A complex relationship exists between autophagy and apoptosis, but the regulatory mechanisms underlying their interactions are largely unknown. We conducted a systematic study of Drosophila melanogaster cell death–related genes to determine their requirement in the regulation of starvation-induced autophagy. We discovered that six cell death genes—death caspase-1 (Dcp-1), hid, Bruce, Buffy, debcl, and p53—as well as Ras–Raf–mitogen activated protein kinase signaling pathway components had a role in autophagy regulation in D. melanogaster cultured cells. During D. melanogaster oogenesis, we found that autophagy is induced at two nutrient status checkpoints: germarium and mid-oogenesis. At these two stages, the effector caspase Dcp-1 and the inhibitor of apoptosis protein Bruce function to regulate both autophagy and starvation-induced cell death. Mutations in Atg1 and Atg7 resulted in reduced DNA fragmentation in degenerating midstage egg chambers but did not appear to affect nuclear condensation, which indicates that autophagy contributes in part to cell death in the ovary. Our study provides new insights into the molecular mechanisms that coordinately regulate autophagic and apoptotic events in vivo.

Introduction

Macroautophagy (hereafter referred to as autophagy) is an evolutionarily conserved mechanism for the degradation of long-lived proteins and organelles. During autophagy, cytoplasmic components are sequestered into double membrane structures called autophagosomes, which then fuse with lysosomes to form autolysosomes, where degradation occurs (for review see Klionsky, 2007). Currently, there are 31 autophagy-related (Atg) genes in yeast, and 18 Atg proteins are essential for autophagosome formation (Mizushima, 2007). Most yeast Atg genes have orthologues in higher eukaryotes and encode proteins required for autophagy induction, autophagosome nucleation, expansion, and completion, and final retrieval of Atg protein complexes from mature autophagosomes (for review see Levine and Yuan, 2005).

Depending on the physiological and pathological conditions, autophagy has been shown to act as a pro-survival or pro-death mechanism in vertebrates (for reviews see Levine and Yuan, 2005; Maiuri et al., 2007). In the case of growth factor withdrawal, starvation, and neurodegeneration, autophagy has been shown to function in cell survival (Boya et al., 2005; Lum et al., 2005; Hara et al., 2006; Komatsu et al., 2006). In contrast, autophagy has been found to act as a cell death mechanism in derived cell lines where caspases or apoptotic regulators are impaired (Shimizu et al., 2004; Yu et al., 2004). The nature and perhaps level of the stress stimulus may also be important in determining whether autophagy promotes cell survival or cell death (Boya et al., 2005; Maiuri et al., 2007; Wang et al., 2008).

Effector caspase Dcp-1 and IAP protein Bruce regulate starvation-induced autophagy during Drosophila melanogaster oogenesis

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2Department of Biology, Boston University, Boston MA 02215

A complex relationship exists between autophagy and apoptosis, but the regulatory mechanisms underlying their interactions are largely unknown. We conducted a systematic study of Drosophila melanogaster cell death–related genes to determine their requirement in the regulation of starvation-induced autophagy. We discovered that six cell death genes—death caspase-1 (Dcp-1), hid, Bruce, Buffy, debcl, and p53—as well as Ras–Raf–mitogen activated protein kinase signaling pathway components had a role in autophagy regulation in D. melanogaster cultured cells. During D. melanogaster oogenesis, we found that autophagy is induced at two nutrient status checkpoints: germarium and mid-oogenesis. At these two stages, the effector caspase Dcp-1 and the inhibitor of apoptosis protein Bruce function to regulate both autophagy and starvation-induced cell death. Mutations in Atg1 and Atg7 resulted in reduced DNA fragmentation in degenerating midstage egg chambers but did not appear to affect nuclear condensation, which indicates that autophagy contributes in part to cell death in the ovary. Our study provides new insights into the molecular mechanisms that coordinately regulate autophagic and apoptotic events in vivo.
Overlaps between components in apoptosis and autophagic pathways have been described. Upstream signal transducers in apoptotic pathways, including TNF-related apoptosis-inducing ligand (TRAIL), TNF, Fas-associated protein with death domain (FADD), and death-associated protein kinase (DAPK), have been shown to play a role in autophagy regulation (Prins et al., 1998; Inbal et al., 2002; Mills et al., 2004; Thorburn et al., 2005), and two apoptotic inducers, including sphingolipid and ceramide, can activate autophagy in mammalian cells (Ghidoni et al., 1996; Scarlatti et al., 2004). In addition, two recent studies demonstrate physical and functional interactions between components of apoptosis and autophagy. First, the antiapoptosis protein, Bcl-2, suppresses autophagy through a direct interaction with Beclin 1, a protein required for autophagy (Pattingre et al., 2005). Second, Atg5, which is cleaved by calpain, associates with Bcl-XL, leading to cytochrome c release and caspase activation (Yousefi et al., 2006). Further examples and discussion of the connections between apoptosis and autophagy can be found in several recent reviews on this topic (Ferraro and Cecconi, 2007; Maiuri et al., 2007; Thorburn, 2008). The current findings indicate that there is a complex relationship between apoptosis and autophagy, but the regulatory mechanisms underlying the crosstalk between the two processes are still largely unknown.

Autophagy is observed in several Drosophila melanogaster tissues during development, and thus D. melanogaster is useful as a model to study autophagy in the context of a living organism. 14 D. melanogaster annotated genes share significant sequence identity with the yeast Atg genes, and, overall, eight D. melanogaster Atg homologues have already been shown to be required for autophagy function (Scott et al., 2004; Berry and Baehrecke, 2007). In addition, recent studies demonstrated the role of autophagy in D. melanogaster physiological cell death. Loss of Atg genes, including Atg1, Atg2, Atg3, Atg6, Atg7, Atg8, Atg12, and Atg18, inhibited proper degradation of salivary glands during development. Overexpression of Atg1 induced premature salivary gland cell death in a caspase-independent manner (Berry and Baehrecke, 2007). In contrast, caspase activity was required for Atg1-mediated apoptotic death in the fat body (Scott et al., 2007). Mutation of Atg7 resulted in an inhibition of DNA fragmentation in the midgut but led to an increase of DNA fragmentation in the adult D. melanogaster brain (Juhasz et al., 2007). Together, these results further suggest that the mechanistic role of autophagy in cell death and the interrelations between autophagy and apoptosis may be tissue and/or context dependent.

