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Detection of Autophagy in *Caenorhabditis elegans*

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Abstract

Autophagy is a dynamic and catabolic process that results in the breakdown and recycling of cellular components through the autophagosomal-lysosomal pathway. Many autophagy genes identified in yeast and mammals have orthologs in *C. elegans*. In recent years, gene inactivation, by RNAi and/or chromosomal mutations, has been useful to probe the functions of autophagy in *C. elegans*, and a role for autophagy has been shown in multiple processes such as, the adaptation to stress, longevity, cell death, cell growth control, clearance of aggregate prone proteins, degradation of P granules during embryogenesis, and apoptotic cell clearance. Here we discuss some of these roles and describe methods that can be used to study autophagy in *C. elegans*.

Specifically, we summarize how to visualize autophagy in embryos, larva, or adults, how to detect the lipidation of LGG-1 by western blot, and how to inactivate autophagy genes by RNAi.

INTRODUCTION

Autophagy in *C. elegans*

Autophagy is a lysosomal-mediated pathway resulting in the degradation and recycling of long-lived proteins, protein aggregates, as well as damaged and old organelles (Klionsky, 2004). It is highly conserved and has been shown to be a fundamental catabolic process in eukaryotes that is required for key developmental and pathological events. Autophagy was first described in mammals, through morphological studies of rat liver cells (Deter et al., 1967). However, it was in yeast where many autophagy genes (*atg*) were discovered, by screening for mutations that decreased the survival of yeast cells under starvation, as well as mutations that disrupted the cytoplasm-to-vacuole targeting (*cvt*) process (Harding, 1996; Harding et al., 1995; Hutchins and Klionsky, 2001; Klionsky et al., 2003; Thumm et al., 1994; Tsukada and Ohsumi, 1993).

The process of autophagy is composed of several distinct steps: formation of a phagophore (also referred to as an isolation membrane or preautophagosomal structure); elongation and closure of the phagophore to form the double membrane autophagosome; transport and fusion of the autophagosome with a lysosome; and finally, degradation of the autophagosomal contents, and recycling of degraded material (FIG. 1) (Mizushima, 2007; Nakatogawa et al., 2009; Xie and Klionsky, 2007). In addition to fusing with a lysosome, an

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autophagosome may also fuse with an endosome to form a hybrid organelle called the amphisome (Jing and Tang, 1999; Liou et al., 1997). When an amphisome or autophagosome fuses with a lysosome, it is referred to as an autophagolysosome (or an autolysosome).

The evolutionary conservation of autophagy genes between yeast and *C. elegans* allowed for the identification of genes that encode core components of the autophagic machinery in *C. elegans*, on the basis of genomic sequence homology (Table 1) (Meléndez and Levine, 2009; Meléndez et al., 2003). Genetic screens for mutations that disrupt the degradation of P granules, has recently discovered autophagy genes not previously identified in *C. elegans* on the basis of sequence homology, including: *epg-1*, the ortholog of yeast *ATG13*, and *epg-8*, the ortholog of yeast *ATG14* (Table 1) (Tian et al., 2009; Yang and Zhang, 2011). Although, the similarities between *S. cerevisiae*, mammals, and *C. elegans* autophagy proteins suggest that the molecular mechanisms of autophagosome formation may be conserved (FIG. 1 and Table 1) (Meléndez and Levine, 2009), genes recently identified in *C. elegans* that do not have a yeast ortholog may indicate that autophagy involves more complex membrane dynamics in higher eukaryotes. It is important to uncover further details about the roles of autophagy genes in autophagosome formation and maturation in *C. elegans*, and the role of these genes in different settings where autophagy is required.

The role of autophagy genes in *C. elegans* development has emerged from studies using chromosomal mutations or RNA interference against autophagy genes. Chromosomal mutations exist for many of the autophagy genes found in *C. elegans* and many RNAi clones are available (Table 1).

