Activation of mTORC1 and Suppression of Autophagy in Muscle Tissue Shortens Lifespan in Mice and Flies

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# Abstract

# Introduction

# Methods and Materials

## Animal Housing and Procedures

Floxed *Tsc1* alleles (Tsc1*tm1Djk*/J1 from the Jackson Laboratory) were crossed with *Ckmm-Cre* driver mice (FVB-Tg(*Ckmm-cre*)5Khn/J2 from the Jackson Laboratory) to generate animals that were heterozygous for the floxed allele, and either hemizygous for the *Cre* allele or wild-type at this locus. These mice were used to generate male littermates that were wild-type at both the *Tsc1* and *Cre* loci, homozygous at the *Tsc1* loci (floxed only), hemizygous at the Cre loci (transgene only) or *Tsc1*fl/fl, *Ckmm-Cre*Tg/+. Animals were housed in a 12h light/dark cycle animal facility with ad libitum access to food (Harlan Teklad) and water according to procedures approved by the University of Michigan University Committee on Use and Care of Animals. Animals were allowed to die naturally, or were euthanized at the advice of veterinary staff.

## Drosophila Breeding and Maintenance

Fly stocks (see Table 1) were purchased from the Bloomington Stock cCnter and maintained and were raised at 25C on standard corn meal food. For crosses, virgin females were collected from the GAL4 driver strains. Ten virgin females were used per cross. Males with the appropriate genotype were chosen from each of the lines and crossed to male UAS-TRiP-shRNA lines as well as a UAS-TRiP control which contains the genomic insertion site but no shRNA3 . Flies were maintained in a humidified (50–60%) incubator at 25C. Ten days after each cross the F1 progeny began to eclose and adults were sorted according to phenotype and gender. Flies bearing the balancer markers were discarded from the analysis. Sorted flies were put into new vials, with males and females separated and with 5–10 flies in each vial. Flies were transferred to fresh food twice weekly with deaths noted from each cross. The person handling the flies was blinded to the genotype of the flies.

## Western Blotting

Muscle samples (20-50 ug) were lysed in 20 uL/mg of RIPA buffer using a Qialyser (5 minutes at 30 Hz). After centrifugation (15 minutes at 14 000 RPM), lysates were boiled in a final concentration of 1X SDS-PAGE sample buffer (BioRad). Proteins were separated on pre-cast gradient gels from BioRad and transferred to nitrocellulose membranes. After blocking in 2% bovine serum albumin (Fisher), proteins were probed with anti-LC3, anti-pS6K, total S6K, anti-pS6 and anti-S6 antibodies. Secondary antibodies were alexa 680/700 conjugated anti-mouse and anti-rabbit secondary antibodies and blots were visualized via a LiCOR Odyssey system. Quantification was performed using ImageStudio Lite (LiCOR).

## Statistics

All statistical tests were performed using the R software package4. For pairwise tests, normality was tested via Shapiro-Wilk tests, and equal variance was tested using Levene’s test. Based on these results, either Wilcoxon tests, Student’s *t* or Welch’s *t*-tests were performed. For mouse studies, the three non-knockout genotypes (floxed allele alone, transgene alone and wild-type at both loci) were analyzed separately and then combined and labeled as “Controls” if not significantly different. For survival analyses and cox proportional hazard tests, the survival package was used (version 2.38-3)5,6. P-values were adjusted for multiple hypothesis testing by the method of Benjamini and Hochberg7. All raw data and reproducible code is available at http://bridgeslab.github.io/DrosophilaMuscleFunction

# Results

## Deletion of *Tsc1* in muscle tissue causes shortened lifespan and increased autophagy

To evaluate the effects of chronic mTORC1 elevation on aging in mice, we deleted the negative regulator of mTORC1, TSC1 via a floxed/Cre recombinase system. As shown in Figure 1A-B, deletion of TSC1 causes elevations in mTORC1 activity in quadriceps from these animals as determined by increased phosphorylation of the mTORC1 targets S6K and S6. To evaluate the effects of mTORC1 activation on autophagy in skeletal muscle, we evaluated the levels of LC3-I and II by western blotting. As shown in Figures 1A/C, the LC3-II/I ratio is much lower in *Tsc1* knockout quadriceps, consistent with previous reports using a different Cre line8.

