Overexpression of Methionine-R-Sulfoxide Reductases Has No Influence on Fruit Fly Aging

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Abstract

Methionine sulfoxide reductases (Msrs) are enzymes that repair oxidized methionine residues in proteins. This function implicated Msrs in antioxidant defense and the regulation of aging. There are two known Msr types in animals: MsrA specific for the reduction of methionine-S-sulfoxide, and MsrB that catalyzes the reduction of methionine-R-sulfoxide. In a previous study, overexpression of MsrA in the nervous system of Drosophila was found to extend lifespan by 70%. Overexpression of MsrA in yeast also extended lifespan, whereas MsrB overexpression did so only under calorie restriction conditions. The effect of MsrB overexpression on lifespan has not yet been characterized in animal model systems. Here, the GAL4-UAS binary system was used to drive overexpression of cytosolic Drosophila MsrB and mitochondrial mouse MsrB2 in whole body, fatbody, and the nervous system of flies. In contrast to MsrA, MsrB overexpression had no consistent effect on the lifespan of fruit flies on either corn meal or sugar yeast diets. Physical activity, fecundity, and stress resistance were also similar in MsrB-overexpressing and control flies. Thus, MsrA and MsrB, the two proteins with similar function in antioxidant protein repair, have different effects on aging in fruit flies.

Keywords: aging, lifespan, methionine sulfoxide reductase, Drosophila melanogaster, protein repair

Abbreviations: Msr, methionine sulfoxide reductase; GSH, glutathione; GSSG, oxidized glutathione; MetO, methionine sulfoxide; Met-SO, methionine-S-sulfoxide; Met-RO, methionine-R-sulfoxide; ROS, reactive oxygen species; SY, sugar yeast food; DR, dietary restriction; DR SY, dietary restriction + sugar yeast food; N SY, normal sugar yeast food; ORF, open reading frame; PBS, phosphate buffer saline; HPLC, high performance liquid chromatography.

1. Introduction

One of the prominent theories of aging is known as the free radical theory (Harman, 1956; Beckman and Ames, 1998). It postulates that an age-associated accumulation of macromolecules (e.g., proteins, nucleic acids, lipids) oxidatively damaged by reactive oxygen species (ROS) results in senescence. Oxidative damage appears from an imbalance among oxidant production, antioxidant defense, and repair processes. A logical prediction based on this theory is that the overexpression of antioxidant/repair enzymes should increase lifespan. Drosophila melanogaster is a short-lived model-organism that has been widely used to examine the correlation between antioxidant defense and aging; however, a number of conflicting data were obtained.

Strong evidence of lifespan extension in flies overexpressing Cu,Zn-superoxide dismutase (SOD) and Mn-SOD (Parkes et al., 1998; Sun and Tower, 1999; Sun et al., 2002, 2004) or neutral effect of catalase overexpression (Sun et al., 2002; Orr and Sohal, 1992) were found. The simultaneous overexpression of these enzymes in different combinations resulted in life-prolonging effects (Orr and Sohal, 1994; Sun et al., 2004). Additionally, flies lacking either SODs (Kirby et al., 2002; Phillips et al., 1989) or catalase (Orr et al., 1992) had reduced lifespan. However, other studies have shown that overexpression of these antioxidant enzymes in long-lived genetic background had no effect (Orr and Sohal, 2003; Seto et al., 1990) on survivorship. The simultaneous overexpression of Cu,Zn-SOD, Mn-SOD and catalase in different combinations in long-lived flies also did not result in lifespan extension (Orr et al., 2003) and even led to a decrease in lifespan by 43% for flies overexpressing Mn-SOD and catalase (Bayne et al., 2005). As the correlation between these enzymes and lifespan was not direct and the observed differences in lifespan of transgenic flies were the function of (1) genetic background, (2) tissue/cell distribution of antioxidants, (3) temporal pattern of expression, and (4) source of transgene and type of expression system, it was suggested that antioxidant defense resulting from antioxidant enzymes is not a
limiting factor for Drosophila aging (Helfand and Inouye, 2003; Mockett et al., 2001; Sohal et al., 2002). Recent studies showed that overexpression of two enzymes, glucose-6-phosphate dehydrogenase (Legan et al., 2008) and glutamate-cysteine ligase (Orr et al., 2005), that increase low molecular weight antioxidants in cells (NADPH and glutathione (GSH), respectively), increases mean and maximum lifespan of long-lived Drosophila strain up to 50%. These studies, performed in one genetic background and with different transgene expression patterns, provide insights for understanding the processes that favor long lifespan.

In Drosophila, concentrations of low molecular weight antioxidants (and their precursors) decline in senescence-associated manner (Mockett et al., 1999; Rebrin et al., 2004). GSH as the most abundant low molecular weight antioxidant is considered as a major determinant of the cellular redox state. The reduced GSH/oxydized GSH (GSSG) ratio was decreased in exponential manner in the whole body of Drosophila (by over 70% from 10 to 60 days of age) (Rebrin et al., 2004). In the same time scale, the concentration of free methionine, which also serves as the source for cysteine production via the transsulfuration pathway, was decreased by 50% (Rebrin et al., 2004). Cysteine is a precursor for the GSH biosynthesis (Stipanuk, 2004). Various studies (reviewed in Stadtmann et al., 2005) revealed an age-related increase in methionine sulfoxide (MetO) levels in different tissues and organisms.

