Atg6 is required for multiple vesicle trafficking pathways and hematopoiesis in Drosophila

Bhupendra V. Shravage
University of Massachusetts Medical School, bhupendra.shravage@umassmed.edu

Jahda H. Hill
University of Massachusetts Medical School

Christine M. Powers
University of Massachusetts Medical School, Christine.Powers@umassmed.edu

See next page for additional authors

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

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

Repository Citation
Shravage, Bhupendra V.; Hill, Jahda H.; Powers, Christine M.; Wu, Louisa; and Baehrecke, Eric H., 'Atg6 is required for multiple vesicle trafficking pathways and hematopoiesis in Drosophila' (2013). University of Massachusetts Medical School Faculty Publications. Paper 157.
http://escholarship.umassmed.edu/faculty_pubs/157

This material is brought to you by eScholarship@UMMS. It has been accepted for inclusion in University of Massachusetts Medical School Faculty Publications by an authorized administrator of eScholarship@UMMS. For more information, please contact Lisa.Palmer@umassmed.edu.
Atg6 is required for multiple vesicle trafficking pathways and hematopoiesis in Drosophila

Authors
Bhupendra V. Shravage, Jahda H. Hill, Christine M. Powers, Louisa Wu, and Eric H. Baehrecke

Comments
Publisher PDF posted as allowed by the publisher's author rights policy at http://dev.biologists.org/site/misc/rights_permissions.xhtml#author

Rights and Permissions
Citation: Development. 2013 Mar;140(6):1321-9. doi: 10.1242/dev.089490. Epub 2013 Feb 13. Link to article on publisher’s site

This article is available at eScholarship@UMMS: http://escholarship.umassmed.edu/faculty_pubs/157
Atg6 is required for multiple vesicle trafficking pathways and hematopoiesis in Drosophila

Bhupendra V. Shravage1*, Jahda H. Hill1,2,*, Christine M. Powers1, Louisa Wu2 and Eric H. Baehrecke1,6

SUMMARY

Atg6 (beclin 1 in mammals) is a core component of the Vps34 complex that is required for autophagy. Beclin 1 (Becn1) functions as a tumor suppressor, and Becn1+/− tumors in mice possess elevated cell stress and p62 levels, altered NF-κB signaling and genome instability. The tumor suppressor function of Becn1 has been attributed to its role in autophagy, and the potential functions of Atg6/Becn1 in other vesicle trafficking pathways for tumor development have not been considered. Here, we generate Atg6 mutant Drosophila and demonstrate that Atg6 is essential for autophagy, endocytosis and protein secretion. By contrast, the core autophagy gene Atg1 is required for autophagy and protein secretion, but it is not required for endocytosis. Unlike null mutants of other core autophagy genes, all Atg6 mutant animals possess blood cell masses. Atg6 mutants have enlarged lymph glands (the hematopoietic organ in Drosophila), possess elevated blood cell numbers, and the formation of melanotic blood cell masses in these mutants is not suppressed by mutations in either p62 or Nfkb genes. Thus, like mammals, altered Atg6 function in flies causes hematopoietic abnormalities and lethality, and our data indicate that this is due to defects in multiple membrane trafficking processes.

KEY WORDS: Autophagy, Endocytosis, Protein secretion, Drosophila

INTRODUCTION

Macroautophagy (autophagy) is an evolutionarily conserved catabolic process that is induced in response to cell stress, such as nutrient restriction, organelle damage and protein aggregation. During autophagy, double-membrane vesicles, known as autophagosomes, sequester cytoplasmic components, such as proteins and organelles, and deliver them to the lysosome for degradation (Mizushima and Komatsu, 2011). Protein turnover by the lysosome enables recycling of amino acids to be utilized for protein synthesis, and breakdown of damaged organelles prevents accumulation of toxic reactive oxygen species in the cell (Yang et al., 2006; Zhang et al., 2007). Autophagy has been implicated in many processes, including the mitigation of cell stress and genome instability, tissue remodeling during development, and clearance of intracellular pathogens (Berry and Baehrecke, 2007; Deretic, 2011; Karantza-Wadsworth et al., 2007).

Genetic screens in the yeast Saccharomyces cerevisiae identified autophagy-related (Atg) genes (Harding et al., 1995; Thurnm et al., 1994; Tsukada and Ohsumi, 1993). These genes are required for autophagy and many are conserved in higher animals, including humans. A class III phosphoinositide 3-kinase (PI3K) complex, which includes the class III PI3K vacuolar protein sorting 34 (Vps34; also known as Pik3c3), the serine-threonine kinase Vps15 (Vps34; also known as Pik3r4), and Atg6/Becn1 (also known as Vps30 in yeast), regulates autophagosome formation in yeast and mammals (Funderburk et al., 2010; Kihara et al., 2001b). The substrate of Vps34, phosphatidylinositol (PtdIns or PI), is converted to PI 3-phosphate [PI3P], and this membrane-associated lipid is bound by proteins containing either FYVE or PX domains (Ellson et al., 2002; Stenmark et al., 2002). PI3P-containing membranes include autophagosome isolation membranes, which recruit other proteins to modulate the specific biological function of this complex. The Atg6, Vps34 and Vps15 complex interacts with Atg14L to promote autophagosome formation, whereas it interacts with Uvrag/Vps38 to regulate vacuolar protein sorting. Recent work also indicates that the complex containing Uvrag is involved in ligand-receptor degradation and cytokinesis (Thoresen et al., 2010). S. cerevisiae and Caenorhabditis elegans Atg6 are also required for retrograde transport from endosomes to the Golgi complex (Ruck et al., 2011; Seaman et al., 1997). In addition, Rubicon, Ambra1 and Bif1 (Zbtb24) function as regulators of these complexes (Fimia et al., 2007; Matsunaga et al., 2009; Takahashi et al., 2007; Zhong et al., 2009).

