Wound-Induced Syncytia Outpace Mononucleate Neighbors during *Drosophila* Wound

Repair

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ABSTRACT:

In response to injury, cells proliferate, migrate and invade to replace missing cells and close wounds. However, the role of other wound-induced cell behaviors is not understood, including the formation of syncytia (multinucleated cells). Here, we use *in vivo* live imaging to analyze wound-induced syncytia in mitotically competent *Drosophila* pupae. We find that almost half the epithelial cells near a wound fuse to form large syncytia. When the autophagy gene *Atg1* is knocked down, fewer syncytia form, and wounds close more slowly. Further, a computational model of tissue fluidity indicates that cell fusion speeds wound closure time by about one third. Syncytia use several routes to speed wound repair: they outpace diploid cells at the wound margin to lead the initial resealing of the wound; they reduce the need for intercalation as the tissue reshapes during closure; and they pool resources of their component cells to concentrate them toward the wound margin. In addition to wound healing, these properties of syncytia are likely to contribute to their roles in development and pathology.

INTRODUCTION

Injury is a constant reality of life, and survival requires all organisms to repair wounds. Wound-induced cell behaviors like proliferation, migration, and invasion replace missing cells and close wounds (Martin et al., 2024). Other cell behaviors are induced around wounds, but their contribution to wound healing is not well understood, *e.g.*, the fusion of cells into syncytia. Syncytia are one type of polyploid cell, and it is generally appreciated that increases in ploidy – number of genomes per cell – is a common response of post-mitotic tissues and cells to injury (Losick et al., 2013; Nandakumar et al., 2020; Tamori and Deng, 2013). Wound-induced epithelial syncytia were first observed around epidermal puncture wounds in *Drosophila* larvae and adults (Galko and Krasnow, 2004; Losick et al., 2013), consistent with the idea of polyploidy induction in non-proliferative cells. However, recent studies have observed syncytia around wounds in mitotically competent tissues: around laser-ablation wounds in *Drosophila* pupal epidermis (Wang et al., 2015) and in zebrafish epicardium damaged by endotoxin, microdissection, or laser ablation (Cao et al., 2017). Further, injury associated with the surgical implantation of biomaterials can cause immune cells to fuse into multinucleated giant cells, which are associated with rejection (Al-Maawi et al., 2017). Similarly, injury induces bone marrow-derived cells to fuse with various somatic cells to promote repair (Alvarez-Dolado et al., 2003; Corbel et al., 2003; Davies et al., 2009; Nygren et al., 2004). The many instances of syncytia being induced by wounds raise the possibility that syncytia offer an adaptive benefit. It is not clear, however, what that benefit is.

Syncytia can form either by endomitosis – mitosis without cytokinesis – or by cell-cell fusion. Fusion is widely observed throughout development in both vertebrates and invertebrates: for example myoblasts fuse into muscles (Kim et al., 2015a; Lehka and Rędowicz, 2020), and

fusions occur in the lineages of the *C. elegans* hypodermis (Podbilewicz and White, 1994) as

well as vertebrate trophoblast (Renaud and Jeyarajah, 2022) and osteoclast (Søe, 2020). Cell

fusions are also observed in disease: pathogen-induced epithelial fusion allows spreading of

many viruses including human respiratory syncytial virus and SARS-CoV-2 (Leroy et al., 2020);

and the fusion of cancer cells with bone-marrow derived cells is implicated in metastasis

(Pawelek and Chakraborty, 2008).

Here, we use live imaging and clonal analysis to understand the behavior of syncytia

following laser wounding in the *Drosophila* pupal notum. The unwounded notum is a monolayer

epithelium composed of mononuclear diploid cells that are mitotically competent. Nonetheless,

during the first several hours after wounding, many of the surrounding cells fuse to form giant

syncytia. We previously reported that after wounding the pupal notum, some wound-adjacent

cells undergo a single round of endoreplication, increasing their ploidy two-fold (White et al.,

2024), but fusion increases ploidy far more, with some wound-induced syncytia observed to have

more than a dozen nuclei. Some cell fusions are obvious with apical borders breaking down

between cells, while others surprisingly appear as shrinking of a cell's apical surface. Combined,

fusion is a common fate of cells near wounds: about half the cells fuse to form syncytia within 70

μm of a wound with 30 μm radius. To understand the role of fusion-mediated syncytia in wound

repair, we undertook two types of analysis, first analyzing an autophagy mutant that reduces

fusion after wounding, and second comparing the behaviors of syncytial and mononuclear cells

within the same wound. Compared to their smaller mononuclear neighbors, syncytia outpace

mononuclear cells to the leading edge. We propose that syncytia accelerate wound repair because

cell fusion limits the need to negotiate cell intercalations as the wound closes, a hypothesis

supported by computational modeling; and because clonal analysis demonstrates that syncytia

mobilize and transport cell resources such as actin from distal cells to the wound margin.

RESULTS:

A mitotic tissue utilizes cell-cell fusions during wound repair.

The pupal notum is a monolayer columnar epithelium that will become the epidermis of the adult fly. At the time of our analysis, 12-18h after puparium formation (APF), it sits atop a basement membrane that is still developing (Mehaffey et al., 2024), and it is composed of diploid cells that undergo regular mitotic cycles (Guirao et al., 2015) (Figure 1—figure supplement 1A-C). To analyze cell behaviors around wounds, we live-imaged after laser ablation. Epithelial cell borders were labeled by the adherens junction protein p120ctnRFP (Ogura et al., 2018) and nuclei were labeled with histone His2GFP. Two hours after wounding, we observed what appeared to be prominent syncytial (multi-nucleated) cells around the wound (Figure 1A); experiments described below demonstrated that these were indeed syncytia. Some appeared to contain over a dozen nuclei within epithelial borders. For both syncytial and mononuclear cells, it was difficult to assign nuclei precisely to cell borders because notum epithelial cells are not oriented at right angles with respect to the surface, and in 2-D projections, a nucleus was frequently observed outside the cell's apical border (Figure 1—figure supplement 1D). Accordingly, using apical area and nuclear density, we estimated the number of nuclei within the 3 largest syncytia in different wounds. The number of nuclei in these syncytia increased over time: at 1 h after wounding the three largest syncytia contained an average 3-13 nuclei, and 2 h after wounding they nearly doubled to 6-20 nuclei (Figure 1B). Interestingly, larger wounds generated syncytia with larger apical areas and more nuclei, proportional to wound size, suggesting syncytium formation is a dynamic and scalable response to injury (Figure 1 C-E).

Live imaging of cells after wounding revealed the gradual loss of p120ctn along the border between two epithelial cells followed by rounding of the resulting syncytium (Figure 1F,I,

and Video 2), such that the initial two-cell morphology gradually became a one-cell morphology.

We termed the visible loss of p120ctn "border breakdown". We determined that as p120ctn was

lost, the adherens junction protein E-cadherin was also lost (Figure 1—figure supplement 1E-H)

indicating adherens junctions disassembly along the border between the cells. Border

breakdowns were found spatially clustered in the first three to four rows of cells, 30-50 μm from

the wound center, and they occurred primarily within the first hour after wounding, some within

10 minutes after wounding (Figure 1G,H). These events could be explained by wound-induced

cell fusion or by wound-induced epithelial-to-mesenchymal transition. To ask whether border

breakdowns represented cell fusions, we analyzed cytoplasmic mixing. Individual GFP-labeled

cells (clones) were generated at random locations using the flip-out Gal4 technique (Pignoni and

Zipursky, 1997). Before wounding, the level of cytoplasmic GFP fluorescence was stable yet

exhibited cell-to-cell variability, allowing some differentiation of cells by intensity (Figure 1I[i]).

Minutes after a nearby laser ablation, GFP was observed to diffuse from labeled cells into

neighboring unlabeled cells. GFP mixing between two cells was followed by the eventual loss of

their shared p120ctn-labeled cell border, confirming that border breakdown is indeed cell fusion,

but that cytoplasmic mixing occurs more than 10 minutes before the border breakdown is first

observed to start (Figure 1I, Video 2). GFP mixing always preceded border breakdowns (n=11).

Cytoplasmic GFP mixing resulted in a consistent level of fluorescence across the two cells,

indicating that GFP mixing is a reliable indicator of plasma membrane fusion. The order of

events demonstrates that plasma membrane fusion occurs many minutes before the visible

disassembly of the apically located adherens junctions. Thus, epithelial fusion is a rapid local

response to wounding, and border breakdown is a lagging indicator of cell fusion.

Apical cell shrinking also represents cell-cell fusion, evident later during wound closure.