The repair of age-related protein damage has, to some extent, been studied in Drosophila (Chavous et al., 2001; Ruan et al., 2002). A balance between oxidative modifications of proteins and their repair was proposed to play an important role in senescence. Almost all amino acids are susceptible to oxidation by radicals that cause damage to amino acid side chains as well as protein backbones (Levine and Stadtman, 1996; Sohal, 2002; Stadtman, 2008). Thus, Drosophila shows an age-related increase in modified and oxidized proteins (Chavous et al., 2001; Orr and Sohal, 1994; Sohal et al., 1993). To repair oxidized side chains of sulfur-containing amino acids, cysteine and methionine, cells have evolved enzymes specific for oxidized forms of these amino acids. For example, two conserved redox systems, the thioredoxin and glutathione systems, maintain intracellular thiol groups of proteins and low molecular weight thiols in the reduced state in organisms from bacteria to humans (Holmgren, 2008; Lou, 2008).

Methionine sulfoxide reductases (Msr) occur in most organisms and catalyze the thioreductin-dependent free and protein-bound MetO to methionine (Brot and Weissbach, 2000; Kim and Gladyshev, 2007; Moskovitz, 2005). Msr enzymes as well as glutathione and thioredoxin reductases are ubiquitously expressed in cells (Holmgren, 2008; Kim and Gladyshev, 2007; Lou, 2008) and together with their substrates and cofactors form repair systems that protect cells from oxidative stress, and maintain cellular redox homeostasis (Holmgren, 2008; Moskovitz, 2005; Kim and Gladyshev, 2007; Levine et al., 2000).

Msr enzymes are classified with respect to their substrate specificity into two types: MsrA that catalyzes the reduction of methionine-S-sulfoxide (MetSO) in both protein-bound and free forms, and MsrB that is specific for the reduction of methionine-R-sulfoxide (MetRO) primarily in proteins. Msr genes are found in most organisms except some parasites and hyperthermophiles (Kim and Gladyshev, 2007). The number of MsrA and MsrB genes varies in different organisms. One MsrA and one MsrB are present in Escherichia coli, Saccharomyces cerevisiae, Caenorhabditis elegans, and D. melanogaster. Mammals have one MsrA and three MsrBs (MsrB1, MsrB2, and MsrB3). Although MsrA and MsrB enzymes have the same function of MetO reduction, they are different not only in substrate specificity, but also in active site composition, protein fold, subcellular localization and evolution (Kim and Gladyshev, 2005, 2006, 2007; Kryukov et al., 2002).

Several studies have provided evidence for an important role of MsrA in aging. An age-related decrease in total Msr activity and MsrA levels was observed in rat liver and kidney (Petropoulos et al., 2001). Expression of MsrA and MsrB2 was decreased in senescent human WI-38 fibroblasts (Picot et al., 2004). MsrA null mutants of yeast (Kryukov et al., 2002; Moskovitz et al., 1997) and mice (Moskovitz et al., 2001) were more sensitive to oxidative stress than wild type organisms and had a shortened lifespan (decreased by ~26% in yeast (Koc et al., 2004) and ~40% in mouse (Moskovitz et al., 1997)). Moreover, overexpression of MsrA in yeast (Moskovitz et al., 1998) and fruit flies (Ruan et al., 2002) led to protection against oxidative stress. In S. cerevisiae, overexpression of host MsrA extended lifespan by 25% (Koc et al., 2004). Most remarkably, expression of GFP-fused bovine MsrA in the nervous system of Drosophila increased the median lifespan of fruit flies by 70% (Ruan et al., 2002). Moreover, the authors observed that the MsrA-overexpressing transgenic flies had better physical activity, reproduction, and resistance to oxidative stress at the old age. Since MsrB is responsible for the reduction of one diastereomer of MetO (i.e., half of total MetO reduction), this enzyme is expected to have the same role as MsrA. However, thus far, the effects of MsrB overexpression and knockout on aging were studied only in yeast (Koc et al., 2004). The knockout of MsrB gene had little effect on the lifespan. Moreover, the overexpression of MsrB in yeast had no effect on the lifespan under standard growth conditions, but prolonged the lifespan under caloric restriction conditions (Koc et al., 2004).

Since the most dramatic effect of MsrA overexpression on lifespan was observed in Drosophila (Ruan et al., 2002), it was of interest to examine whether MsrB overexpression affects lifespan in this organism. Further considering the findings on the roles of MsrA and MsrB on aging in yeast, it was important to determine the effects of MsrB overexpression under both regular and caloric restriction conditions. In this study, we developed transgenic fruit flies overexpressing mouse mitochondrial MsrB2 or Drosophila cytosolic MsrB, and used them to address these questions.
2.3. Fly culture media

Two food types were used in the lifespan experiments. The first was corn meal food (85.7 g corn meal, 4,000 mg A’Antu Jemina’; The Quaker Oats Company, Chicago, IL), 50 ml golden A unsulfured molasses (Groeb Farms Inc., Onsted, MI), 71.4 g Torula yeast (MP Biomedicals, Solon, OH), 2.66 g p-hydroxybenzoic acid methyl ester (Sigma), 6.4 g agar (Natexagar Inc., Loomis, CA) and 5.7 ml propionic acid (Sigma) per liter water. The second type was sugar yeast food. It included 20 g agar, 3 g p-hydroxybenzoic acid methyl ester, 3 ml propionic acid, and variable amounts of sugar and yeast per liter of water. 50 g/dxrose was present in the dietary restriction sugar yeast food (DR SY) and 100 g in normal food (N SY). Autolyzed yeast powder (T.P. Drewitt, London, UK) was added in quantity 50 g per liter of water in DR SY food and 100 g in N SY food (Chapman and Partridge, 1996).