Two distinct Atg6/Becn1 protein complexes have been described in yeast and mammals (Itakura et al., 2008; Kihara et al., 2001b; Liang et al., 2008). Atg6, Vps34 and Vps15 form a core complex, which recruits other proteins to modulate the specific biological function of this complex. The Atg6, Vps34 and Vps15 complex interacts with Atg14L to promote autophagosome formation, whereas it interacts with Uvrag/Vps38 to regulate vacuolar protein sorting. Recent work also indicates that the complex containing Uvrag is involved in ligand-receptor degradation and cytokinesis (Thoresen et al., 2010). S. cerevisiae and Caenorhabditis elegans Atg6 are also required for retrograde transport from endosomes to the Golgi complex (Ruck et al., 2011; Seaman et al., 1997). In addition, Rubicon, Ambra1 and Bif1 (Zbtb24) function as regulators of these complexes (Fimia et al., 2007; Matsunaga et al., 2009; Takahashi et al., 2007; Zhong et al., 2009).

The function of beclin 1 as a tumor suppressor has influenced our understanding of the role of autophagy in cancer. BECN1 is monoallelically deleted in sporadic breast, ovarian and prostate cancers (Aita et al., 1999), and allelic loss of Becn1 in mice leads to lymphomas and carcinomas (Qu et al., 2003; Yue et al., 2003). At the cellular level, Becn1+/− tumors have decreased autophagy, elevated cell stress and genome instability (Mathew et al., 2007). Moreover, decreased beclin 1 function in oncogene-expressing tissues is associated with the accumulation of the autophagy cargo binding protein p62 (SQSTM1), altered NFκB signaling, and inflammation (Mathew et al., 2009). Combined, these results...
indicate that the tumor suppressor function of beclin 1 is related to its role in autophagy, but do not consider the potential functions of Atg6/Beclin1 in other vesicle trafficking pathways for tumor initiation and progression.

*Drosophila* has a single beclin 1 ortholog, Atg6, which shares 71% amino acid identity with the evolutionarily conserved domain of mammalian beclin 1, and 50% overall identity. Atg6 protein interacts with Vps34 (P3K39F – FlyBase) in vivo, and co-expression of Atg6 with either Vps34 or Vps15 (ird1 – FlyBase) is sufficient to induce autophagy (Juhász et al., 2008). Both Vps34 and Vps15 are required for starvation-induced autophagy and adult viability in *Drosophila* (Juhász et al., 2008; Lindmo et al., 2008; Wu et al., 2007). However, the lack of a null Atg6 mutant has precluded full functional analysis of the Vps34 complex in flies.

Here, we use gene targeting to generate a *Drosophila Atg6* null mutant, and show that Atg6 mutant fat body cells exhibit defects in autophagy and endocytosis. In addition, we show that Atg6, Vps34 and Atg1 function in protein secretion. Consistent with the role of beclin 1 as a tumor suppressor, loss of Atg6 caused over-production of blood cells, a failure in proper blood cell differentiation and the formation of melanotic blood cell masses.

**MATERIALS AND METHODS**

**Fly stocks and culture**

Flies were reared at 25°C on standard cornmeal/molasses/agar media. The following *Drosophila melanogaster* stocks were used: P[2] Atg6(T2) w hs-FLP; FRT82B ubi-GFP, w; SgsΔGAL4, w hs-FLP; FRT42D mRFPnls, y w hs-FLP; FRT80B mRFPnls, y w hs-FLP; FRT80B ubi-GFP, FRT80B mRFP-nls, y w hs-FLP; +; FRT80B ubi-nlsGFP, y w hs-FLP; +; FRT80B ubi-mRFP, y w hs-FLP; +; FRT82B Ubi-nlsGFP, y w hs-FLP; CgGAL4; FRT82B UAS-mCherry and y w hs-FLP; FRT42D Ubi-nlsGFP. Four-hour egg layers were maintained at 37°C for 1 hour to induce clones in the larval salivary glands, and 10-hour egg layers were maintained at 37°C for 1 hour to induce clones in the larval fat body.

**Nutrient restriction**

Second and third instar larvae were fed 20% sucrose in PBS, pH 7.4, and maintained at 25°C for 4 hours.

**Texas Red-avidin assay**

To visualize endocytosis, the fat body was dissected from third instar larvae and incubated *ex vivo* with Texas Red-avidin (Invitrogen) diluted in Schneider’s media to a concentration of 80 μg/ml for 20 minutes, then chased with 0.5% BSA in cold PBS for 10 minutes prior to overnight fixation in 4% formaldehyde. The tissue was washed three times (10 minutes per wash) with 0.1% Tween-20 in PBS and mounted in Vectashield (Vector Laboratories). Images were collected on a Zeiss Axiosmager Z1 equipped with an Apotrime. Images were acquired with AxioCam and processed using Zeiss Axiosvision Suite 4.8 and Photoshop CS4 and Adobe Illustrator CS4 14.0.0.