The adult D. melanogaster ovary contains 15–20 ovarioles comprised of developing egg chambers, which consist of 16 germ line cells (15 nurse cells and 1 oocyte) surrounded by a layer of somatic follicle cells. The germ line cells originate from stem cells that undergo mitosis to form 16-cell cysts in a specialized region called the germarium. In the late stage of oogenesis, the nurse cells support the development of the oocyte by transferring to it their cytoplasmic contents. After this “dumping” event, the nurse cells undergo cell death, and their remnants are engulfed by the surrounding follicle cells (King, 1970; Spradling, 1993). In addition to this late-stage developmental cell death, egg chambers can be induced to die at two earlier stages, during germarium formation (in region 2) and mid-oogenesis, by factors such as nutrient deprivation, chemical insults, and altered hormonal signaling (Drummond-Barbosa and Spradling, 2001; McCall, 2004). In some respects, cell death during D. melanogaster oogenesis is similar to the death of D. melanogaster larval salivary glands. Both nurse cells and salivary gland cells are large and polyploid, and the entire tissues undergo cell death simultaneously (McCall, 2004). Notably, morphological features of autophagy have been described during mid-oogenesis cell death in a related species, Drosophila virilis (Velentzas et al., 2007), which suggests that the cell death process in ovaries and salivary glands share additional similarities.

Previous studies have focused on characterizing the role of autophagy genes in cell death and determining the paradoxical functions of autophagy (pro-survival and pro-death) in various cell lines and organisms. However, a systematic approach that investigates the involvement of cell death genes in starvation-induced autophagy has not been conducted. Here, we present RNAi analyses to determine whether known cell death–related genes in D. melanogaster play a role in autophagy regulation in the lethal (2) malignant blood neoplasm (l(2)mbn) cell line. We also used D. melanogaster genetics to investigate a role for the effector caspase death caspase-1 (Dcp-1) and the inhibitor of apoptosis (IAP) family member Bruce in autophagy regulation in vivo during D. melanogaster oogenesis. Further, we examine the function of autophagy genes Atg7 and Atg1 in starvation-induced germ line cell death in the D. melanogaster ovary.

**Results**

The RNAi screening assay identifies known positive and negative regulators of starvation-induced autophagy in D. melanogaster l(2)mbn cells

To quantify starvation-induced autophagy, we used a D. melanogaster tumorsropic larval hemocyte cell line, l(2)mbn (Ress et al., 2000), and used LysoTracker green (LTG) dye, which has been shown previously to label lysosomes and autolysosomes in D. melanogaster (Scott et al., 2004; Kliouisky et al., 2007). Flow cytometry was used to acquire LTG fluorescence of individual cells. Under nutrient-full medium conditions, we detected a basal level of LTG labeling in l(2)mbn cells (Fig. 1 A). When cells were transferred into amino acid–deprived medium for 2 h, we observed a detectable increase in LTG labeling. After 4 h of amino acid deprivation, a further increase in the percentage of cells with high LTG fluorescence levels (LTG$^{high}$) population) was observed (Fig. 1 A). To confirm that autophagy is indeed up-regulated under nutrient-deprived conditions in l(2)mbn cells, we constructed a stable l(2)mbn cell line expressing mammalian microtubule-associated protein 1 light chain 3 (LC3)/Atg8 fused to GFP protein, a widely used marker for autophagy (Kliouisky et al., 2007). During autophagy, LC3 conjugates to phosphatidylethanolamine, which then inserts into the autophagosomal membrane. Thus, localization of GFP-LC3 changes from a diffuse cytoplasmic pattern to a punctate autophagosomal membrane-bound pattern that can be monitored by microscopy (Mizushima
et al., 2001; Klionsky et al., 2007). As expected, the percentage of cells with more than three GFP-LC3 puncta (GFP-LC3 positive) was increased from 9% (n = 216) in the nutrient-full condition to 32% (n = 200) in the nutrient-starved condition for 2 h (Fig. 1B). Further, to confirm that LTG labeling correlates with autophagy in l(2)mbn cells, we used the pharmacological autophagy inhibitors 3-methyladenine (3MA) and bafilomycin A1 (Baf). 3MA blocks autophagy by inhibiting phosphoinositide 3-kinase (PI3K) activity (Seglen and Gordon, 1982). Baf is a specific inhibitor of lysosomal proton pumps and prevents the fusion of autophagosomes with lysosomes (Yamamoto et al., 2001; Klionsky et al., 2007). In l(2)mbn cells, both autophagy inhibitors significantly reduced LTG fluorescence levels after starvation treatment (Fig. 1, C and D). Consistently, the addition of 3MA also decreased the numbers of GFP-LC3–positive cells after starvation treatment. As expected, the addition of Baf, which is known to increase the autophagy levels in D. melanogaster l(2)mbn cells starved for 2 h (2h S) or 4 h (4h S) showed an increase in LTG fluorescence levels (x axis) compared with control cells in full-nutrient medium (C). The gate shown on the histogram represents the LTGhigh population. (B) Representative images of GFP-LC3 puncta in control and 2-h starved l(2)mbn cells. An increase in GFP-LC3 puncta was observed in the starved cells (left). Bar, 10 μm. (C) Flow cytometry analysis of 4-h starved cells were incubated with 3MA (4h S + 3MA) and Baf (4h S + Baf). Both autophagy inhibitors reduced the LTG fluorescence levels compared with starved cells (4h S). Control cells in nutrient-full medium (C) are represented by the brown line. (D) Both autophagy inhibitors, 3MA and Baf, reduced the LTGhigh population significantly. [3MA, P = 0.00001; and Baf, P = 0.00006]. (E) RNAi of representative Atg genes decreased the LTG fluorescence levels compared with control. [Atg1, P = 0.01; Atg5, P = 0.01; Atg7, P = 0.002; Atg8a, P = 0.008; Atg8b, P = 0.006; and Atg12, P = 0.02]. (F) RNAi of all tested genes in the TOR–PI3K pathways had a statistically significant effect on LTG fluorescence levels. Known negative regulators of autophagy are shown with gray bars; positive regulators are shown with white bars. [Pten, P = 0.007; Tsc1, P = 0.027; Tsc2, P = 0.025; RheB, P = 0.005; Tor, P = 0.016; and S6k, P = 0.012]. dsRNA corresponding to a human gene (Hs) was used as a negative control in E and F. Results represent the mean value ± SD from at least three independent experiments.