2.4. Genetic crosses and Drosophila husbandry

The GAL4–UAS binary system (Brand and Perrimon, 1993) was used to drive overexpression of mouse mitochondrial MsrB2 and fruit fly cytosolic MsrB in Drosophila. To obtain heterozygous flies expressing mouse Mrer2 or Drosophila MsrB2, homozygous mMsrb2B/A, mMsrb2B1, dMsrb2, and dMsrb2 virgin males were crossed to the corresponding virgin females containing the GAL4-driver. F1 offspring were crossed between GAL4 drivers and white flies (GAL4-activator/+) and between white flies and homoygous MsrB lines (u[1118]w;wMrER2+) or (u[1118]w;wMsrb2+) were obtained for control concurrently. Experimental flies were reared on corn meal food from vials seeded with less than 70 eggs per vial. Newly emerged flies were transferred to fresh corn meal food and allowed to mate for 1–2 days. 3-day-old mated flies were collected using ether, sorted by sex, and used for lifespan studies, parapat resistance test, and starvation test. Unless otherwise stated, flies used in the experiment were held on the corn meal food and transferred to fresh vials without anesthesia every 2–3 days. Embryonic, larval, pupal, and adult animals were kept in temperature-controlled chamber at 25 °C with 12 h light/dark cycle and approximately 60% humidity.

2.5. Lifespan study

Newly eclosed adult animals were collected within 4 h and kept on corn meal food at density of 50 animals per vial. In a typical lifespan trial, 3-day-old mated flies were placed in cages. The cage was made from 1 L plastic container with a grommet for changing of fresh food vials and a slit for removal of dead flies (for the experimental and 50–60% humidity. The control and experimental group trials were all performed concurrently.

2.6. Parapat resistance test

Male flies overexpressing mouse Mrer2 or Drosophila Mrer2 in nervous system were prepared as described above (Section 2.4) and cultured in half pint bottles on corn meal food at a density of 150 animals per bottle. 17 days old flies were sorted in groups of 10 or 20 animals with etherization 3 days before the test. The test vials were set up with sponge soaked with 2 ml of 20 mM or 30 mM freshly prepared parapat (Sigma) and 5% sucrose (Sigma) solution and covered with a 3 MM filter paper circle. On the day of the test, flies were transferred without etherization to the test vials for the experiment with 20 mM parapat or to vials with 5% agar and kept starved for 6 h (for the experiment with 30 mM parapat). The starved flies were transferred to the test vials without etherization and the number of dead animals was counted at indicated time points. For the test with 20 mM parapat, 8 replicates of 10 animals were used. For the test with 30 mM parapat, 18 replicates of 20 animals were performed for each cross except for control cross clas-GAL4/u[1118] where 9 replicates were examined. All data are reported as the means ± S.D.

2.7. Starvation resistance test

Male flies were prepared by standard techniques (Section 2.4) and maintained on corn meal food for 20 days prior to the test. Groups of 20 flies were transferred without etherization to vials with 6 ml 1% agar and kept in 12 h light/dark cycle at 25 °C. Total number of flies tested for each genotype was 140 animals. Dead animals were counted every 8 h. All data are reported as the means ± S.D.

2.8. Reproduction

Age-specific changes in pupa production were determined from counts of pupal progeny produced by 5 females in 24 h. Females were placed in vials along with 5 males. 10 replicates of each vial were tested. Flies were transferred to vials with fresh food without anesthetization every 2–3 days. Females laid eggs for 24 h, then animals were removed and the number of pupa was counted after eclosion. All data are reported as the means ± S.D.

2.9. Enzyme activity assays

Homogenates of flies were prepared using the same procedure for enzyme activity assays, HPLC-based assay and Western blot analyses. Flies were homogenized in liquid nitrogen. Homogenate was resuspended in PBS buffer containing protease inhibitor mixture (Roche), incubated on ice for 20 min and centrifuged at 16,000 × g for 20 min at 4 °C. Total protein concentration in supernatant was measured by the Bradford method using bovine serum albumin as a standard. 35 six-day-old males were resuspended in 350 μl of PBS buffer for activity measurements. MsrB activity was assayed in the supernatant by a standard procedure (Kumar et al., 2002). Briefly, the reaction mixture (100 μl) contained 20 mM dithiothreitol, 200 μM dabsyl-Met-RO, and 200 μg of total protein in PBS, pH 7.4. The reaction was carried out at 37 °C for 30 min and stopped by adding 200 μl of acetonitrile. The reaction product, dabsyl-Met, was analyzed by an HPLC procedure using a C18 column (Zorbax Eclipse XDB, USA). Measurements for each sample were performed in triplicate. All data are reported as the means ± S.D.

2.10. Analysis of Met/MetO content in proteins and free amino acid forms

Homogenates of 70 female flies in 500 μl of PBS buffer containing protease inhibitors were prepared as described in Section 2.9. Two sets of independent preparations were prepared. Proteins (2 μg) were precipitated from the homogenates by 5% trichloroacetic acid (Sigma) on ice for 10 min. Samples were centrifuged at 16,000 × g for 20 min at 4 °C, supernatants were used for measurements of Met content immediately (or stored at −80 °C), and pellets were purified with d-1-300μM p-toluenesulfonic acid, p-Toluenesulfonic acid (Sigma, 98.5% purity) was prepared as described (Bayer et al., 1985). Pellets were treated with 0.5 ml of 3 M p-toluenesulfonic acid under anaerobic conditions at 110 °C for 22 h, acidic samples were neutralized with equal volumes of 2 M NaOH and stored at −20 °C. The analysis of Met/MetO content in protein-free and hydrolyzed samples by HPLC was carried out as described (Lee et al., 2008). p-Phthalaldehyde derivatization of amino acids were detected using a Zorbax Eclipse XDB-C8 column (for Met content) or Zorbax Eclipse XDB-C8 column (for MetO content). Measurements for each sample were performed in triplicate. All data are reported as the means ± S.D.