**Immunostaining**

For fat body immunofluorescence experiments, tissues were dissected in PBS and fixed overnight in 4% formaldehyde in PBS, pH 7.4, at 4°C. Following fixation, tissues were washed with 0.1% Triton X-100 in PBS (PBST) for 2 hours, then blocked in 0.5% BSA in PBST (PBSBT) for 2 hours at room temperature. Primary antibody incubations were performed overnight at 4°C in PBSBT followed by washing in PBSBT for 2 hours at room temperature. Secondary antibody was added at a dilution of 1:200, and tissues were incubated for 4 hours at room temperature. Following a series of short PBSBT washes, tissues were mounted in Vectashield with DAPI (Vector Laboratories). The following primary antibodies were used: rabbit anti-Ref (2)P (1:1000; I. Nezis) (Nezis et al., 2008), mouse anti-P1/NimC1 (1:10; I. Ando) (Ando et al., 2003), and mouse anti-L1 (1:10; I. Ando) (Ando et al., 2003). Secondary antibodies from Invitrogen were used at 1:200: goat anti-rabbit Oregon Green 488, goat anti-rabbit Alexa Fluor 546, goat anti-mouse Alexa Fluor 546 and donkey anti-rat FITC.

For lymph gland analyses, larval fillets were prepared as previously described (Budnik et al., 2006), and lymph glands were dissected and stained as previously described (Lebestky et al., 2000).

For immunohistochemistry of paraffin sections, third instar larvae were fixed and dehydrated for histology according to published methods (Muro et al., 2006). Histological sections were de-waxed with a series of xylene series of short PBSBT washes, tissues were mounted in Vectashield with DAPI (Vector Laboratories). The following primary antibodies were used: rabbit anti-Ref (2)P (1:1000; I. Nezis) (Nezis et al., 2008), mouse anti-P1/NimC1 (1:10; I. Ando) (Ando et al., 2003) and mouse anti-L1 (1:10; I. Ando) (Ando et al., 2003). Secondary antibodies from Invitrogen were used at 1:200: goat anti-rabbit Oregon Green 488, goat anti-rabbit Alexa Fluor 546, goat anti-mouse Alexa Fluor 546 and donkey anti-rat FITC.

**Generation of Atg6 targeting construct**

The 'ends-out' gene disruption approach (Rong and Golic, 2000) was used to target the open reading frame (ORF) of Atg6 in the isogenic w^108 parental line. The resultant strain contained a w^− mini-gene in place of the Atg6 ORF.

**RT-PCR**

RNA was collected from third instar larvae (n=10) using Trizol Reagent (Invitrogen) and was treated with DNase. cDNA was generated from 1 μg of RNA, using Superscript II Reverse Transcriptase (Invitrogen), following standard protocols. cDNA was used as PCR template, using the following primers to amplify Atg6 and flanking gene sequences: Atg6: 5’-CGACAGCAGCTGGAGAAGATT-3’ and 5’-CGGTGATATCCTGAG-CCAGTC-3’; CG5991-RA: 5’-CATTTGGCTAATGTGGC-3’ and 5’-GGAGATTTGGCAGATCG-3’; CG5991-RB: 5’-GGACACGCC-ATACGGAAGAC-3’ and 5’-GGAGATTTGGCAGATCG-3’; CG5991-RC: 5’-GCCCTTCTGAGATT-3’ and 5’-GGAGAA-TTGGCGCGATAGTGC-3’; CG5986: 5’-GGCGATAACGCTTGGCATC-3’ and 5’-CGTGTATCCGGCAGAACCG-3’. Quantitative real-time PCR was performed as described (Denton et al., 2009).

**Induction of mutant clones of cells**

Standard methods were used for the induction of mutant clones of cells (Xu and Rubin, 1993). To induce loss-of-function mutant cell clones, we used y w hs-Flp; FRT42D Ubi-nlsGFP, y w hs-Flp; FRT42D mRFP-nls, y w hs-Flp; FRT80B ubi-nlsGFP, y w hs-Flp; +; FRT80B ubi-mRFP, y w hs-Flp; +; FRT82B Ubi-nlsGFP, y w hs-Flp; CgGAL4; FRT82B UAS-mCherry and y w hs-Flp; FRT42D Ubi-nlsGFP. Four-hour egg layers were maintained at 37°C for 1 hour to induce clones in the larval salivary glands, and 10-hour egg layers were maintained at 37°C for 1 hour to induce clones in the larval fat body.

**DEVELOPMENT**

**140 (6)**

**DEVELOPMENT**

**1322**

**RESEARCH ARTICLE**

**Development 140 (6)**
Hemocyte quantification
Individual third instar larvae of similar age (± 3 hours) were bled into 20 μl of PBS. From this, 10 μl was loaded onto a standard hemocytometer and the average number of cells per milliliter was calculated for 20 animals per genotype. A one-tailed Student’s t-test was used to determine statistical significance.

Quantification and statistical analyses
Zeiss Image Measurement Software was used for the quantification of Atg8a, Ref(2)P and Rab5 puncta, as well as the eye-antennal disc area and the lymph gland area. Statistical analyses were performed using GraphPad prism software. Student’s t-test for two samples assuming unequal variances was used to determine the statistical significance of the data.

Transmission electron microscopy
Tissues were dissected and fixed overnight at 4°C in 4.0% paraformaldehyde, 2.0% glutaraldehyde, 1% sucrose and 0.028% CaCl2 in 0.1 M sodium cacodylate, pH 7.4, thoroughly washed in cacodylate buffer, post-fixed in 2.0% osmium tetroxide for 1 hour, and embedded in SPI-pon/Araldite resin (Polysciences) according to manufacturer’s recommendations. Ultrathin sections (80 nm) were stained with uranyl acetate and lead citrate before examination in a Philips CM10 transmission electron microscope.

