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

Bhupendra V. Shrvage1,*, Jahda H. Hill1,2,*, Christine M. Powers1, Louisa Wu2 and Eric H. Baehrecke1,§

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 NfκB 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; Thumml et al., 1994; Tsukada and Ohsunami, 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 (p150 in mammals; 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 autophagosomal isolation membranes, which serve as precursors to double-membrane autophagosomes prior to membrane expansion (Kirisako et al., 1999; Simonsen et al., 2004). In addition to their functions in autophagy, Vps34 and PI3P also regulate sorting of hydrolases to the yeast vacuole and mammalian lysosome, endocytic trafficking, and potentially multiple other vesicle trafficking processes (Juhasz et al., 2008; Thoresen et al., 2010).

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; Matsuura 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

1Department of Cancer Biology, University of Massachusetts Medical School, Worcester, MA 01605, USA. 2Department of Cell Biology and Molecular Genetics, University of Maryland, College Park, MD 20742, USA.

*These authors contributed equally to this work

†Present address: National Heart, Lung, and Blood Institute, National Institutes of Health, Bethesda, MD 20892, USA

§Author for correspondence (Eric.Baehrecke@umassmed.edu)

Accepted 11 January 2013
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/Becn1 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 (P3K59F- FlyBase) in vivo, and co-expression of Atg6 with either Vps34 or Vps15 (irdl – 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[PZ] Atg6<sup>6006</sup>, y w hs-FLP; FRT82B ubi-GFP, w;Sgs3-GFP, y w hs-FLP; FRT42D GFPnls, y w hs-FLP; FRT80B mRFPnls, y w hs-FLP; FRT80B ubi-GFP, y w hs-FLP; FRT80B ubi-GFP, y w hs-FLP; FRT80B ubi-GFP; actin >cd2 >GAL4::UAS-dsRed and y w hs-FLP; FRT82B UAS-GFPnls, UAS-GFP-2x-FYVE, UAS-Rab5-GFP, y w hs-flp; r4GAL4>FRT82B UAS-mCherry, y w hs-FLP; FRT80B Atg6<sup>113d</sup> (all from T. Neufeld, University of Minnesota, MN, USA; y w hs-FLP; FRT42D Fps25n53 y+;CyO actin GFP (from A. Bergmann, University of Massachusetts Medical School, MA, USA); Atg6<sup>606</sup> (TID 22123) (from Vienna *Drosophila* RNAi Center); Ref(2)P<sup>602b</sup>, Ref(2)P<sup>603</sup> (both from I. Nezis, University of Warwick, UK); w; ref(2)P<sup>603</sup> w;Dff<sup>4</sup> on bw/CyO; w; J4/CyO, dff<sup>4</sup> (all from T. Ip); w; Atg7<sup>477</sup> /CyO actin GFP, w; Atg7<sup>477</sup> /CyO actin GFP, y; Atg6<sup>86</sup> K07569/FM7 actin-GFP, Atg13<sup>2</sup>-Atg13<sup>674</sup> (all from T. Neufeld); and FRT42D Vps32<sup>653</sup>/CyO twist-Gal4 UAS-GFP (from D. Bilder, University of California, Berkeley, CA, USA).

**Larval staging**

For lymph gland analyses, larvae were obtained from collections of 4-hour-old eggs and aged at 25°C. Classification of third instar larvae was based on the number of teeth on the mandibular hooks (Bodenheim, 1965) and developmental age. For eye imaginal disc experiments, larvae were raised on food supplemented with 0.05% Bromophenol Blue (Maroni and Stamey, 1983). Stationary larvae with clear guts were used for dissection of eye imaginal discs from Atg6 and Vps mutants.

