Journal of Cell Science

An autophagy-dependent tubular lysosomal network synchronizes degradative activity required for muscle remodeling

Tadayoshi Murakawa, Amy A. Kiger, Yuriko Sakamaki, Mitsunori Fukuda and Naonobu Fujita
DOI: 10.1242/jcs.248336

Editor: Tamotsu Yoshimori

Review timeline
Original submission: 30 April 2020
Editorial decision: 22 May 2020
First revision received: 3 August 2020
Editorial decision: 25 August 2020
Second revision received: 8 September 2020
Editorial decision: 23 September 2020
Third revision received: 29 September 2020
Accepted: 1 October 2020

Original submission

First decision letter

MS ID#: JOCES/2020/248336

MS TITLE: An Autophagy-Dependent Tubular Lysosomal Network Synchronizes Degradative Activity Required for Muscle Remodeling

AUTHORS: Tadayoshi Murakawa, Amy A Kiger, Yuriko Sakamaki, Mitsunori Fukuda, and Naonobu Fujita
ARTICLE TYPE: Research Article

We have now reached a decision on the above manuscript.

To see the reviewers' reports and a copy of this decision letter, please go to: https://submit-jcs.biologists.org and click on the 'Manuscripts with Decisions' queue in the Author Area. (Corresponding author only has access to reviews.)

As you will see, the reviewers raise a number of substantial criticisms that prevent me from accepting the paper at this stage. I think, however, that a revised version might prove acceptable, if you can address their concerns. If you think that you can deal satisfactorily with the criticisms on revision, I would be pleased to see a revised manuscript. We would then return it to the reviewers.

We are aware that you may currently be unable to access the lab to undertake experimental revisions. If it would be helpful, we encourage you to contact us to discuss your revision in greater detail. Please send us a point-by-point response indicating where you are able to address concerns raised (either experimentally or by changes to the text) and where you will not be able to do so within the normal timeframe of a revision. We will then provide further guidance. Please also note that we are happy to extend revision timeframes as necessary.

Please ensure that you clearly highlight all changes made in the revised manuscript. Please avoid using 'Tracked changes' in Word files as these are lost in PDF conversion.

I should be grateful if you would also provide a point-by-point response detailing how you have dealt with the points raised by the reviewers in the 'Response to Reviewers' box. Please attend to all of the reviewers' comments. If you do not agree with any of their criticisms or suggestions please explain clearly why this is so.

Reviewer 1

Advance summary and potential significance to field

This work may provide a new insight into how lysosomal function is regulated through its morphological alterations.

Comments for the author

In this study, the authors found the transient emergence of tubular autolysosomal network (tAL) in Drosophila muscles during metamorphosis. The formation of tAL required several ATG-genes. The data shown in Fig6/7 are interesting to show that the tubular network shares the continuous luminal space.

The study lacked the identification of genes required for tubulation process other than ATG-genes, therefore, it is difficult, in principle, to dissect the specific role of "tubulation" of lysosomes from that of autophagy-dependent degradation by lysosomes. Although to reveal the function of "tubular" AL in tissue remodeling may not be the primal aim of the study, this reviewer thinks that to show the causative relationship between the "tubulation" of lysosomes and the proper tissue remodeling is critical to publish this work in JCS.

The following critiques may help the authors amend the study.
(1) The authors did not show the mechanistic insight how spherical lysosomes are converted into tubular structures during metamorphosis in wild-type Drosophila. Are spherical lysosomes first tubulated at the onset of metamorphosis and fused together? or does that process need the fusion with Atg8-positive compartments? The authors have to analyze in detail the tubulation process of lysosomes in wild-type Drosophila and provide some mechanistic insight. The data in Figure 2F is neat, but the fusion was only demonstrated between tAL and Atg8-positive compartment, which could not address to the reviewer concern.

(2) What is the consequence of the knockdown of SPIN or TRPML in tissue remodeling? The lysosomes in these cells do not fuse with autophagy-related compartments?

(3) How are the degradation activity (with DQ-BSA) and the pH (with Lysotracker) of non-tubulated lysosomes in ATG-deficient mutants?