Protein secretion assay
Salivary glands were dissected from control and mutant animals at 4 hours after puparium, fixed for 30 minutes in 4% paraformaldehyde in PBS, washed three times (5 minutes per wash) in PBS, and mounted in Vectashield with DAPI.

RESULTS
Atg6 is required for autophagy in Drosophila
A transposable P-element, P[PZ]Atg600096, is located in the 5’ untranslated regions of Atg6 and the neighboring gene CG5991 (Fig. 1A). Starvation-induced autophagy was not consistently altered in the fat body of homozygous P[PZ]Atg600096 larvae (Scott et al., 2004). Based on this result and the fact that P[PZ]Atg600096 does not disrupt the Atg6 ORF, we generated an Atg6 mutant using a gene-targeting approach (Rong and Golic, 2000).

Homologous recombination was used to replace the Atg6 ORF with a w+ mini-gene (Fig. 1A). RT-PCR confirmed the absence of Atg6 RNA in homozygous third instar larvae, whereas the RNA levels of neighboring genes were not altered in the homozygous mutant Atg6 (hereafter termed as Atg66) mutant larvae (Fig. 1B). In addition, PCR was used to confirm the presence of a w+ mini-gene in the Atg6 genomic locus (data not shown). Both homozygous Atg66 and animals transheterozygous for Atg66 and the Df(3R)Exel 6197 deficiency for this region died during the late third larval instar and early pupal stages of development (supplementary material Fig. S1A; data not shown). Significantly, expression of a UAS-GFP-Atg6 transgene under the control of a ubiquitously expressed actin-GAL4 driver rescued the lethality of Atg66 homozygous (supplementary material Fig. S1A). In addition, Atg66 complements P[PZ]Atg600096 even though this is a lethal P-element insertion, indicating that P[PZ]Atg600096 is not an Atg6 mutant. These data indicate that we have isolated a loss-of-function Atg66 mutant.

Atg6, Vps15 and Vps34 are core components of all known Vps34 complexes (Funderburk et al., 2010), and loss of either Vps34 or Vps15 inhibits starvation-induced autophagy in the larval fat body of Drosophila (Juhász et al., 2008). To determine whether Atg6 is required for starvation-induced autophagy, we monitored the localization of the autophagosome marker mCherry-Atg8a in larval fat body. Atg8a, the Drosophila ortholog of mammalian LC3 (microtubule-associated protein 1 light chain 3), displays diffuse cytoplasmic localization in the fat body of feeding Drosophila larvae, but becomes incorporated into autophagosome membranes during starvation and is visualized as punctate spots in the cytoplasm (Scott et al., 2004). We utilized FLP recombination-mediated recombination at FLP recombination target (FRT) sites to generate Atg66 mitotic mutant cell clones in the fat body, resulting in tissue composed of control (either wild type or heterozygous Atg66/wild type) and homozygous Atg66/Atg66 mutant cells. Following 4 hours of starvation, control fat body cells, which were marked by the presence of green fluorescent protein (GFP) contained several mCherry-Atg8a puncta, whereas homozygous Atg66 mutant cells (lacking GFP) displayed diffuse localization of mCherry-Atg8a (Fig. 1C–C’).

Two additional approaches were used to determine the influence of Atg6 function on autophagy. We used transmission electron microscopy to determine the statistical significance of the data.
microscopy (TEM) to investigate Atg61 mutants at the ultrastructural level. Following 4 hours of starvation, many autophagosomes (Fig. 1E, arrowhead) and autophagolysosomes (Fig. 1E, arrow) were observed in control fat body cells, whereas homozygous Atg61 mutant fat body cells lacked these autophagic structures (Fig. 1F). Ref(2)P is the Drosophila ortholog of p62 (SQSTM1) and is known to bind ubiquitylated substrates and aid in their recruitment into autophagosomes to be targeted for degradation (Nezis et al., 2008). Homozygous Atg61 mutant cells lacking GFP accumulated Ref(2)P compared with neighboring control fat body cells (Fig. 1G-G’; supplementary material Fig. S1B). Importantly, the accumulation of Ref(2)P aggregates could be rescued by expressing an Atg6 transgene in the Atg61 mutant cells (supplementary material Fig. S1C-C’). These results indicate that Atg6 is required for autophagy in vivo.

**Atg6 functions in multiple vesicle trafficking processes**

Vps34 is required for the formation of PI3P in Drosophila and other species (Juhász et al., 2008; Lindmo and Stenmark, 2006). To examine the influence of Atg6 function on PI3P, we used a transgenic reporter consisting of GFP fused to the FYVE domain of hepatocyte growth factor regulated tyrosine kinase substrate (Hrs) (Gillooly et al., 2000). GFP-FYVE localized to punctate structures in the cytoplasm of control (red) cells of the larval fat body (Fig. 2A-A’). By contrast, homozygous Atg61/Atg61 mutant cells (lacking red) had no detectable GFP-FYVE puncta (Fig. 2A-A’).

Vps34 is required for endocytosis in Drosophila (Juhász et al., 2008). To test whether Atg6 functions in endocytosis, uptake of Texas Red (TR)-avidin was used to monitor fluid-phase endocytosis in larval fat body. Control (GFP-positive) cells contained TR-avidin-positive puncta throughout the cytosol, whereas homozygous Atg61 mutant (GFP-negative) cells possessed little to no endocytic tracer (Fig. 2B-B’ and instead TR-avidin was often more abundant on the surface of these mutant cells (Fig. 2C-C’).