2.11. Western blotting

6-day-old flies were prepared as described in Section 2.9. 100 μg of total protein was electrophoresed on NuPAGE® Novex 10% Bis-Tris gels, transferred onto PVDF membranes, and immunoblotted with antibodies specific for mouse Mrer2 (Kim and Gladyshev, 2005), Drosophila MsrB (Kumar et al., 2002) or Drosophila β-actin (ab8224, Abcam). Dilution 1:1000 was used for anti-mouse Mrer2 antibodies, 1:2000 for anti-Drosophila MsrB antibodies and 1:1000 for anti-β-actin. Immunoblot signals were visualized using ECL detection system (Sigma).

2.12. Statistical analysis

The significance of the difference between the survivor curves was determined separately for each 3 replicates of transgenic flies and their corresponding control (GAL4-activator/v[1118], UAS-MsrB2/+/u[1118]) using SAS software v. 9.1 (SAS Institute Inc., Cary, NC). To compare the survivor curves of the MsrB-expressing and control flies the non-parametrical estimates of the survivor functions by Kaplan–Meier method were applied using the procedure LIFETEST provided by SAS. The PROC LIFETEST calculated statistics for testing the null hypothesis that the survivor functions are the same for testing and control flies; statistical parameters (χ2 and p-value) of log rank test were used for estimation of accuracy of the null hypothesis. To get the mean and maximum (90% mortality) lifespans for each set of replicates (transgenic and control flies) the procedure MEANS provided by SAS software was used.

3. Results

3.1. Overexpression of fruit fly MsrB and mouse MsrB2 in Drosophila

We used the GAL4–UAS binary system to drive overexpression of mouse mitochondrial MsrB2 and fruit fly cytosolic MsrB in Drosophila as described in Section 2.4. Two independent homozygous UAS-MsrB2-responder lines for each MsrB were used, designated mMsrb2B/A and mMsrb2B/A for mouse Mrer2 and dMsrb2B/A and dMsrb2B/A for Drosophila Mrer2.
Figure 1. Expression of mouse MsrB2 in fruit flies. (A–D) Western blot analyses of Drosophila total homogenates with anti-mouse MsrB2 antibodies. mMsrB2\(^{2A}\) (lanes 1, 2) and mMsrB2\(^{2B}\) (lanes 3, 4) lines were crossed to GAL4-activator lines to drive mouse MsrB2 expression. Control flies were obtained by crossing white flies (\(w^{1118}\)) with mMsrB2\(^{2A}\) (lanes 5, 6), mMsrB2\(^{2B}\) (lanes 7, 8) and GAL4-activator (lane 9) lines. Expression of mouse MsrB2 (lanes 1–4) in whole body was achieved by crossing UAS-mMsrB2 lines and tubP-GAL4 (A) and da-GAL4 (B) drivers, in fatbody by crossing UAS-mMsrB2 with fatbody-GAL4 driver (C), and in the nervous system by crossing UAS-mMsrB2 with elav-GAL4 driver (D). Migration of the 19 kDa band corresponding to mouse MsrB2 is indicated on the left in panels A–D. (E) Protein loading control (42 kDa Drosophila \(\beta\)-actin) for the Western blotting experiment shown in A. Gender of 6-day-old females and males analyzed is shown by the corresponding symbols below panel E. (F) MsrB activity of total homogenates of male flies used for Western blot analyses. Designations 3A, 2A, and letter \(w\) refer to mMsrB2\(^{2A}\), mMsrB2\(^{2B}\), and \(w^{1118}\) lines that were crossed with the GAL4-driver. Measurements of each sample were performed in triplicates. All data are reported as the means ± S.D.

Figure 2. Expression of Drosophila MsrB in fruit flies. (A–D) Western blot analyses of fruit fly total homogenates with anti-Drosophila MsrB antibodies. dMsrB\(^{2B}\) (lanes 1, 2) and dMsrB\(^{2A}\) (lanes 3, 4) flies were crossed to GAL4-activator lines to overexpress Drosophila MsrB. Controls were obtained by crossing white flies with dMsrB\(^{2A}\) (lanes 5, 6), dMsrB\(^{2B}\) (lanes 7, 8), and GAL4-activator (lane 9) lines. F1 progeny of crosses between tubP-GAL4 (A), da-GAL4 (B), fatbody-GAL4 (C), and elav-GAL4 (D) drivers and UAS-dMsrB (lanes 1–4) and white flies \(w^{1118}\) (lane 9) were analyzed. Adult animals used were 6 days old. Migration of the 17 kDa band corresponding to fruit fly MsrB is shown by arrows on the left in panels A–D. (E) Protein loading control (42 kDa Drosophila \(\beta\)-actin) for the Western blotting experiment presented in A. Gender of 6-day-old females and males analyzed is shown by the corresponding symbols below panel E. (F) MsrB activity of total homogenate of fruit flies used for Western blot analyses. Designations 2A, 2B, and letter \(w\) refer to mMsrB2\(^{2A}\), mMsrB2\(^{2B}\), and \(w^{1118}\) lines that were crossed with the indicated GAL4-driver. Measurements were performed in triplicate. All data are reported as the means ± S.D.
the homogenates of flies expressing MsrB in the nervous system show lower levels of this enzyme in comparison, for example, with the homogenates of fruit flies expressing MsrB in the whole body. The highest MsrB activity was found in both ubiquitous GAL4-activator lines. Total body homogenates prepared from flies ubiquitously expressing mouse MsrB2 had almost 40-fold higher MsrB activity than the background activity due to endogenous fruit fly MsrB (Figure 1F). Homogenates prepared from fruit flies overexpressing Drosophila MsrB in whole body had almost 20-fold increase in activity (Figure 2F). No difference between two ubiquitous GAL4-activator lines (tubP-GAL4 and da-GAL4) was found with regard to MsrB activity or expression (Figure 1A, B, and F), although the da-GAL4 line is considered as a weaker driver. Fruit flies expressing MsrBs in the nervous system had statistically significant elevation in total MsrB activity (up to 6 times for mouse MsrB2 and up to 2 times for fruit fly MsrB overexpression) in comparison with controls. Clearly, efficient expression of active enzymes was achieved with both mouse MsrB2 and Drosophila MsrB transgenes. Background activity due to endogenous Drosophila MsrB was 13.2 ± 1.9 pmol/min mg.

