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Genetic Regulation of Caenorhabditis elegans Lysosome Related Organelle Function

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Abstract

Lysosomes are membrane-bound organelles that contain acid hydrolases that degrade cellular proteins, lipids, nucleic acids, and oligosaccharides, and are important for cellular maintenance and protection against age-related decline. Lysosome related organelles (LROs) are specialized lysosomes found in organisms from humans to worms, and share many of the features of classic lysosomes. Defective LROs are associated with human immune disorders and neurological disease. Caenorhabditis elegans LROs are the site of concentration of vital dyes such as Nile red as well as age-associated autofluorescence. Even though certain short-lived mutants have high LRO Nile red and high autofluorescence, and other long-lived mutants have low LRO Nile red and low autofluorescence, these two biology are distinct. We identified a genetic pathway that modulates aging-related LRO phenotypes via serotonin signaling and the gene kat-1, which encodes a mitochondrial ketothiolase. Regulation of LRO phenotypes by serotonin and kat-1 in turn depend on the proton-coupled, transmembrane transporter SKAT-1. skat-1 loss of function mutations strongly suppress the high LRO Nile red accumulation phenotype of kat-1 mutation. Using a systems approach, we further analyzed the role of 571 genes in LRO biology. These results highlight a gene network that modulates LRO biology in a manner dependent upon the conserved protein kinase TOR complex 2. The results implicate new genetic pathways involved in LRO biology, aging related physiology, and potentially human diseases of the LRO.


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Introduction

Lysosomes are ubiquitous, dynamic, membrane-bound organelles that serve a major degradative role within cells. Lysosomes receive material through the endocytic pathway and are its terminal compartment [1–3]. Lysosomes also receive material via the secretory pathway and directly from the cytoplasm [1–5]. Proteins, lipids, nucleic acids, and oligosaccharides received from endocytic, secretory, and cytoplasmic compartments are degraded within lysosomes, and breakdown products are exported to cellular anabolic or catabolic processes [4–6]. Lysosome function in diverse cellular processes including cell surface receptor turnover, destruction of pathogens, antigen processing, digestion, starvation responses, tissue remodeling, ion storage, autophagy, aging, and plasma membrane repair [2,3,7].

Lysosome related organelles (LRO), also known as gut granules in Caenorhabditis elegans [8], are a heterogeneous group of specialized, membrane-bound cellular compartments that share many of the features of classical lysosomes [3,9]. Specifically, they have acidic pH, contain acid hydrolases, and lack mannose-6-phosphate receptors [4,9]. LROs subserve a specialized set of functions such as the production and storage of pigment (melanosomes), immune defense (neutrophil azurophilic granules), and blood clotting (platelet dense granules) [9]. Human disorders of LRO biogenesis or function are characterized by defects in pigmentation (melanosome), immunodeficiency (neutrophil), bleeding diathesis (platelet), and neurological disease [3]. In Drosophila, defects in LRO biogenesis or function lead to altered eye color, caused by defects in the trafficking of pigment granules [3,9].

In C. elegans, lysosome-related organelles are the site of microscopic autofluorescence which accumulates as animals age [10]. LROs are easily recognized in the worm by their autofluorescence and birefringence under polarized microscopy, and mutations that disrupt LRO function also disrupt age-dependent accumulation of autofluorescence [8]. C. elegans LROs also serve as a cellular reservoir for zinc, preventing toxicity of high dietary zinc [11].

C. elegans LROs are the site of accumulation of the vital dyes Nile red and BODIPY-labeled fatty acids when these substances are fed to living C. elegans with E. coli as a nutrient source [3,12–14]. This, together with the lipophilic properties of Nile red and BODIPY-labeled fatty acids, led to the erroneous conclusion these dyes reveal the storage of neutral lipids and that the Nile red stores are the site of fat storage in C. elegans [15–19]. By a number of microscopic and cell-biological techniques, LROs do not co-
Lysozyme-related organelles (LROs) are specialized, membrane-bound organelles that share many common features of canonical lysosomes. Mutations in critical components of LRO biogenesis lead to human diseases of immunity, blood clotting, and pigmentation. In Caenorhabditis elegans, LROs are the site of accumulation of aging-related autofluorescence and the vital dye Nile red when fed to living C. elegans. Through classical genetics we show that the LRO is regulated by a conserved genetic pathway involving serotonin, a mitochondrial ketothiolase, and a proton-coupled solute transporter. Though previously thought to be linked in an obligatory manner, through systems level analysis we show that accumulation of C. elegans LRO Nile red and autofluorescence are mechanistically distinct processes. Contrary to the prior notion that LRO Nile red indicates lipid stores, we show that LRO Nile red is not correlated with, and may be antirelated with, C. elegans lipid stores. Using hundreds of candidate gene inactivations that disrupt Nile red accumulation, we determined which LRO regulatory genes specifically interact with 6 genetic mutants known to have altered LRO biology, identifying changes specifically dependent upon target of rapamycin complex 2 signaling. These data reveal relationships between LRO biology and aging and metabolism in C. elegans.

To identify other regulators of LRO function, we surveyed by high LRO Nile red and autofluorescence in wild type C. elegans animals in the presence of a level of exogenous serotonin that causes a decrease LRO Nile red in wild type animals yielded ~100 high LRO Nile red mutant strains. We mapped the mutants harboring the brightest residual LRO Nile red signal and identified 6 alleles of the mitochondrial ketothiolase kat-1 (Figure 2A). kat-1 mutations elevate LRO Nile red in strains that also carry a mutation in the C. elegans homologue of mammalian tubby gene, tub-1 [18]. kat-1 mutations were also identified in a genetic screen for elevated intestinal autofluorescence [29].