Autophagy in *C. elegans* Development and Aging

L1 arrest after starvation: Autophagy plays a role mediating the developmental changes associated with survival during extracellular and/or intracellular stress, such as starvation (Levine and Klionsky, 2004). In the absence of food, L1 larvae undergo a reversible developmental arrest and can survive for 1–2 weeks (Johnson et al., 1984). The insulin/IGF-1 signaling pathway, composed of the insulin-like/IGF-1 receptor *daf-2* and the FOXO transcription factor *daf-16*, is involved in regulating L1 arrest triggered by starvation (Baugh and Sternberg, 2006; Fukuyama et al., 2006; Gems, 1998). Interestingly, reduced levels of autophagy have been shown to greatly decrease the survival of starved L1 larvae, emphasizing the importance of autophagy during early stages of development (Alberti et al., 2010; Kang et al., 2007; Lu et al., 2011; Tian et al., 2009; Tian et al., 2010; Yang and Zhang, 2011).

Dauer development: During the first larval molt, animals that are exposed to a limited food supply develop into an alternate L3 larval stage termed dauer (Albert et al., 1981). Dauer development is associated with morphological and behavioral changes that allow for survival under harsh conditions and stress (Cassada and Russell, 1975; Golden and Riddle, 1984). The regulation of dauer development has been well characterized and requires the IGF-1/insulin-like, guanylyl cyclase, and TGF- β signaling pathways, as mutations in any of these pathways can result in a dauer constitutive phenotype (Daf-c) or a dauer defective

phenotype (Daf-d) (Birnby et al., 2000; da Graca et al., 2004; Estevez et al., 1993; Gottlieb and Ruvkun, 1994; Inoue and Thomas, 2000; Patterson et al., 1997; Ren, 1996; Schackwitz, 1996; Thomas et al., 1993). Dauer development is associated with an increase in autophagy, which appears to be required for the cell remodeling associated with proper dauer formation (Meléndez et al., 2003).

Longevity pathways: In *C. elegans*, aging is controlled by multiple longevity pathways, such as insulin-like growth factor signaling, TOR signaling, dietary restriction, mitochondrial activity, and germline signaling (Antebi, 2007). Recent genetic studies suggest that autophagy interacts with many of these longevity signals to regulate *C. elegans* aging (Hansen et al., 2008; Lapierre et al., 2011; Meléndez et al., 2003; Toth et al., 2008). Insulin/IGF-1R/*daf-2* mutants display an increase in autophagy, as detected by an increase in the number of punctate structures labeled by the autophagy marker, GFP::LGG-1, in hypodermal seam cells, a cell type commonly used to visualize autophagy in *C. elegans* (FIG. 2) (Hansen et al., 2008; Meléndez et al., 2003). A reduction in autophagy during development, or only during adulthood, shortens the long lifespan of *daf-2* mutants (Hansen et al., 2008; Hars et al., 2007; Meléndez et al., 2003). Reduced food intake without malnutrition, otherwise referred to as dietary restriction, occurs in *eat-2* mutants (Avery, 1993). These animals lack a nicotinic acetylcholine receptor specific to the pharynx, thereby exhibiting reduced pharyngeal pumping, and have an extended lifespan phenotype (Lakowski and Hekimi, 1998; Raizen et al., 1995). Consistent with a role for TOR in dietary restriction, *eat-2* mutants have reduced TOR signaling, display an increase in autophagy, and require autophagy for their long-lived phenotype (Hansen et al., 2008; Jia and Levine, 2007; Toth et al., 2008). The reduction in mitochondrial respiration in *isp-1* mutants extends lifespan (Dillin et al., 2002; Lee et al., 2003), and this phenotype is also dependent on autophagy (Toth et al., 2008). Finally, *glp-1*/Notch germline-less mutants induce autophagy, and require autophagy for lifespan extension (Lapierre et al., 2011). Interestingly, HLH-30, the ortholog of the mammalian TFEB transcription factor, is required for the lifespan extension associated with the longevity pathways described above, and also regulates autophagy (Lapierre et al., 2013). In conclusion, autophagy is required as part of most longevity pathways in *C. elegans*, the only exception thus far being the longevity associated with a reduction in protein translation (Hansen et al., 2008; Pan et al., 2007).