3.2. Overexpression of mouse MsrB2 has no effect on lifespan on corn meal food

Expression of MsrB2 in whole body had no life-prolonging effect; in contrast, a small reduction in the mean lifespans (Table 1; Figure 3B, E and F) or no effect (Table 1; Figure 3A) in MsrB2-expressing flies was observed. The longevity of females in which the expression of mouse MsrB2 was driven by tubP-GAL4 activator line (tubP-GAL4/mMsrB2\(^{2A}\)) was not significantly different compared to driver line control tubP-GAL4/\(^{u118}\) (Figure 3A; Table 1, column 5). However, male progeny of a cross tubP-GAL4/mMsrB2\(^{2A}\) showed a reduction (13%) in the mean lifespan in comparison with tubP-GAL4/\(^{u118}\) control (\(\chi^2 = 68.73, p < 0.0001\); Table 1, column 5 and Figure 3E). These three lines also demonstrated 10–20% reduction (\(p < 0.0001\); Table 1, column 8) in the mean lifespan in comparison with the corresponding responder line controls (females tubP-GAL4/mMsrB2\(^{2A}\) vs. \(^{u118}\)/mMsrB2\(^{2A}\), females tubP-GAL4/mMsrB2\(^{2A}\) vs. \(^{u118}\)/mMsrB2\(^{2A}\), and males tubP-GAL4/mMsrB2\(^{2A}\) vs. \(^{u118}\)/mMsrB2\(^{2A}\)). One male line tubP-GAL4/mMsrB2\(^{2A}\) displayed an 8% increase (\(\chi^2 = 10.76, p = 0.001\) and 30% increase (\(\chi^2 = 68.73, p < 0.0001\)) in mean lifespan in comparison with driver line control and responder line control, respectively (Figure 3A; Table 1, columns 5 and 8). This was the only line in this study that showed lifespan extension with both controls.

When tubP-GAL4 activator line was replaced with da-GAL4 line, females expressing mouse MsrB2 lived significantly shorter (\(p < 0.0001\)) than driver control da-GAL4/\(^{u118}\). Experimental flies had 24% decrease in mean lifespan for cross da-GAL4/mMsrB2\(^{2A}\) vs. da-GAL4/\(^{u118}\) (\(\chi^2 = 39.42, p < 0.0001\)) and 19% decrease for cross da-GAL4/mMsrB2\(^{2A}\) vs. da-GAL4/\(^{u118}\) (\(\chi^2 = 57.18, p < 0.0001\)) (Figure 3B and Table 1, column 5). In males, respective 3% and 12% reductions in mean lifespan were observed (Figure 3F and Table 1, column 5). However, when a larger group was used (i.e., 210 males instead of 105) in the experiment with using sugar yeast (DRoSY) food, no significant decrease in the mean lifespan for males with the same genotypes was observed (Figure 5B; Table 3).

Table 1. Statistical analysis of survivor curves presented in Figure 3 for mouse MsrB2-expressing flies and their controls.

<table>
<thead>
<tr>
<th>1. Panel in Figure 3</th>
<th>2. Genotype</th>
<th>3. Sex</th>
<th>4. Mean (days)</th>
<th>5. % vs. driver/(^{u118})</th>
<th>6. (\chi^2)</th>
<th>7. (p &gt; \chi^2)</th>
<th>8. % vs. responder/(^{u118})</th>
<th>9. (\chi^2)</th>
<th>10. (p &gt; \chi^2)</th>
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<td>(^{u118})/mMsrB2(^{2A})</td>
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<td>64.4</td>
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<td>0.62*</td>
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<td>6.66*</td>
<td>0.0099*</td>
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<tr>
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<td>+8</td>
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<td>+30</td>
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<td></td>
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<td>0.52</td>
<td>+13</td>
<td>30.38</td>
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</tbody>
</table>