Reviewer 2

Advance summary and potential significance to field

In this manuscript, Murakawa et al. found an extensive tubular autolysosomal network in Drosophila abdominal muscle remodeling during metamorphosis. The formation of Stx17-positive tubular autolysosomal network depends on autophagy core machinery except Atg5, Atg7, and Atg12. The tubular autolysosomal network provides greater degradative capacity for muscle remodeling during metamorphosis. Overall, the findings on autophagy-dependent tubular lysosomal network for Drosophila muscle remodeling are very interesting. The experiments are well controlled and the manuscript is elegantly written. The conclusion of the manuscript will be greatly improved, if the following experimental data are provided:

Comments for the author

1. Previous studies showed that the SNARE Stx17 localizes to the autophagosome and detaches after fusion with the lysosome. Whereas the authors found that Stx17 marks tubular autolysosomal

network. Do other SNARE proteins involved in autophagosome-lysosome fusion also localize to the tubular autolysosomal network during muscle remodeling?
2. It's likely that tubular autolysosomal network is a dynamic structure with constant tabulation/elongation, fusion and fission. It has been reported that microtubule and motor proteins kinesin and dynein, and small GTPases Rab7 and Arl8b are required for lysosome tabulation. What's their involvement in tubular autolysosomal network formation during muscle remodeling?
3. Fig2, the authors should explain (or discuss) on the large vacuolated structures accumulated upon Spin RNAi. Are they autophagosomes or autolysosomes? Do similar phenotypes occur in STX17 RNAi and other SNARE mutants?
4. Fig3 and 5, additional RNAi lines should be used to confirm the Atg5, Atg7 or Atg12 knockdown experiments.
5. Besides DIOM shape changes, is there a functional assay that can be used to test the muscle function in Atg5 and Atg9 knockdown flies?
6. Please mark mitochondria in Fig 5G-I.
7. As several studies have implicated the involvement of Tor signaling in regulating autolysosomal tabulation (PMID:26139536 PMID:26582390), the authors should confirm their results in Fig S3 using additional RNAi lines or by mutant clones.

Minor:
Typo in page 6 line 3 "Syntaxin 17 marks aa tubular network in remodeling muscle cells".

First revision

Author response to reviewers' comments

Reviewer 1 Comments for the Author:

This work may provide a new insight into how lysosomal function is regulated through its morphological alterations.
In this study, the authors found the transient emergence of tubular autolysosomal network (tAL) in Drosophila muscles during metamorphosis. The formation of tAL required several ATG-genes. The data shown in Fig6/7 are interesting to show that the tubular network shares the continuous luminal space.
The study lacked the identification of genes required for tubulation process other than ATG-genes, therefore, it is difficult, in principle, to dissect the specific role of "tubulation" of lysosomes from that of autophagy-dependent degradation by lysosomes. Although to reveal the function of "tubular" AL in tissue remodeling may not be the primal aim of the study, this reviewer thinks that to show the causative relationship between the "tubulation" of lysosomes and the proper tissue remodeling is critical to publish this work in JCS.

We agree with the reviewer that both the mechanism of lysosomal tubulation and the significance of this tubulation to muscle remodeling are two interesting questions raised by our novel findings. We also agree that uncovering of autophagy genes required for the tubular lysosome do not each all directly address the mechanisms of tubulation. However, our finding that the autophagy pathway is a key basis for the formation of the tubular lysosome, and the requirement for progression through this step for muscle remodeling, are significant findings. With respect to how lysosomal tubulation occurs, we now have illuminated through live imaging in intact muscle and mutant analysis that autophagosome fusion is required for tubulation, that tubules extend from spherical lysosomes, and that tubular lysosomes can be joined to create a bigger tubulated network (detailed below, 1).

(1) The authors did not show the mechanistic insight how spherical lysosomes are converted into tubular structures during metamorphosis in wild-type Drosophila. Are spherical lysosomes first tubulated at the onset of metamorphosis and fused together? or does that process need the fusion with Atg8-positive compartments? The authors have to analyze in detail the tubulation process of lysosomes in wild-type Drosophila and provide some mechanistic insight. The data in Figure 2F is

neat, but the fusion was only demonstrated between tAL and Atg8-positive compartment, which could not address to the reviewer concern.