Rab5, a small GTPase of the Ras superfamily, is associated with endosomes and functions as a key regulator of vesicle trafficking (Wucherpfennig et al., 2003). To monitor Rab5 localization in fat body cells, we used a GFP-Rab5 transgenic reporter. In control fat body cells, GFP-Rab5 localizes to the plasma membrane and has characteristic puncta with perinuclear localization. In cells with RNAi knockdown of Atg6 (Atg66), GFP-Rab5 localized to the plasma membrane in most fat body cells; however, the perinuclear localization was significantly reduced (supplementary material Fig. S2A-D). These data suggest that in larval fat body cells, Atg6 is required for either recruitment of or stable association of Rab5 with the perinuclear endosomal compartment.

To determine whether the endocytosis phenotypes observed in Atg6 and Vps34 mutant cells are due to defects in autophagy, we performed the TR-avidin uptake assay in Atg1 mutant fat cells. Atg1 is a kinase and a core component of the autophagy pathway that is both necessary and sufficient for inducing autophagy (Scott et al., 2007). Both control (GFP-positive) cells and homozygous Atg1Δ3D (GFP-negative) mutant cells contained TR-avidin-positive puncta throughout the cytosol (Fig. 2D-D’). Furthermore, TR-avidin did not accumulate at the surface of these cells (Fig. 2E-E’), indicating that Atg1 function is not required for fluid-phase endocytosis. These results indicate that Atg6, but not Atg1, is required for fluid-phase endocytosis in vivo.

Endosomal sorting complex required for transport (ESCRT) proteins are required for recruitment of ubiquitylated cargo proteins to the endosome, sorting to multivesicular bodies (MVBs), and subsequent degradation by the lysosome (Henne et al., 2011). Like Atg6 mutant cells, mutations in either Vps32 (ESCRT-II; shrb – FlyBase) (GFP-negative) or Vps32 (ESCRT-III; shrb – FlyBase) (GFP-negative) cells suppressed the overgrowth of either Vps25 or Vps32 mutant eye tissue (Fig. 3C,E,F). Combined, our data indicate that Atg6 is required for fluid-phase endocytosis, and suggest the possibility that an important relationship might exist between Atg6 and the ESCRT pathway.

Recent work has implicated autophagy in protein secretion (Deretic et al., 2012), but direct genetic analyses of the role of key autophagy regulatory factors, including Atg6, in protein secretion within animals are lacking. The Drosophila larval salivary gland secretes large quantities of glue proteins in response to steroid at
is possible that this
Atg61
salivary gland cells homozygous for melanotic blood cell masses are often present in the phenotype (visible as black masses) (Fig. 5A-C). Although single melanotic blood cell masses are often present in homozygous Atg61 type animals exhibited no obvious phenotypes, all homozygous Atg61 mutant late third larval instar eye tissue (neighboring (GFP-positive) cells leading to overgrowth of the developing eye tissue (n=11). (E) Homozygous loss of Atg61 suppressed overgrowth of the eye caused by Vps25 mutant cells (GFP negative) (n=8). (D) Vps32Δ43 mutant clones (GFP negative) in late third larval instar eye imaginal disc cause non-autonomous overproliferation of neighboring (GFP-positive) cells leading to overgrowth of the developing eye tissue (n=11). (F) Vps32Δ43 mutant clones (GFP negative) in Atg61 mutant eye disc leads to suppression of overgrowth of the eye discs (n=10). Scale bars: 1 mm in A,C; 50 μm in E-G.

the end of larval development. A transgenic fusion of the secreted glue protein Sgs3 and GFP proteins provides an excellent means to follow protein secretion in this in vivo (Biyasheva et al., 2001). Both control (Fig. 4A,A') and homozygous Atg6Δ1 mutant animal (Fig. 4C,C') salivary glands are able to synthesize glue protein in the salivary glands based on the presence of GFP. By 4 hours after puparium formation, control animals had secreted most of the glue protein, based on the absence of GFP (Fig. 4B,B'), whereas homozygous Atg6Δ1 mutant animals retained GFP, suggesting that they have a protein secretion defect (Fig. 4D,D'). It is possible that this Atg6Δ1 mutant animal defect is caused by a failure to arrest protein synthesis that is associated a general delay in development. To address this possibility, homozygous Atg6Δ1 mutant clones of cells (mCherry negative) were produced in salivary glands. These Atg6Δ1 mutant cells retained Sgs3-GFP, whereas neighboring control cells (mCherry positive) lacked expression of Sgs3-GFP at 0 hour (n=12), but are unable to secrete it 4 hours after puparium formation (D-D'). Control cells (mCherry positive) are able to secrete Sgs3-GFP whereas homozygous Atg6Δ1 mutant cells (mCherry negative) retain Sgs3-GFP in the cytoplasm (n=12). Control cells (mCherry positive) secrete Sgs3-GFP whereas Vps32Δ43 mutant cells retain Sgs3-GFP granules in the cytoplasm (n=11). Control cells (mCherry positive) secrete Sgs3-GFP whereas Atg1Δ3D expressing cells retain Sgs3-GFP granules in the cytoplasm (n=10). Scale bars: 1 mm in A,C; 50 μm in E-G.

Loss of Atg6 leads to melanotic blood cell mass formation

Whereas the parental control w1118 and heterozygous Atg6Δ1/wild-type animals exhibited no obvious phenotypes, all homozygous Atg6Δ1 mutant larvae displayed a striking melanotic blood cell mass phenotype (visible as black masses) (Fig. 5A-C). Although single melanotic blood cell masses are often present in Atg6Δ1 mutant larvae (Fig. 5C), many homozygous mutant animals possess multiple melanotic blood cell masses (Fig. 6B). Significantly, this homozygous Atg6Δ1 mutant melanotic blood cell tumor phenotype was completely rescued by ubiquitous expression of Atg6 (Fig. 5D).