Degradation of paternal mitochondria: Directly after fertilization, autophagy is induced resulting in the elimination of spermatozoon specific organelles, including paternal mitochondria (Al Rawi et al., 2011; Sato and Sato, 2011). Whether autophagy also acts in higher eukaryotes to degrade paternal mitochondria is not known, however, an increase in ubiquitination and the localization of LC3 near the sperm mid-piece at the point of entry, may suggest that this is the case in fertilized mouse zygotes (Al Rawi et al., 2011).

Autophagy in apoptosis, necrosis and cell clearance: Although autophagy has a role in homeostasis as an important pro-survival mechanism in response to stress, an excess in autophagy may result in cell death (Kang et al., 2007). Autophagy is also required for necrotic cell death, a type of cell death characterized by the loss of plasma membrane integrity (Samara et al., 2008; Toth et al., 2007). Additionally, similar to mammals, BEC-1, a

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component of the class III Phosphatidylinositol 3-Kinase (PI3K) complex (FIG. 1), interacts with the anti-apoptotic ortholog of Bcl-2, CED-9, suggesting cross-talk between autophagy and apoptosis (Erdelyi et al., 2011; Takacs-Vellai et al., 2005). Autophagy proteins have been shown to play a role in the proper degradation of apoptotic cell corpses in *C. elegans*, since in autophagy deficient animals, apoptotic cells are internalized, but not properly degraded (Li et al., 2012; Ruck et al., 2011). Interestingly, rescue experiments indicate that autophagy genes are required within the engulfing cell to promote apoptotic cell degradation (Li et al., 2012).

Detecting autophagy in *C. elegans*: Autophagy can be monitored by transmission electron microscopy (TEM), fluorescent image analysis of the GFP::LGG-1 reporter or other autophagy reporters (Table 2), and by western blot, evaluating LGG-1 lipidation. It should be noted that an increase in the number of autophagosomes does not necessarily reflect an induction of autophagy (Klionsky, 2012), and is therefore important to distinguish between induction of autophagy, an increase in autophagic flux, and the accumulation of autophagosomes due to inefficient or blocked autophagy (Klionsky, 2012). Usually, it is useful to infer the turnover of autophagosomes in the presence and absence of lysosomal degradation. In *C. elegans*, this may be achieved by RNAi knockdown of genes with lysosomal function, such as *cup-5* (Fares and Greenwald, 2001; Kostich et al., 2000; Sun et al., 2011), or the addition of inhibitors such as bafilomycin A1, or chloroquine, routinely used in mammalian cells, which have also been successful in *C. elegans* (Ji et al., 2006; Oka and Futai, 2000; Pivtoraiko et al., 2010). Clearly, the use of multiple assays to verify an increase in functional autophagy is recommended. A comprehensive list of guidelines was recently reported (Klionsky et al., 2012). Here we describe four protocols for the basic study of autophagy in *C. elegans*: detection of autophagy using GFP::LGG-1, autophagy in embryos, western blotting to evaluate lipidation of LGG-1, and RNAi as a method to target the knockdown of autophagy genes.