LRO Nile red in kat-1 mutants without serotonin treatment is more than twice that of wild-type animals at day 1 of adulthood (Figure 2B). When treated with serotonin, wild-type animals lose virtually all LRO Nile red over 48–72 hours. However, serotonin-treated strains bearing either of two independent kat-1 alleles show retention of approximately half of their starting levels of LRO Nile red (Figure 2C), although the absolute decrease in LRO Nile red is similar between wild type and kat-1 mutants. tub-1 mutant animals maintain sensitivity to exogenous serotonin and show decreased LRO Nile red upon serotonin treatment (Figure 2D). As in the case of the kat-1 single mutant, kat-1;mut-1 double mutants retain high LRO Nile red even when treated with serotonin (Figure 2D).
Figure 1. Exogenous serotonin reduces LRO Nile red. (A) Exogenous serotonin suppresses LRO Nile red in a dose dependent manner. Animals were treated for 48 hours with doses indicated. (B) A representative image of an animal treated with 5 mM serotonin shows near complete absence of LRO Nile red. (C) Mutants lacking serotonin do not have a large effect on LRO Nile red. A null mutant in tph-1 (tryptophan hydroxylase) causes a modest decrease in LRO Nile red whereas a null cat-4 mutant (GTP-cyclohydrolase) which lacks dopamine and serotonin has a small but significant increase in LRO Nile red. cat-2 mutants have defective dopamine production but preserve normal serotonin synthesis. (N>25; significance by ANOVA with Bonferroni correction.)
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Thus in a kat-1 mutant, Nile red uptake into the LRO is partially resistant to exogenous serotonin. But the kat-1 mutation induced increase in Nile red in the LRO remains responsive to a tub-1 mediated output of the ciliated neurons, because null mutations in tub-1 strongly enhance the LRO Nile red storage phenotype of many kat-1 alleles [18].

We investigated the means by which the serotonin response depends on the KAT-1 thiolase. kat-1 mRNA levels after treatment with exogenous serotonin did not change (Figure 3A). kat-1 mRNA was also unchanged in both tph-1 mutants and tub-1 ciliary mutants (Figure 3B). Thus kat-1 is not transcriptionally regulated by serotonin.

High LRO Nile red of kat-1 mutants is suppressed by loss of function in the 9-transmembrane domain transporter skat-1

To determine which of our ~100 mutants with altered LRO Nile red might be in a pathway with kat-1 and serotonin, we inactivated kat-1 by RNAi in each of the newly isolated mutants. The majority of mutants showed an additive increase in LRO Nile red when kat-1 was inactivated. However, one mutant with slightly low LRO Nile red in a kat-1(+) background showed a near disappearance of LRO Nile red when kat-1 was inactivated by RNAi. We mapped this mutation and identified a missense mutation in the annotated transporter F59B2.2, which we named skat-1.

- skat-1 encodes a predicted 9-transmembrane domain protein orthologous to yeast and mammalian proton-coupled amino acid transporters (Figure S1, A and B). As skat-1 is predicted to be in an operon with two upstream genes F59B2.5, and F59B2.3, we constructed a GFP promoter fusion to the most upstream gene in the operon, F59B2.5 to determine the site of expression of skat-1. This revealed expression in head, tail, body and ventral nerve cord neurons, muscles of the vulva, and intestine (Figure S1C).

While skat-1 single mutants show a non-significant trend towards decreased LRO Nile red, double kat-1;skat-1 mutants manifest nearly absent LRO Nile red, far lower than skat-1 single mutants (Figure 4A). Given that skat-1 could potentially suppress the large increase in LRO Nile red in kat-1 mutants, and since serotonin and kat-1 are in a genetic pathway with each other, we also hypothesized that skat-1 might interact with serotonin pathway mutants. In tub-1 mutants, loss of skat-1 has a small, nonsignificant effect in LRO Nile red (Figure 4B). However, in kat-1;skat-1 mutants, kat-1;skat-1;tub-1 mutants, skat-1;tph-1 serotonin-deficient mutants or cat-4;skat-1;tub-1 serotonin deficient mutants, LRO Nile red was reduced 3–4 fold, and microscopically to levels much less than wild type (Figure 4B). All that was visible in kat-1;skat-1;3tub-1 triple mutants was a Nile red streak in the intestinal lumen, with essentially no detectable LRO Nile red (Figure 4B, right). This indicates either in animals lacking serotonin or kat-1 that skat-1 synergistically reduces LRO Nile red, and provides further evidence that kat-1 and serotonin lie in a genetic pathway regulating lysosome-related organelles.

We used expression information to guide construction of tissue-specific skat-1 rescue constructs. As we observed both neuronal and intestinal expression with the F59B2.3p::GFP transgenic strain, we attempted intestinal rescue of skat-1 with a vha-6 intestine-specific promoter and rescue in the nervous system using a rab-3 pan-neuronal promoter. We injected SKAT-1::GFP rescue constructs into kat-1;skat-1 double mutants in order to see re-animination of intestinal LRO Nile red in rescued animals. Only with intestinal rescue constructs did we observe an elevation in LRO Nile red, indicating that similar to kat-1 [18], skat-1 regulates lysosome related organelles in the intestine in a cell autonomous manner (Figure 4C). Based upon prediction algorithms, SKAT-1 is predicted to be cytoplasmic and localized either in the plasma membrane or in a membrane-bound structure (Psort II, http://psort.hgc.jp/). SKAT-1::GFP was visualized in spherical, autofluorescent, cytoplasmic gut granules (Figure 4D), but more brightly in smaller cytoplasmic structures that did not co-localize with intestinal autofluorescence. These structures were abundant and excluded from the nucleus (Figure 4D). These data suggest that SKAT-1 at least partially localizes to the LRO and might directly regulate LRO physiology.