In response to this concern, we performed live imaging of Spin:RFP in 14 h APF DIOMs, at a time when the tAL network was not fully developed yet. As shown in Fig. 5A and B, we observed in wildtype DIOMs examples where initially spherical lysosomes became actively tubulated. We also observed examples where two short tubules fused together and became a network (Fig. 5C). In sharp contrast to wildtype, the lysosome tubulation was not observed in the Stx17 RNAi condition (Fig. 5D). Moreover, the spherical lysosomes in Stx17 RNAi were smaller than the Spin:RFP-positive non-tubulated lysosomes in wildtype (Fig. 5A,B,D). Collectively, these data suggest that fusion with autophagosomes is a prerequisite for the lysosomal tubulation, that tubulation occurs as extensions from spherical lysosomes, and that tubulated lysosomes can be joined together to build an extended tubulated network. Since the data provide mechanistic insight into the formation of tAL network, we included the data as the main figure. Thank you for this constructive comment.

(2) What is the consequence of the knockdown of SPIN or TRPML in tissue remodeling? The lysosomes in these cells do not fuse with autophagy-related compartments?

To analyze the phenotypes of SPIN or TRPML RNAi in the muscle remodeling, we observed the ultrastructure of SPIN or TRPML RNAi DIOMs at 4 d APF. As shown in new supplemental data (Fig. S5F and G), both SPIN and TRPML RNAi induced the accumulation of autolysosomes and autophagosomes. This result suggests that non-tubulated lysosomes in SPIN or TRPML RNAi DIOMs can fuse with autophagosomes, albeit at reduced efficiency, but that the tAL network is important for the complete execution of autophagy during muscle remodeling.

(3) How are the degradation activity (with DQ-BSA) and the pH (with Lysotracker) of non-tubulated lysosomes in ATG-deficient mutants?

To evaluate the lysosomal pH and degradation activity in ATG-deficient DIOMs, control and Atg18 RNAi animals were injected with Lysotracker or DQ-BSA. As shown in Fig. 8E and 8G, both of the dyes stained small discontinuous puncta in ATG-deficient DIOMs at 24 h APF. Since the intensities of these markers were comparable between wildtype and knockdown conditions, we conclude that the non-tubulated lysosomes in loss of ATGs still possess degradative activity. Strikingly, we found the intensity of Lysotracker or DQ-BSA puncta was more heterogeneous in Atg18 RNAi than in control DIOMs. This result strengthens our model and significantly improve our manuscript; therefore, we include the data in Fig. 8E-H. Thank you.

Reviewer 2 Comments for the Author:
In this manuscript, Murakawa et al. found an extensive tubular autolysosomal network in Drosophila abdominal muscle remodeling during metamorphosis. The formation of Stx17-positive tubular autolysosomal network depends on autophagy core machinery except Atg5, Atg7, and Atg12. The tubular autolysosomal network provides greater degradative capacity for muscle remodeling during metamorphosis. Overall, the findings on autophagy-dependent tubular lysosomal network for Drosophila muscle remodeling are very interesting. The experiments are well controlled and the manuscript is elegantly written. The conclusion of the manuscript will be greatly improved, if the following experimental data are provided:

1. Previous studies showed that the SNARE Stx17 localizes to the autophagosome and detaches after fusion with the lysosome. Whereas the authors found that Stx17 marks tubular autolysosomal network. Do other SNARE proteins involved in autophagosome-lysosome fusion also localize to the tubular autolysosomal network during muscle remodeling?

We have performed an experiment to test colocalization between Spin:RFP and GFP:SNAP29 or GFP:Vamp7 in 20 h APF DIOMs. First, GFP:SNAP29 mostly localized to the cytosol and hardly localized to the tAL network (Figure X for reviewers, Left panel,). Since membrane localization of SNAP29 (Qbc) depends on Stx17 (Qa), an excess amount of GFP:SNAP29 might localize to the cytosol. Second, overexpression of GFP:VAMP7 severely affected the tAL network (Figure X_Right for reviewers); therefore we could not judge whether VAMP7 localizes to the tAL network. The tAL network fused with autophagosomes (Fig. 2F), and GFP:VAMP7 colocalized with the Spin:RFP-positive tubule remnants (Figure X, Right panel, arrow); therefore, we predict that VAMP7 also

localizes to the tAL network. To further test this possibility in future study, we would like to explore endogenous protein localization.