Figure 1. Quantification of starvation-induced autophagy in D. melanogaster l(2)mbn cells. (A) Flow cytometry analysis of l(2)mbn cells starved for 2 h (2h S) or 4 h (4h S) showed an increase in LTG fluorescence levels (x axis) compared with control cells in full-nutrient medium (C). The gate shown on the histogram represents the LTGhigh population. (B) Representative images of GFP-LC3 puncta in control and 2-h starved l(2)mbn cells. An increase in GFP-LC3 puncta was observed in the starved cells (left). Bar, 10 μm. (C) Flow cytometry analysis of 4-h starved cells were incubated with 3MA (4h S + 3MA) and Baf (4h S + Baf). Both autophagy inhibitors reduced the LTG fluorescence levels compared with starved cells (4h S). Control cells in nutrient-full medium (C) are represented by the brown line. (D) Both autophagy inhibitors, 3MA and Baf, reduced the LTGhigh population significantly. [3MA, P = 0.00001; and Baf, P = 0.00006]. (E) RNAi of representative Atg genes decreased the LTG fluorescence levels compared with control. [Atg1, P = 0.01; Atg5, P = 0.01; Atg7, P = 0.002; Atg8a, P = 0.008; Atg8b, P = 0.006; and Atg12, P = 0.02]. (F) RNAi of all tested genes in the TOR–PI3K pathways had a statistically significant effect on LTG fluorescence levels. Known negative regulators of autophagy are shown with gray bars; positive regulators are shown with white bars. [Pten, P = 0.007; Tsc1, P = 0.027; Tsc2, P = 0.025; RheB, P = 0.005; Tor, P = 0.016; and S6k, P = 0.012]. dsRNA corresponding to a human gene (Hs) was used as a negative control in E and F. Results represent the mean value ± SD from at least three independent experiments.
Figure 2. Identification of known cell death–related genes in autophagy regulation in l(2)mbn cells using RNAi. (A) The percentage of LTG-high cells was reduced by hid-RNAi (P = 0.006) but not by rpr, grim, and skl-RNAi. (B) Knockdown of Ras, Phl, and rl expression by RNAi resulted in an increase in the percentage of LTG-high cells. (Ras, P = 0.003; Phl, P = 0.001; and rl, P = 0.028). (C) th-RNAi treatment (24 h) had no significant effect on LTG levels; in contrast, RNAi of Bruce resulted in an increase in LTG fluorescence levels (P = 0.01). (D) Reduction of debcl, Buffy, or p53 expression by RNAi resulted in a decrease in LTG fluorescence levels. (debc1, P = 0.018; Buffy, P = 0.006; and p53, P = 0.004). (E) RNAi of effector caspase Dcp-1 resulted in a significant decrease in the LTG-high population (P = 0.001). (F) Representative images of GFP-LC3 puncta in cells treated with the indicated RNAi after a 2-h starvation treatment. Bar, 10 μm. (G) Quantification of cells with GFP-LC3 puncta after RNAi treatment. Cells with more than three GFP-LC3 punctate dots were considered to be GFP-LC3–positive cells. Cells treated with the RNAi indicated here all showed a significant difference (P < 0.05) in the percentage of GFP-LC3–positive
autophagy in l(2)mbn cells, we designed double-stranded RNAs (dsRNAs) against several genes in these pathways. RNAi of Tor or RheB, negative regulators of autophagy, showed an increase in LTG<sup>hi</sup> cells compared with Hs-dsRNA (negative control)-treated cells after starvation treatment (Fig. 1 F). In contrast, RNAi of Pten, Tsc1, Tsc2, and S6k, positive regulators of autophagy, showed a reduction in the LTG<sup>hi</sup> population (Fig. 1 F). These results indicate that components of TOR and PI3K pathway are essential to regulate starvation-induced autophagy in <i>D. melanogaster</i> l(2)mbn cells. These results also demonstrate that our primary screening method, a flow cytometry–based LTG assay, is capable of detecting alterations induced by RNAi-mediated knockdown of positive and negative regulators of autophagy. Thus, this method can be used to identify novel components in starvation-induced autophagy. To ensure that the changes in LTG fluorescence levels were caused by alterations in autophagy, we used GFP-LC3 to track changes in autophagosome formation in cells. RNAi of Tor showed an increase in the numbers of GFP-LC3 positive cells after starvation treatment (Fig. 2 G). In contrast, reduction of Pten expression by RNAi resulted in a decrease in the number of the GFP-LC3–positive cells (Fig. 2 G). Together, these two methods allow us to monitor the dynamic steps, formation of autophagosomes (GFP-LC3), and autophagosome-lysosome fusion (LTG), during autophagy.

### Identification of cell death-related genes that regulate starvation-induced autophagy in l(2)mbn cells

To better understand the relationship between autophagy and apoptosis, we investigated whether known cell death genes were required for starvation-induced autophagy in l(2)mbn cells. dsRNAs were designed against the <i>D. melanogaster</i> core cell death effectors, <i>rpr</i>, <i>hid</i>, <i>grim</i>, and <i>skl</i>, and autophagy was evaluated by our flow cytometry–based LTG assay. Only dsRNA corresponding to <i>hid</i> but not <i>rpr</i>, <i>grim</i>, or <i>skl</i> showed an effect on autophagy by this assay. RNAi of <i>hid</i> decreased the percentage of LTG<sup>hi</sup> cells after starvation treatment (Fig. 2 A). Previous studies showed that the Ras–Raf–MAPK pathway specifically inhibits the proapoptotic activity of <i>hid</i> (Bergmann et al., 1998). To determine whether the Ras–Raf–MAPK pathway also plays a regulatory role in autophagy in l(2)mbn cells, we designed dsRNAs to target these three components. RNAi of <i>Ras</i>, <i>phi</i> (also known as <i>raf</i>), or <i>rl</i> (also known as <i>MAPK</i>) all further enhanced the LTG fluorescence levels, suggesting that, like in apoptosis, they have an inhibitory role in autophagy regulation (Fig. 2 B). A second set of dsRNAs, nonoverlapping with the first set of dsRNAs, was designed to validate these new findings, and consistent results were observed (Fig. S1 B). In addition, GFP-LC3 was used to track changes in autophagosome formation in cells. RNAi of <i>hid</i> showed a decrease in the numbers of cells with GFP-LC3 puncta (Fig. 2, F and G), whereas RNAi of <i>Ras</i>, <i>phi</i>, or <i>rl</i> all resulted in a significant increase in the numbers of GFP-LC3–positive cells after starvation treatment (Fig. 2 G).