We investigated whether mutations in other core autophagy genes results in melanotic blood cell mass formation. All homozygous Atg7 and Atg13 mutant animals lack melanotic blood cell masses (supplementary material Fig. S4A; data not shown). Although 18% of Atg8aΔK067569 mutant pupae possess melanotic masses (supplementary material Fig. S4A-C), such blood cell masses were not observed in Atg8 mutant larvae. Combined, these data indicate that Atg6 mutants are different from other autophagy mutants in their predisposition to the formation of melanotic blood cell masses.

We investigated whether blood cells are the source of melanotic masses in Atg6 mutant larvae. Blood cell-specific hemolectin (hmlΔ)-GAL4 was used to drive GFP expression in parental w1118 control, heterozygous Atg6Δ1/wild-type and homozygous Atg6Δ1 mutant larvae. Immunohistochemical analyses of paraffin sections with a GFP antibody revealed that these masses were indeed composed of blood cells in homozygous Atg6Δ1 mutants, whereas significantly fewer blood cells were observed in either w1118 or Atg6Δ1/wild-type control animals (Fig. 5E-G). Quantification of blood cells revealed that Atg6Δ1/wild-type animals contained approximately twice as many blood cells as parental w1118 larvae, and homozygous Atg6Δ1/Atg6Δ1 mutants contained nearly ten times as many blood cells as control w1118 animals (Fig. 5H). These data indicate that loss of Atg6 results in an increase in blood cell formation.
numbers, and like beclin 1 mutant mice, loss of Atg6 causes an increase in the number of circulating blood cells.

Two approaches were taken to determine whether the melanotic mass phenotype is blood cell autonomous. First, we expressed UAS-Atg6 using two different blood cell-specific drivers, either hmlA-Gal4 or croquemort-Gal4, in Atg61 mutant animals. Expression of the Atg6 transgene using these approaches failed to rescue the phenotype, suggesting that ectopic blood cell masses are either due to a blood cell-independent effect of Atg6 or that these Gal4 drivers are expressed too late during blood cell development to rescue the mutant phenotype (data not shown). Second, we induced Atg6 loss-of-function mutant cell clones in lymph glands using hs-FLP. Although these animals possess melanotic masses (data not shown), they also have Atg6 mutant cell clones in other tissues. Thus, we cannot conclude that the Atg6 melanotic mass phenotype is blood cell lineage specific.

The current model for beclin 1 function during tumor progression suggests that decreased autophagy leads to elevated p62 signaling and activation of the NFkB pathway (Mathew et al., 2009). In addition, the NFkB pathway has been implicated in the formation of melanotic blood cell masses in Drosophila (Minakhina and Steward, 2006). Therefore, we investigated whether mutations in either ref(2)P (Drosophila p62) or different combinations of NFkB genes suppress melanotic blood cell mass formation in homozygous Atg61 mutant larvae. All homozygous Atg61 mutant larvae possessed melanotic blood cell masses (black masses), whereas control larvae did not contain such structures (Fig. 6A,B). Significantly, homozygous ref(2)P mutants failed to suppress the Atg6 mutant melanotic mass phenotype (Fig. 6C). Drosophila has three NFkB proteins named Dif, Dorsal and Relish. Double mutant analyses of homozygous Atg61 with either homozygous dif, dorsal or Relish mutants indicated that mutations in each individual NFkB failed to suppress the Atg6 mutant melanotic mass phenotype (Fig. 6D-F). Therefore, we constructed a triple mutant containing homozygous dif, Relish and Atg6, and mutation of these two NFkB genes failed to suppress the formation of melanotic masses associated with Atg61 (Fig. 6G). Finally, we constructed a strain containing homozygous dif, Relish and Atg6 and also lacking one allele of dorsal (loss of all four genes was lethal at an earlier developmental stage), and this combination of NFkB mutations failed to suppress the Atg61 melanotic blood cell mass phenotype (Fig. 6H). These results suggest that neither Ref(2)P nor NFkB proteins play a role in melanotic blood cell mass formation in Atg61 mutants.

To gain insight into the kinetics of melanotic blood cell mass formation, we followed the lymph gland (the larval hematopoietic organ) and melanotic mass development. We used hmlA-GAL4 to drive GFP in blood cells in control (n=107) and homozygous Atg61 mutant (n=157) larvae. Compared with synchronized control animals, homozygous Atg61 mutant larvae displayed enlarged lymph glands (yellow boxes) between 80 hours and 104 hours after egg lay (Fig. 7A,B,E). During the same developmental interval, homozygous Atg61 mutant larvae progressively accumulated GFP-positive blood cell masses, whereas control animals lacked these structures. By 126 hours, all of the Atg61 mutant larvae contained numerous ectopic blood cell masses that were absent in controls
Fig. 7. Loss of Atg6 leads to enlargement of lymph gland and altered blood cell development. (A) Control larva at 104 hours after egg lay expressing GFP in blood cells. (B) Homozygous Atg61 mutant larva at 104 hours after egg lay expressing GFP in blood cells. Note the enlarged lymph gland (yellow box). (C) Same control animal as in A at 126 hours after egg lay has formed a prepupa. (D) Same Atg61 mutant animal as in B at 126 hours after egg lay did not pupariate, and appeared to have an increased number of circulating blood cells. (E) Graph showing progression of different phenotypes exhibited by Atg6 mutants during larval development. The larval stage-specific numbers of teeth on mouth hooks of control and Atg6 mutant larvae were used to normalize development of these genotypes. As larvae progress through development there is an increase in formation of blood cell aggregates followed by melanotic masses (n=157). (F) Control hmlΔ-GAL4 UAS-GFP lymph gland at third instar larval stage (n=10). (G) Atg61 mutant hmlΔ-GAL4 UAS-GFP lymph gland at third instar stage (n=10). (H) Control third instar lymph gland stained for NimrodC1 (NimC1) showing expression in the cortical zone (n=7). (I) Atg61 mutant third instar lymph gland stained for NimC1 showing a complete lack of expression in the cortical zone (n=7). (J) Control third instar larval lymph gland stained for lamellocyte specific antigen L1 showing no expression in the cortical zone (n=7). (K) Atg61 mutant third instar larval lymph gland with increased expression of L1 in the cortical zone (n=7). (L) Control hmlΔ-GAL4 UAS-GFP animal showing sessile blood cells that are located in a reiterated pattern along abdominal segments (n=7). (M) hmlΔ-GAL4 UAS-GFP expressing Atg61 mutant animals possess less patterned sessile blood cells along the abdominal segments than controls (n=7). (N) NimC1 staining of animal shown in L. (O) NimC1 staining of animal shown in M indicates that this blood cell antigen is missing in sessile blood cells. Yellow boxes in A-D delineate lymph glands. Scale bars: 250 μm in A; 100 μm in F, 50 μm in H, I; 200 μm in L, N.