Column 1 indicates the letter of the corresponding panel in Figure 3. The genotypes and gender (female, F; males, M) are shown in columns 2 and 3, respectively. The mean lifespan is shown in column 4. The percent change in the mean lifespan compared with corresponding driver controls (GAL4-driver/\(^{u118}\)) is displayed in column 5 and compared with corresponding responder control in column 8. Comparison of two types (transgenic and control) of survivor curves (three curves in each group, 105 flies total) was performed with SAS software (see Section 2.12). Statistics of non-parametrical log rank test (\(\chi^2\)) for comparison with driver control lines is shown in column 6; \(p\)-value in column 7 and for comparison with responder control line in columns 9 and 10. Star marks a comparison of two responder lines.
Figure 3. Survivorship curves of mouse MsrB2 expressing flies on corn meal food. 35 female and 35 male animals were housed together in plastic cages; three replica cages were used for each lifespan curve. Survivorship distribution presented shows the average of those independent replicas (105 females and 105 males for each curve). Fresh corn meal food was supplied and surviving animals were counted every 3–4 days. Expression of mouse MsrB2 in whole body was activated by using tubP-GAL4 (A and E) or da-GAL4 (B and F) activator lines; in fatbody by using fatbody-GAL4 driver (C and G); in the nervous system by using elav-GAL4 line (D and H). Genotypes and sexes are indicated on the plots. All trials were performed concurrently.
Figure 4. Survivorship curves of *D. melanogaster* MsrB-overexpressing flies on corn meal food. Males and females were kept together during lifespan study. Each survivorship curve represents 105 flies. Expression of *Drosophila* MsrB in whole body was driven by using *tubP-GAL4* (A and E) or *da-GAL4* (B and F) activator lines; in fatbody by using *fatb-GAL4* driver (C and G); in the nervous system by using *elav-GAL4* line (D and H). Genotypes and sexes are shown on the plots. All trials were performed concurrently.
Although two ubiquitous GAL4-activator lines were used, conflicting data obtained does not allow making definitive conclusions with regard to negative influence of mouse MsrB2 overexpression in whole body on longevity of fruit flies. One of the possible reasons of such variations in lifespan could be the hybrid effect of two genetic backgrounds. Although both UAS-mMsr2 flies and GAL4-drivers had white genetic background, they were not isogenic with experimental flies. The substantial effect of variations in genetic background was observed on responder line controls (Table 1, column 8). Although responder line controls had similar mean lifespan (* 65 days for females, \( \chi^2 = 0.23, p = 0.62 \); 58 and 61 days for males, \( \chi^2 = 6.66, p = 0.0099 \); Table 1), they showed statistically significant difference (\( \chi^2 > 20, p < 0.0001 \)) in mean lifespan in comparison with the GAL4-activator line control and experimental flies. The responder line controls \( w^{1118}/UAS-mMsrB2 \) had white genetic background. However, both the GAL4-activator line control and experimental flies had the same mixture (50:50) of GAL4-driver and white line chromosomes. Therefore, an identical genetic background was achieved only in the driver line control, which should be viewed as the best control for the analysis of the effect of mMsrB2 expression on longevity. It was shown previously that genetic background itself could influence lifespan (Toivonen et al., 2007); our data obtained for ubiquitous drivers are consistent with this idea. It should be noted that life-prolonging effect of MsrA overexpression in whole body (40% increase in median lifespan in comparison with homozygous GAL4-activator line UbI-GAL4 and 80% increase in comparison with homozygous UAS-MsrA responder line) was obtained on non-backcrossed animals. Also, no responder line and driver line controls were analyzed in comparison with the flies overexpressing MsrA in the whole body (Ruan et al., 2002).

Mouse MsrB2 ectopic expression in fatbody-GAL4 activator line had no effect on lifespan in comparison with GAL4-activator line control (Figure 3Cand G; Table 1, column 5). Male and female progeny of MsrB2-expressing flies had the similar mean lifespan as GAL4-fatbody/\( w^{1118} \) controls and their survivor curves were undistinguishable by statistical analysis (Table 1, column 5). The fatbody-GAL4 flies (Grönke et al., 2003) were generated on the basis of long-lived flies with yellow and white genetic background, \( y w \). Long-lived flies expressing transgenes usually show more reproducible and reliable data than their short-lived counterparts (Orr et al., 2003). Two heterozygous controls \( w^{1118}/mMsrB2^{BA} \) and \( w^{1118}/mMsrB2^{BA} \) were tested concurrently with the experimental flies; no lifespan extension for MsrB2-expressing flies compared with their genetically matched \( w^{1118}/MsrB2^{BA} \) and \( w^{1118}/MsrB2^{BA} \) controls was found (Table 1, column 8). The positive effect of combination of different genetic backgrounds \( w^{1118} \) and \( y w \) on lifespan was observed. The heterozygotes combined \( w^{1118} \) and \( y w \) chromosomes lived for approximately 13% (females) and 32% (males) longer than the responder line control with only white genetic background.

Table 2. Statistical analysis of survivor curves presented in Figure 4 for flies overexpressing Drosophila MsrB and their controls.