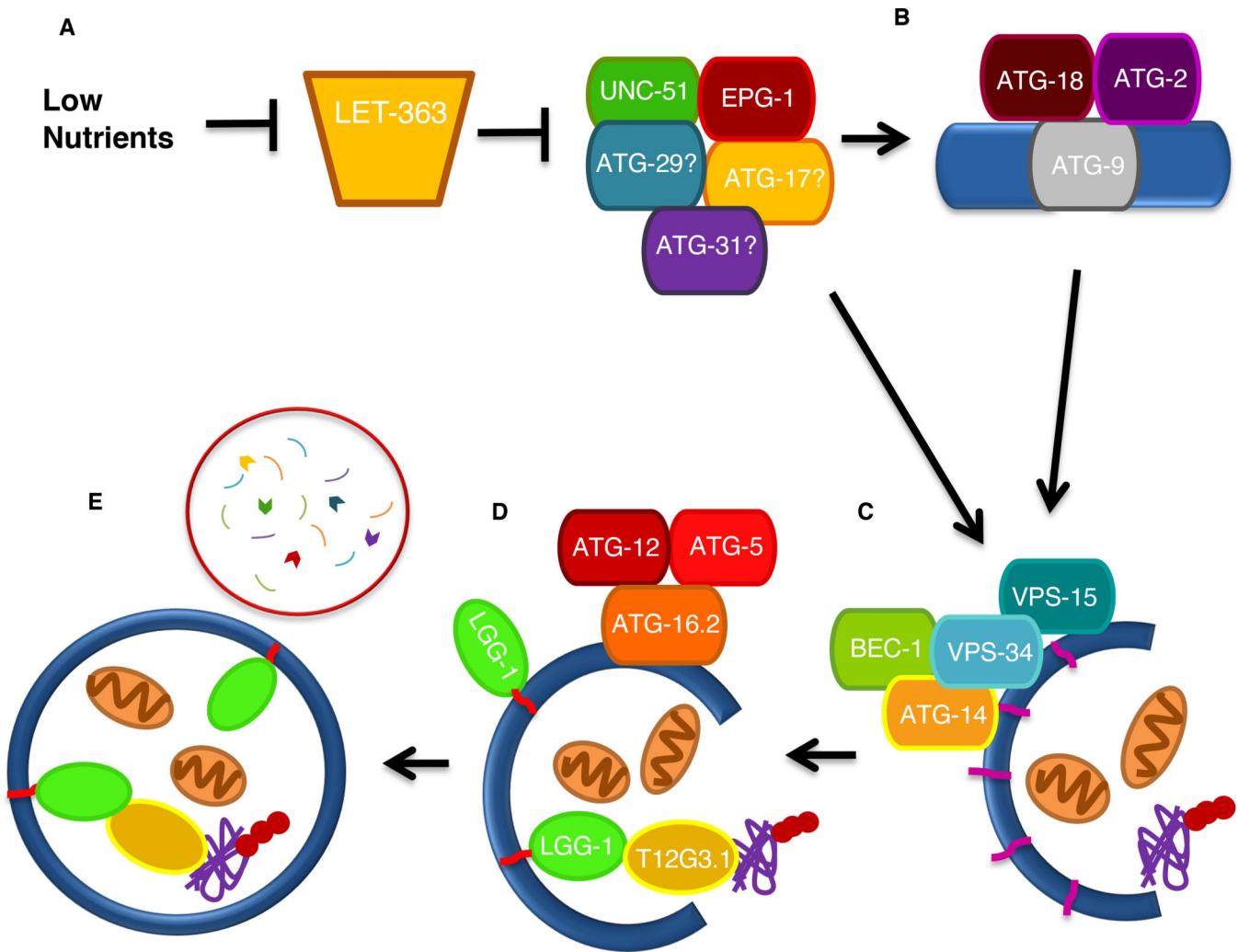
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**Figure 1.**

Autophagy in *C. elegans*. A. The process of autophagy has been delineated by studies in yeast and mammalian cells. We presume that induction of autophagy begins with the activation of UNC-51. B. Autophagosome formation requires the integral protein ATG-9, thought to contribute membrane to the developing autophagosome. C. Nucleation requires the Class III PI3K complex, which recruits downstream autophagy proteins to the isolation membranes (IM) in mammals or pre-autophagosomal structure (PAS) in yeast, through the production of PI3P (light purple). D. Two conjugation complexes (LGG-1 and ATG-12) are required for elongation of the isolation membranes and completion of the developing autophagosome. LGG-1 conjugated to phosphatidylethanolamine (PE, red) binds to both the inner and outer membranes of the autophagosome. LGG-1 also has the ability to bind to the autophagic adaptor proteins, such as SQST-1 which bind poly-ubiquitinated aggregates. E. The complete autophagosome eventually fuses with the lysosome leading to the degradation of cargo within the autophagosome.