**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<sup>118</sup> parental line. The resultant strain contained a w<sup>+</sup> 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 1μg 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’-CCAGCAGCTGGAGAAGATTAGG-3’ and 5’-GCGTTGATCTCTGAGCCAGTC-3’; CG5991-RA: 5’-CATTGCCAATAATGCTGGC-3’ and 5’-GGAGAATTTCGCGCAATGAC-3’; CG5991-RB: 5’-GGAGACGCGATACCGGAAAGC-3’ and 5’-GGAGATTTGGCGAAATGAC-3’; CG5991-RC: 5’-GCTCTTCTCGATCTGGAC-3’ and 5’-GGAGATTGTGCGCAATGAC-3’; CG5986: 5’-GGGCTAAACGCTTGCATTAC-3’ and 5’-CGTGTATATCGCGAAGCGG-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 hsFlp; FRT42D Ubi-nslGFP, y w hsFlp; FRT42D mRFP-nls, y w hs-FLP; +; FRT80B Ubi-nslGFP, y w hs-FLP; +; FRT80B Ubi-mRFP, y w hs-FLP; +; FRT82B Ubi-nslGFP, y w hsFlp; CgG4A; FRT82B UAS-mCherry and y w hsFlp; FRT42D Ubi-nslGFP. Four-hour egg lays were maintained at 37°C for 1 hour to induce clones in the larval salivary glands, and 10-hour egg lays 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 larva 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 Axiolmager Z1 equipped with an Apotome. Images were acquired with Axioscam and processed using Zeiss Axiovision 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/Imc1 (1:10; I. Ando) (Asha et al., 2003) and mouse anti-L1 (1:10; I. Ando) (Asha 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 washes, and rehydrated through a series of decreasing percentage ethanol washes, and rehydrated through a series of decreasing percentage ethanol washes.
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 SPIpon/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 untranslatable 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]Atg60096 larvae (Scott et al., 2004). Based on this result and the fact that P[PZ]Atg60096 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 larva, whereas the RNA levels of neighboring genes were not altered in the homozygous mutant Atg6 (hereafter termed as Atg6p) 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 Atg6p and animals transheterozygous for Atg6p 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 Atg6p homozygous mutants (supplementary material Fig. S1A). In addition, Atg6p complements P[PZ]Atg60096 even though this is a lethal P-element insertion, indicating that P[PZ]Atg60096 is not an Atg6 mutant. These data indicate that we have isolated a loss-of-function Atg6 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 recombinase-mediated recombination at FLP recombinase target (FRT) sites to generate Atg6p mitotic mutant cell clones in the fat body, resulting in tissue composed of control (either wild type or heterozygous Atg6p/wild type) and homozygous Atg6p/Atg6p 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 Atg6p mutant cells (lacking GFP) displayed diffuse localization of mCherry-Atg8a (Fig. 1C–E).

Two additional approaches were used to determine the influence of Atg6 function on autophagy. We used transmission electron
microscopy (TEM) to investigate Atg6<sup>+</sup> 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 Atg6<sup>+</sup> 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 Atg6<sup>+</sup> mutant cells lacking GFP accumulated Ref(2)P compared with neighboring control fat body cells (Fig. 1G; supplementary material Fig. S1B). Importantly, the accumulation of GFP-positive puncta throughout the cytosol of control (Fig. 1D-D<sup>+</sup>); supplementary material Fig. S1C-C<sup>+</sup>–) were observed in control fat body cells, whereas homozygous Atg6<sup>+</sup> mutant (GFP-negative) cells possessed little to no endocytic tracer (Fig. 2B-B<sup>+</sup>) and instead TR-avidin was often more abundant on the surface of these mutant cells (Fig. 2C-C<sup>+</sup>–). 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 (Atg6<sup>+</sup>), 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 Atg1<sup>Δ3D</sup> (GFP-negative) mutant cells contained TR-avidin-positive puncta throughout the cytosol (Fig. 2D-D<sup>+</sup>). Furthermore, TR-avidin did not accumulate at the surface of these cells (Fig. 2E-E<sup>+</sup>–), 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 Vps25 (ESCRT-II) or Vps32 (ESCRT-III; shrb – FlyBase) (GFP-negative) cells suppress TR-avidin fluid-phase endocytic tracer uptake compared with control cells (GFP-positive) (supplementary material Fig. S3A–D<sup>+</sup>). Loss of ESCRT components in the developing Drosophila eye impairs MVB formation and leads to defects in receptor degradation that cause tissue overgrowth (Fig. 3A,D) (Herz et al., 2006; Herz et al., 2009; Thompson et al., 2005; Vaccari and Bilder, 2005; Vaccari et al., 2009). By contrast, eye imaginal disc tissue isolated from homozygous Atg6<sup>+</sup> animals at the same third larval instar stage is normal in size (Fig. 3B). Although Atg6 and ESCRT component double mutant eye tissue is disorganized, loss of Atg6 significantly 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