2. It's likely that tubular autolysosomal network is a dynamic structure with constant tabulation/elongation, fusion and fission. It has been reported that microtubule and motor proteins kinesin and dynein, and small GTPases Rab7 and Arl8b are required for lysosome tabulation. What's their involvement in tubular autolysosomal network formation during muscle remodeling?

We have tried knockdown of a series of genes that are mentioned by the reviewer. 1) Rab7 or Arl8 RNAi severely blocked the tAL network formation, the same as Stx17 RNAi (Figure Y for reviewers). Since both Rab7 and Arl8 are critical for the AP-LY fusion in Drosophila (PMID; 27559127, 30590083), we cannot judge whether Rab7 and Arl8 function in the tubulation per se. 2) Muscle-targeted RNAi of a series of kinesins, such as kinesin 1, was lethal at the larval stage. Thus, we could not investigate whether kinesin motors are required for the lysosome tubulation in the pupal period. To explore the involvement of microtubules, motor proteins, and the small GTPases in the tAL network formation, we need to establish a system for temporal genetic perturbation in the Drosophila muscle. It is a very critical question that we want to tackle in future studies.

3. Fig2, the authors should explain (or discuss) on the large vacuolated structures accumulated upon Spin RNAi. Are they autophagosomes or autolysosomes?

We think the large vacuolated structures induced by Spin RNAi are autolysosomes from these reasons: (1) TEM showed that the vacuoles were single-membraned structures and filled with other organelles (Fig. 4G), (2) the size of the vacuole induced by Spin RNAi depended on both autophagosome formation and the AP-LY fusion (Fig. 3I and J), and (3) The Spin RNAi-induced vacuoles had cathepsin L (Cp1:mKO) in the lumen (Fig. 7D). To describe it more clearly, we added the following sentence, "The large vacuolated structures were single-membraned and contained other cytoplasmic organelles, such as mitochondria; therefore, they shared the features of autolysosomes." on page 10 line 1-3.

Do similar phenotypes occur in STX17 RNAi and other SNARE mutants?

STX17, SNAP29, or VAMP7 RNAi blocked the fusion between AP and LY, and resulted in autophagosome accumulation. Therefore, the loss of SNARE phenotypes are much different from Spin RNAi.

4. Fig3 and 5, additional RNAi lines should be used to confirm the Atg5, Atg7 or Atg12 knockdown experiments.

To address the reviewer's concern, we tested another Atg7 or Atg12 RNAi on the formation of the tAL network (Figure Z for reviewers). Consistent with Fig. S3A-B, Atg7 or Atg12 RNAi induced a minor defect on the tAL network. Since the loss of Atg5 phenotype had been confirmed in the null condition (Fig. 3B), we did not test another Atg5 RNAi line. Collectively, we could confirm that the two ubiquitin-like conjugation systems are dispensable for the tAL network.

5. Besides DIOM shape changes, is there a functional assay that can be used to test the muscle function in Atg5 and Atg9 knockdown flies?

To assess the contractile function of DIOMs at 4 d APF, we performed live imaging of GCaMP6S, a biosensor of Ca2+. DIOMs expressing GCaMP6S with either LacZ (control), Atg5, or Atg18 RNAi constructs were observed by confocal microscopy. As shown in Fig. S4, Atg5 RNAi hardly affected the DIOM contraction upon the elevation of Ca2+ levels; in contrast, Atg18 RNAi severely disrupted DIOM contraction. This data shows a clear correlation between DIOM morphological changes and the contractile function. We included the data as a new supplemental figure (Fig. S4).