Mutation of skat-1 regulates LRO accumulation of age pigment and vital dyes

The lysosome-related organelle is not only the principle site of feeding-Nile red accumulation, but also the site of autofluorescent material that may represent age pigment or lipofuscin accumulation [8,13]. To determine if the accumulation of age pigment in the LRO is also regulated by kat-1 and skat-1, we examined intestinal autofluorescence in these mutants. Intestinal autofluorescence accumulates in wild type C. elegans with age, and in progeric strains of C. elegans such as daf-16 and rct-1, intestinal autofluorescence is elevated [10,30]. Intestinal autofluorescent material emits fluorescence in both blue and green wavelengths. We examined the effects of kat-1 and skat-1 mutations on both spectra. kat-1 mutants have elevated autofluorescence in the blue spectrum, and much like the Nile red synergistic phenotype, kat-1;skat-1 double mutants show full suppression of the increased blue fluorescence in the kat-1 mutant (Figure 5A). Both the kat-1 loss of function allele isolated in this study (mg449) and the reference allele previously identified (mg360) show quantitatively similar increases in LRO Nile red and blue spectrum autofluorescence (Figure 2C and Figure 5A, respectively). Conversely, skat-1 mutants had elevated green spectrum intestinal autofluorescence, and this was synthetically exaggerated in double kat-1;skat-1 mutants (Figure 5, B and C). This analysis indicated that skat-1 synergistically increases intestinal green-spectrum autofluorescence while reducing the accumulation of blue spectrum autofluorescence and Nile red in that compartment.

To determine the physiological handling of diverse vital dyes by the LRO in kat-1 mutants, we examined accumulation of the labeled fatty acid C1-BODIPY-C12 and the Vital dye Lyso-Tracker Red. C1-BODIPY-C12 accumulates similarly to Nile red.
and blue spectrum autofluorescence in a \textit{kat-1} mutant, and the C1-BODIPY-C12 accumulation is fully suppressed in a \textit{kat-1;skat-1} double mutant (Figure 5D). In contrast, accumulation of the vital dye LysoTracker Red in the LRO [13] is reduced in \textit{kat-1} and \textit{skat-1} mutants and is additive in the \textit{kat-1;skat-1} double mutant. Thus, \textit{kat-1} and \textit{skat-1} do not globally increase the uptake of vital dyes in a non-specific manner into the LRO.

In order to confirm that Nile red, LysoTracker Red, and autofluorescence accumulate in the LRO, we analyzed PGP-2::GFP transgenic animals fed Nile red as a vital dye and conducted imaging for blue spectrum autofluorescence, PGP-2::GFP, and Nile red (Figure S2A). These data confirm that Nile red and autofluorescence perfectly overlap with PGP-2::GFP in the LRO (Figure S2A) [8,12–14]. We also analyzed PGP-2 overlap with LysoTracker Red, finding that while all LysoTracker Red positive granules also contain PGP-2, not all PGP-2 positive granules contain LysoTracker Red (Figure S2, B and C).

Autofluorescence accumulates with age. Confirming that the animals being compared were at an equivalent age, we found egg to egg time for the following strains to be within 1–2 hours of 70 hours at 20°C: wild type N2, \textit{kat-1}(mg368), \textit{kat-1}(mg447), \textit{kat-1}(mg449), \textit{skat-1}(mg459), \textit{skat-1;tub-1}(nr2004), \textit{kat-1}(mg368);\textit{skat-1}(mg449);\textit{tub-1}(nr2004), and \textit{kat-1}(mg449);\textit{skat-1}(mg459). At 72 hours after egg lay, all strains examined had laid eggs and adults had 6–8 corporal eggs and oocytes, a further confirmation of equivalent developmental timing into early adulthood. Thus, \textit{skat-1} decouples the LRO from Nile red import induced for example by a defect in KAT-1 ketothiolase activity, reducing blue autofluorescence while

Figure 3. \textit{kat-1} mRNA is not transcriptionally regulated by serotonin, and \textit{tub-1} regulates LRO Nile red in parallel with serotonin and \textit{kat-1}. (A) \textit{kat-1} mRNA abundance does not change with exogenous serotonin treatment. (B) \textit{kat-1} mRNA abundance is identical in \textit{tph-1} and \textit{tub-1} mutants. (A and B, N = 3; significance by ANOVA with Bonferroni correction.)

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C. elegans Lysosome Related Organelle Genetics

A

**Mean Lysosomal Nile Red Intensity (\% of Wild type)**

- **Wild type**
- **kat-1(mg459)**
- **skat-1(mg439)**
- **kat-1;skat-1**

**P < 0.0001**

B

**Mean Lysosomal Nile Red Intensity (\% of Wild type)**

- **Wild type**
- **kat-1;skat-1, tub-1**
- **kat-1;skat-1, tub-1, tph-1**
- **kat-1;skat-1, tub-1, cal-4**
- **kat-1;skat-1, tub-1, sdr-1**
- **kat-1;skat-1, tub-1, skat-1**
- **kat-1;skat-1, tub-1, kat-1**
- **kat-1;skat-1, tub-1, kat-1, skat-1**
- **kat-1;skat-1, tub-1, kat-1, skat-1, tub-1**

**P < 0.0001**

C

- **kat-1;skat-1**
- **Ex[vha-6p::SKAT-1]**
- **Ex[rab-3p::SKAT-1]**

No Rescue

Intestinal Rescue

Neuronal Rescue

D

- **SKAT-1::GFP**
- **Autofluorescence**
- **Merge**
more strongly inducing the accumulation of green autofluorescence.