We next observed these animals without manipulation as they aged. We observed increased signs of aging including hunched and scruffy appearances at an earlier age in the knockout animals but not any of the control littermates. As shown in Figure 1D, muscle-specific *Tsc1* knockout mice died of natural causes at a higher rate. Based on a Cox-proportional hazard model the hazard ratio was 4.17 compared to non-knockout littermates (p=2.0 x 10-5).

As previous reports implicated cardiac hypertrophy in cardiac muscle-specific knockout of *Tsc1*9,10 we evaluated cardiac mass and histology from these mice. We did not observer any evidence of rhabdomyomas, as was present in previous reports, but we did observe increased cardiac mass (Figure 1E).

## Knockdown of *Tsc1* in drosophila muscle tissue reduces lifespan

Our previous studies had shown that knockdown of the obligate mTORC1 component Raptor in fly muscles causes early lethality and muscle weakness, but that *Tsc1* knockdown resulted in viable adult flies11. To test whether gain of function of dTORC1 decreases lifespan in flies, we used the UAS-shRNA/GAL4 system to knockdown *Tsc1* in fly muscles. These knockdowns were driven by *24B*-GAL4 which is expressed in wing disks and adult fly muscles12. As shown in Figure 2A-D, knockdowns driven by two shRNA’s targeting *Tsc1* increase the rates of natural deaths for both strains and both sexes (shRNA #1, 3.8 fold for females, 3.4 fold for males; shRNA #2: 2.6 fold for females, 1.9 fold for males all with adjusted p-values<1 x10-5).

To test whether cardiac-specific knockdown of *Tsc1* has a similar phenotype we used a *Hand*-GAL4 driver which is expressed in fly cardiac tissue13. In contrast to the *24B* driven knockdowns, we did only observed modest increases in mortality (20-30% increase in hazard ratios, Figure 2E-F). Together, these data support the hypothesis that muscle-specific ablation of *Tsc1* results in early lethality in both mice and flies.

# Knockdown of Atg8a in fly muscles reduces lifespan

To test whether chronically impaired autophagy in muscle tissue can reduce Drosophila lifespan, we used a similar approach to reduce the levels of *Atg5*, *Atg8a* and *Atg8b* in fly muscles using the *24B*-GAL4 driver. We found that there

# Discussion

In this study we report that in both mice and flies, deletion or knockdown of *Tsc1* specifically in muscle tissue reduces lifespan. Cardiac-specific ablation of Tsc1 using *Tagln-Cre* showed early lethality of these mice, at approximately 3 weeks of age10 or 6 months of age in the case of *Myl-Cre*9. These mice exhibited dramatic cardiac hypertrophy and sudden death at a much earlier age than our animals. In addition, there was only very modest reductions in lifespan in the fly cardiac-specific knockdown model presented here. Together these data support the hypothesis that in these animals, the cause of early lethality may be distinct from cardiac defects, but our approach cannot conclusively show that cardiac *Tsc1* ablation plays no role in reductions in lifespan.

Skeletal muscle tissue is an extremely important organ for aging, as participants with the highest baseline grip strength had 20-217% decreased risk of all-cause mortality, irrespective of gender or body mass index14–19. Candidate gene studies have also implicated genes with important role in muscle tissue such as *IGF1R*, *AKT1* and *FOXO3A*20,21. For example, in humans, polymorphisms in *FOXO3A* have been associated with lengthened lifespan21–27. Both mouse and fruit fly models of *FOXO3A* loss of function result in stronger and longer living model organisms28–30. Furthermore, fruit fly studies have implicated improved muscle proteostasis as a key element co-ordinating lifespan extension31. TORC1 also plays a key role in protein homeostasis, through inhibiting autophagy and proteosomal regulation while promoting protein synthesis in an evolutionarily conserved manner.

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