All RHG family members, <i>Rpr</i>, <i>Hid</i>, <i>Grim</i>, and <i>Skl</i>, bind to <i>D. melanogaster</i> IAP-1 (DIAP1) and inhibit its antiapoptotic activities (Hay et al., 2004). To test whether DIAP1 (encoded by <i>th</i>) is a putative downstream mediator of Hid-dependent autophagy in l(2)mbn cells, dsRNA was designed specifically to target <i>th</i>. We found that <i>th</i>-dsRNA–treated cells showed no difference in LTG fluorescence levels compared with Hs-dsRNA (negative control)–treated cells (Fig. 2 C). Interestingly, our data showed that reduced expression of Bruce, another IAP family member protein, further increased the LTG fluorescence levels after starvation treatment (confirmed using nonoverlapping dsRNAs; Fig. 2 C; see Fig. S1 C). RNAi of Bruce expression also resulted in an increase in GFP-LC3 puncta after starvation treatment (Fig. 2 G). These results suggest that Bruce, instead of DIAP1, could be the downstream target of Hid during starvation-induced autophagy in l(2)mbn cells.

Next, we investigated whether the transducers of apoptotic signals, <i>Ark</i>, <i>Buffy</i>, and <i>debcl</i>, are required for starvation-induced autophagy. Reduced expression of <i>Ark</i>, the <i>D. melanogaster</i> homologue of mammalian Apaf-1, did not affect the LTG fluorescence levels (Fig. 2 D). RNAi of two Bcl-2 family members, <i>Buffy</i> or <i>debcl</i>, resulted in a decrease in the percentage of LTG<sup>hi</sup> cells after starvation treatment (Fig. 2 D). Consistently, reduction of <i>Buffy</i> and <i>debcl</i> expression by RNAi decreased the percentage of GFP-LC3–positive cells after starvation treatment (Fig. 2, F and G). Reduced expression of <i>Ark</i>, <i>Buffy</i>, and <i>debcl</i> was determined using quantitative RT-PCR (QRT-PCR; Fig. S1 D). In addition, we reduced expression of the tumor suppressor <i>p53</i> by RNAi and found that starvation-induced autophagy was inhibited (Fig. 2 D). Results were further confirmed using nonoverlapping dsRNAs (Fig. S1 C).

To investigate the requirement of caspases, the final effectors of apoptosis, in starvation-induced autophagy, we designed gene-specific dsRNAs corresponding to seven different <i>D. melanogaster</i> caspases. RNAi of just one caspase, <i>Dcp-1</i>, but not others resulted in a decrease in the percentage of LTG<sup>hi</sup> cells after starvation treatment (Fig. 2 E). A second dsRNA against <i>Dcp-1</i>, nonoverlapping with the first dsRNA, yielded a similar result (Fig. S1 C). Reduction of <i>Dcp-1</i> expression by RNAi was determined using QRT-PCR (Fig. S1 D). Consistent with the LTG derived data, RNAi-mediated knockdown of <i>Dcp-1</i> resulted in a decrease in GFP-LC3–positive cells after starvation treatment (Fig. 2, F and G). These results indicate that <i>Dcp-1</i> functions as a positive regulator of autophagy in <i>D. melanogaster</i> l(2)mbn cells.

### Autophagy occurs in response to nutrient deprivation in germline and midstage egg chambers in the <i>D. melanogaster</i> ovary

To further characterize the requirement of <i>Dcp-1</i> and Bruce in autophagy regulation, we studied <i>D. melanogaster</i> oogenesis in vivo. We used a transgenic fly line that expresses a GFP-LC3 fusion protein under the control of the upstream activating
sequence (UASp) promoter (Rusten et al., 2004). Coexpression of UASp-GFP-LC3 with the germ line–specific nanos-GAL4 driver resulted in detectable GFP-LC3 expression in the germ line (nurse cells and oocyte cells) but not in somatic (follicle) cells (Fig. 3 A; Rorth, 1998; Rusten et al., 2004). When UASp-GFP-LC3; nanos-GAL4 flies were subjected to nutrient deprivation, we observed numerous GFP-LC3 puncta in region 2 within the gerarium (Fig. 3 B). In contrast, flies raised in the presence of yeast paste (Fig. 3 B, well-fed) had a diffuse GFP-LC3 pattern (Fig. 3 B). In addition, we found an increased in punctate LysoTracker red (LTR) staining in gerarium of nutrient-deprived wild-type (w1118) flies compared with well-fed wild-type flies (Fig. 3 B and Table I). We also observed numerous GFP-LC3 puncta in nutrient-deprived degenerating stage 8 chambers, but a diffuse GFP-LC3 pattern was detected in healthy egg chambers (Fig. 3 C). Similarly, degenerating stage 8 egg chambers had numerous LTR-positive dots in the nurse cells, whereas healthy egg chambers had a low level of LTR staining (Fig. 3 C and Table II). In starved Atg7 mutants (Atg7d77/Atg7d14), there was a significant decrease in punctate LTR staining in region 2 of the gerarium and in stage 8 degenerating egg chambers compared with flies with the genotype CG3353d30/Atg7d14, which were used previously as controls in Juhasz et al. (2007; Fig. 3 D and Tables I and II). These results indicated that nurse cells lacking the core autophagy regulator Atg7 failed to induce autophagy in response to nutrient deprivation. Overall, our observations showed that nutrient deprivation induces autophagy in region 2 germaria and in degenerating stage 8 egg chambers in D. melanogaster.