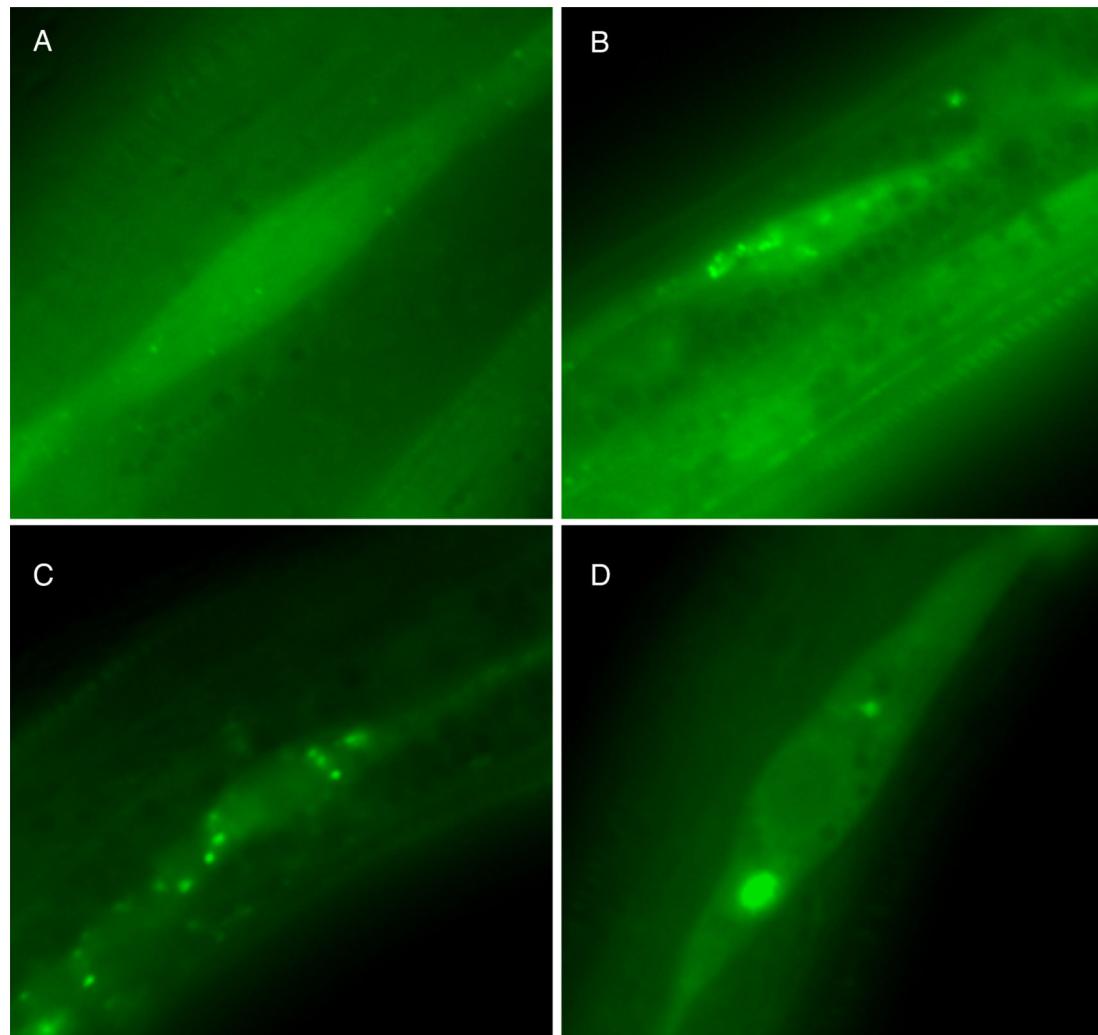


Figure 2.

GFP::LGG-1 expression in hypodermal seam cells of *daf-2(e1370)* mutants. A. *daf-2(e1370)* mutants grown on OP50 *E. coli*, at 15°C, display a diffuse localization of GFP::LGG-1. B. *daf-2(e1370)* mutants grown on OP50 *E. coli*, at 25°C, display an increase in GFP::LGG-1 positive puncta (up to 12 GFP::LGG-1 positive puncta/seam cell) that represent early autophagic structures or autophagosomes. C. *daf-2(e1370)* mutants grown on control RNAi *E. coli* (transformed with empty vector, L4440), at 25°C, display the characteristic GFP::LGG-1 positive punctate structures. D. *daf-2(e1370)* mutants fed *bec-1* RNAi, and raised at 25°C, display an increase in GFP::LGG-1 expression and large GFP::LGG-1 positive aggregates