**Fig. 2. Loss of Atg6 leads to defects in PI3P formation and endocytosis.** (A–A<sup>+</sup>) GFP-FYVE localizes to perinuclear puncta, reflecting Vps34 activity and PI3P formation in control (mCherry-positive) fat body cells, but remains cytoplasmic in Atg6<sup>+</sup> mutant (mCherry-negative) fat body cells (n=24). (B–B<sup>+</sup>) Texas Red-avidin is endocytosed by control (GFP-positive) fat body cells, but is largely excluded from Atg6<sup>+</sup> mutant fat body cells (Fig. 1G; supplementary material Fig. S1B). Importantly, the accumulation of Ref(2)P aggregates could be rescued by expressing an Atg6 transgene in the Atg6<sup>+</sup> mutant cells (supplementary material Fig. S1C–C<sup>+</sup>). These results indicate that Atg6 is required for autophagy in vivo.
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 (Biyaasheva et al., 2001). Both control (Fig. 4A,A′) and homozygous Atg6Δ 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 Atg6Δ mutant animals retained GFP, suggesting that they have a protein secretion defect (Fig. 4D,D′). It is possible that this Atg6Δ 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 Atg6Δ mutant clones (mCherry negative) were devoid of GFP expressing cells (mCherry positive) as well as in cells with RNAi knockdown of Vps34Δ mutant cells retain Sgs3-GFP granules in the cytoplasm (n=11). (G-G′) Control cells (mCherry positive) secrete Sgs3-GFP whereas homozygous Atg6Δ mutant cells (mCherry negative) retain Sgs3-GFP in the cytoplasm (n=12). (F-F′) Control cells (mCherry positive) secrete Sgs3-GFP whereas Vps34Δ mutant cells retain Sgs3-GFP granules in the cytoplasm (n=12). (E-E′) Control cells (mCherry positive) secrete Sgs3-GFP whereas Atg8Δ 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 Atg6Δ/wild-type animals exhibited no obvious phenotypes, all homozygous Atg6Δ 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 Atg6Δ mutant larvae (Fig. 5C), many homozygous mutant animals possess multiple melanotic blood cell masses (Fig. 6B). Significantly, this homozygous Atg6Δ 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 Atg8Δ K0117506 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 (hmhΔ)-GAL4 was used to drive GFP expression in parental w1118 control, heterozygous Atg6Δ/wild-type and homozygous Atg6Δ mutant larvae. Immunohistochemical analyses of paraffin sections with a GFP antibody revealed that these masses were indeed composed of blood cells in homozygous Atg6Δ mutants, whereas significantly fewer blood cells were observed in either w1118 or Atg6Δ/wild-type control animals (Fig. 5E-G). Quantification of blood cells revealed that Atg6Δ/wild-type animals contained approximately twice as many blood cells as parental w1118 larvae, and homozygous Atg6Δ/Atg6Δ 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.
Fig. 5. Loss of Atg6 leads to melanotic blood cell mass formation. (A-D) White-light images of wandering third instar larvae. Parental control w1118 (A) and heterozygous Atg6+/ (B) larvae are phenotypically similar. Homozygous Atg6+/ mutant larvae (C) contain melanotic blood cell masses (yellow ring), and this phenotype is rescued by ubiquitous expression of a GFP-Atg6 transgene (D). (E-G) Hemocytes were visualized by immunohistochemistry in third instar larvae expressing GFP, driven by hmlΔ-GAL4 (arrowheads). Histological sections of w1118 (E) and Atg6+/ heterozygous (F) larvae contain few hemocytes (brown) and no visible melanotic masses, whereas sections of homozygous Atg6 mutant larvae (G) reveal many hemocytes, which surround melanotic masses (black ring). (H) Quantification of hemocytes from w1118, Atg6+/+ and Atg6+/Atg6−/ larvae revealed a significant increase in hemocyte number in both heterozygous and homozygous Atg6 mutant larvae compared with control w1118 larvae. For each genotype, n=20 animals. Error bars represent s.e.m. A one-tailed t-test was used for statistical analysis and P: values relative to w1118 are: Atg6+/+, P=0.0004; Atg6+/Atg6−, P=2.6×10⁻⁶. Scale bars: 500 µm in A,C; 100 µm in E.

