC^{GluR1} ablation.

(**F**) Mean pixel area of adult wings from late L3 discs ablated with DC^{rpr} (n = 31), DC^{rpr}>>*miRHG* (n = 13), DC^{GluR1} (n = 21) and DC^{GluR1}>>*miRHG* (n = 18). ns: not significant, * $p < 0.0439$, *** $p = 0.0004$, data analyzed by one-factor ANOVA and Tukey's multiple comparisons tests**.**

Figure 7

A

Induced Apoptosis

Wound edge

Distant pouch

JNK activity
↓
Wg, Dpp, Egf
↓
Apoptosis/Proliferation

Egr, ROS

B

Induced Necrosis

?

JNK activity

Apoptosis   Proliferation

Necrosis-induced Apoptosis (NiA)

DAMPs

Figure 7. NiA cells promotes regeneration in DC^{GluR1} ablated discs

(**A-B**) Schematics depicting the cell signaling events that occur resulting from apoptotic

ablation with DC^{hepCA} (**A**) and necrotic ablation with DC^{GluRI} (**B**). Dying cells release

reactive oxygen species (ROS) and promote Egr release via hemocytes and potentially

other mechanisms, inducing high levels of JNK signaling at the wound edge. In turn,

wound edge apoptotic cells and surviving cells with lower JNK signaling release

mitogens including Wg, Dpp, and Egf, to promote regenerative signaling in the adjacent

wound edge tissue. In cells undergoing necrosis, low levels of ligand-independent JNK

signaling occurs at the wound edge, likely through pathways related to polarity

disruption, mechanical stress or immediate stress signals such as ROS. This signaling

induces sporadic apoptosis at the wound edge that potentially contributes to

proliferation and recovery. Necrotic cells also release an as yet unidentified long-range

signal that could be a damage associated molecular pattern (DAMP), resulting in the

formation of NiA cells in the distant pouch. These cells promote proliferative blastema

formation and regeneration.

Figure S1

Supplemental Figure Legends

Figure S1. Related to Figure 3

Blocking apoptosis with P35 leads to wing overgrowth phenotypes

(**A**) A wing disc labelled with a TUNEL (red) following $DC^{rpr}>>p35$ ablation. DAPI, blue. The lack of signal demonstrates the ability of P35 to inhibit cell death.

(**B**) Adult wing showing the overgrown phenotype accompanied by blistering and ectopic vein tissue observed following $DC^{GluR1}>>p35$ ablation.

(**C**) A graph representing the frequency of overgrown wings following ablation with $DC^{rpr}>>p35$, $DC^{hepCA}>>p35$ and $DC^{GluR1}>>p35$. No overgrown wings were observed in $DC^{rpr}>>p35$.

(**D-F**) Wing imaginal discs stained for Wg (red) and DCP1 (gray) following ablation by DC^{hepCA} (**D**), $DC^{hepCA}>>p35$ (**E**) or $DC^{GluR1}>>p35$ (**F**). Ectopic Wg overlaps with the diffuse DCP1 signal in $DC^{hepCA}>>p35$, discs however, little Wg is associated with the blocked apoptotic cells of $DC^{GluR1}>>p35$ discs.

Figure S2

A DC^{GluRI} hep^{r75}/y
Mmp1
DCP1
DAPI
DCP1
Mmp1

B DC^{GluRI} $>>bsk^i$
Mmp1
DCP1
DAPI
DCP1
Mmp1

C DC^{GluRI} $>>egr^i$
Mmp1
DCP1
DAPI
DCP1
Mmp1

D DC^{GluRI} $>>grnd^i$
Mmp1
DCP1
DAPI
DCP1
Mmp1

E $egr>GFP$
GFP
DCP1
DAPI
DCP1
GFP

F DC^{GluRI} $egr>GFP$
GFP
DCP1
DAPI
DCP1
GFP

G DC^{GluRI} $>>rpr^i$
Mmp1
DCP1
DAPI
DCP1
Mmp1

H DC^{GluRI} $>>miRHG$
Nub
DCP1
DAPI
DCP1
Nub

Figure S2. Related to Figure 5.

Manipulation of JNK pathway elements in *DC^{GluRl}* ablated discs.

(**A**) A wing imaginal disc stained for DCP1 (gray) and Mmp1 (red) following *DC^{GluR1}* ablation in a *hep^{r75}* hemizygous background. Wound edge apoptosis and NiA cells are still observed in this background, although are overall reduced. DAPI, blue. As in other panels, the dashed line outlines the ablated *salm* domain, indicated by the change in DAPI appearance.

(**B**) A wing imaginal disc stained for DCP1 (gray) and Mmp1 (red) following *DC^{GluR1}>>bsk^{RNAi}* ablation. DAPI, blue. Wound edge apoptotic cells are largely absent following *bsk* knockdown, while NiA cells remain unaffected,.

(**C**) A wing imaginal disc stained for DCP1 (gray) and Mmp1 (red) following *DC^{GluR1}>>egr^{RNAi}* ablation. DAPI, blue. Both wound edge apoptotic cells and NiA cells remain unaffected by *egr* knockdown.

(**D**) A wing imaginal disc stained for DCP1 (gray) and Mmp1 (red) following *DC^{GluR1}>>grnd^{RNAi}* ablation. DAPI, blue. As in (C), both wound edge apoptotic cells and NiA cells remain unaffected following *grnd* knockdown.

(**E-F**) Discs bearing an *egr* reporter (*egr-Gal4; UAS-GFP*, green) in an undamaged disc (**D**) and following ablation by *DC^{GluR1}* (**E**). Reporter activity is not observed in the pouch with or without ablation, but is seen in the notum.

(**G**) A wing imaginal disc stained for DCP1 (gray) and Mmp1 (red) following *DC^{GluR1}>>rpr^{RNAi}* ablation. DAPI, blue. Knockdown of *rpr* leads to a mild reduction of both wound edge apoptotic cells and NiA cells (open arrowheads).

(**H**) A wing imaginal disc stained for DCP1 (gray) and Nub (red) following *DC^{GluR1}>>miRHG* ablation. Tissue loss indicated by loss of Nub (arrowhead) is still observed following ablation with *DC^{GluR1}* despite apoptosis inhibition by knockdown of *rpr, hid,* and *grim.*

Figure S3

Figure S3. Related to Figure 6.

(**A-B**) Wing imaginal discs bearing the *CycE-GFP* reporter (green) at 18 hr (**A**) and 24 hr (**B**) of recovery following ablation by DC^{GluR1}. The open arrowhead in (A) indicates a lack of reporter activity in the *salm* domain, while the arrowhead in (B) highlights stronger reporter activity at 24 hr.