<table>
<thead>
<tr>
<th>1. Panel</th>
<th>2. Genotype</th>
<th>3. Sex</th>
<th>4. Mean (days)</th>
<th>5. % vs. driver/( w^{1118} )</th>
<th>6. ( \chi^2 )</th>
<th>7. ( p &gt; \chi^2 )</th>
<th>8. % vs. responder/( w^{1118} )</th>
<th>9. ( \chi^2 )</th>
<th>10. ( p &gt; \chi^2 )</th>
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<td>A</td>
<td>tubP-GAL4/dMsrB2(^A)</td>
<td>M</td>
<td>60.9</td>
<td>-5*</td>
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<td>0.12*</td>
<td>-5*</td>
<td>-3.17*</td>
<td>0.12*</td>
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<td>-5*</td>
<td>-3.17*</td>
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<tr>
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<td>M</td>
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<td>-3.17*</td>
<td>0.12*</td>
<td>-5*</td>
<td>-3.17*</td>
<td>0.12*</td>
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<tr>
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<td>M</td>
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<td>-5*</td>
<td>-3.17*</td>
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<td>M</td>
<td>65.5</td>
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<td>-3.17*</td>
<td>0.12*</td>
<td>-5*</td>
<td>-3.17*</td>
<td>0.12*</td>
</tr>
<tr>
<td>C</td>
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<td>M</td>
<td>71.2</td>
<td>-5*</td>
<td>-3.17*</td>
<td>0.12*</td>
<td>-5*</td>
<td>-3.17*</td>
<td>0.12*</td>
</tr>
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<td>clw-GAL4/dMsrB2(^A)</td>
<td>M</td>
<td>62.6</td>
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<td>-3.17*</td>
<td>0.12*</td>
<td>-5*</td>
<td>-3.17*</td>
<td>0.12*</td>
</tr>
<tr>
<td>D</td>
<td>clw-GAL4/dMsrB2(^B)</td>
<td>M</td>
<td>66.2</td>
<td>-5*</td>
<td>-3.17*</td>
<td>0.12*</td>
<td>-5*</td>
<td>-3.17*</td>
<td>0.12*</td>
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<tr>
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<td>M</td>
<td>66.1</td>
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<td>-3.17*</td>
<td>0.12*</td>
<td>-5*</td>
<td>-3.17*</td>
<td>0.12*</td>
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<td>-5*</td>
<td>-3.17*</td>
<td>0.12*</td>
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<td>M</td>
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<td>0.12*</td>
<td>-5*</td>
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<td>F</td>
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<td>71.5</td>
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<td>-3.17*</td>
<td>0.12*</td>
<td>-5*</td>
<td>-3.17*</td>
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<td>-3.17*</td>
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<td>M</td>
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<td>G</td>
<td>fatb-GAL4/dMsrB2(^B)</td>
<td>M</td>
<td>77.2</td>
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<td>-5*</td>
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<td>M</td>
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<td>-1.56*</td>
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<td>M</td>
<td>65.5</td>
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<td>0.214</td>
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Column 1 indicates the letter of the corresponding panel in Figure 4. The genotypes and gender (female, F; male, M) are shown in columns 2 and 3, respectively. The mean lifespan is shown in column 4. The percent change in the mean lifespan compared with corresponding driver controls (GAL4-driver/\( w^{1118} \)) is displayed in column 5 and compared with corresponding responder control in column 8. Comparison of two types (transgenic and control) of survivor curves (three curves in each group, 105 flies total) was performed with SAS software (see Section 2.12). Statistics of non-parametrical log rank test (\( \chi^2 \)) for comparison with driver control lines is shown in column 6; \( p \)-value in column 7 and for comparison with responder control lines in columns 9, 10. Stars mark a comparison of two responder lines.
Ectopic expression of mouse MsrB2 in neurons by elav-GAL4 driver had not revealed any effect of MsrB2 expression on lifespan in comparison with the GAL4-activator line control, elav-GAL4/w1118 (Figure 3D and H; Table 1, column 5). No statistically significant difference in survivor curves was observed (Table 1, column 5). Survivor curves of two other control lines, which do not express MsrB2 (w1118/mMsrB2A and w1118/mMsrB2A), were also obtained in a parallel experiment. Female responder line controls had the mean lifespans that were similar to those of the tested lines (Table 1, column 8). Consequently, we conclude that neither ubiquitous nor ectopic expression of mitochondrial mouse MsrB2 in flies had the dramatic and consistent effect on lifespan on corn meal food.

3.3. Overexpression of Drosophila MsrB has no effect on lifespan on corn meal food

Similar results were obtained with flies overexpressing Drosophila MsrB (Figure 4 and Table 2, columns 5 and 8). Variations in mean lifespan (reduction up to 20%) were observed between
MsrB-overexpressing flies and their controls for both ubiquitous drivers (Figure 4A, B, E, F and Table 2). The most significant decrease in the mean lifespan in comparison with GAL4-activator line control was found for crosses da-GAL4/dMsrB2A and da-GAL4/dMsrB2A.1118. Females with respective genotype had 14% and 8% reduction in the mean lifespan, and males had 20% and 6% reduction in the mean lifespan (Figure 4B and F and Table 2, column 5). However, this effect was not seen with female progeny of a cross between UAS-dMsrBs lines and another ubiquitous driver tubP-GAL4 (compare Figure 4A and B; Table 2, column 5). In addition, when more da-GAL4/dMsrBs males were studied on DR SY food (210 males instead of 105), no changes in mean lifespan of the experimental and the driver and control line flies were found (Figure 5D; Table 3). The survivor curves of animals overexpressing Drosophila MsrB in fatbody as well as the mean lifespans were not changed significantly when compared with fatbody-GAL4/w1118 control (Figure 4C and G; Table 2, column 5).

In the case with expression of mouse MsrB2, responder line controls for fatbody-GAL4/dMsrB lines showed statistically significant (p < 0.0001) difference with experimental flies (Table 2, column 8). No dramatic effect of MsrB expression in the nervous system in comparison with driver line and responder line controls was detected (Figure 4D and H; Table 2, columns 5 and 8). In conclusion, strong MsrB overexpression in the nervous system, fatbody, or whole body of flies had no dramatic and consistent lifespan-prolonging effect on corn meal food.

3.4. Overexpression of MsrBs has no effect on lifespan on sugar yeast food

A link between overexpression of host MsrB in yeast and extended lifespan under caloric restriction was previously reported (Koc et al., 2004). Under caloric restriction conditions, MsrB-overexpressing cells divided twice as many times (lifespan was assessed by replicative assays of yeast aging) (Koc et al., 2004). Our initial purpose was to examine whether or not dietary restriction (DR) influences the lifespan of MsrB transgenic flies. It was demonstrated (Chapman and Partridge, 1996; Mair et al., 2005; Kabil et al., 2007) that sugar yeast diet (SY) regulated lifespan of flies in response to dietary dilution of sugar, but yeast dilution had a stronger effect on lifespan (Mair et al., 2005). Dietary dilution in two fold provided up to 50% increase in the median lifespan for D. melanogaster females (the effect was less pronounced for males) (Mair et al., 2005; Chapman and Partridge, 1996). To confirm that dietary restriction works for our flies, the diet containing twice less sugar and yeast (DR SY food, Section 2.3) in comparison with normal sugar yeast food (NSY) was tested for da-GAL4/w1118 female flies. As expected, these females had 52% increase in the mean lifespan (χ² = 187.7, p < 0.0001; Table 1, column 5 and Figure 5A). However, the mean lifespan of these flies on NSY (69.2 days) was significantly lower than that on corn meal food tested previously (36.3 days on N SY diet against 65.5 days on corn meal diet). The mean lifespan of tested females on DR SY diet (69.2 days) was comparable to that on corn meal food. We have not compared the nutritional composition and caloric content of corn meal diet and DR SY diet by analytical methods, but the lifespan showed that both foods had approximately the same calorie content. This finding led us to an additional test of MsrB-expressing flies on the other diet; however, even if we kept designation of this diet (DR SY) as accepted in the literature, this diet could not be considered as dietary restriction diet in comparison with corn meal food.