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 hmlΔ-Gal4 or croquemort-Gal4, in Atg6+/ 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 Atg6+/ mutant larvae. All homozygous Atg6+/ 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 Atg6+/ with either homozygous dif, dorsal or Relish mutants indicated that mutations in each individual NFkB gene 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 Atg6+/ (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 Atg6 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 Atg6 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 hmlΔ-GAL4 to drive GFP in blood cells in control (n=107) and homozygous Atg6+/ mutant (n=157) larvae. Compared with synchronized control animals, homozygous Atg6+/ 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 Atg6+/ mutant larvae progressively accumulated GFP-positive blood cell masses, whereas control animals lacked these structures. By 126 hours, all of the Atg6+/ mutant larvae contained numerous ectopic blood cell masses that were absent in controls...
Homozygous Atg6\textsuperscript{1} mutant larvae 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 Atg6\textsuperscript{1} 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. (F) Control hml\textsubscript{Δ}-GAL4 UAS-GFP lymph gland at third instar larval stage. (G) Atg6\textsuperscript{1} mutant hml\textsubscript{Δ}-GAL4 UAS-GFP lymph gland at third instar stage. (H) Control third instar lymph gland stained for NimrodC1 showing expression in the cortical zone. (I) Atg6\textsuperscript{1} mutant third instar lymph gland stained for NimrodC1 showing a complete lack of expression in the cortical zone. (J) Control third instar larval lymph gland stained for lamellocyte specific antigen L1 showing no expression in the cortical zone. (K) Atg6\textsuperscript{2} mutant third instar animal lymph gland with increased expression of L1 in the cortical zone. (L) Control hml\textsubscript{Δ}-GAL4 UAS-GFP animal showing sessile blood cells that are located in a reiterated pattern along abdominal segments. (M) hml\textsubscript{Δ}-GAL4 UAS-GFP-expressing Atg6\textsuperscript{1} mutant animals possess less patterned sessile blood cells along the abdominal segments than controls. (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,J; 200 μm in L,N.

**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 Atg6\textsuperscript{1} 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 Atg6\textsuperscript{1} 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. (F) Control hml\textsubscript{Δ}-GAL4 UAS-GFP lymph gland at third instar larval stage. (G) Atg6\textsuperscript{1} mutant hml\textsubscript{Δ}-GAL4 UAS-GFP lymph gland at third instar stage. (H) Control third instar lymph gland stained for NimrodC1 (NimC1) showing expression in the cortical zone. (I) Atg6\textsuperscript{1} mutant third instar lymph gland stained for NimrodC1 showing a complete lack of expression in the cortical zone. (J) Control third instar larval lymph gland stained for lamellocyte specific antigen L1 showing no expression in the cortical zone. (K) Atg6\textsuperscript{2} mutant third instar animal lymph gland with increased expression of L1 in the cortical zone. (L) Control hml\textsubscript{Δ}-GAL4 UAS-GFP animal showing sessile blood cells that are located in a reiterated pattern along abdominal segments. (M) hml\textsubscript{Δ}-GAL4 UAS-GFP-expressing Atg6\textsuperscript{1} mutant animals possess less patterned sessile blood cells along the abdominal segments than controls. (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,J; 200 μm in L,N.

**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 \textit{Atg6} mutant eye over-growth phenotype suggests that \textit{Atg6} mutants are different from ESCRT pathway mutants. In addition, unlike ESCRT mutants, \textit{Atg6} mutant cell clones neither accumulated Notch intracellular domain antigen nor possessed altered the expression of the \textit{m2.61lacZ} Notch reporter (data not shown). An alternative explanation for the difference between \textit{Atg6} and ESCRT mutants is that maternally contributed \textit{Atg6} mRNA may enable normal \textit{Atg6} mutant eye imaginal disc development. Although loss of \textit{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 \textit{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 \textit{Atg6} regulating protein secretion. In addition, we show that loss of either \textit{Vps34} or \textit{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 Sgs3-GFP vesicles in \textit{Atg6}, \textit{Vps34} and \textit{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 Vps34 and Atg6 are part of a third Vps34 complex that can regulate protein secretion, although it is also possible that the Vps34 complex that regulates autophagy participates in this process. \textit{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 cuticular remodeling in the blood cells (Kadandale et al., 2010). Although blood cells clearly surround the melanotic masses in \textit{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 \textit{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 \textit{Atg6} in \textit{Drosophila} results in expansion of the hematopoietic lineage. NF-\kappaB are known to regulate hematopoesis in both \textit{Drosophila} and mammals. In flies, \textit{Toll} and \textit{cactus} are key regulators of NF-\kappaB 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-\kappaB (Mathew et al., 2009), we speculated that the melanotic mass phenotype in \textit{Atg6} mutants could be due to misregulation of p62 and NF-\kappaB. We systematically removed either \textit{ref(2)p} (By p62) or the three \textit{Drosophila} NF-\kappaBs \textit{dorsal}, \textit{diff} and \textit{Rel} in combination with loss of \textit{Atg6}. Surprisingly, mutations in these genes failed to suppress the \textit{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 \textit{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 \textit{Atg6} influences multiple trafficking pathways in flies, and that \textit{Atg6} mutant animals possess hematopoietic defects and melanotic blood cell masses. Future studies of \textit{Drosophila} \textit{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. Stenmark, 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 S10RR027897 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/lookup/suppl/doi:10.1242/dev.089490/-/DC1