Border breakdowns, representing cell fusion events, occurred mostly within 1 h after

wounding, so it was unclear how syncytia grew in size and nuclear number between 1-2 h after

wounding. However, an unexpected cell behavior was frequently observed during this time: the

apical area of diploid epithelial cells shrank until they disappeared from the epithelial sheet, a

phenomenon we termed "apical shrinking" (Figure 2A). Although the appearance of apical

shrinking suggested cell extrusion, we were surprised at its high frequency around wounds

(Figure 2E), as wounds have already lost many cells and would be expected to prioritize cell

survival to speed barrier repair. To understand the fate of apical-shrinking cells, we tracked their

nuclei and determined that they did not extrude; rather, all apical-shrinking cell nuclei moved

laterally within the plane of the epithelium to join neighboring syncytia (n=7, Figure 2B),

suggesting that apical shrinking is an indicator of cell fusion. To better understand this behavior,

we analyzed individual GFP-labeled cells so that we could observe the fate of the cytoplasm.

Like with border breakdowns, GFP mixing in the X-Y plane of the epithelium was observed to

precede the initiation of apical shrinking, although the interval between GFP mixing and apical

shrinking was longer, one or more hours (Figure 2C, Video 3). In X-Z projections, GFP labeled

cytoplasm associated with apical shrinking shifted laterally to join with a neighboring cell as

shown for two apical-shrinking cells in Figure 2D. For the cell labeled with the yellow arrow,

before apical shrinking at 60 min post wound, its GFP-labeled cytoplasm extended from the

plane of the adherens junctions (Z_{AJ}) basally over 8 μm; when apical shrinking was underway at

120 min post wound, its cytoplasm extended less than 5 μm down from the apical plane; and

when shrinking was almost complete at 150 min post wound, it extended only 1-2 μm down

from the apical plane, appearing as a whisp of cytoplasm connecting the shrinking apical surface

with the neighboring syncytia. A similar loss of basal depth over time is observed in the cell

labeled with the white arrow. In both these cells, as the cell lost its basal volume, cytoplasm

moved laterally to join the neighboring syncytia. Thus, analysis of both nuclei and cytoplasm

demonstrated that apical shrinking represented cell fusion events. The spatial distribution of

apical shrinking around wounds was similar to border breakdowns, but fusions associated with

apical shrinking occurred later and were more numerous (Figure 2E,F). Thus, cell fusion is

evident as either border breakdown or apical shrinking, which both occur after GFP sharing.

To determine what percentage of cells around a wound will fuse, we analyzed over 100

single epithelial cells randomly-labeled with cytoplasmic GFP within the radius of observed

fusion (80 µm), tracking them for 6.5 h to assess their fate (Figure 3A,B): a full quarter of the

cells fused (25%), sharing GFP before borders breakdown or apical shrinking; 67% persisted as

diploid cells, most with stable GFP, but infrequently (n=3) with GFP mixing and no subsequent

cell fusion; the remaining 7% could not be tracked (Figure 3—figure supplement 1A). All GFP-

labeled cells with apical shrinking had previously shared cytoplasm, indicating that all apical

shrinking represents fusion. The observation of rare diploid cells with previous cytoplasmic

mixing confirms that plasma membrane fusion occurs before the later steps of border

breakdown/apical shrinking, as these cells represent fusion initiation events (fusion pore) but

were unable to productively stabilize and expand the site of fusion and so returned to the diploid

state. Fusing cells were strongly skewed toward the center of the wound: within 70 µm, about

half the cells (47%) underwent fusion (Figure 3A, left), and fusion continued for over 300 min

after wounding (Figure 3—figure supplement 1B,C). Apical shrinking accounts for more than

half of all fusing cells (Figure 3C), and the spatial distribution of fusing cells that shrank vs. lost

borders was similar (compare Figures 1G and 2E). However, apical shrinking began later than

border breakdowns (Figure 2F, Figure 3—figure supplement 1C), continued for several hours

after wounding (Figure 2F, Figure 3—figure supplement 1C), and took longer to complete

(Figure 3—figure supplement 1D). Thus, fusion associated with apical shrinking accounted for

continuing syncytial growth after border breakdowns subsided. Further, cell fusion is a persistent

behavior over the course of wound closure.

Our individual cell tracking indicated that syncytia were the result of epithelial cell

fusions. However, phagocytic hemocytes are known to migrate to the sites of pupal wounds

(Antunes et al., 2013). To determine if hemocytes fused with epithelial syncytia around wounds,

we labeled hemocytes with cytoplasmic GFP (*hml>GFP*) and observed their behavior in live

imaging. In six wounds, we observed GFP-labeled hemocytes at the basal side of the wound

margin; however, we did not observe any events where GFP was transferred from hemocytes to

the epithelium, ruling out the fusion of hemocytes with epithelia in pupal wounds (Supplemental

Video 4) .

Syncytia close wounds faster.

To evaluate the role of cell fusion and syncytia in repairing wounds, we wanted to

analyze a mutant that blocked syncytia formation. It has been reported that several individual

autophagy (*Atg*) genes are required for syncytia formation around small laser ablation wounds in

the polyploid *Drosophila* larval epithelium (Kakanj et al., 2022), so we asked if autophagy

promotes fusion around laser wounds in the diploid pupal epithelium. Using a dsRNA line

known to disrupt syncytia in larvae, we knocked down *Atg1* on one side of the wound expressing

pnr-Gal4, as illustrated in Figure 4A, reserving the other side of the wound as an internal control,

modifying an internally controlled wounding system we have previously reported (O'Connor et

al., 2021b). Visualizing Ecad-labeled cell borders across the wound, we found that indeed *Atg1* is

required for syncytia formation in pupal wounds, like it is in larval wounds (Figure 4B).

Specifically, we observed a reduction in cell fusion, both reductions of border loss and apical

shrinking (Figure 4C). We next compared wound closure rates on the two sides of the wound

(Figure 4D,E). Because leading edge migration is slightly delayed on the *pnr-Gal4* side of the

wound even in control wounds (*pnr>+*), we compared the difference in wound radii on the two

sides, comparing control wounds to *pnr>Atg1^{RNAi}* wounds. By 5h after wounding, the *pnr>+* side

lagged behind the other side by only about 10 µm, yet the *pnr>Atg1^{RNAi}* side lagged behind the

other side by an average of about 25 µm, a reproducible, significant, and large reduction in

wound closure when syncytia formation was reduced (Figure 4E). These results suggest that

syncytia speed wound closure. It is difficult, however, to disentangle the roles of autophagy and

syncytia in this experiment, as the *Atg1* knockdown cells may move more slowly because they

are defective in the essential cellular function of autophagy and/or lacking syncytia. To address

this question, we found a strong correlation between the size of the cell/syncytium and the

distance it had moved from the start, measured at the time when the wound was half-closed.

This correlation was true for cells/syncytia in control wounds as well as for those when *Atg1* was

knocked down (Figure 4F,G respectively). These data indicate that syncytia formed through cell

fusion speed wound closure.

Syncytia outcompete mononucleate cells at the leading edge of repair.

To understand this phenomenon better, we further investigated control wounds. Because

about half the cells fused to form syncytia around wounds, we were able to compare the behavior

of syncytial to non-syncytial cells within the same wound, providing a well-controlled

environment for assessing how syncytia contribute to wound closure. In live imaging, we

observed that syncytia frequently moved faster than mononucleated cells toward the wound,

overtaking unfused cells as the wound closed. Figure 5A tracks four GFP-labeled cells near a

wound, with cell 1 furthest from and cell 4 closest to the wound (Figure 5A[i]). Middle cells 2 and

3 fuse with five others into a large syncytium, which advances toward the wound faster than both

non-fusing cells, and by 400 min after wounding the syncytium extends well beyond the unfused

cells (Figure 5A[iii]). This behavior was evident even without GFP labeling: Figure 5B-C show a

group of cells at the leading edge of the wound (the wound is recognized by the lack of p120ctn).

At 90 min after wounding, this region of the leading edge comprises three mononuclear cells

flanked on either side by syncytia (outlined in yellow); the middle of the three mononuclear cells

is outlined in orange (5B) and white (5C). By 150 min, the syncytia have pushed out all three

mononuclear cells from the leading edge, and at 360 min two of these mononuclear cells are

visible about 20 μm back from the wound edge. Indeed, we observed that several hours after

wounding, the entire leading edge was occupied by syncytia. To investigate how syncytia came

to occupy this position at the front lines of wound healing, we expressed MyoIIGFP/Zip-GFP,

which along with actin forms the contractile purse string and makes the leading edge visible,

along with p120ctnRFP to label cell borders. We analyzed the persistence of all mononuclear

and syncytial cells at the leading edge over the course of closure for three wounds, starting when

the leading edge was first visible about 30 min after wounding (Figure 5D-G). At the start, 75%

of the perimeter was occupied by syncytia with the rest occupied by 10-13 mononuclear cells

(Figure 5D). As the wound closed, the syncytia became larger and displaced all the mononuclear

cells, with the last mononuclear cell removed from the leading edge 20-160 min before closure

(Figure 5E-G). No mononuclear cell persisted at the leading edge through wound closure,

indicating that syncytia outcompete unfused cells to close the wound.

Radial border fusion reduces intercalation, the rate-limiting step of wound closure

Why do syncytia move faster? To address this question, we considered the geometry of

fusion because different fusion orientations could provide different benefits for wound repair.