Table 1:*C. elegans* autophagy genes

| <i>C. elegans</i> A _{tg} gene | Allele | Yeast/Mammalian ortholog | Phenotype in <i>C. elegans</i> | Reference |
|--|----------------------|-------------------------------|--------------------------------|---|
| <i>let-363</i> ^R | <i>h98</i> | <i>TOR1/2</i> mTOR | Let, LL | (Brown et al. 1994; Noda and Ohsumi 1998; Vellai et al. 2003; Jia et al. 2004; Hansen et al. 2007; Hansen et al. 2008) |
| <i>unc-51</i> ^R | <i>e369</i> | <i>ATG1/ULK1</i> 2 | Unc, AbD, Pg, Egl | (Hedgecock et al. 1985; Ogura et al. 1994; Matsura et al. 1997; Kuroyanagi et al. 1998; Meléndez et al. 2003; Zhang et al. 2009) |
| <i>epg-1</i> ^R | <i>bp414</i> | <i>ATG1/3</i> / <i>Atg13</i> | Dv, Pg | (Funakoshi et al. 1997; Chan et al. 2009; Tian et al. 2009) |
| <i>bcc-1</i> ^R | <i>ok691</i> | <i>ATG6/VPS30/beclin 1</i> | Let, AbD, St, SL, Pg pQ | (Seaman et al. 1997; Kametaka et al. 1998; Khara et al. 2001; Meléndez et al. 2003; Takacs-Vellai et al. 2005; Jia et al. 2007; Hansen et al. 2008; Zhao et al. 2009; Ruck et al. 2011) |
| <i>let-512/vps-34</i> ^R | <i>h797</i> | <i>VPS34/Vps34</i> | Let, SL, Pg | (Seglen and Gordon 1982; Volinia et al. 1995; Roggo et al. 2002; Zhao et al. 2009; Ruck et al. 2011) |
| <i>ZK930.1</i> ^R | <i>ok3132</i> | <i>VPS15/p150</i> | ND | (Panaretou et al. 1997; Khara et al. 2001; Kovács et al. 2003) |
| <i>epg-8</i> ^R | <i>bp251</i> | <i>ATG1/4/Atg14L</i> , Barkor | Dv, Pg | (Kihara et al. 2001; Obara et al. 2006; Sun et al. 2008); (Fan et al. 2011; Yang and Zhang 2011) |
| <i>epg-6</i> | <i>bp242</i> | -/ <i>WIP14</i> | Dv, Pg | (Lu et al. 2011) |
| <i>epg-3</i> ^R | <i>bp405</i> | -/ <i>VMP1</i> | Dv, Pg | (Tian et al. 2010) |
| <i>epg-4</i> ^R | <i>bp425</i> | -/ <i>E124/PIG8</i> | Dv, Pg | (Tian et al. 2010) |
| <i>atg-3</i> | <i>bp412</i> | <i>ATG3/Atg3</i> | Pg | (Tanida et al. 2002; Zhang et al. 2009) |
| <i>atg-4.1</i> ^{*R} | <i>tm3949</i> | <i>ATG4/Atg4</i> | Pg | (Kirisako et al. 2000; Tanida et al. 2004; Zhang et al. 2009) |
| <i>atg-4.2</i> ^{*R} | <i>tm3948</i> | <i>ATG4/Atg4</i> | ND | (Kirisako et al. 2000; Tanida et al. 2004; Zhang et al. 2009) |
| <i>atg-5</i> | <i>bp545</i> | <i>ATG5/Atg5</i> | ND | (Mizushima et al. 1998; Mizushima et al. 2001; Tian et al. 2010) |
| <i>atg7/M7.5</i> ^R | <i>tm831</i> | <i>ATG7/Atg7</i> | AbD, SL, Pg, pQ | (Kim et al. 1999; Tanida et al. 2001; Meléndez et al. 2003) |
| <i>Igg-1</i> ^R | <i>bp500, tm3489</i> | <i>ATG8/LC3</i> | Let, Dv, AbD, SL, Pg | (Kirisako et al. 2000; He et al. 2003; Meléndez et al. 2003; Zhang et al. 2009; Alberti et al. 2010) |
| <i>Igg-2</i> ^R | - | <i>ATG8/LC3</i> | Let, Dv, AbD, SL, Pg | (Kirisako et al. 2000; He et al. 2003; Meléndez et al. 2003; Tian et al. 2010) |
| <i>atg-10</i> ^R | <i>bp588</i> | <i>ATG10/Atg10</i> | ND | (Takahiro Shintani 1999; Mizushima et al. 2002; Meléndez et al. 2003; Tian et al. 2010) |
| <i>Igg-3</i> ^R | <i>gk1857</i> | <i>ATG12/Atg12</i> | SL, Pg | (Mizushima et al. 1998; Meléndez et al. 2003; Hars et al. 2007) |
| <i>atg-16.1</i> ^{*R} | - | <i>ATG16/Atg16L1</i> | ND | (Kuma et al. 2002; Mizushima et al. 2003; Tian et al. 2010) |