(Fig. 7C,D,E). These Atg61 mutant animal blood cell masses initiated melanization 104 hours after egg lay (following the formation of GFP-positive blood cell aggregates) and continued to do so until 160 hours after egg lay (Fig. 7E). Whereas control animals formed prepupa by 120 hours after egg lay, most Atg61 mutants did not pupariate.

We analyzed the lymph glands of age-matched control and homozygous Atg61 mutant third instar larval animals to obtain a better understanding of how hematopoiesis is altered. Homozygous Atg61 mutant lymph glands were larger than those of control animals (Fig. 7F,G; supplementary material Fig. S5). As expected, the plasmacytocyte-specific blood cell differentiation marker NimrodC1 (NimC1) could be detected in the cortical zone in control lymph gland of control animals (Fig. 7H), but this marker could not be detected in the lymph glands of homozygous Atg61 mutant animals (Fig. 7I). L1 is a lamellocyte-specific blood cell differentiation marker that we did not detect in the cortical zone of control animal lymph glands (Fig. 7J). By contrast, homozygous Atg61 mutant lymph glands displayed increased L1 staining (Fig. 7K). In addition, blood cells that are present in clusters in abdominal segments expressed NimC1 in control animals, whereas those in Atg61 mutant animals appeared to lack the NimC1 antigen (Fig. 7L-O). Taken together, these data indicate that Atg6 plays an important role in blood cell development, and that an altered differentiation program probably contributes to melanotic blood cell masses.

DISCUSSION

Here we describe the genetic characterization of Atg6 in Drosophila. Atg6 is an essential gene, and most homozygous Atg6 null mutant animals die at the end of larval development. Drosophila lacking Atg6 function possess melanotic blood cell masses, as well as defects in several vesicle trafficking pathways.

Atg6 is a core component of the Vps34 complex. Studies in yeast and mammalian systems have identified Vps34 as an essential protein regulating a wide variety of vesicular trafficking events, including autophagy, endocytosis, and anterograde and retrograde transport between Golgi and the lysosome (Lindmo and Stenmark, 2006). Therefore, it is logical that Atg6 mutant cells not only have a defect in starvation-induced autophagy, but also fail to produce PI3P and have defects in endocytosis and protein secretion. Our data are consistent with reports from other animal systems in which beclin 1 mutants exhibit endocytosis defects (Ruck et al., 2011; Thoresen et al., 2010).

The accumulation of an endocytic tracer at the periphery of homozygous Atg6 mutant cells suggests that Atg6 functions at an early step of endocytosis. This conclusion is supported by the similarity between Atg6 and ESCRT II and III endocytic tracer phenotypes in the fat body. Therefore, it is possible that loss of Atg6 is similar to ESCRT mutants in flies, and that the Vps34 complex
regulates receptor downregulation because of similar defects in endocytosis (Herz et al., 2006; Herz et al., 2009; Thompson et al., 2005; Vaccari and Bilder, 2005; Vaccari et al., 2009). However, the lack of an obvious \( \text{Atg6} \) mutant eye over-growth phenotype suggests that \( \text{Atg6} \) mutants are different from ESCRT pathway mutants. In addition, unlike ESCRT mutants, \( \text{Atg6} \) mutant cell clones neither accumulated Notch intracellular domain antigen nor possessed altered expression of the \( m2.61lacZ \) Notch reporter (data not shown). An alternative explanation for the difference between \( \text{Atg6} \) and ESCRT mutants is that maternally contributed \( \text{Atg6} \) mRNA may enable normal \( \text{Atg6} \) mutant eye imaginal disc development. Although loss of \( \text{Atg6} \) suppresses ESCRT mutant developing eye tissue size, the pattern of these structures remains disrupted, suggesting that some aspects of the ESCRT phenotype cannot be suppressed. It is tempting to speculate that \( \text{Atg6} \) functions at an earlier stage than these ESCRT genes in endocytosis, but additional studies are needed to understand the relationship of these factors during endocytosis.