We observed that fusions sometimes occur between two adjacent cells equidistant from the

wound, as diagramed in the top panel of Figure 6A and exemplified in Figure 1I[iii]-I[iv] (cells 1,2).

This breakdown of a radial border produces a syncytium elongated along the wound edge.

Alternatively, fusion may occur between adjacent cells at different distances from the wound, as

diagramed in the lower panel of Figure 6A and exemplified in Figure 1F (cells 3,4). This

breakdown of a tangential border produces a spoke-like syncytium pointing into the wound. To

analyze the frequency and timing of these two different axes of fusion, we calculated the

orientations of all lost borders in four wounds. (The angle of the lost border can be determined

for border breakdowns; it is difficult to determine for apical shrinking because the other fusion

partner is hard to identify). In four analyzed wounds, we identified 235 border breakdowns: 39

radial borders and 196 tangential borders (Figure 6B). Thus, there were about five-fold more

tangential borders lost to fusion than radial. Nonetheless, the two types had similar temporal and

spatial distributions around the wounds (Figure 6—figure supplement 1).

As a wound closes, fewer cells can occupy the ever-smaller leading edge, necessitating a

rearrangement of cell adhesions to allow cell intercalation, as depicted in the top of Figure 6C.

Indeed, when cells do not fuse after wounding, as in *Drosophila* wing discs, the impact of

intercalations on tissue fluidity is known to be a rate-limiting step of wound repair (Tetley et al.,

2019). As shown in the bottom of Figure 6C, the requirement for cell intercalation would be

reduced specifically by radial border fusion.

To consider the contribution of radial border fusions to wound closure, we took three

approaches. First, we analyzed existing data from the three wounds shown in Figure 5D-G, and

asked how many leading-edge cells fused radially vs. intercalated: 17-41% of cells removed

from the leading edge were removed through fusion, reducing the burden of intercalation

substantially (Figure 6D). Interestingly, the larger the percentage of cells that fused rather than

intercalated, the faster the wound closed (Figure 6D).

Second, we analyzed tissue fluidity as measured by the cell shape index, $\rho = P/\sqrt{A}$,

where P is cell perimeter and A is cell area. This dimensionless index characterizes the cell

jamming transition in vertex models of epithelia: for $\rho < 3.81$, a modeled isotropic epithelium is

in a jammed state with energy barriers that limit intercalations, giving rise to a solid-like tissue;

but for $\rho > 3.81$, the energy barriers vanish, yielding an unjammed fluid-like tissue (Bi et al.,

2016; Park et al., 2015). In real epithelia, the solid-fluid transition may take place at different

values of ρ (Wang et al., 2020), but higher ρ still implies greater tissue fluidity. We segmented

images of the pupal notum before and after wounding and calculated the distributions of cell

shape index for both syncytia and non-syncytial cells (Figure 7A-B). The mean cell shape index

increased significantly after wounding with syncytia having a higher shape index than nearby

post-wound non-syncytial cells ($p = 0.001$) and both having higher shape indices than pre-wound

cells ($p < 10^{-6}$). The post-wound epithelium is thus substantially more fluid-like than it was

before wounding

Third, we adapted the computational vertex model from Tetley et al. (2019) to include

probabilistic cell-cell fusions to directly investigate the role of cell fusion in tissue fluidity and

wound closure. We generated four initial cell configurations with similarly sized wounds and

used these to run four matched pairs of simulations – one that proceeded to close without any

cell fusions and the other that allowed fusions to occur with spatiotemporal probabilities that

matched our experimental observations (Figure 6B, Figure 6—figure supplement 1A). On

average, the probabilistic fusion-allowed simulations had 68 ± 14 (mean $\pm$ SD) fusions and

closed the wound in about 1/3 less time than those without fusions (Figure 7C). Selected frames

from one of the matched simulation pairs are shown in Figure 7D-E and full videos of this pair

are available as Video 5. Importantly, the modeled syncytia had no special properties: same

contractility as other cells, same target shape index, and same target area as the sum of the fused

pair. Just the presence of these larger cells reduced the need for intercalations during wound

closure and thus sped up the process.

Tangential border fusions allow resources from distant cells to be mobilized to the wound

edge.

In contrast to radial border fusions, tangential border fusions might provide a way for

cellular resources that would be trapped in distal cells to move toward the wound to contribute to

closure. To test this hypothesis, we generated small flip-out clones expressing actin-GFP and

wounded such that unlabeled cells intervened between the labeled cell and the leading edge

(Figure 8). Like cytoplasmic GFP in Figures 1I and 2C, we observed actin-GFP to equilibrate

between cells soon after fusing. For syncytia that did not have access to the leading edge (n =2),

actin-GFP levels remained uniform (Figure 8A,B). In contrast, syncytia with access to the

leading edge (n = 10) first uniformly distributed actin (Figure 8C[ii]), but once the leading edge

was contacted, they redistributed actin-GFP to it (Figure 8C,D). Kymographs of actin-GFP

confirm that regardless of location, actin equilibrates between fusing cells within 5 minutes

(Figure 8B^{iii}, D^{iv}); however, nearly all actin that originated in the distal cell is redistributed to the

leading edge in a syncytium positioned there (Figure 8D^{iv}). In one striking instance, actin-GFP

appeared to travel through three cells to arrive at the leading edge from its initial location three

rows back (Figure 8E-G, Video 6). Importantly, although actin is labeled from only one of the

fusing cells, it likely represents the location of actin from all fusing cells, explaining why

syncytia are better able to occupy the leading edge. We envision that other resources would also

be concentrated in subcellular regions as needed by syncytia. This ability of syncytia to

concentrate pooled actin to the leading edge may allow syncytia to outcompete their smaller

mononuclear neighbors and close wounds more rapidly.

DISCUSSION:

Previous work established that polyploid cells – both cells with multiple nuclei and cells

with enlarged nuclei – are important for closing epithelial wounds in post-mitotic tissues (Losick

et al., 2013). Here we have used live-imaging to analyze the response to wounds of a diploid

mitotic tissue, the epithelial monolayer of the pupal notum. We found that syncytia form around

wounds by cell fusion at a remarkably high rate, with almost half the epithelial cells within 5

cells of the wound fusing with neighbors over the course of hours. Syncytial size increases with

wound size, indicating syncytia formation is a dynamic and scalable response to wounding.

Several lines of evidence demonstrate that syncytia are faster at closing wounds than unfused

cells. Knockdown of the autophagy gene *Atg1* reduces fusion around pupal wounds as was

previously reported for larval wounds; *Atg1* knockdown also reduces the rate of wound closure.

In both *Atg1* knockdowns and in controls, there was a consistent observation that the bigger the

syncytium, the faster it moved. Within control wounds, syncytia completely displace unfused

cells of the same genotype at the leading edge of the wound, such that wounds are closed entirely

by syncytia, even though there is a smaller number of syncytia than unfused cells. Finally,

computational modeling of wound closure with and without cell fusion shows that wounds with

fusion-based syncytia close faster because of the reduced need for cell intercalations.

Thus, wound-induced polyploidy is a generalized strategy for wound closure, used by

both mitotic and non-mitotic tissues. Although one might have wondered if polyploidy was a

wound response limited to tissues that cannot use mitosis to increase nuclear content, both

endoreplication and cell fusion into syncytia occur after wounding in this mitotically active

diploid tissue (Wang et al., 2015; White et al., 2024; this study). The requirement for *Atg1* for

fusion in both polyploid larval tissue and in diploid pupal tissue suggests that the fusion

mechanisms are common, despite the altered cell cycle of the starting cells. Further, our finding

that larger syncytia travel faster suggests that syncytia – and by extension perhaps cell

enlargement via endoreplication –occur as adaptations to close wounds faster.

We identified two unique properties of syncytia that may improve their wound-closing

ability. First, syncytia are larger than neighboring diploid cells and their presence enhances tissue

fluidity. Previous studies have determined that the rate-limiting step in epithelial wound healing

is the process of cell intercalation or rearrangement (Tetley et al., 2019). As the wound closes

and the leading edge encircling the wound gets smaller, fewer cells can occupy the leading edge.

The cells leaving the leading edge must remodel their cellular junctions, requiring time and

energy. Overall, tissue solidity slows closure, so enhancing fluidity promotes faster closure. By

fusing into larger syncytia, cells reduce the need for adhesion remodeling and intercalation and

instead just change shape as the leading edge becomes smaller. Moreover, the resulting larger

cells can have significantly more fluidity and less epithelial tension than their diploid

progenitors, as recently demonstrated in syncytia formed by age-induced epidermal cell fusion

(Dehn et al., 2023). As our computational modeling demonstrates, fusion can speed wound

closure by ~33% even when the resulting syncytia have no special properties besides being

larger than neighboring diploid cells. Making the syncytia individually more fluid would be

expected to speed closure even more.