Dcp-1 and Bruce regulate autophagy in germaria and degenerating midstage egg chambers

To determine whether Dcp-1 is required for autophagy at these two specific stages during oogenesis, we used the LTR staining in nutrient-deprived Dcp-1P0 mutant flies. We observed a decrease in punctate LTR staining in region 2 of the germarium and in stage 8 degenerating egg chambers (Fig. 4, A and B; and Tables I and II) compared with nutrient-deprived wild-type flies. Consistent results were observed using GFP-LC3. Degenerating stage 8 egg chambers in nutrient-deprived Dcp-1P0 mutants containing the GFP-LC3 transgene had a diffuse GFP-LC3 pattern instead of punctate GFP-LC3 structures (Fig. 4 C). Together, these results indicate that nurse cells lacking Dcp-1 function are severely impaired in the ability to induce autophagy in response to starvation.

To determine whether Dcp-1 was also sufficient to induce autophagy in vivo, we generated transgenic flies that express the full-length Dcp-1 (fl-Dcp-1) under the control of the UASp promoter. In the presence of a nutrient-rich food source, degenerating stage 8 egg chambers are observed only rarely in wild-type flies (Drummond-Barbosa and Spradling, 2001). However, under nutrient-rich conditions, we observed an abundance of degenerating stage 8 egg chambers in nanos-GAL4/UASp-fl-Dcp-1 flies with increased levels of punctate LTR staining (Fig. 4 D and Table II). Further, we expressed an activated form of Dcp-1 (missing the prodomain) and GFP-LC3 in the germ line using the UASp/nanos-GAL4 system and observed numerous degenerating...
stage 8 egg chambers with GFP-LC3 puncta (Fig. 4 E), which indicates that 
activity of effector caspase Dcp-1 is sufficient to induce autophagy during 
mid-oogenesis even under nutrient-rich conditions.

We identified the IAP protein Bruce as a negative regulator of 
autophagy in I(2)mbn cells. We next asked whether Bruce is able 
to inhibit autophagy during D. melanogaster oogenesis. We 
monitored the LTR staining in ovaries of BruceE81 flies that have a deletion 
in the baculoviral IAP repeat (BIR) domain, which binds to 
caspases (Arama et al., 2003). In the presence of a nutrient-rich food source, we observed an increase in punctate LTR staining in 
region 2 of the germarium in BruceE81 flies compared with controls 
(BruceE81/TM3; Fig. 5 A and Table I). Similarly, we observed nu-
ergous degenerating stage 8 egg chambers with increased levels of 
punctate LTR staining in BruceE81 flies, resembling overexpression of 
Dcp-1 (Fig. 5 B and Table I). In well-fed conditions, we ob-
erved no degenerating stage 8 egg chambers in control BruceE81/ 
TM3 flies (n = 187 ovarioles; Table II). Punctate LTR staining was 
similarly observed in region 2 germaria (Table I) and degenerating 
stage 8 egg chambers (not depicted) in well-fed BruceE81 flies 
that have a 10-kb deletion in the 3’ end of the Bruce gene sequence 
(Vernooy et al., 2002). Our results demonstrate that Bruce is nor-
mally required to inhibit autophagy under nutrient-rich conditions.

Table I.  Quantification of autophagy in region 2 germaria

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Nutritional status</th>
<th>LTR positive</th>
<th>Number</th>
<th>Percentage of autophagy</th>
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<td>53</td>
<td>32</td>
</tr>
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<td>67</td>
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<td>Nutrient deprivation</td>
<td>14</td>
<td>65</td>
<td>22</td>
</tr>
<tr>
<td>CG5335g30/Atg714</td>
<td>Nutrient deprivation</td>
<td>37</td>
<td>68</td>
<td>54</td>
</tr>
</tbody>
</table>

Numbers in the fourth column refer to the numbers of individual germariums scored in at least seven different animals.

Dcp-1 and Bruce mutants have altered 
TUNEL staining in germaria and 
degenerating midstage egg chambers

Our previous work showed that nutrient-deprived Dcp-1 mut-
tants (Dcp-1Prev) have defects in mid-oogenesis germ line cell 
death (Laundrie et al., 2003). To determine whether Dcp-1 is 
also required for germ line cell death in region 2 within the 
germarium, we used the TUNEL assay to detect levels of DNA 
fragmentation as an indication of cell death. We found that 
nutrient-deprived Dcp-1 mutants had decreased levels of TUNEL-
positive cells in region 2 within the germarium compared with 
nutrient-deprived wild-type flies (Fig. 6 A and Table III), which 
indicates that Dcp-1 is also required for germarium stage 
cell death.

We also investigated the role of Bruce in cell death during 
oogenesis. In well-fed BruceE81 flies, we observed a degenerating 
avary phenotype that has been shown previously in ovaries with 
partial loss of another IAP protein, DIAP1 (Xu et al., 2005). This 
avary phenotype may be a consequence of excess cell death. 
Consistent with this possibility, we observed an increased num-
ergous of cells with TUNEL-positive staining in region 2 within the 

germarium compared with controls (Fig. 6 A and Table III). 