**Systems level analysis of LRO autofluorescence, LRO Nile red accumulation, and fat storage**

To examine the broader genetic architecture regulating lysosome-related organelle biology, we re-visited a set of 407 gene inactivations reported to positively or negatively affect Nile red accumulation [16]. We added another 164 genes to this list encoding genes annotated to regulate metabolism in *C. elegans* (Table S1). To determine the most robust regulators of LRO Nile red among this group we examined the Nile red phenotype after gene inactivation of each gene by RNAi in an enhanced RNAi mutant (*eri-1*) using a quantitative microscopy assay for feeding LRO Nile red at day 1 of adulthood. Genes were tested using 6 biological replicates to ensure reproducibility of the observations. This analysis identified 79 gene inactivations that induce quantitatively different LRO Nile red compared to control RNAi. 56 of which were from the original 407 reported LRO Nile red regulatory genes (Figure 6 and Table S1). This was a stringent cutoff, correcting for multiple hypothesis testing. If criteria were loosened to significance at an uncorrected $P<0.05$, a total of 210 genes met the cutoff, comprising 131 of the original 407 genes previously reported affect Nile red staining and 79 annotated metabolic regulators (Table S1).

Nile red, when fed to *C. elegans*, was assumed to be an indicator of fat mass [16,31,32] but it is now thought that the LRO Nile red compartment is distinct from neutral lipid storage in *C. elegans* [14,20–23]. However, fixation-based methods of staining lipids do highly correlate with biochemically measured lipid mass [14,20]. To systematically study how the regulation of LRO Nile red may correlate with changes in *C. elegans* lipid levels, we utilized a validated, fixation-based staining protocol for highlighting fat stores in the worm [33]. We knocked down all 571 genes by RNAi in the 1 worms and stained for lipid in biological quadruplicate (Figure 6B and Table S2). Fixative based staining with Nile red unlike vital staining with Nile red reveals true lipid droplets [20,21,33]. To avoid confusion, we refer to the fixative Nile red result as lipid droplet staining. This analysis indicated that there is a negative correlation between LRO Nile red and lipid levels in the worm (Figure 6A and Table S2). Few gene inactivations caused correlated changes in LRO Nile red and lipid levels. Among them were *elt-2* and the protein kinase A (PKA) catalytic subunit ortholog *kin-1*.

To determine the systematic relationship between LRO Nile red accumulation and LRO autofluorescence, we assessed the effect of RNAi knockdown of the most robust LRO Nile red regulators with significance scores passing a corrected threshold of $P<0.05$, or 79 genes, in wild type worms, rather than the *eri-1* enhanced RNAi mutant used in our primary screen, in biological quadruplicate and assessed LRO Nile red and autofluorescence (Figure 6B). Under these conditions, many gene inactivations in wild type caused less pronounced effects on LRO Nile red than inactivations in the *eri-1* background, and some, e.g. *elt-2*, *obr-2*, *kat-2*, and *daf-9*, had opposite effects in N2 versus *eri-1* worms (Figure S3). However, overall, these results indicate that while a large number of canonical LRO regulatory genes, e.g. *glo-3*, *pgp-2*, and adaptin subunits *apb-3* and *apm-3* cluster together and demonstrate low LRO Nile red and autofluorescence, a large number of genes demonstrate dissociation between LRO Nile red and autofluorescence. Perhaps the most extreme example was inactivation of the GATA transcription factor *elt-2*, which leads to a ~3 fold increase in LRO Nile red but a ~4 fold reduction in intestinal autofluorescence (Figure 6B). In contrast, knockdown of the related transcription factor *elt-7* led to a decrease in LRO Nile red and an increase in autofluorescence. Thus there are many examples of separation of LRO Nile red and autofluorescence as it might represent age pigment.

**Gene network regulating LRO autofluorescence and LRO Nile red accumulation**

The 79 genes that significantly modulate LRO autofluorescence and LRO Nile red when knocked down by RNAi in the 1 worms were also knocked down by RNAi in wild-type *C. elegans* (N2 Bristol) and a set of 6 genetic backgrounds with altered lysosome-related organelle phenotypes: *kat-1*, *skat-1*, *tub-1*, *vps-54*, and *apm-3*. These can now be studied for their role in LRO biology in a manner dependent upon the evolutionarily conserved heteromeric kinase target of rapamycin (TOR) complex 2. Nonsense mutations in gene encoding the essential TOR complex
Figure 5. LRO autofluorescence and vital dye accumulation are regulated by skat-1. (A) A kat-1 mutant has high blue spectrum autofluorescence, which is concordant with the high LRO Nile red phenotype. Mutation of skat-1 in kat-1 mutants fully suppresses accumulation of LRO blue spectrum autofluorescence with age. kat-1(mg368) and kat-1(mg449) show similar phenotypes in blue spectrum autofluorescence. (B) kat-1 and skat-1 both show elevated green spectrum autofluorescence that is synergistic in the kat-1;skat-1 double mutant. (C) Green autofluorescence in a representative day 1 adult animal for each genotype. (D) C1-BODIPY-C12, which is accumulated in the LRO, is also increased in kat-1 mutants and fully suppressed like Nile red in the kat-1;skat-1 double mutant. (E) In contrast, LysoTracker Red is decreased in kat-1 and skat-1 single mutants and synthetically decreased in the kat-1;skat-1 double mutant. (N>25; *, P<0.05; **, P<0.0001 by one-way ANOVA with Bonferroni correction.) doi:10.1371/journal.pgen.1003908.g005
Figure 6. LRO Nile red is not equivalent to and most often discordant with blue autofluorescence and fat mass. (A) LRO Nile red versus fixation-based lipid staining for 571 gene inactivations in *eri-1* enhanced RNAi mutant worms show that LRO Nile red is not equivalent to lipid mass. There are a limited number of gene inactivations that show concordant changes in LRO Nile red and lipid mass as determined by fixation staining.
2 subunit Rictor (*C. elegans* rict-1) lead to shortened lifespan, high fat mass, elevated LRO Nile red and high levels of age-associated autofluorescence [30,34]. We found one gene inactivation, of the predicted solute transporter *K09C4.5*, that increased LRO Nile red in all strains examined except for the TOR complex 2 mutant rict-1, indicating that rict-1 is genetically downstream of *K09C4.5* regulating LRO Nile red and LRO biology (Figure 7, A and C). Conversely, RNAi to the catalytic subunit of protein phosphatase 2C, *tax-6*, increases LRO Nile red synergistically only in *rict-1* mutants (Figure 7, B and E). These effects are limited to LRO Nile red as a co-regulated change in autofluorescence was not seen. There are additional genes in a cluster with *tax-6* that show similar biology and can now be studied with regard to their interaction with *rict-1* (full dataset in Table S3).