The second unique property of syncytia is their ability to pool and concentrate the cellular

resources of the many constituent cells into a subcellular location within the large syncytium. We

explored this concept by monitoring the localization of actin within syncytia. Actin is important

for wound healing, as epithelial wounds close through the action of two actin-dependent

processes: the cinching of a multicellular actin cable at the leading edge that surrounds the

wound, sometimes called a purse string (Abreu-Blanco et al., 2012; Bement et al., 1993; Martin

and Lewis, 1992; Tamada et al., 2007), and the protrusion of actin-rich projections into the

wound (Abreu-Blanco et al., 2012; Farooqui and Fenteany, 2005). Pupal wounds have been

shown to use both processes, with the actin cable developing early and actin protrusions

appearing later in wound closure (Antunes et al., 2013). By labeling actin in individual cells

(clones), we were able to follow it redistribution in syncytia after fusion. As expected, at first

labeled actin diffuses and equilibrates throughout the new large cell. Remarkably however, when

the syncytium is in contact with the leading edge, labeled actin is concentrated at the leading

edge, even if the actin originated several cells away from the leading edge. Without fusion, the

labeled actin would have been trapped in a distal cell without access to the leading edge, but after

fusion, the syncytium can concentrate the actin of its many component cells at the wound front.

If N represents the number of cells that fused, our results suggests that syncytia can apply up to

N times more actin to the leading edge; considering that we observed syncytia with dozens of

nuclei, this could represent a significant enhancement of actin at the leading edge. Increased

actin might explain the ability of syncytia to outcompete diploid cells at the leading edge.

Presumably, other resources such as mitochondria and ribosomes could also be pooled and

concentrated by syncytia at cellular locations where they promote wound healing. It is known

that mitochondrial fragmentation is localized to the site of cellular injury (Horn et al., 2020), and

that ribosomes are localized at the tips of severed neurons (Noma et al., 2017), and syncytia

would have access to a larger pool of mitochondria and ribosomes than their component cells. By

pooling the cellular resources of component cells, syncytia may also allow lethally damaged cells

to survive by providing them with needed survival factors originating in cells further from the

wound. Thus, the concept of resource sharing that we demonstrate with actin may have

ramifications for many resources. Interestingly, it has been demonstrated that wound-induced

endoreplicating cells also increase protein levels of some wound-repair resources, such non-

muscle myosin, presumably possible because of the many copies present in the polyploid

genome (Losick and Duhaime, 2021).

Two visibly distinct cellular behaviors attended fusion in the apical plane of the adherens

junctions: border breakdowns and apical shrinking. Both processes were confirmed as fusion by

expressing GFP in clones and analyzing GFP sharing at fusion. Border breakdowns occurred

sooner after wounding than apical shrinking and appeared to be a faster process, as apical

shrinking started later and took hours to complete. It is unclear whether these differences in

appearance and timing indicate different mechanisms, as both require the autophagy gene Atg1.

For border-breakdown, it is simple to envision that fusion initiates near the apical adherens

junctions, which are under more tension than the basolateral membranes, and this may explain

why fusion proceeds more quickly there. We recently found that although epithelial tension

drops after laser wounding, it is restored within about 10 min (Han et al., 2023), consistent with

the timing of apical border breakdown. Also consistent with this model, in the *C. elegans*

hypodermis, developmental cell fusion has been observed to initiate at the apical side and travel

in the apical-to-basal direction (Mohler et al., 1998). It is also possible that fusion initiates at a

more basal site, and that fusion proceeds apically, with adherens junction disassembly occurring

later. Regardless of the site of fusion initiation, fusion seems to be a relatively equal process

when border breakdown is observed, with the resulting syncytium occupying the same footprint

that the two fusion partners did, at least initially. For apical shrinking, however, one cell appears

to transfer its cytoplasmic contents and nucleus into another recipient cell, with both cytoplasm

and nucleus moving laterally to the location of the fusion recipient, while the apical surface of

the donor cell shrinks. It is possible that apical shrinking may indicate a different location for the

initial fusion pore below the plane of the adherens junctions; it is also possible that this may

reflect a difference in the starting pressure of the two fusion partners, so that one subsumes the

other.

It is unclear what triggers either border breakdown or apical shrinking fusion. Many

developmentally programmed cell fusions are mediated by fusogens, cell surface proteins that

bring opposing membranes into close contact with each other, as in the *C. elegans* hypodermis

(Chernomordik and Kozlov, 2008; Iosilevskii and Podbilewicz, 2021; Markvoort and Marrink,

2011; Mohler et al., 2002; Podbilewicz et al., 2006; Sapir et al., 2007; Shemer et al., 2004). For

other cell fusions, the fusogen is elusive and may not exist, as none has been identified yet in

Drosophila myoblast fusions, which occur when a fusion competent myoblast generates actin-

rich podosome-like membrane protrusions that invade a founder cell (Kim et al., 2015b; Lee and

Chen, 2019; Petrany and Millay, 2019; Rushton et al., 1995; Sens et al., 2010). Wound-induced

fusion may be a response to the plasma membrane damage that occurs around wounds; indeed,

plasma membrane damage has been documented around both laser wounds and puncture wounds

(McNeil and Steinhardt, 2003; Shannon et al., 2017). Interestingly, in the large syncytial cells of

the *C. elegans* hypodermis, plasma membrane repair after a puncture wound requires the fusogen

EFF-1 (Meng et al., 2020).

Polyploidy as a wound response has begun to get increased recognition. In adult

Drosophila, epithelial puncture wounds are repaired by both endoreplication and syncytia

formation (Bailey et al., 2020; Besen-McNally et al., 2021; Grendler et al., 2019; Losick, 2016;

Losick et al., 2013; Losick et al., 2016). In the zebrafish epicardium, genetic ablation is repaired

by a wavefront of multinucleated polyploid cells formed by endomitosis, and these lead diploid

cells to encompass the heart (Cao et al., 2017). In adult mammalian cardiomyocytes, polyploidy

may be an adaptive response to maintain growth after the cardiomyocytes lose their ability to

complete mitosis. Mouse cornea endothelial cells endoreplicate to increase polyploidy to restore

tissue ploidy following genetic ablation (Losick et al., 2016). Mammalian hepatocytes are known

to become increasingly polyploid with age (Carriere, 1969; Wheatley, 2008) and in response to

various types of injury and disease (Gentric et al., 2015; Madra et al., 1995; Muramatsu et al.,

2000; Sigal et al., 1999; Toyoda et al., 2005; Wilkinson et al., 2019). All mechanisms that

promote polyploidy – fusion, endomitosis, endoreplication – result in larger cells with the

potential to localize more resources; of these, fusion would act the fastest after wounding

because there is no need for DNA replication. Interestingly, in *Drosophila* embryos, wounds

induce the surrounding cells to become larger by increasing their volume alone and not their

ploidy (Scepanovic et al., 2021), suggesting that simply an increase in size is important.

Although many examples of wound-induced polyploidy exist, it is still likely to be an

underreported phenomenon, as endpoint analysis might miss a transient polyploid response to

injury; live imaging is the surest way to identify a polyploid wounding response.

Another polyploid response to injury can occur after surgical implantation of biomaterials

for the purpose of guiding regeneration, as reviewed previously (Al-Maawi et al., 2017). In some

cases, only mononuclear cells of the immune system respond to the implant, and in these cases

the biomaterial is integrated into the body; in other cases, the implant triggers the fusion of

immune cells into multinucleated giant cells, and in these cases the material is degraded and

rejected. These multinucleated giant cells seem to share properties with the syncytia of the pupal

notum, as they are formed by fusion in response to an environmental trigger and they have an

aggressive ability to protect the animal in response to wounding. As these studies highlight,

understanding the formation, maintenance, and regulation of polyploid cells may improve our

ability to successfully implant biomaterials to aid tissue regeneration.

It is often noted that wound responses are similar to cancer cell behaviors. This similarity

extends to wound-induced syncytia and their counterparts, polyploid giant cancer cells, as both

cell types are highly aggressive and invasive. Chemotherapeutics induce the formation of

polyploid giant cancer cells (Illidge et al., 2000; Mosieniak et al., 2015; Ogden et al., 2015;

Wang et al., 2013), and some studies indicate that they can form through cell-cell fusion in

tumors (Melzer et al., 2018; Noubissi et al., 2015; Powell et al., 2011; Song et al., 2021; Zhang et

al., 2021). Once formed polyploid giant cancer cells are hypothesized to escape further

chemotherapy treatments due to increased resistance to genotoxic stress (Weihua et al., 2011).

These polyploid giant cancer cells and their progeny also exhibit increased migration and

invasion potential (Qu et al., 2013; Zhao et al., 2021). The parallels between the behaviors of

polyploid giant cancer cells and the wound-induced syncytia of the pupal notum highlight the

importance of understanding wound induced syncytia formation in a highly reproducible system,

as a basic understanding of how these cells form in the *Drosophila* notum could inform how they

become dysregulated in cancer.