| <i>C. elegans</i> Atg gene | Allele | Yeast/Mammalian ortholog | Phenotype in <i>C. elegans</i> | Reference |
|-------------------------------|---------------|--------------------------------|--------------------------------|---|
| <i>atg-16.2</i> ^{3R} | <i>ok3224</i> | <i>ATG1/6</i> / <i>Atg16L1</i> | ND | (Kuma et al. 2002; Mizushima et al. 2003; Tian et al. 2010) |
| <i>atg-2</i> | <i>bp576</i> | <i>ATG2</i> / <i>Atg2</i> | | (Shintani 2001; Wang et al. 2001; Lu et al. 2011) |
| <i>atg-9</i> ^R | <i>bp564</i> | <i>ATG9</i> / <i>Atg9</i> | | (Noda et al. 2000; Yamada et al. 2005; Reggioli 2006) |
| <i>atg-18</i> ^R | <i>gk378</i> | <i>ATG18/WIP1/2</i> | Let, AbD, Pg, pQ | (Barth 2001; Meléndez et al. 2003; Jia et al. 2007); (Polson et al. 2010; Tian et al. 2010) |
| <i>epg-2</i> | <i>bp287</i> | -/- | Pg | (Tian et al. 2010) |
| <i>epg-5</i> ^R | <i>bp450</i> | -/ KIAA1632 | Dv, Pg | (Tian et al. 2010) |
| <i>sepa-1</i> | <i>bp402</i> | -/- | Pg | (Zhang et al. 2009) |
| <i>T12G3.1</i> | <i>ok2892</i> | -/pG2(SQSTM1) | | (Tian et al. 2010; Lu et al. 2011) |

Let= Lethal; Unc= uncoordinated; Dv = Decreased viability of L1s during starvation; AbD= Abnormal Dauer; St= Sterile; LL= Long lifespan; SL= Short Lifespan; Pg= P granule accumulation; Egl= Egg laying defective; pQ= polyQ expansion susceptibility; ND= Not determined

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Paralogs in *C. elegans*

R RNAi clone available

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Table 2.Fluorescent reporters for monitoring Autophagy in *C. elegans*