Recent work indicates that autophagy regulates protein secretion (Deretic et al., 2012). To our knowledge, this is the first report of \( \text{Atg6} \) regulating protein secretion. In addition, we show that loss of either \( \text{Vps34} \) or \( \text{Atg1} \) in salivary gland cells also leads to disruption of protein secretion. Therefore, our data indicate that protein secretion might be an autophagy-dependent process. Interestingly, we noted differences in the size of \( \text{Sgs3-GFP} \) vesicles in \( \text{Atg6} \), \( \text{Vps34} \) and \( \text{Atg1} \) mutant cells (Fig. 4E-G). Although these genes might function at distinct steps in the maturation of secretory vesicles, it is also possible that differences in maternal contribution of mRNAs in these mutants are responsible for the differences in these mutant phenotypes. Beclin 1 and PI3P localize to the trans Golgi network (Gillooly et al., 2000; Kihara et al., 2001a). Thus, it is also possible that \( \text{Vps34} \) and \( \text{Atg6} \) are part of a third \( \text{Vps34} \) complex that can regulate protein secretion, although it is also possible that the \( \text{Vps34} \) complex that regulates autophagy participates in this process.

\( \text{Atg6} \) mutant larvae possess excess hemocytes, the \textit{Drosophila} equivalent of macrophages, and contain melanotic blood cell masses prior to their death. Melanotic masses are thought to be caused by at least two possible mechanisms: (1) tissue damage that recruits blood cells to encapsulate the unhealthy tissue and potentially protect the organism, and (2) over-proliferation of the blood cell lineage due to a defect in the hematopoietic stem cell niche (Minakhina and Steward, 2006). In support of the latter possibility, a recent study showed that hemocytes with decreased autophagy have decreased recruitment to epidermal wounds because of impaired cortical remodeling in the blood cells (Kadandale et al., 2010). Although blood cells clearly surround the melanotic masses in \( \text{Atg6} \) mutant larvae, it is unclear whether the masses themselves are composed strictly of hemocytes and whether the masses result from hemocyte over-proliferation, or if hemocytes are induced to proliferate by the presence of melanotic masses. Our data indicate that \( \text{Atg6} \) mutants have enlarged hematopoietic organs, more blood cells and altered blood cell differentiation and that blood cell aggregations precede the formation of melanotic masses. However, we cannot exclude the possibility that cells that are not of hematopoietic origin are involved in the initiation of melanotic masses.

It is interesting that, like beclin 1 mutant mice, loss of \( \text{Atg6} \) in \textit{Drosophila} results in expansion of the hematopoietic lineage. NF-\( \kappa B \)s are known to regulate hematopoiesis in both \textit{Drosophila} and mammals. In flies, \textit{Toll} and \textit{cactus} are key regulators of NF-\( \kappa B \) signaling, and either \textit{Toll} gain-of-function or \textit{cactus} loss-of-function mutants lead to over-proliferation of hemocytes, in particular lamellocytes, resulting in the formation of melanotic masses (Qiu et al., 1998). Given the connection between beclin 1, p62 and NF-\( \kappa B \) (Mathew et al., 2009), we speculated that the melanotic mass phenotype in \( \text{Atg6} \) mutants could be due to misregulation of p62 and NF-\( \kappa B \). We systematically removed either \textit{rel(2)p} (\textit{fly p62}) or the three \textit{Drosophila} NF-\( \kappa B \)s \textit{dorsal}, \textit{dif} and \textit{Rel} in combination with loss of \( \text{Atg6} \). Surprisingly, mutations in these genes failed to suppress the \( \text{Atg6} \) melanotic mass phenotype.

Numerous reports indicate that beclin 1 plays an important role in cancer, and most studies attribute this function to a defect in autophagy (White and DiPaola, 2009). Although autophagy is likely to contribute to tumor progression, it is also possible that the influence of beclin 1 on other vesicle trafficking pathways may promote tumor development. Consistent with this possibility, loss of \( \text{Atg3} \) and autophagy leads to benign adenomas in livers that fail to cause cancer, but this phenotype is not observed in other tissues (Takamura et al., 2011). Here, we show that \( \text{Atg6} \) influences multiple trafficking pathways in flies, and that \( \text{Atg6} \) mutant animals possess hematopoietic defects and melanotic blood cell masses. Future studies of \textit{Drosophila} \( \text{Atg6} \) mutants should resolve a number of questions that are relevant to both the fundamental cellular function of this protein, as well as potentially advance our understanding of how beclin 1 functions as a tumor suppressor.

Acknowledgements

We thank Y. Rong for advice about gene targeting; C. Evans and U. Banerjee for advice about lymph gland analyses; I. Anda, A. Bergmann, D. Bilder, M. Freeman, T. Ip, T. Neufeld, I. Nezis, N. Silverman, H. Stemmark, the Bloomington Stock Center and the Vienna \textit{Drosophila} RNAi Center for flies and antibodies; T. Fortier for technical support; and the Baehrecke lab for constructive comments.

Funding

This work was supported by National Institutes of Health grants [CA159314 to E.H.B. and S01RR027897 to the UMass EM Core]. E.H.B. is an Ellison Medical Foundation Scholar and a member of the UMass DERC [DK32520]. Deposited in PMC for release after 12 months.

Author contributions

B.V.S., J.H.H. and E.H.B. designed experiments; B.V.S., J.H.H. and C.M.P. performed experiments; and all authors wrote and discussed the manuscript.

Competing interests statement

The authors declare no competing financial interests.

Supplementary material

Supplementary material available online at http://dev.biologists.org/supplメント/doi:10.1242/dev.0894900-DC1

References


Henne, W. M., Buchkovich, N. J. and Emr, S. D.

Herz, H. M., Chen, Z., Scherr, H., Lackey, M., Bolduc, C. and Bergmann, A.