FIGURE LEGENDS:

Figure 1. Wounds induce epithelial syncytia via cell fusion.

A) Syncytia form within 2 h post wounding, evident by the clustering of multiple nuclei within

cell borders.

B) The number of nuclei per syncytia increases over time after wounding. Number of nuclei was

estimated based on area and nuclear density (see text) for the 3 largest syncytia of 3 different

wounds, mean and SD.

C-D) Larger wounds generate larger syncytia. Images are at 3 h post wounding, single syncytium

outlined.

E) Syncytial apical area is proportional to initial wound size. Each dot represents a wound, made

with either low or high laser energy as sown. For each wound, the mean area of the three largest

syncytia is plotted. Bars represent SD.

F) A time course of six cells fusing within 30 min after wounding. Apical borders are lost (white

arrowhead) as syncytia form. Original cells are numbered.

G) All borders lost to cell fusion (white) mapped to cells in the first frame after wounding. The

leading edge of wound closure will form at dashed line; cells within the shaded area were

damaged by the wound and will be dismantled.

H) Distance from the wound center vs time for all border breakdowns in 3 wounds. Each symbol

represents a cell border. Leading-edge locations indicated by solid lines.

I) Cytoplasmic GFP is expressed in cell 1 before wounding and mixes with neighboring cells 2-4

by 2 min after wounding. Cytoplasmic sharing is followed by the lagging fusion indicator of

visible border breakdown (white arrow). The fates of cells 3 and 4 are shown at later times in

Figure 2D. Maximum intensity projections in A, C-D, G; single Z slices in F, I. Scale bars:

A,C,D,G = 20 μm, F,I = 10 μm. W and red star indicate wound.

Figure 2: Cell fusion often appears as apical shrinking.

A) The apical footprint of an epithelial cell shrinks in the epithelial plane after wounding (yellow

arrow).

B) Same sample as A, showing that the nucleus (asterisk) of the apically shrinking cell enters a

neighboring syncytium, outlined in B[iv].

C) Cell 1 expresses actin-GFP before wounding. After wounding, cell 1 fuses with cells 2-6

evidenced by GFP sharing, then the apical surface of cell 1 shrinks.

D) Two cells undergoing apical shrinking are identified in the X-Y plane with white and yellow

arrows, shown at three times after wounding. Below, two X-Z projections are shown for each, at

Y1 and Y2 as indicated, with the Z-plane of the adherens junctions (Z_{AJ}) indicated by dotted

lines. Rather than extrude, cytoplasm moves to the right as the cell depth in the Z-axis

diminishes, so that cytoplasm joins with the neighboring wound-proximal syncytium. These

video frames are a continuation of the sample shown in Figure 1I.

E) All cells displaying apical shrinking mapped to first frame after wounding.

F) All apical shrinking and border breakdowns were tracked in 3 wounds. Border-breakdown

fusions happen sooner after wounding than apical-shrinking fusions. A, B, C, D (top), and E

show maximum intensity projections. Lower panels in D show X-Z projections. Scale bar for all

panels A and B shown in B[iv.] A, B, C, D (top),E = 10 µm; D (X-Z projections) = 5 µm.

Figure 3: Half the cells near the wound fuse to form syncytia, demonstrated by tracking

individual cell fates.

A) All GFP labeled cells in the region of fusion (80 µm) were tracked in 5 wounds over 6.5 h

after wounding to determine frequency of fusion initiation (GFP mixing) and later morphological

changes into syncytia. All morphological fusion events were preceded by GFP sharing, and 90%

of GFP sharing events were followed by morphological fusion. Untrackable cells lost GFP, see

Figure 3—figure supplement 1A.

B-C) Pre-wound location of persisting and fusing cells from panel A is shown with respect to the

wound center. Panel B shows that fusion is common within 70 μm. Panel C shows that apical-

shrinking fusion and border-breakdown fusion occur at similar distances from the wound.

Figure 4: *Atg1* promotes wound-induced fusion and faster wound closure.

A) Overview: *Atg1* was knocked down in central *pnr* domain (pink), visualized by nls-mCherry

(not shown). A laser pulse was targeted to the edge of the *pnr* domain (right or left) so that the

wound extended into both *Atg1* knockdown and control domains, allowing the symmetry of

response to be analyzed.

B-C) Inhibition of *Atg1* decreased the frequency of wound-induced fusion in the *pnr* domain. For

border loss, n = 11 pupae, p < 0.0001. For apical shrinking, n=9 pupae, p = 0.0008 (paired T-

test).

D-E) Wound closed more slowly when *Atg1* was knocked down. (D) Radius of the wound was

calculated by the distance between the wound center and the leading edge in *pnr* or control

domains. (E) Difference in the wound radius between *pnr* and control domains over time (i.e.,

wound asymmetry) is shown. Each dot represents one wound. With no genetic manipulation in

either domain (black), wound radius was slightly larger in *pnr* than in control domain. When

Atg1 was knocked down in the *pnr* domain, the asymmetry grew over time indicating slower

wound closure on the *Atg1* knockdown side. p = 0.0031 (5 hr) calculated from two-way

ANOVA, fit full model, comparing each cell mean with the other cell mean in that row. error bar

= 1 +/- SEM.

F-G) Larger cells (*i.e.* syncytia) move further during wound closure, evident in control wounds

(F) or with *Atg1* knockdown (G). Each data point represents a cell or syncytium present at the

leading edge when the wound is half closed. The curve of square root area was overlaid for

comparison, as it represents the amount of movement expected based on reshaping of a

cell/syncytium from an initial round state to one strongly elongated towards the wound.

Figure 5: Syncytia outpace mononuclear cells.

A) Before wounding, two clusters of cells are labeled with GFP, 1-2 and 3-4 (white numbers).

After wounding, cells 2 and 3 fuse with neighbors 5-9 to form a syncytium (dashed leading edge

in A^{iii}), which advances toward the wound, passing unfused cell 4 (arrow).

B-C) Unfused cell (outlined in orange and white) is replaced at leading edge by neighboring

syncytia (S and yellow outline).

D) Leading-edge perimeter was analyzed over time for three wounds, also analyzed in panel G.

Percent leading edge occupied by syncytia increased over time to 100%.

E) Images of sample 1 from graph D. Unfused cells (arrows) were tracked over the course of

wound closure; 30 min after wounding, 10 unfused cells at the wound leading edge are indicated

by arrows.

F) At 120 min, the last unfused cell was ejected from leading edge (arrow). The wound closed at

140 min.

G) The loss of unfused cells was analyzed over time in the three wounds from panel D. All

unfused cells are excluded from leading edge by syncytia well before each wound closed 20-160

min later.

Images are single Z slices in A^{i}-A^{ii} and maximum intensity projections in A^{iii}-F. Scale bar for

B,C shown in C^{iv} and for E,F shown in F. Scale bars in A,E,F = 20 μm, B,C = 10 μm.

Figure 6: Cells fuse along different axes at different frequencies, reducing the number of wound-proximal cell intercalations.

A) Illustration of tangential vs radial border breakdown. **B)** More tangential than radial borders break down after wounding. Data are from four wounds, with a total of 235 border breakdowns: 39 radial and 196 tangential. Individual counts are shown per wound with mean and SEM. **C)** Fusions across radial borders reduce intercalation at a wound. **D)** Quantification of intercalations and fusions around the three wounds of Figure 5D,G.

Figure 7: Computational modeling indicates that fusion speeds the rate of wound closure because of reduced cell intercalation.

(A-B) Experimental observations of cell shape index (perimeter divided by square root of area). By two hours after wounding, the cell shape index has increased for both syncytia and non-syncytial cells within two rows of the wound margin. These increases indicate an increase in tissue fluidity. (A) Cells and syncytia were segmented, and cell shape index calculated, as shown for this image at 115 min after wounding; cell shape index indicated by color-coding. (B) Pre- and post-wound cell-shape distributions were compiled from 6 pupae. The red dashed line represents the critical cell shape parameter, 3.81, for the solid-to-fluid transition in vertex models of epithelia. Grey boxes span the interquartile range with a line at the median; whiskers extend out 1.5x the median-to-closest-quartile range; and outliers beyond the whiskers are plotted as individual points. Distributions include 1304 pre-wound mononucleate cells, 168 post-wound mononucleate cells, and 52 post-wound syncytia; **** denotes $p < 10^{-6}$ level; *** denotes $p < 0.001$.

(C-E) Vertex model simulations of wound closure with cell fusion allowed or suppressed. When

the spatial and temporal probabilities for cell fusion match experimental observations, the model

yielded 55 ± 22 fusions per wound (mean $\pm$ standard deviation), with 15 ± 6 of these occurring at

radially aligned edges. As shown in C, fusions in the model speed wound closure: four

simulations per condition; shaded regions denote standard deviation; time normalized to the

average time to closure when fusion is suppressed. Panels D-E show a series of still frames from

a matched pair of simulations in which fusion is allowed or suppressed. Corresponding videos

are available as Video 5.