| Protein | Function | Tissue Expression ^Y | Transgenes ^Φ | References |
|----------|--|---|---|--|
| LGG-1 | Microtubule – associated protein-1/ Ubiquitin-like protein | Intestine, Hypodermis, Muscle, Pharynx, Neurons, Vulva, Somatic Gonad, Germline | <i>adls2122[Plgg-1::GFP::LGG-1; rol-6(su1006) izEx1[Plgg-1::GFP::LGG-1; rol-6(su1006) izEx5[Plgg-1::GFP::LGG-1; Podr-1::RFP] vkEx1093[Pnhx-2::mCherry::LGG-1] dkls399[Ppie-1::GFP::lgg-1, unc-119(+)] Is(Ppie-1::GFP::mCherry::LGG-1; unc-119(+)) Ex[Plgg-1::DsRED::LGG-1; Pmyo-2::GFP]</i> | (Melendez et al. 2003; Kang et al. 2007; Samara et al. 2008; Gosai et al. 2010; Manil-Segalen et al. 2014) |
| LGG-2 | Ubiquitin-like protein | Hypodermis, Intestine, Vulva, Pharynx, Neurons, Muscle | <i>RD108 Ex[Plgg-2::GFP::LGG-2; rol-6(su1006) RD217 unc119(ed3)III; Ex[unc-119(+); Ppie-1::gfp::mcherry::lgg-1] VIG9 unc119(ed3)III; Is[unc-119(+); Plgg-2::gfp::lgg-2]</i> | (Alberti et al. 2010; Manil-Segalen et al. 2014) |
| DFCP1 | Double FYVE-Containing Protein | Head, Tail, Vulva, Neurons | <i>bpIs168[Pnfy-a-1::DFCPI::GFP; unc-76(+)]</i> | (Derubeis et al. 2000; Cheung et al. 2001; Axe et al. 2008; Tian et al. 2010) |
| ATG-16.1 | WD repeat-containing protein | Intestine, Head, Pharynx, Muscle, Neurons | <i>[Patg-16.1::ATG-16.1::GFP; rol-6(su10006)]</i> | (Zhang et al. 2013) |
| ATG-16.2 | WD repeat-containing protein | Intestine, Head, Pharynx, Muscle, Neurons | <i>[Patg-16.2::ATG-16.2::GFP; rol-6(su10006)]</i> | (Zhang et al. 2013) |
| ATG-9 | Integral Membrane Protein | Head, Tail, Vulva, Neurons | <i>bpIs211[Pnfy-a-1::ATG-9::GFP; unc-76(+)]</i> | (Noda et al. 2000; Lu et al. 2011; Liang et al. 2012; Lin et al. 2013) |
| EPG-1 | Atg13 homolog | Neurons, Pharynx, Muscle | <i>bpIs175[Pepg-1::EPG-1::GFP; rol-6(su1006)]</i> | (Tian et al. 2009) |
| EPG-9 | Atg101 homolog | Intestine, Pharynx, Neurons | <i>bpIs214[Pepg-9::EPG-9::GFP; unc-76(+)]</i> | (Liang et al. 2012) |
| BEC-1 | Coiled-Coil protein | Intestine, Hypodermis, Vulva, Neurons, Somatic Gonad | <i>swEx520 [Pbec-1::BEC-1::GFP; rol-6(su1006)] grEx129[Pbec-1::BEC-1::mRFP; lin-15(+)] Ex[Pced-1::mCherry::BEC-1; rol-6(su1006)] Ex[Pegl1::mCherry::BEC-1; rol-6(su1006)]</i> | (Takacs-Vellai et al. 2005; Rowland et al. 2006; Ruck et al. 2011; Huang et al. 2012) |
| SQST-1 | p62/Autophagy adaptor protein | Hypodermis, Neurons, Intestine, Vulva, Muscle | <i>bpIs151[Psqst-1::SQST-1::GFP; unc-76(+)]</i> | (Hunt-Newbury et al. 2007; Pankiv et al. 2007; Tian et al. 2010) |
| SEPA-1 | Autophagy adaptor protein | Intestine, Head, Tail | <i>bpIs131[Psepa-1::SEPA-1::GFP; unc-76(+)]</i> | (Zhang et al. 2009; Tian et al. 2010) |
| PGL-1 | RNA-binding protein/P-granule component | P-granules, Intestine | <i>bnIs1[Ppie-1::GFP::PGL-1; unc-119(+)] bnIs26[Pelt-2::PGL-1::GFP; Pmyo-2::mCherry]</i> | (Cheeks et al. 2004; Zhang et al. 2009; Updike et al. 2011) |

^Y Tissue expression may vary depending on the specific promoter used

^Φ Transgenes shown are those found in autophagy studies or those which may be beneficial in autophagy studies; Additional transgenes may be available for each gene

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