6. Please mark mitochondria in Fig 5G-I.

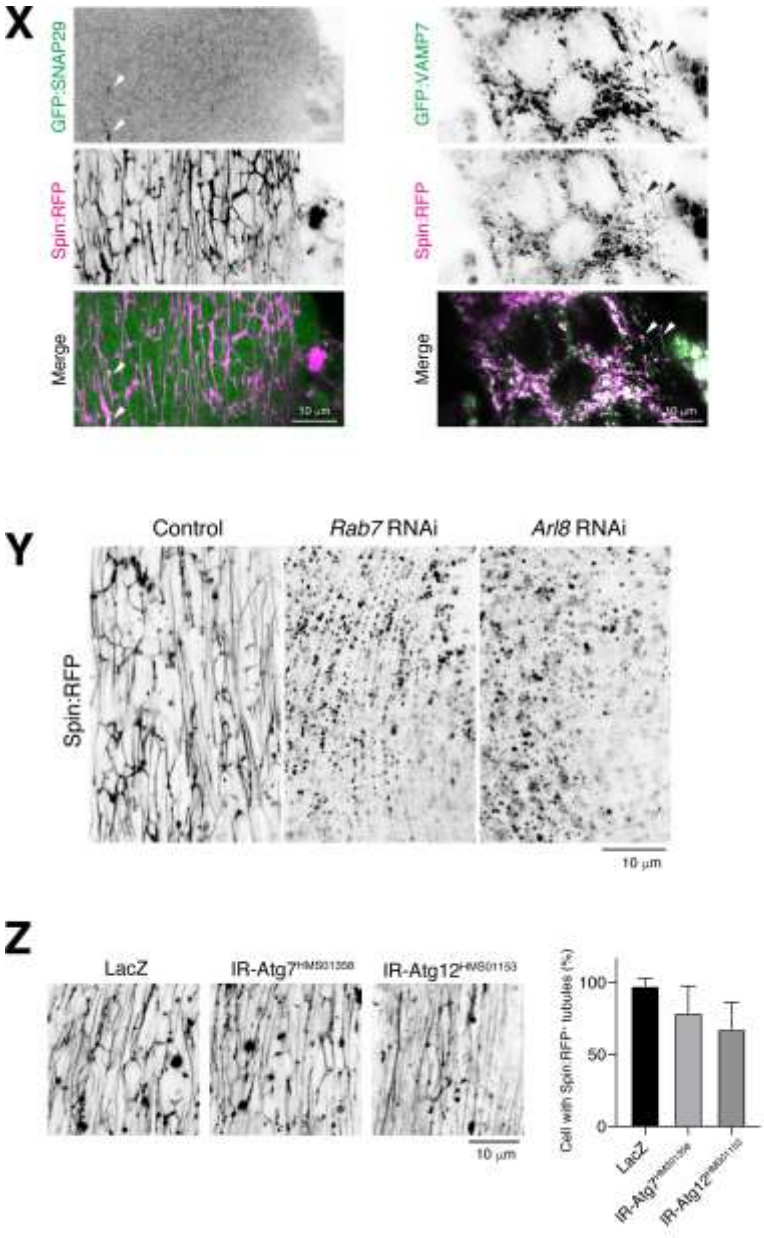
Thank you for this comment. We labeled mitochondria as "M" in Fig. 6G-I.

7. As several studies have implicated the involvement of Tor signaling in regulating autolysosomal tabulation (PMID:26139536 PMID:26582390), the authors should confirm their results in Fig S3 using additional RNAi lines or by mutant clones.

To confirm the Tor RNAi phenotype in the muscle remodeling, an additional Tor RNAi line was tested. As shown in Fig. S2B and S2D, two independent RNAi lines for Tor showed a consistent phenotype on the DIOM shape (Fig. S2B) and Spin:RFP-positive tAL network (Fig. S2D). Hence, we conclude that mTOR activity is not essential for the formation of the tAL network.

Minor:
Typo in page 6 line 3 “Syqntaxin 17 marks aa tubular network in remodeling muscle cells”.

Thank you. We corrected the typo.



Figures for reviewers

Second decision letter

MS ID#: JOCES/2020/248336

MS TITLE: An Autophagy-Dependent Tubular Lysosomal Network Synchronizes Degradative Activity Required for Muscle Remodeling

AUTHORS: Tadayoshi Murakawa, Amy A Kiger, Yuriko Sakamaki, Mitsunori Fukuda, and Naonobu Fujita
ARTICLE TYPE: Research Article

We have now reached a decision on the above manuscript.