Figure 8: Syncytia concentrate pooled resources at the leading edge.

Random scattered cells expressing Actin-GFP were generated by heat-shock mediated flip-out

expression of Gal4. **A-B)** Labeled actin is expressed in cell 1 before wounding (A^i, B^i). These

cells are not close to the wound (inset in A^{ii}). By 28 min after wounding, actin-GFP equilibrated

between cells 1 and 2 (A^{ii}, B^{ii}), demonstrating cytoplasmic fusion. The resulting syncytium had

no access to the leading edge, and actin remained equilibrated, as shown in the kymograph (B^{iii})

generated from actin-GFP intensity over time at the yellow line in B^{ii}. Fusion was confirmed at

180 min after wounding by apical shrinking of cell 2 (not shown). **C-D)** Labeled actin is

expressed in cell 1 before wounding (C^i, D^i) and equilibrates between cells 1 and 2 by 6 minutes

after wounding, demonstrating cytoplasmic fusion (C^{ii}, D^{ii}). The resulting syncytium contacts the

leading edge, and by 28 min after wounding actin from cell 1 is redistributed to the wound

margin (C^{iii}, D^{iii}), as shown in the kymograph (D^{iv}) of actin intensity over time at the yellow line

in D^{iii}. Fusion was confirmed at 55 min after wounding, by apical shrinking of cell 1 (not

shown). **E-F)** Before wounding, actin-GFP in cell 1 is three cells away from the future leading

edge. After wounding, fusion of cells 1-4 allows actin-GFP to be subcellularly localized to the

leading-edge actin cable. Border breakdown is visible between cells 1-2 at 30 min after

wounding (E^v) and apical shrinking occurs later (see Video 6). **G)** Mean profile plot of actin-

GFP comparing the syncytia in F^v at 30 min after wounding (dark line) with the cells in F^i before

wounding (dotted line) demonstrating that nearly all actin-GFP has been relocalized to the

leading edge from its starting position 20-30 μm away. Single Z slices for E$^{i \, - \, ii}$, F$^{i \, - \, ii}$; maximum

intensity projections for A-D, E$^{iii \, - \, v}$, F$^{iii \, - \, v}$. Scale bar for panels in A-B shown in B^{ii}, 10 μm. Scale

bar for panels in C-D shown in D^{iii}, 5 μm. Scale bar for panels E-F shown in F^v, 10 μm.

Figure 1—figure supplement 1: Characteristics of the pupal notum epithelium.

A-C) An example of mitosis occurring ~80 μm from the wound. Scale bar for A-C shown in C^v,

10 μm. **D)** Z-slices at different depths of GFP-labeled cells reveal that the apical area (red

outline) does not reflect the position of cells at basal slices (yellow arrows). The nuclear shadow

in panel D^{ii} demonstrates the location of the nucleus. Scale bar, 10 μm. **E-H)** Ecad-GFP and

p120ctnRFP colocalize and behave similarly during border breakdown. Arrowheads in F-H

points to borders breaking down in first hour after wounding. Scale bar for F-H shown in H^v, 10

μm.

Figure 3—figure supplement 1: Temporal analysis of fusion events

A) An example of an untrackable cell is shown. After wounding, cell 1 loses cytoplasmic GFP,

but there is no obvious recipient cell. Cell 1 then shrinks. Scale bar = 10 μm.

B) Cells individually labeled with GFP reveal the timing and frequency of fusion or GFP loss

(untrackable). **C)** Fusion cells from panel B were divided into two types of fusion events,

shrinking cells and border breakdowns, to compare the temporal onset of each type of fusion. **D)**

Cell shrinking was a lengthy and variable process, lasting up to hundreds of minutes. 274

shrinking cell events from three wounds were identified by p120ctnRFP, mean and SD indicated.

Figure 6—figure supplement 1: Comparisons of tangential and radial border breakdowns

A) The distance of tangential and radial border breakdown events from the wound, compared

over time binned into 10 min intervals. The data is the same as in Figure 6B, from four wounds,

with a total of 235 border breakdowns: 39 radial and 196 tangential. Border breakdown events

were identified by p120ctn. B) The timing of tangential vs radial border breakdown fusion events

observed in single GFP-labeled cells.

Video 1: Syncytial cells form after wounding in the *Drosophila* pupal notum. Epithelial cell

borders in red (p120ctnRFP) and nuclei in green (HistoneGFP). White box on first frame denotes

field of view in Figure 1A. Video begins before wounding and extends to 2 h after wounding.

Video 2: GFP mixing precedes border breakdown after wounding. Arrow in first frame

points to cell border between cells that will fuse after wounding. GFP diffusion into the

unlabeled cell precedes visible border breakdown. w, wound region. Cell borders are labeled

with p120ctnRFP. Video begins before wounding and extends to 2 h 10 min after wounding.

Same cells as Figure 1I and 2D.

Video 3: Shrinking cells contribute to syncytia. Arrow in first frame points to an individual

cell labeled with Actin-GFP that fuses by shrinking after wounding. This cell contributes its

actin-GFP to neighboring cells minutes after wounding then shrinks much later; shrinking is first

evident about 1.5 h after wounding and is nearly complete by 3.5 h after wounding. w, wound

region. Cell borders are labeled with p120ctnRFP. Same cells as Figure 2C.

Video 4: Blood cells labeled with *hml-Gal4, UAS-GFP* were observed migrating to and along

the basal side of the wounded pupal notum. Video is a Z-stack maximum projection. Wound is

indicated by w in the first frame. No GFP was observed to enter the epithelium, indicating that

blood cells do not fuse with the wounded epithelium. Six similar wounds were analyzed, with no

evidence of fusion.

Video 5: Computational vertex models show that incorporating cell fusion speeds wound

closure. When fusion occurs with spatiotemporal and edge-orientation probabilities that match

experimental observations, wound closure in the model with fusion is 33% faster than when

fusion is suppressed.

Video 6: Syncytia pool actin and concentrate it at the leading edge of repair. An individual

cell labeled with actin-GFP fuses with wound proximal cells and contributes its actin to the

leading edge of the syncytium. w, wound region. The original source cell and its immediate

neighbor go on to shrink into wound proximal cells. Cell borders are labeled with p120ctnRFP.

Same cells as Figure 6E,F.

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Resource availability

Lead contact

Requests for fly lines, reagents, and additional questions should be directed to Dr. Andrea Page-

McCaw (andrea.page-mccaw@vanderbilt.edu)

Materials availability

Fly lines generated in this study are available from the Bloomington *Drosophila* Stock Center or

from the lead contact.

Data availability

All primary microscopy videos are available through OSF.

Experimental model and subject details

Drosophila melanogaster

Drosophila lines used in this study are in Table S1. All *Drosophila* lines were maintained on

standard cornmeal-molasses media supplemented with dry yeast. All flies, except those used in

heat-shock flip clonal analysis, were raised at room temperature. For clonal analysis experiments

flies were raised at 18 degrees Celsius until the 3rd instar stage when they were heat shocked in a

circulating water bath at 37°C for 3 minutes. They were then allowed to develop at room

temperature to 15-18hr after puparium formation (APF) before wounding experiments (described

below) were conducted. To knock down *Atg1*, *Atg1^{RNAi}* was crossed to the stock for internally

controlled wounding analysis, expressing *Ecad-GFP* and *TubP-Gal80^{ts}* ubiquitously and *pnr-*

Gal4, UAS-nls-mCherry in the central region of the notum, similar to our previous system

(O'Connor et al., 2021b). Crosses were moved to 29° for 6 days to allow expression of the RNAi

construct and dissected between 12-15 hr APF.

Method details

Pupal mounting

At room temperature, white prepupae were identified and marked within plastic food vials. 15-18 APF pupae were removed from the vial onto a piece of double-sided tape (Scotch brand, catalogue #665) applied to a microscope slide. Using fine forceps, the anterior pupal case was removed exposing the head and notum of all pupae applied to the tape, as previously described (O'Connor et al., 2022; Shannon et al., 2017). The tape was carefully removed from the microscope slide and inverted onto a pre-prepared cover glass (Corning 2980-246, 24 mm x 64 mm) (O'Connor et al., 2022). The pupae were carefully pressed down onto the cover glass by adhering the section of tape above the pupal head. Once the notum was visibly pressed onto the cover glass an oxygen permeable membrane (YSI, standard membrane kit, cat#1329882) was applied to prevent the pupae from drying out during imaging.

Pupal survival

Following imaging, pupae were kept mounted as described above and allowed to continue to develop and eclose for 3-4 days. Pupae that continued developing until they were able to crawl out of the partially dissected case were classified as 'survived' and their data acquired form these samples were used for analysis. If a pupae did not survive to eclosion, the associated datasets were not used in the study.