Table II.  Quantification of autophagy in stage 8 degenerating egg chambers

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Nutritional status</th>
<th>LTR positive</th>
<th>Number</th>
<th>Percentage of autophagy</th>
</tr>
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<td>w1118</td>
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Numbers in the fourth column refer to the number of individual degenerating stage 8 egg chambers scored in at least seven different animals.

a n = 4 animals scored for this genotype.
b No degenerating stage 8 egg chambers detected.
lethality; thus, we first analyzed the fully viable Atg7 mutant flies (Scott et al., 2004; Juhasz et al., 2007). We found that nutrient-deprived Atg7 mutants had reduced levels of TUNEL-positive cells in region 2 within the germarium compared with control flies (Table III). Further, degenerating stage 8 egg chambers in starved Atg7 mutants showed low or no TUNEL-positive staining compared with controls (Fig. 7, A and B; and Table IV). However, nuclear DNA condensation was still observed in the degenerating stage 8 egg chambers of starved Atg7 mutants (Fig. 7 B). To further investigate the role of autophagy in starvation-induced germ line cell death, we generated Atg1 germ line clones (GLCs), as mutations in Atg1 result in lethality at the pupal stage of development (Scott et al., 2004, 2007). Consistent with our Atg7 mutant observations, nutrient-deprived Atg1 GLC ovaries had decreased levels of TUNEL staining in both germaria and degenerating stage 8 egg chambers, which indicates a suppression of DNA fragmentation (Fig. 7, A and B; and Table IV). However, nuclear DNA condensation was still observed in the degenerating stage 8 egg chambers of starved Atg7 mutants (Fig. 7 B). To further investigate the role of autophagy in starvation-induced germ line cell death, we generated Atg1 germ line clones (GLCs), as mutations in Atg1 result in lethality at the pupal stage of development (Scott et al., 2004, 2007). Consistent with our Atg7 mutant observations, nutrient-deprived Atg1 GLC ovaries had decreased levels of TUNEL staining in both germaria and degenerating stage 8 egg chambers, which indicates a suppression of DNA fragmentation (Fig. 7, A and B; and Table IV). Also consistent with Atg7, we observed nuclear DNA condensation in the Atg1 GLC degenerating stage 8 egg chambers (Fig. 7 D). Our results show that lack of autophagy results in a reduction of DNA fragmentation during starvation-induced cell death in the germaria and midstage egg chambers, which suggests that autophagy contributes to the cell death process at these stages.

Discussion

Key outstanding questions that need to be addressed are how autophagy and apoptosis pathways interact with each other, and whether common regulatory mechanisms exist between these two processes. We have shown here that six known cell death
genes and the Ras–Raf–MAPK signaling pathway not only function in apoptosis but also act to regulate autophagy in *D. melanogaster* l(2)mbn cells. We cannot rule out the possibility that additional cell death genes that we screened may also function in autophagy but were not detected in our assay because of insufficient knockdown by RNAi, a long half-life of the corresponding proteins, and/or functional redundancy.

Consistent with our in vitro data, the involvement of Hid in autophagy regulation has been demonstrated in *D. melanogaster*. Overexpression of Hid induced autophagy in the fat body, larval epidermis, midgut, salivary gland, Malpighian tubules, and trachea epithelium (Juhasz and Sass, 2005). Further, expression of the constitutively active Ras form (RasV12), which has been shown to inhibit Hid activity in apoptosis (Bergmann et al., 1998), can also block Hid-induced autophagy (Juhasz and Sass, 2005). In *D. melanogaster* salivary glands, the Ras signaling pathway has also been shown to inhibit the autophagy process (Berry and Baehrecke, 2007). Based on our loss-of-function findings and these previous gain-of-function studies, we speculate that the Ras–Raf–MAPK pathway acts upstream to inhibit Hid activity in autophagy.

Poor nutrition has a dramatic effect on egg production in *D. melanogaster*. Flies fed on a protein-deprived diet showed an increase in cell death in germaria and midstage egg chambers (Drummond-Barbosa and Spradling, 2001). These two stages have been proposed to serve as nutrient stress checkpoints where defective egg chambers are removed before the investment of energy into them. The molecular mechanisms of germarium cell death are still largely unknown, and Daughterless, a helix-loop-helix transcription factor, was the only known regulator involved in cell death of germaria (Smith et al., 2002). Nurse cell death during mid-oogenesis is also different from most developmental cell death in other *D. melanogaster* tissues because apoptotic regulators such as rpr, hid, or grim are not required for cell death in these cells (Peterson et al., 2007). However, the activity of caspases, particularly Dcp-1, was shown to be required for mid-oogenesis cell death (Laundrie et al., 2003; Baum et al., 2007). Our findings implicate several additional genes, Dcp-1, Bruce, Atg7, and Atg1, in nutrient deprivation–induced cell death in the germarium, as well as during mid-oogenesis.

Other forms of cell death, such as autophagic cell death, have been proposed previously to be involved in the elimination of defective egg chambers during mid-oogenesis. Known signaling pathways, including the insulin and ecdysone pathways, have been shown to be required not only for the survival of nurse cells in mid-oogenesis; they are also known to regulate the autophagy process, supporting the notion that autophagy plays a role in mid-oogenesis cell death (Drummond-Barbosa and Spradling, 2001; McCall, 2004). Features of autophagy were observed during *D. virilis* mid-oogenesis cell death as shown by monodansylcadaverine staining and transmission electron microscopy (Velentzas et al., 2007). Our results using GFP-LC3 and LTG demonstrate that autophagy occurs in degenerating midstage egg chambers and also in germaria of nutrient deprived *D. melanogaster*. We found that mutation of Atg7 results in a significant decrease of autophagy in dying mid-stage egg chambers and in germaria of starved flies, further supporting the presence of autophagy during these stages.

The role of autophagy in cell survival or cell death is still not well resolved and is likely to be context dependent. Our results show that autophagy contributes to the cell death process in the ovary. Loss of Atg7 or Atg1 activity in both dying mid-stage egg chambers and germaria leads to decreased TUNEL staining, which indicates a reduction in DNA fragmentation.

<table>
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<tr>
<th>Genotype</th>
<th>Nutritional status</th>
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<th>Number</th>
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<td>Nutrient deprivation</td>
<td>53</td>
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</table>

Numbers in the fourth column refer to the number of individual germaria scored in at least seven different animals.
Consistent results were observed previously in the larval midguts of Atg7 mutants, which also showed an inhibition of DNA fragmentation (Juhasz et al., 2007). Interestingly, lack of autophagy function does not appear to affect nuclear DNA condensation in nurse cells. Nurse cells in degenerating stage 8 egg chambers of starved Atg7 mutants or Atg7 GLCs appeared to still have condensed nuclei, as shown by DAPI staining (Fig. 7, B and D). Thus, based on Atg7 and Atg1 mutant analyses, autophagy contributes to DNA fragmentation but not all aspects of nurse cell death. Future studies are required to determine how autophagy is connected to known pathways leading to DNA fragmentation and chromatin condensation during cell death.