To see the reviewers' reports and a copy of this decision letter, please go to: https://submit-jcs.biologists.org and click on the 'Manuscripts with Decisions' queue in the Author Area. (Corresponding author only has access to reviews.)

As you will see, the reviewer 2 is satisfied by the revision but the reviewer 1 raised some critical points that will require amendments to your manuscript. I hope that you will be able to carry these out, because I would like to be able to accept your paper.

We are aware that you may currently be unable to access the lab to undertake experimental revisions. If it would be helpful, we encourage you to contact us to discuss your revision in greater detail. Please send us a point-by-point response indicating where you are able to address concerns raised (either experimentally or by changes to the text) and where you will not be able to do so within the normal timeframe of a revision. We will then provide further guidance. Please also note that we are happy to extend revision timeframes as necessary.

Please ensure that you clearly highlight all changes made in the revised manuscript. Please avoid using 'Tracked changes' in Word files as these are lost in PDF conversion.

I should be grateful if you would also provide a point-by-point response detailing how you have dealt with the points raised by the reviewers in the 'Response to Reviewers' box. Please attend to all of the reviewers' comments. If you do not agree with any of their criticisms or suggestions please explain clearly why this is so.

Reviewer 1

Advance summary and potential significance to field

This work may provide a new insight into how lysosomal function is requlated through its morphological alterations.

Comments for the author

Reviewer1 still has one critical concern on the revised manuscript.

In the new Figure 5A-C, the authors showed the active tubulation process of lysosomes. In contrast, knockdown of Stx17 suppressed the tubulation process. Based on these observations, the authors suggested that the fusion of lysosomes with autophagosomes is required for the lysosomal tubulation. But this is a speculation and the direct assessment is necessary.

The authors have to perform "dual" color live imaging of lysosomes and autophagosomes at 14h APF like Figure 2 (Spin-RFP vs GFP-Atg8) to show that the fusion precedes the tubulation process. Ideally, this set of experiments will be performed in Spin RNAi and/or Stx17 RNAi flies. The experiment should provide direct mechanistic insights how lysosomal tubulation occurs.

Reviewer 2

Advance summary and potential significance to field

In this manuscript, Murakawa et al. found an extensive tubular autolysosomal network in Drosophila abdominal muscle remodeling during metamorphosis. Overall, the findings on autophagy-dependent tubular lysosomal network for Drosophila muscle remodeling are very interesting.

Comments for the author

The authors have address my concerns and I recommend it for publication.

Second revision

Author response to reviewers' comments

Below is a point-by-point response to the reviewers' comments.

Reviewer 1 Comments for the author
Reviewer1 still has one critical concern on the revised manuscript.
In the new Figure 5A-C, the authors showed the active tubulation process of lysosomes. In contrast, knockdown of Stx17 suppressed the tubulation process. Based on these observations, the authors suggested that the fusion of lysosomes with autophagosomes is required for the lysosomal tubulation. But this is a speculation and the direct assessment is necessary.
The authors have to perform "dual" color live imaging of lysosomes and autophagosomes at 14h APF like Figure 2 (Spin-RFP vs GFP-Atg8) to show that the fusion precedes the tubulation process. Ideally, this set of experiments will be performed in Spin RNAi and/or Stx17 RNAi flies. The experiment should provide direct mechanistic insights how lysosomal tubulation occurs.

To address the reviewer's concern, we first observed colocalization between Spinster:Gamillus and mCh:Atg8 in 12 h APF DIOMs. As shown in figure S4A, almost all of the non-tubulated Spin-positive lysosomes were positive for mCh:Atg8. The colocalization indicates that the non-tubulated structures at 12 h APF are autolysosomes. Also, dual-color live imaging of Spin:RFP and GFP:Atg8 showed that the spherical autolysosomes tubulated without further fusion with GFP:Atg8-positive autophagosomes (Fig. S4B). These new data indicate that the fusion precedes the initial tubulation process. However, our data do not exclude the possibility that the fusion with autophagosomes contributes further development of the tAL network. As the reviewer 1 suggested, it is ideal for including the RNAi condition. However, we could not perform the experiment because it requires combining several transgenes in Drosophila, which will take several months.
We added a new data set (Fig. S4) and described that on page 10, lines 22 to 28 (red-colored).