References
Henne, W. M., Buchkovich, N. J. and Emr, S. D. 2008. Beclin 1 forms two

Juhász, G., Hill, J. H., Yan, Y., Sass, M., Baehrecke, E. H., Backer, J. M. and


of Drosophila hematopoiesis by efficient isolation of ESCRT mutants. 
Dev. Cell 9, 711-720.


Fig. S1 Atg6 is required for development and autophagy. (A) Atg6 is required for development, as homozygous Atg6 mutant animals die during development. Most homozygous Atg6 mutant lethality occurs prior to puparium formation, and lethality can be rescued by expressing an atg6 transgene ubiquitously in the whole animal. (B) Quantification of Ref(2)P (fly p62) puncta in control and homozygous Atg6 mutant fat body cells as in Fig. 1G. A two-tailed t-test was used for statistical analysis, and the P-value relative to control was 5.07×10⁻⁹. The error bars represent s.d. (C-C″) Ref(2)P aggregates did not accumulate Atg6-mutant clone cells (mCherry negative) expressing a myc-tagged Atg6 transgene in the entire fat body (n=7). Scale bar: 50 μm.
Fig. S2. Loss of Atg6 leads to defects in Rab5 localization. (A) GFP-Rab5 distribution in control fed fat body cells is prominent at the plasma membrane and perinuclear region (n=11). (B) Fat body cells expressing Atg6IR have fewer GFP-Rab5 puncta in the perinuclear region and at the plasma membrane (n=13). (C) Quantification of GFP-Rab5 puncta in the perinuclear region (2 μm diameter ring surrounding the nucleus). Two tailed t-test was used for statistical analysis, and the P-value relative to control was 1.48×10⁻⁸. (D) Graph showing relative Atg6 mRNA level normalized to rp49 mRNA in control and Atg6IR. Error bars represent s.d. Scale bar: 50 μm.
Fig. S3. Vps25 and Vps32 mutant cells possess defects in fluid phase endocytosis. (A-A’’) Texas Red-avidin is endocytosed by control (GFP-positive) fat body cells, but is excluded from Vps25n55 mutant cells (GFP negative) (n=10). (B-B’’) Surface view of the fat body depicted in A showing accumulation of Texas Red-avidin at the surface of the Vps25n55 mutant cells but not in control cells. (C-C’’) Texas Red-avidin is endocytosed by control (GFP-positive) fat body cells, but is excluded from Vps32G5 mutant cells (GFP negative) (n=10). (D-D’’) Surface view of the fat body depicted in C showing accumulation of Texas Red at the surface of the Vps32G5 cells but not in control cells. Scale bars: 50 μm.
**Fig. S4. Mutations in core autophagy genes do not lead to melanotic mass formation.** (A) Graph showing percentage of larvae/pupae exhibiting melanotic tumor phenotype in w1118 (n=145) and Atg6 (n=157), Atg7 (n=113), Atg8a (n=101), Atg13 (n=99) mutant animals. Note that melanotic tumors in Atg8a mutant are observed only after pupariation, and that all homozygous Atg6 mutant larvae possess melanotic tumors. (B) Parental control Atg8a KG07569/+ pupae do not have melanotic masses (n=94). (C) Atg8a KG07569/Y (n=18/101) pupae contains melanotic masses. Scale bar: 250 μm.

**Fig. S5. Atg6 mutants have enlarged lymph glands.** Quantification of lymph gland area in control (n=10) and homozygous Atg6+/y (n=10) mutants shown in Fig. 7F,G. A two-tailed t-test was used for statistical analysis, and the P-value relative to control was 6.3×10⁻⁵. Error bars represent s.d.