The IAP family member Bruce was shown previously to repress cell death in the D. melanogaster eye (Vernooy et al., 2002). Bruce was also shown to protect against excessive nuclear condensation and degeneration, perhaps by limiting excessive caspase activity, during sperm differentiation (Arama et al., 2003). Other IAP family members have been shown to bind caspases via a BIR domain and inhibit apoptosis (Riedl and Shi, 2004). The presence of a BIR domain in Bruce suggests that it may also have caspase-binding activity. We found that lack of Bruce function resulted in an increase in both LTR and TUNEL staining of nuclei in stage 8 defective egg chambers, which indicates a block in both DNA fragmentation and nuclear condensation, and further supports a dual regulatory role for Dcp-1 in mid-oogenesis cell death. Dcp-1 might function to induce autophagosome formation while coordinately acting upon alternate proteolytic targets to complete execution of apoptosis. Future studies to elucidate upstream regulators and downstream substrates of Dcp-1 in cells undergoing autophagy or apoptosis will help to establish the regulatory mechanisms governing the crosstalk between these two cellular processes. Given the multiple cellular effects associated with autophagy, our results also have important therapeutic implications for the use of modulators of caspase or IAP activity in the treatment of cancer and other diseases.

Materials and methods

Cell culture conditions

D. melanogaster (l(2)mbn) cells (provided by A. Dorn, Institute of Zoology, Johannes Gutenberg University, Mainz, Germany) were maintained in Schneider’s D. melanogaster medium (Invitrogen) supplemented with 10% FBS in 25-cm² suspension flasks (Sarstedt) at 25°C (Ress et al., 2000). All the experiments were performed 3 d after passage and the cells were discarded after 25 passages.
dsRNA synthesis

Individual PCR products containing coding sequences for the transcripts to be targeted were generated by RT-PCR using Superscript one-step RT-PCR kit with platinum taq (Invitrogen). Each primer used in the RT-PCR contained a 5’ T7 RNA polymerase-binding site (TAATACGACTCAC-TATAGG) followed by sequences specific for the targeted genes (Table S2, available at http://www.jcb.org/cgi/content/full/jcb.200712091/DC1). For in vitro transcription reactions, 50 μl of each of the RT-PCR products was ethanol-precipitated and resuspended in 8 μl of nuclease-free water and then used as template. In vitro transcription reactions were performed using T7 RiboMax Express RNAi systems (Promega) according to the manufacturer’s instructions. dsRNAs were ethanol-precipitated and resuspended in 50 μl of nuclease-free water. A 5-μl aliquot of 1:100 dilution was analyzed by 1% agarose gel electrophoresis to determine the quality of dsRNA. The dsRNA was quantitated using the PicoGreen dsDNA detection assay (Invitrogen) and adjusted to 200 ng/μl with nuclease-free water.

RNAi

66 μl of cells (10^6 cells/ml in SFM922 medium) were seeded into each well of a 96-well plate. 2 μg of dsRNA (20 μM) was added into each well. After 1 h of incubation at room temperature, the cells received Schneider’s medium supplemented with 10% FBS to achieve a final volume of 200 μl. Cells were incubated for 72 h at 25°C.

Because RNAi of ih triggered a massive amount of apoptosis at the standard incubation time of 72 h, we instead used a 24-h incubation period. After 24 h of ih-dsRNA treatment, there was already a significant amount of apoptotic cells present, which indicates an efficient knockdown by RNAi, but a sufficient number of healthy cells (>10,000) remained for LTG analysis.

Flow cytometry–based LTG assay

For drug treatments, 10 mM 3MA or 0.1 μM Baf was added when nutrient-full medium was replaced with 2 mg/ml glucose in PBS. After a 4-h incubation at 25°C, cells were incubated for 20 min at room temperature with 50 nM LTG for quantification of autophagy levels and 2 μg/ml propidium iodide (PI) to eliminate dead cells. The cells were then analyzed using flow cytometry (FACSCalibur; Becton Dickinson). A minimum of 10,000 cells per sample was acquired for triplicate samples per experiment. LTG fluorescence levels of cells (excluding PI-positive cells) were analyzed using Flowjo software.

For RNAi experiments, the RNAi-treated cells, after a 72-h incubation, were transferred into a U-bottom 96-well plate and centrifuged at 800 rpm for 5 min. Nutrient-full medium was replaced with 20 μM dsRNA for a 4-h starvation treatment, then cells were labeled with LTG and PI for 20 min at room temperature and finally analyzed as described in the previous section.

GFP-LC3 detection

The p2ZOp2F-EGFP-LC3 plasmid was generated by restriction digestion of EGFP-LC3 from pUASP-EGFP-LC3 (Rusten et al., 2004) and cloning into the p2ZOp2F vector (a gift from T. Grigliatti, University of British Columbia, Vancouver, British Columbia, Canada; Hegedus et al., 1998). To create a stable cell line, D. melanogaster l(2)mbn cells were transfected with p2ZOp2F-EGFP-LC3 and selected for the presence of the construct using zeocin. The resulting p2ZOp2F-EGFP-LC3 stable (GFP-LC3) l(2)mbn cells were maintained in Schneider’s D. melanogaster medium supplemented with 10% FBS and 10 μg/ml zeocin. 66 μl of these GFP-LC3 l(2)mbn cells (2.5 x 10^6 cells/ml in SFM922 medium) were seeded into each well of an 8-well CC2-coated chamber slide (LabTek). Cells were incubated with dsRNAs as described in the previous section. Following a 4-h starvation treatment, cells were fixed with 2% paraformaldehyde for 20 min and incubated with anti-GFP antibody (1:200; JL8; Clontech Laboratories, Inc.), followed by anti-mouse immunoglobulin Alexa 488 conjugates (Invitrogen). Cells were mounted with antifade reagent with DAPI at room temperature (SlowFade Gold; Invitrogen). Images were obtained using a 63x objective on a microscope (AxioPlan2; all from Carl Zeiss, Inc.) and captured with a cooled mono 12-bit camera (QImaging) and Northern Eclipse image analysis software (Empix Imaging, Inc.). Cells with more than three GFP-LC3 punctate dots were analyzed as autophagy-positive.