Reviewer 2 Comments for the author
The authors have addressed my concerns and I recommend it for publication.

Thank you very much for reviewing our manuscript.

Third decision letter

MS ID#: JOCES/2020/248336

MS TITLE: An Autophagy-Dependent Tubular Lysosomal Network Synchronizes Degradative Activity Required for Muscle Remodeling

AUTHORS: Tadayoshi Murakawa, Amy A Kiger, Yuriko Sakamaki, Mitsunori Fukuda, and Naonobu Fujita
ARTICLE TYPE: Research Article

We have now reached a decision on the above manuscript.

To see the reviewers' reports and a copy of this decision letter, please go to: https://submit-jcs.biologists.org and click on the 'Manuscripts with Decisions' queue in the Author Area. (Corresponding author only has access to reviews.)

As you will see, the reviewer 1 still raises one concern. I hope that you will be able to answer it by carrying out the experiment or by changing text, because I would like to be able to accept your paper.

We are aware that you may currently be unable to access the lab to undertake experimental revisions. If it would be helpful, we encourage you to contact us to discuss your revision in greater detail. Please send us a point-by-point response indicating where you are able to address concerns raised (either experimentally or by changes to the text) and where you will not be able to do so within the normal timeframe of a revision. We will then provide further guidance. Please also note that we are happy to extend revision timeframes as necessary.

Please ensure that you clearly highlight all changes made in the revised manuscript. Please avoid using 'Tracked changes' in Word files as these are lost in PDF conversion.

I should be grateful if you would also provide a point-by-point response detailing how you have dealt with the points raised by the reviewers in the 'Response to Reviewers' box. Please attend to all of the reviewers' comments. If you do not agree with any of their criticisms or suggestions please explain clearly why this is so.

Reviewer 1

Advance summary and potential significance to field

This study may provide a novel insight into how lysosomal morphological changes affect its degradative ability.

Comments for the author

At the 2nd revision, the authors performed dual-color imaging in 12 h APF and found that spherical lysosomes (positive with Spin:RFP) was already positive with GFP:Atg8. Thus, the results clearly indicate that fusion of lysosomes with autophagosomes is not sufficient for lysosomal tubulation.

This reviewer thinks that the specific tubulation mechanism(s) and/or molecule(s) should be provided by this study, as I commented at the first review, and this study still fails to address this.

Third revision

Author response to reviewers' comments

Reviewer 1 Comments for the author
At the 2nd revision, the authors performed dual-color imaging in 12 h APF and found that spherical lysosomes (positive with Spin:RFP) was already positive with GFP:Atg8. Thus, the results clearly indicate that fusion of lysosomes with autophagosomes is not sufficient for lysosomal tubulation.

This reviewer thinks that the specific tubulation mechanism(s) and/or molecule(s) should be provided by this study, as I commented at the first review, and this study still fails to address this.

We appreciate the reviewer's helpful suggestion. We agree with the reviewer that the specific mechanism of lysosomal tubulation is the next critical question raised by this study. However, as we have already stated in the last sentence in the Discussion "Identification of such factors would be the next crucial step and answer the fundamental question, why the lysosomes dynamically change shape in certain conditions", we think that identification of the specific factors is out of scope of the present manuscript. Thus, we would like to address the issue in our future studies. Moreover, the reviewer commented at the first review as follows "The authors have to analyze in detail the tubulation process of lysosomes in wild-type Drosophila and provide some mechanistic insight". So, that's why we analyzed the tubulation process of lysosome in wild-type in the first (Fig. 5) and second revisions (Fig. S4). We therefore believe that we could properly respond the reviewer's request.

Fourth decision letter

MS ID#: JOCES/2020/248336

MS TITLE: An Autophagy-Dependent Tubular Lysosomal Network Synchronizes Degradative Activity Required for Muscle Remodeling

AUTHORS: Tadayoshi Murakawa, Amy A Kiger, Yuriko Sakamaki, Mitsunori Fukuda, and Naonobu Fujita
ARTICLE TYPE: Research Article

I am happy to tell you that your manuscript has been accepted for publication in Journal of Cell Science, pending standard ethics checks.