Alternatively, we found many unique interactions of TOR complex 2 mutant *rict-1* with the 79 LRO genes when aging-related autofluorescence was investigated. Autofluorescence is specifically increased by *kel-1* RNAi only in TOR complex 2 mutants (Figure 7, B and E). *Kel-1* is a member of the kelch-family group of genes, and regulates pharyngeal development and likely affects feeding [35]. Given that *kel-1* is expressed in the pharyngeal gland and *rict-1* acts to regulate aging in the intestine in a cell-autonomous manner [30], it is likely that these genes act in parallel pathways regulating autofluorescence. Given the synergistic increase only seen in *rict-1* animals, it is possible that *kel-1* is part of a compensatory pathway that protects against premature aging in *rict-1* mutants. We see another cluster of genes exemplified by the acyl-coenzyme A synthetase gene *acs-6* that lead to increases in aging-related autofluorescence in a manner dependent upon *rict-1* (Figure 7, B and F). As autofluorescence accumulates with age, this may be a group of genes that depends upon TOR complex 2 to produce accelerated aging phenotypes (full dataset in Table S4). Similarly, loss of function of *acs-3* has previously been shown to have an impact on LRO Nile red [36].

**Discussion**

Lysosome-related organelles have specific functions and share many common features with canonical lysosomes. Disrupted lysosome related organelle biology leads to human Chediak-Higashi and Hermansky-Pudlak Syndromes [3]. In mice, mutations in LRO biogenesis genes lead to alterations in coat color. In *C. elegans*, LROs are responsive to aging as they are the site of age-associated increases in autofluorescence. LROs are also the site of concentration of the vital dye Nile red when fed to the worm. We identified that serotonin regulates LRO biology in a manner that is disrupted in a mutant for the ketothiolase *kat-1*. By orthology, *kat-1* encodes a predicted 9-transmembrane domain protein targeted either to the LRO and to additional cytoplasmic structures of unclear identity. *skat-1* acts to suppress LRO Nile red entirely via expression in the intestine, so we conclude that the increased Nile red uptake into LRO defect induced in a *kat-1* mutant is disabled by the *skat-1* mutation. Much like Nile red, mutation of *skat-1* also fully suppresses the high blue autofluorescence evident in a *kat-1* mutant, but markedly increases the green autofluorescence. One model for this interaction is that the SKAT-1 transmembrane protein in the intestine directly modulates the pH of the LRO. This is not unreasonable given that SKAT-1 localizes to the LRO and is orthologous to proton-coupled amino acid transporters. We suggest that by altering the pH of the LRO, that SKAT-1 prevents accumulation of Nile red, and shifts the emission peak of intestinal autofluorescent material from blue to green.

The nature of the autofluorescent substance in *C. elegans* that accumulates with age was previously thought to be lipofuscin, or oxidation products of cellular proteins and lipids resistant to canonical degradation pathways [7,10]. Recent findings suggest that rather than lipofuscin, that the autofluorescent substance in *C. elegans* LROs is anthranilate, a breakdown product of tryptophan [37]. In *Drosophila*, kynurenine synthesis as a product of tryptophan catabolism produces autofluorescent globules in the fat body [38]. A role for tryptophan catabolism in the accumulation of intestinal blue autofluorescence has been suggested [39], and, decreased L-kynureninase activity is associated with a shift in autofluorescent material from the blue to the green spectrum [40]. As tryptophan may be metabolized in part in a *kat-1* dependent manner, it is possible that accumulation of kynurenine, anthranilate, or their metabolites is responsible for the high LRO blue autofluorescence in a *kat-1* mutant. This possibility remains to be investigated. Consistent with the notion that mutation of *skat-1* affects LRO pH, tryptophan metabolites are known to undergo shifts in fluorescence excitation and emission at different pH values [41]. Given that serotonin is a tryptophan derivative, it is possible that the mode of serotonin action in the LRO to decrease LRO Nile red is through alteration of tryptophan catabolism in the intestine. This could explain why ambient levels of serotonin have little effect on LRO Nile red but rather elevated exogenous levels or those seen in
Figure 7. Gene-gene interaction network underlying LRO accumulation of Nile red and autofluorescence. (A) Seventy-nine genes affecting LRO Nile red were inactivated by RNAi in wild type worms and 6 genetic mutants with altered LRO Nile red phenotypes to determine gene-gene interactions. Genes were clustered by mean clustering, with the heatmap indicating genes that increase LRO Nile red in yellow and decrease LRO Nile red in blue. No inference can be made on the absolute magnitude of the effect from the heatmap as data from each mutant for all 79 genes are normalized and scaled (see methods and table S3 for absolute fold change differences). Genes knocked down by RNAi are along the vertical axis and mutant backgrounds are along the horizontal axis. Two clusters of genes that show decreases in all mutants tested are indicated by the black bars to the immediate right of the heatmap. Mutants are organized by hierarchical clustering, indicating that overall kat-1 and tph-1 which lacks serotonin cluster most closely to each other (dendrogram on top of the heatmap). (B) The same 79 genes were inactivated in the same seven genetic backgrounds, imaged for blue autofluorescence and organized by cluster analysis as in A. Three clusters of genes that have known regulators of LRO biogenesis are indicated by the black bars along the vertical axis to the right of the heatmap (see also table S4). (C) The solute transporter K09C4.5 RNAi increases LRO Nile red in all strains tested except the TOR complex 2 mutant rict-1. (D) RNAi to the catalytic subunit of the protein phosphatase calcineurin, tax-6, led to a decrease in LRO Nile red in all strains tested except rict-1 in which there was a small but measureable increase. (E) RNAi to the Kelch domain protein kel-1 increases blue autofluorescence only in a rict-1 mutant. (F) RNAi to acyl-coenzyme A synthetase acc-6 increases blue autofluorescence in a manner genetically dependent upon TOR complex 2 mutant rict-1. (C-F, N as in tables S3 and S4; significance by unequal variance, two-tailed Student’s t-test with Bonferroni step-down correction.)