Live imaging

Images were collected using a Nikon Ti2 Eclipse with X-light V2 spinning disc (Nikon, Tokyo, Japan) with a 40X 1.3 NA oil-immersion objective or 60X 1.4 NA oil-immersion objective. Unless otherwise noted samples were imaged pre-wounding, immediately after wounding, every 2 min for 30 min, and then every 10 min for 6 h. Images were pre-processed in NIS-Elements using combinations of background subtraction, rolling ball correction, local contrast, and

Denoise a.i. Assembly of figure panels was done using Affinity Designer and frames were

centered on the entity in focus, compensating for frame shift due to wounding.

Laser ablation

A single pulse of a 3rd harmonic (355 nm) Q-switched Nd:YAG laser (5 ns pulse-width,

Continuum Minilite II, Santa Clara, CA) was used for laser ablation. Laser pulse energies were

kept to 1.9 μJ +/- 0.1 μJ, increased from our previous report (O'Connor et al., 2021b) to keep the

wound size similar between old and new ablation rig.

Border breakdown and tangential vs radial assignment analysis

Individual border breakdown events were manually observed using FIJI by identifying syncytia

late in the video and back-tracking to determine which borders broke down to form each

syncytium. These borders were traced back to the first frame after wounding to develop the map

on Fig 1G. For each border breakdown event, distance from the center of the wound and time

after wounding were recorded in Microsoft Excel. These events were categorized as tangential or

radial based on the orientation of the border-to-be-lost relative to a vector pointing outward from

the center of the wound. Specifically, the line tool in FIJI was used to measure both the angle of

the border with respect to the horizon, θ, and the angle of the line from the center of the wound

to the center of the border with respect to the horizon, α. If $|\cos(\alpha - \theta)| \geq \cos 45°$, then the

border was classified as radial; otherwise, the border was classified as tangential.

Shrinking cell initiation / duration analysis

Shrinking cells were identified in live microscopy videos by beginning at the end of the video

and playing backwards in FIJI. Backwards, a shrinking cell appears to bloom from the epithelial

layer, characterized by the expansion of a bright puncta of p120ctnRFP. Each cell that underwent

this behavior was marked on a single frame of the video, then the distance from the center of the

wound when shrinking started was denoted as well as the time that the shrinking started and

completed. All cells that shrank were then manually traced back to the first frame after wounding

to develop the map of shrinking cells (Fig 2E).

Approximating nuclei per syncytia

Nuclei and cell borders do not align in Z-projections of the pupal notum as the cells are non-

prismatic. To estimate the number of nuclei per syncytium, the pre-wounding density of nuclei

per unit area was determined for the circular region where syncytia form after wounding. Next,

the apical area of the three largest syncytia/cells around a wound was measured at 0h, 1 h and 2 h

post wounding. The area of each syncytia was multiplied by the nuclear density to yield the

approximate number of nuclei per syncytia. The number of nuclei in each of the three syncytia

was averaged to give a value for each of three samples in Figure 1B.

Measuring apical area of syncytia across varied wound sizes

The three largest syncytia were determined by eye in FIJI for six samples, three ablated at 1.9 μJ

and three ablated at 3 μJ ablation. The apical area of syncytia was measured 3 h post wounding

using the p120ctnRFP signal. Initial wound size was calculated by measuring Myosin II marked

leading edge when it became apparent 30-160 min post wounding.

Unfused cells at leading edge: count and percent analysis

Unfused cells at the leading edge were identified using FIJI by a lack of border breakdowns.

Each unfused cell was manually observed over the duration of wound closure and the time at

which it departed from the leading edge was noted. A count of unfused cells at the leading edge

was created in Excel and formal graphs were generated using Prism 9. To measure percent of the

leading edge comprised of unfused vs. syncytial cells, each unfused cell's leading edge contact

was measured in FIJI using the polygon line tool. The total circumference of the wound was

measured using the polygon line tool and unfused cell measurements were subtracted from the

total to infer the syncytial occupancy at the leading edge. Formal histograms were generated

using Prism 9.

Analyzing GFP labeled cells

107 individually labeled GFP cells were analyzed across 5 wounds over 6.5 h. The position of

the ablation was optimized to place as many individually labeled cells within 40-80 μm from the

center of the wound as possible. After wounding it was possible to identify a mixing event by the

decrease in intensity from the source cell with a corresponding increase in intensity of a

previously unlabeled neighbor. Intensity differences made it possible to distinguish instances

where two source cells were adjacent to each other but only one had a mixing event. However,

large patches of source cells were not evaluated because inter-patch mixing was not

distinguishable. To evaluate if border breakdowns were preceded by mixing, the 11 individually

labeled cells that had border breakdowns were tracked back to the start of the video and

confirmed to have a mixing event. There was never an instance where a labeled source cell had a

border breakdown without a prior mixing event occurring.

Wound closure analysis

A pigmented scar forms at the site of laser ablation making identifying the exact moment a

wound is closed difficult. Since the scar is approximately the same size in each sample, the time

point at which the Myosin II signal disappeared below the scar was used as a proxy for closure.

Fusion analysis

A cell border was counted as a location of wound-induced fusion if it met three criteria: (1)

adherens junctions along the cell border were lost; (2) the lost adherens junctions were not

restored; and (3) the loss of adherens junctions was accompanied by a morphological change of

the neighboring cells, for example, the moving apart of tri-cellular junctions previously

connected by the lost cell border. Since border-breakdown fusions are observed most frequently

within 1 hr after wounding, we counted all such fusions occurring within 1 hr 40 min of

wounding.

When comparing the fusion frequency in *pnr* versus control domains, we used a

landscape-oriented rectangle centered on the wound with its height defined by the inner radius of

the zone of nuclear membrane damage visualized by the release of nls-mCherry from the

nucleus, which is approximately the same as the zone of lysis (O'Connor et al., 2021a).

Replacing the annular region with an extended rectangle excludes possible heterotypic fusions

along the *pnr*-control border just above and below the wound. To calculate the frequency of

fusion, in addition to the raw number of fusion borders, the total number of cell borders was also

estimated by area-based scaling of the border count within a randomly selected 60-x-60-pixel

(16.8-x-16.8-µm) region in the pre-wound image.

Since fusions can also appear as apical shrinking rather than border breakdown, we also

quantified the number of apical-shrinking cell fusions in *pnr* versus control domains. Apical-

shrinking cell fusions were defined as diploid cells that decreased in surface area over time and

fully disappeared within a 5-hr movie. As with fusion analysis, cells near the *pnr*-control border

were excluded. Apical shrinking cells were counted manually and their spatial locations marked

using FIJI's "Multi-point" tool.

Determining the effect of syncytia on wound closure

The distance between the leading edge and the wound center over time was used to calculate the

speed of wound closure. The distance was calculated using the coordinates of the wound center

and fixed points on the leading edge. To identify fixed positions on the leading edge that are

unbiased and consistent over time, four reference lines, all crossing the center of the wound,

were drawn using the red channel with only the nuc-mCherry signal: line 1 along the edge of the

pnr domain labeled by nuc-mCherry, line 2 perpendicular to line 1, and line 3

and 4 are 30° from line 2. These references lines were then overlaid on the green channel with

the E-cadherin signal.

To determine the speed of wound closure, the intersection of E-cadherin marked leading

edge and reference lines 2-4 were used as the position of the leading edge. That is, at each time

point, a total of 6 positions of the leading edge were recorded, among which 3 will be in the *pnr*

domain and the other 3 in the ctrl domain. The average distance (d) between the leading edge and

the center of the wound were calculated at each time point for both the *pnr* domain (d_{pnr}) and the

control domain (d_{ctrl}). The difference between control and *pnr* distance ($\Delta d = d_{pnr} - d_{ctrl}$) was

calculated over time for both the control pupae with no genetic manipulation in the *pnr* domain

(*pnr > +*) and experimental animals with *Atg1* knocked down in the *pnr* domain (*pnr >*

Atg1^{RNAi}). To determine whether Δd is statistically different between control and experimental

pupae at each time point, two-way ANOVA (fit using full model) was used, comparing each cell

mean with the other cell mean in that row.

To determine the distance syncytia covered during wound healing, syncytia were

analyzed (1) at the leading edge when wound is half closed and (2) within the bow-tie region

between reference line 3 and 4. ROIs were drawn along syncytia of interest using the "Freehand

selections" tool of FIJI. In addition to syncytia location when wound is half closed, the starting

position of cells that later fuse to form syncytia were also recorded in live-imaging videos,

tracking the syncytia back in time. In addition to area, the coordinates of ROIs outlining syncytia

at different time points were obtained using a self-written FIJI Macro. Within each ROI, the

coordinate closest to the center of the wound was recorded using python, as the location of the

syncytia. The distance a certain syncytium moved was calculated by subtracting the distance

between the syncytium and the wound center when the wound was half closed from the distance

between the syncytium and the wound center immediately after injury.