Figure 7. Lack of Atg7 or Atg1 function reduces DNA fragmentation during mid-oogenesis cell death. (A) TUNEL-positive staining was observed in dying stage 8 egg chambers (arrows) from nutrient-deprived control flies (CG5335 /Atg7 '). DAPI staining of nuclei (white) is shown on the right. (B) In nutrient-deprived Atg7 mutants (Atg7 '/Atg7 '), degenerating stage 8 egg chambers (arrows) showed no or low levels of TUNEL staining. Nuclear DNA condensation, detected by DAPI, was still observed. (C) Dying stage 8 egg chambers (arrows) from nutrient-deprived control siblings (Atg1 '130/TM3) generated from the same cross in D had abundant TUNEL-positive staining. (D) In nutrient-deprived Atg1 GLCs, degenerating stage 8 egg chambers (arrows) showed no or low levels of TUNEL staining. Nuclear DNA condensation (DAPI, right) in degenerating egg chambers appeared to occur as in the controls. Bars, 50 μm.
considered to be GFP-LC3-positive cells. A minimum of 200 cells per sample were counted manually for triplicate samples per experiment.

**Statistical analysis**

Two-tailed student’s t test (equal variances) was used to compare mean levels. n = 3. P < 0.05 was considered statistically significant.

**Generation of transgenic flies**

The UASp-fulllength-Dcp-1 construct was generated by PCR amplification of the coding region from a Dcp-1 cDNA clone (Song et al., 1997) and cloning into the UASp vector (Rorth, 1998). Transgenic flies were generated using standard procedures. To express fulllength Dcp-1 in the germ line, flies were crossed to NGT; nanosGAL4 flies (Cox and Spradling, 2003), and the resulting progeny were analyzed. To express truncated Dcp-1 and GFP-LC3 in the germ line, yw; nanosGAL4 UASp-Dcp-1 were crossed to UASp-GFP-LC3; nanos GAL4, and the resulting progeny were analyzed (Peterson et al., 2003).

**Fly strains**

w1118 was used as the wild-type stock. Other fly stocks were used as follows: Dcp-1Δ1-58 and UASp-GFP-LC3; nanos-GAL4 (from H. Stemmark, Norwegian Radium Hospital, Oslo, Norway), BruceβIII (from H. Steller, the Rockefeller University, New York, NY), BruceβIII (from B.A. Calvi, California Institute of Technology, Pasadena, CA), Atg7R77, Atg7R14, CG33536, and Atg1R120 (from T. Neufeld, University of Minnesota, Minneapolis, MN).

**Generation of Atg1 GTCs**

To generate germ line clones, FRT2A was recombined onto the Atg1R120 correct. Recombinants were confirmed by failure to complement DM(3)Basc10 and Atg1R105D. Germ line clones were generated with the FLP/FRT/ovoD technique as described previously (Chou and Perrimon, 1996). Larvae of the genotype HSsp; ovoD FRT2A/Atg1R120 FRT2A were heat-shocked on days 4 and 5 for 1 h at 37°C.

**LTR staining**

For nutrient-deprivation experiments, flies were conditioned on yeast paste for 2 d and then placed in a dry vial with access to a 10% sucrose solution for 4–5 d (Peterson et al., 2003).

Ovaries were dissected in PBS and immediately transferred into PBS containing 0.8 μM LTR (Invitrogen) for 5 min at room temperature in the dark. The ovaries were then stained with 0.1 mg/ml DAPI for 30 s. The ovaries were washed three times with PBS and mounted with SlowFade antifade reagent at manufacturer’s instructions. Images were captured with a cooled mono 12-bit camera and Northern Eclipse image analysis software. Egg chambers with >10 LTR positive spots were considered to be LTR positive. Stage 8 degenerating egg chambers in w1118 flies were scored by the presence of condensed nurse cell nuclei. The degenerating egg chambers in Dcp-1Δ1-58 flies were characterized by a disappearance of follicle cells and a persistence of nurse cell nuclei, as described previously (Laundrie et al., 2003).

**FLP/FRT/ovoD technique as described previously.**

**For expression of Dcp-1 in ovaries**

Ovaries were dissected in PBS and immediately transferred into PBS containing 0.8 μM LTR (Invitrogen) for 5 min at room temperature in the dark. The ovaries were then stained with 0.1 mg/ml DAPI for 30 s. The ovaries were washed three times with PBS and mounted with SlowFade antifade reagent at room temperature. Images were obtained using a 20 or 40x objective (Carl Zeiss, Inc.) on an Axiosplan2 microscope and captured with a cooled mono 12-bit camera and Northern Eclipse image analysis software.

**QRT-PCR**

Cells (~2 × 10^5 cells in 600 μl) were incubated with dsRNAs as described (see “RNAi”) at 25°C for 72 h, followed by a 4-h starvation treatment. Cell cultures were transferred to RNase-free Eppendorf tubes (Ambion), and cells were pelleted at 1,000 rpm for 10 min. Cells were lysed in 1 ml Trizol (Invitrogen), and total RNA was extracted according to manufacturer’s instructions. Isolated RNA was treated with RNase-free DNase, and 50 ng of total RNA was used in a 15-μl QRT-PCR reaction. QRT-PCR was performed using the one-step SYBR green RT-PCR reagent kit (Applied Biosystems) on a sequence detection system (7900; Applied Biosystems). Expression levels were calculated using the Comparative Ct method with D. melanogaster rp49 as the reference. All samples were analyzed in triplicate. The knockdown efficiency was determined by comparing the fold change in expression between target dsRNA treated and untreated cells.

**Online supplemental material**

Fig. S1 includes representative images of GFP-LC3 puncta in I(2)mmb cells after starvation and treatment with autophagy inhibitors. Quantitative ligation detection (QTD) data for additional nonoverlapping dsRNAs is also presented, along with assessment of target knockdown by QRT-PCR for selected genes. Table S1 shows a comparison of essential autophagy genes in the D. melanogaster larval fat body and I(2)mmb cells. Table S2 contains all primer sequences used for the preparation of dsRNAs. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200712091/D1.

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**References**


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