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C. elegans Lysosome Related Organelle Genetics

...RNAi resistant tissues in the LRO, we have identified a number of phenotypic clusters of regulatory genes in different tissues, and illuminate potential future directions for investigation of non-cell autonomous modes of regulation of LRO biology.

By systematic examination of a set of 79 genes that affect LRO Nile red, we have identified a number of phenotypic clusters of LRO regulatory genes. These genes, like skat-1, may identify components in the sorting of Nile red to the LRO or the sorting of endogenous lipids and other macromolecules such as the autofluorescent gut molecules to the LRO. The clusters of particular gene interactions may correspond to modules of biological function in the LRO. We find that there are many gene inactivations that affect Nile red sorting to the LRO but not sorting of endogenous autofluorescent molecules, and vice versa. There are other gene inactivations that disrupt both processes. Thus while in some instances, for example in the case of genes involved in the biogenesis of the LRO and for kat-1 mutants, LRO Nile red and autofluorescence are concordant, there are many instances where discordant effects are seen. We also find that LRO Nile red is not concordant with changes in fat mass as determined by fixation-based lipid staining. If anything the data suggest an anticorrelation with LRO Nile red and fat mass. And we found that LRO biology is strongly dependent upon the genetic background examined. We found multiple instances where changes in autofluorescence or LRO Nile red were specific to a given genetic background. Specifically, we found effects of inactivation of the solute transporter K09C4.5, calcineurin phosphatase catalytic subunit tax-6 and the Kelch domain protein kel-1 to be dependent upon the function of TOR complex 2. As the LRO, like the lysosome, plays a key role in trafficking of proteins and degradation products around the cell, it is likely that exploration of these genetic interactions will inform our knowledge of processes such as autophagy, protein synthesis and turnover, and potentially inform human diseases of lysosomes or lysosome related organelles.

Materials and Methods

Strains used

N2 Bristol was used as the wild type strain. The following mutant strains were used: GR1373 eri-1(mg360), MGH53 daf-16(mgDf47), MGH112 tph-1(n422), MGH102 kat-1(mg449), MGH104 skat-1(mg459), MGH34 tub-1(nr2004), MGH33 kat-1(mg368) tub-1(nr2004), LC35 cat-4(ok342), CB1112 cat-2(e1112), MGH1 rict-1(mg451). For tissue distribution of skat-1, MGH273 alxEx50: Ex[F59B2.5p::mRFP myo-2p::GFP]. 1.4 kb of upstream F59B2.5 promoter sequence was used. For intestinal skat-1 rescue.
experiments, MGH129 kat-1(mg449);skat-1(mg459);akxEx6[cha-6::
kat-1::GFP mny-2::xmCherry], and MGH130 kat-1(mg449);kat-
1(mg459);akxEx5[cha-6::kat-1::GFP mny-2::xmCherry] with 0.8 kb
of upstream cha-6 promoter; for neuronal skat-1 rescue, MGH133
kat-1(mg449);skat-1(mg459);akxEx10[rab-3p::skat-1::GFP mny-2::GFP]
and MGH134 kat-1(mg449);skat-1(mg459);akxEx11[rab-3p::skat-
1::GFP mny-2::GFP] 2.2 kb of upstream rab-3 promoter was used.

Vital dye assays for lysosome related organelle Nile red, LysoTracker Red, and C1-BODIPY-C12

The feeding Nile red assay for LRO Nile red was conducted by
seeding wild-type or mutant C. elegans on NGM plates containing
either E. coli OP50 or HT115 supplemented with either 30 ng/mL
M Nile red final (diluted fresh into 100 μL M9 media per plate
from 500 μg/mL stock in acetone and added to the top of E. coli
plates and allowed to dry), 20 ng/mL C1-BODIPY 500/510-
C12 final (diluted fresh into 100 μL M9 media per plate from
200 μg/mL stock in DMSO), or 1 μM LysoTracker Red (diluted
fresh into 100 μL M9 media from 1 mM stock in DMSO) (all from
Invitrogen) as L1 following overnight hatching and synchronization
at 20°C in minimal media. Imaging and quantitation was
done after growth at 20°C as day 1 adults using a Zeiss
Axioplan microscope and Axiovision software (Figures 1–4), or a
Leica DM6000 microscope and MMAF software (Figures 5–7).
For Figures 1–5, at least 30 animals were imaged on at least 2
separate occasions, and results were consistent between experi-
ments. For figures 6 and 7, wild type or mutant animals treated
with RNAi were imaged in 96-well format in biological
quadruplicate or 6x replicates as indicated in the text. All LRO
Nile red analyses were carried out on animals grown at 20°C.

Autofluorescence assay

Autofluorescence in day 1 adult worms was quantified by after
growth at 20°C by picking worms from plates into M9 buffer
containing levamisole as a paralytic, and mounting animals in
multwell Teflon-masked microscope slides. Images were acquired
with a Leica DM6000 microscope outfitted with a standard DAPI
filter set (for blue spectrum auto fluorescence) or GFP filter set (for
green spectrum auto fluorescence and MMAF software (Figure 5).
Identical exposure times were used for each set of animals imaged
within an experiment. At least 30 animals were imaged on at least
2 separate occasions, and results were consistent between
experiments.