Calculating intercalation in live imaging

The change in the number of cells when the leading edge forms at 30 min (N_{start}) to when the

wound is closed ($N_{end)}$ is equal to the number of intercalations plus the number of radial fusion

events. Thus, (intercalations = ΔN – radial fusions). For the same three samples used in Fig

4D,G, we determined ΔN from N_{start} at 30 min and N_{end} when the wound had closed. Radial

fusions were tallied by manually observing border breakdown events between the leading-edge

cells and intercalations were calculated. Each radial fusion was counted as one prevented

intercalation event.

Calculating cell shape index

Images of pupae labeled with Ecad-GFP were segmented into individual cells with Cellpose

(Stringer et al., 2021); cells that were not readily segmented were excluded from subsequent

analysis. To avoid perimeter inflation due to pixelation, the boundaries of segmented cells were

smoothed by taking the midpoint between every other pair of boundary pixels. Smoothing and

calculation of perimeters, areas and cell shape indices ($P/\sqrt{A}$) were performed in Mathematica

(Wolfram Research Inc., Champaign, IL).

Vertex models with cell fusion

Simulations of wound healing were run using vertex models implemented in Mathematica

(Wolfram Research Inc., Champaign, IL) following the methods of Tetley et al. (2019)and using

parameters that match experimental observations from the *Drosophila* pupal notum as detailed in

Han et al. (2024) with the following exceptions: the mean line tension on each edge (Λ) was

specified in terms of a target shape parameter (ρ_0) such that $\Lambda = -2\rho_0\Gamma\sqrt{A_0}$, where the

contractility (Γ) and target cell area (A_0) were taken from Han et al. (2024) and $\rho_0 = 3.745$ was

chosen so that the actual cell shape index matched experimental pre-wound measurements; and

the line tension variability (σ_m) was decreased from 1.0×10^{-2} to 9.3×10^{-4} so that the

intercalation rate in unwounded cell sheets matched experimental observations. Pre-wound

configurations were generated by performing a Voronoi tessellation of a circular area with 320

randomly distributed seed points and then equilibrating the cell configuration without stochastic

fluctuations until it reached a steady state. Wounds were introduced by removing all cell borders

within a circular patch ~8 cells across and removing the wound's contributions to the energy

Hamiltonian. To handle wound closure and fusion, the following additions were made to the

model: (1) purse-string tension on the leading edge of the wound was incorporated as in Tetley et

al. (2019) with a normalized strength of 0.115; (2) traction/crawling forces of cells on the leading

edge of the wound were incorporated as a uniform tensile stress acting inwardly on the edges and

vertices of the wound area (similar to the uniform stress applied to the outer edge of the patch to

represent tension from surrounding cells); this inward stress had a normalized strength of

$\Sigma_{in}/KA_0 = 0.13$, where K is the area elasticity modulus; (3) the cell-cell interfaces at which

fusion would occur were selected stochastically with probabilities that depended on time,

distance from the wound, and the radial or tangential orientation of the interface – all chosen to

match experimental observations reported here; and (4) the fusion of two cells was handled by

eliminating the interface between those cells and setting the target area of the fused cell to the

sum of the target areas of its two progenitors. All cells, fused or not, had the same contractility

and target shape parameter.

Kymograph and plot profile analysis

Actin-GFP intensity was analyzed using the kymograph tool in FIJI after drawing a 11-pixel line

through the middle of the syncytia. Profile plot values were exported from NIS elements to Excel

and graphs were generated using Prism.

Key Resources Table				
Reagent type (species) or resource	**Designation**	**Source or reference**	**Identifiers**	**Additional information**
Fly line (*Drosophila melanogaster*)	"HistoneGFP"	BDSC:	24163	w^*; $P\{w^{+m} =His2Av\text{-}EGFP.C\}2/$ SM6a
Fly line (*Drosophila melanogaster*)	"p120ctnRFP"	gift from Shigeo Hayashi (Ogura et al., 2018)		y; $ubiP\text{-}p120ctn\text{-}TagRFP$
Fly line (*Drosophila melanogaster*)	"Ecad-GFP"	Kyoto Drosophila stock center	109007	w^*; $\{w^+*=ubi\text{-}p63E\text{-}shg.GFP\}5$
Fly line (*Drosophila melanogaster*)	"AyGal4"	BDSC:	3953	w^{1118}; $P\{w^{+mC}=AyGAL4\}25/CyO$
Fly line (*Drosophila melanogaster*)	"hsFLP"	BDSC:	55813	w^{1118}; $P\{y^{+t7.7} w^{+mC}=hs\text{-}FLPD5\}attP2$
Fly line (*Drosophila melanogaster*)	"GFP"	BDSC:	1522	w^*; $P\{w^{+mC}=UAS\text{-}GFP.S65T\}eg^{T10}$
Fly line (*Drosophila melanogaster*)	"Actin-GFP"	BDSC:	7310	w^{1118}; $P\{w^{+mC}=UASp\text{-}Act5C.T:GFP\}2$; $l(3)^*/TM6C, Sb^1 Tb^1$
Fly line (*Drosophila melanogaster*)	"MyosinII-GFP"	BDSC:	51564	w^*; $P\{w^{+mC}=PTTGC\}zip^{CC01626}/SM6a$

Fly line (*Drosophila melanogaster*)	"HistoneRFP"	BDSC:	23651	*y w; His2AvRFP / CyO*
Fly line (*Drosophila melanogaster*)	"UAS-Atg1^{RNAi}"	BDSC	26731	*y^1 v^1; P{y$^{+t7.7}$v$^{+t1.8}$=TRiP.JF02273}attP2*
Fly line (*Drosophila melanogaster*)	internally controlled knockdown for wounding	this study		*w*; Ecad-GFP; pnr-Gal4, tub-Gal80^{ts}, UAS-nls-mCherry/SM6-TM6B*
Fly line (*Drosophila melanogaster*)	hml-Gal4	BDSC	30139	*w^{1118}; P{w^{+mC} =Hml-GAL4.Delta}2*
Software	FIJI	Schindelin et al., 2012	RRID: SCR_002285	
Software	NIS Elements	Nikon Instruments Inc.	RRID: SCR_002285	
Software	Microsoft Excel	Microsoft	https://www.microsoft.com/en-us/microsoft-365/excel	
Software	GraphPad Prism 9	GraphPad	https://www.graphpad.com/scientific-software/prism/	
Software	Affinity Designer	Affinity Serif	https://affinity.serif.com/en-us/designer/	

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Figure 1

A^i Pre-wound   A^ii 30 min   A^iii 2 hr
p120ctnRFP
Histone GFP

B Syncytia grow over time
Sample 1
Sample 2
Sample 3
max [nuclei / cell]
Time (hr)
PreW   1   2

C 1.5 μJ   D 3 μJ
p120ctnRFP
Histone GFP
W   W

E Larger wounds make larger syncytia
○ 1.5 μJ ablation
● 3.0 μJ ablation
Syncytia area (μm²)
Initial wound size (μm²)

F^i 0 min   F^ii 10 min   F^iii 20 min   F^iv 30 min
p120ctnRFP
W   W   W   W

G Border breakdowns
p120ctnRFP

H Border breakdown events
Sample 1
Sample 2
Sample 3
Sample 4
Distance (μm)
Approximate leading edges
Time (min)
0-9 10-19 20-29 30-39 40-49 50-59 60-69 70-79 80-89 90-99 100-109 110-120 120-130

I^i Pre-wound   I^ii 2 min   I^iii 16 min   I^iv 60 min
p120ctnRFP
GFP
W   W   W

Figure 2

Figure 3

Figure 4

A *Drosophila* notum
*pnr>Atg1^RNAi^*
ctrl **X** wound ctrl

B ctrl   *pnr > Atg1^RNAi^*
Ecad-GFP
0 min
30 min
1 hr
2 hr
20 μm

C
% borders lost to fusion — ****
ctrl   *Atg1^RNAi^*

shrinking cells — ***
ctrl   *Atg1^RNAi^*

D ctrl   *Atg1^RNAi^*
Wound radius (μm)
Time (hr)

E • *pnr > +*   • *pnr > Atg1^RNAi^*
Δ wound radius (pnr - control)
ns   ns   ns   **
2 hr   3 hr   4 hr   5 hr
Time post wound (hr)

F
Distance moved (μm)
ctrl
pnr > +
sqrt (area)
Individual cell area (μm²)

G
Distance moved (μm)
ctrl
*pnr > Atg1^RNAi^*
sqrt (area)
Individual cell area (μm²)

Figure 5

Figure 6

Figure 7

A

Cell Shape Index

B

Cell Shape Index

Pre-Wound Non-Syncytia   Post-Wound Non-Syncytia   Post-Wound Syncytia

****

****

***

C

Normalized Wound Area (A/A$_0$)

Fusion allowed

Fusion suppressed

Normalized Time (t / <t$_{close\ w/o\ fusion}$>)

D Fusion allowed

E Fusion suppressed

0.0   0.17   0.33   0.50   0.67   0.84   1.0

Normalized Time

Figure 8

Figure 1—figure supplement 1

Figure 3 —figure supplement 1

Figure 6 —figure supplement 1

A

B