Serotonin treatment of C. elegans and isolation of serotonin resistant mutants

Synchronous populations of wild type or mutant worms at the
L1 stage were dropped on to NGM plates containing E. coli
bacteria. After 36 hours at 20°C, serotonin at the concentrations
indicated was added to the top of the bacterial lawn in M9
minimal media, allowed to dry in the dark in a laminar flow hood,
and worm plates were returned to the 20°C incubator. Worms
were imaged after an additional 48 or 72 hours, and 48 hours was
chosen as the time point for further study based upon the effect on
LRO Nile red being maximal. For isolation of serotonin resistant
mutants, 120,000 haploid genomes were screened in the F2
generation by EMS mutagenesis. Synchronous F2 animals at the
L1 stage were dropped on to E. coli OP50 lawns containing 1 μM
Nile red on 10 cm NGM plates and grown at 20°C for 36 hours.
Thereafter serotonin to a final concentration of 2.5 mM in the
agar was added to the top of the bacterial lawn containing worms,
allowed to dry, and incubated for an additional 48 hours prior to
screening for individual worms with elevated residual LRO Nile
red staining. Six independent mutants with elevated LRO Nile red
staining were mapped using the multiply polymorphic strain
CB4836 to mid chromosome II. After narrowing the interval,
RNAi, complementation, and direct sequencing were used to
identify causal mutations in kat-1.

Quantitative PCR for kat-1 mRNA

All assays were conducted in biological triplicate on 5000 worms
per sample. Wild type C. elegans were dropped as synchronous L1
larvae onto NGM agarose plates containing E. coli OP50 and
allowed to grow for 36 hours prior to the addition of 2.5 mM
serotonin in M9 minimal media or M9 as vehicle. Worms were
incubated for an additional 24 or 48 hours on serotonin or vehicle
plates prior to harvest for RNA preparation. For mutant analysis,
N2, tph-1 or tub-1 animals were dropped as synchronous L1 larvae
onto NGM agarose plates with OP50 and allowed to grow to the
mid-L4 stage prior to harvest for RNA preparation. Serotonin
treated or mutant worms were harvested by washing off of plates
with M9 buffer, allowing worms to settle by gravity with
washes. Worms were flash frozen in liquid nitrogen until RNA
preparation with TriRezol (Invitrogen) per manufacturer instructions.
RNA was treated with DNase free RNAse and reverse transcribed with the
Quantitect reverse transcription kit (Qiagen) prior to real-time
PCR. Real time PCR was conducted on kat-1 mRNA or sub-1
mRNA (control) using Quantitect SYBR Green PCR reagent
(Qiagen) according to manufacturer instructions, and fold change
of kat-1 expressed following normalization to the abundance of
sub-1 mRNA by the 2ΔCt method using experimentally
determined efficiency values. Primer sequences used were: kat-1
F primer 5'-tcacgctctgagtggcgg-3', kat-1 R primer 5'-
tctcgctccgaaccaagagga-3' (product 107 nt); sub-1 F primer
5'-cggataacGctttgcgg-3'; and sub-1 R primer 5'- gaacctcat-
caacGctccg-3' (product 121 nt).

Isolation of skat-1 (F59822.2) mutant

C. elegans N2 Bristol strain was mutagenized with EMS, and the
resultant F2 generation was screened for decreased staining with
the vital dye Nile Red [18]; skat-1(mg459) was identified by back-
crossing three times to N2 Bristol and positionally cloned based
upon polymorphisms between N2 and the multiply polymorphic
C. elegans strain CB4308. Following narrowing of the genetic
interval to ~300 genes, skat-1 was cloned by direct sequencing
following phenocopy of the very low LRO Nile red phenotype
with skat-1 RNAi in a kat-1(mg449) mutant.

Systems level analysis of LRO auto fluorescence and LRO
Nile red

RNAi clones were isolated from a genome-wide E. coli feeding
RNAi library and fed to C. elegans as previously described [43] in
96-well format using NGM agarose supplemented with 5 mM
IPTG (US Biologicals) and 100 μg/mL carbenicillin. Plates also
contained 1 μM Nile red, for LRO Nile red analysis or no
additional additive for auto fluorescence analysis. Synchronous
populations of wild type or mutant worms were obtained by
bleach treatment of gravid adults [44], dropped onto 96-well
RNAi plates as synchronous L1 and at day 1 of adulthood, washed
from RNAi plates, paralysed with 30 mM 2,3-butanedione
monoxime (Sigma) or 10 μg/mL L-tetramisole (Sigma), mounted
on a 96-well teflon slide (Trevigen) and imaged on a Leica
DM6000 microscope in brightfield and fluorescent channels with
uniform exposure times (DAPI for auto fluorescence, Texas Red
filter set for Nile red) at 25x magnification. This magnification
was specifically chosen as the depth of field of the objective captures the entire worm in focus. Image analysis was carried out using custom MATLAB (The Mathworks) scripts, parallelized for speed. Full well images were built by tiling raw brightfield images.

**Well finding.** Full well images were built by tiling raw brightfield images. Each full well image was blurred using a (30 x 30 pixel) Gaussian, scaled to account for its 12 bit dynamic range within a 16 bit image, then converted to 8 bit to facilitate rapid thresholding. The threshold level was determined as L*F, where L is the threshold determined using Otsu’s method, and F is an empirical factor equal to 0.9. After thresholding, holes are filled and the largest connected region is chosen as the well. Then well is eroded with a (30 pixel diameter) disk structuring element. To avoid edge effects due to partial well images, we first pad the well with a (30 pixel) border before the erosion, then restore the original image size after erosion.

**Object finding.** The well is segmented into three masks characterized as background, junk (foreground objects that should not be quantified), and objects. First, each full well brightfield image is bottom hat filtered, using a (20 pixel diameter) disk structuring element, to give an image with much less variability in background intensity. The background-stabilized image is scaled to produce 1% saturation and then quantized to 8 bits. Otsu’s method is then applied to the well region only, to give the Otsu threshold L. If the level L and effectiveness E are adequate, we threshold using the level 1-F*(1-L), where L is the threshold determined using Otsu’s method, and F is an empirical factor equal to 0.9. F < 1 biases this operation towards decreased false positive rate of object identification at the expense of reduced well area. We also perform image closure (3 pixel disk) to eliminate small holes. We typically trigger a second “outlier” method when the effectiveness E is low (<0.7). In this method we blur the image (3x3 pixel Gaussian filter) and identify outlier pixels as those that have intensities beyond a specified boxplot whisker value (nominally 3, which corresponds to >4.6 standard deviations). Next, we filter to eliminate small objects, with the upper and lower size limits allowed to vary between the “threshold” and “outlier” methods, typically with smaller size limits for the “outlier” method. If the largest connected region is very small, a separate “small object” size filter is used. The “threshold”, “outlier” and “small object” methods thus allow progressive detection of smaller and smaller objects (e.g. small worms) while retaining the ability to reject junk (e.g. debris, eggs). Regions that pass all filtering are classified as objects, whereas regions that pass the initial thresholding or outlier analysis but fail the size filter are classified as junk; regions that fail the initial thresholding or outlier analysis are classified as background. Binary masks are then stored for the objects, junk, and background, with the bitwise OR of these three masks equal to the well mask. The identified regions of interest are also flagged for review based on a number of criteria including low thresholding effectiveness or level, low object count, and high junk to object area. All regions of interest are manually reviewed if flagged and excluded from further analysis if poorly indicative of true worm area.

**Quantification.** Summary statistics are computed based on each of the objects, junk, and background masks including intensity histograms and, as a default, the mean, median and 90th percentile intensity for each mask. Because the background intensity distribution is well approximated by a normal distribution with small standard deviation, we calculate adjusted estimates by subtracting the background mean.

**Systems level analysis of body fat mass using fixation-lipid staining**

Fixation based staining with Nile red, which reliably stains neutral lipid droplets, was conducted as previously indicated [33]. In brief, following feeding RNAi in 96-well format as above, animals are washed from RNAi plates, fixed in 40% isopropanol, stained in 3 μg/mL Nile red in 40% isopropanol, washed in PBS with 0.01% Triton-X100, mounted on 96-well Teflon slides and imaged as above for LRO Nile red, except rather than Texas red imaging, GFP filter sets are used. Images are analysed as above.

**Statistical and k-means cluster and statistical analysis**

Statistical differences between groups were determined using ANOVA, Bonferroni corrected for multiple hypothesis testing. For systems level analysis of LRO Nile red, autofluorescence, and body fat mass, the 90th percentile intensity was used. Differences between RNAi treatments and vector control were determined by unequal variance T test Bonferroni corrected for multiple hypothesis testing. k-means cluster analysis was conducted following log2 transformation and quantile normalization using R/Bioconductor. Data were visualized using the heatmap.2 function.

**Supporting Information**

Figure S1 Analysis of SKAT-1 protein and skat-1 expression. (A) SKAT-1 homology to yeast, mouse, and human vacuolar, proton-coupled, solute transporters. (B) Predicted membrane topology for 9 transmembrane segments of SKAT-1. (C) Expression of green fluorescent protein driven by the skat-1 promoter (upstream gene in intron F59B2.5p). Head and tail neurons (top), intestine and tail neurons (middle), ventral nerve cord, intestine, and vulvar muscles (bottom) show expression. (PDF)

Figure S2 LRO accumulation of Nile red, autofluorescent material, and LysoTracker red. (A) Perfect overlap is seen between LRO compartments decorated by PGP-2::GFP, Nile red fed as a vital dye, and intestinal autofluorescence. (B) While most LRO that are decorated by PGP-2::GFP are also positive for LysoTracker red and autofluorescence, we identified distinct populations of intestinal PGP-2 positive granules that did not stain with LysoTracker red (C, arrows). (PDF)

Figure S3 LRO accumulation of Nile red in eri-1 versus wild type (N2) C. elegans. Seventy-nine genes affecting LRO Nile red were inactivated by RNAi in wild type worms (N2) versus eri-1, shown plotted on a logarithmic scale with diagonal equal to unity. (PDF)

Figure S4 Least squares and principal component analysis of k-means clustered data from Figure 7. Least squares analysis of data for 79 genes affecting LRO Nile red indicate a local minimum at 10 clusters for LRO Nile red (A) and plateau at 11 clusters for autofluorescence (C). Principle component analysis of clusters from Nile red (B) and autofluorescence (D) k means clusters indicating good separation between clusters. Identity of genes within each cluster is indicated in Table S3 for Nile red and Table S4 for autofluorescence. (PDF)

Table S1 LRO Nile red in eri-1 mutants treated with RNAi to 407 genes previously annotated to have feeding Nile red phenotypes and 164 metabolic genes. (XLSX)
Table S2 | Lipid droplet staining in mir-1 mutants treated with RNAi to 407 genes previously annotated to have feeding Nile red phenotypes and 164 metabolic genes.

Table S3 | LRO Nile red in wild type and 6 genetic mutants with altered LRO Nile red treated with top 79 RNAi affecting LRO phenotypes and 164 metabolic genes.

Table S4 | Autofluorescence in wild type and 6 genetic mutants with altered LRO biology treated with top 79 RNAi affecting LRO Nile red.

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Author Contributions

Conceived and designed the experiments: AAS CEC GR. Performed the experiments: AAS. Analyzed the data: AAS CEC GR. Wrote the paper: Christopher Webster. Thank you to Eyleen O'Rourke for sharing the data: AAS CEC GR.

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