Overexpression of mouse MsrB2 or host MsrB in the nervous system (Figure 5C and E; Table 3) or the whole body (Figure 5B and D; Table 3) had no significant effect on lifespan on DR SY food. Slight reduction in the mean lifespan of elav-GAL4/mMsrB2A females (11%, χ² = 41.25, p = 0.0001; Table 3, column 5) was not observed on previously tested corn meal food (compare Figure 3D and Figure 5C) and therefore appeared not to be the result of mouse MsrB2 expression. Again, the responder control lines showed a statistically significant difference (p < 0.0001) in mean lifespan (data not shown). Differences in metabolic pathways, MsrB expression levels, and MsrB localization between flies and yeast could possibly explain different outcomes of MsrB expression in these organisms.

3.5. Methionine/methionine sulfoxide content of MsrB-overexpressing flies

Methionine sulfoxide content in proteins is considered as a measure of oxidative damage in cell (Stadtman, 1993; Chapman and Partridge, 1996). To confirm that dietary restriction influences the lifespan of MsrB transgenic flies. It was demonstrated (Chapman and Partridge, 1996; Mair et al., 2005; Kabil et al., 2007) that sugar yeast diet (SY) regulated lifespan of flies in response to dietary dilution of sugar, but yeast dilution had a stronger effect on lifespan (Mair et al., 2005). Dietary dilution in two fold provided up to 50% increase in the median lifespan for D. melanogaster females (the effect was less pronounced for males) (Mair et al., 2005; Chapman and Partridge, 1996). To confirm that dietary restriction works for our flies, the diet containing twice less sugar and yeast (DR SY food, Section 2.3) in comparison with normal sugar yeast food (NSY) was tested for da-GAL4/w1118 female flies. As expected, these females had 52% increase in the mean lifespan (χ² = 187.7, p < 0.0001; Table 1, column 5 and Figure 5A). However, the mean lifespan of these flies on NSY (69.2 days) was significantly lower than that on corn meal food tested previously (36.3 days on N SY diet against 65.5 days on corn meal diet). The mean lifespan of tested females on DR SY diet (69.2 days) was comparable to that on corn meal food. We have not compared the nutritional composition and caloric content of corn meal diet and DR SY diet by analytical methods, but the lifespan showed that both foods had approximately the same calorie content. This finding led us to an additional test of MsrB-expressing flies on the other diet; however, even if we kept designation of this diet (DR SY) as accepted in the literature, this diet could not be considered as dietary restriction diet in comparison with corn meal food.

Overexpression of mouse MsrB2 or host MsrB in the nervous system (Figure 5C and E; Table 3) or the whole body (Figure 5B and D; Table 3) had no significant effect on lifespan on DR SY food. Slight reduction in the mean lifespan of elav-GAL4/mMsrB2A females (11%, χ² = 41.25, p = 0.0001; Table 3, column 5) was not observed on previously tested corn meal food (compare Figure 3D and Figure 5C) and therefore appeared not to be the result of mouse MsrB2 expression. Again, the responder control lines showed a statistically significant difference (p < 0.0001) in mean lifespan (data not shown). Differences in metabolic pathways, MsrB expression levels, and MsrB localization between flies and yeast could possibly explain different outcomes of MsrB expression in these organisms.

| Table 3. Statistical analysis of survivor curves presented in Figure 5 for flies overexpressing mouse MsrB2 and Drosophila MsrB and their controls. |
|---|---|---|---|---|---|---|---|---|
| 1. Panel in Figure 5 | 2. Genotype | 3. Sex | 4. Mean (days) | 5. % vs. driver/w1118 | 6. Max (days) | 7. % vs. driver/w1118 | 8. χ² | 9. p > χ² |
| A | da-GAL4/w1118 N SY | F | 36.3 | -52 | 64.4 | -15 | 187.7 | <0.0001 |
| A | da-GAL4/w1118 DR SY | F | 69.2 | 76.1 |
| B | da-GAL4/mMsrB2A | M | 44.7 | -5 | 51.8 | 0 | 12.7 | 0.0004 |
| B | da-GAL4/mMsrB2A | M | 49.7 | +6 | 59.9 | +16 | 35.99 | <0.0001 |
| B | da-GAL4/w1118 | M | 46.9 | 51.8 |
| D | da-GAL4/dMsrB2A | M | 47.5 | -1 | 59.9 | +16 | 3.12 | 0.08 |
| D | da-GAL4/dMsrB2A | M | 46.2 | -1 | 54.5 | +5 | 0.75 | 0.39 |
| D | da-GAL4/w1118 | M | 46.9 | 51.8 |
| C | elav-GAL4/mMsrB2A | F | 52.6 | -9 | 70.7 | 0 | 3.64 | 0.06 |
| C | elav-GAL4/mMsrB2A | F | 51.4 | -11 | 67.9 | -4 | 41.25 | <0.0001 |
| C | elav-GAL4/w1118 | F | 57.8 | 70.7 |
| E | elav-GAL4/dMsrB2A | F | 54.2 | -6 | 67.1 | -5 | 49.7 | 0.02 |
| E | elav-GAL4/dMsrB2A | F | 55.0 | -5 | 70.7 | 0 | 4.7 | 0.26 |
| E | elav-GAL4/dMsrB2A | F | 57.8 | 70.7 |

Column 1 indicates panel in Figure 5. The genotypes and gender (female, F; males, M) of flies are shown in columns 2 and 3, respectively. The mean lifespan is indicated in column 4 and percent change in the mean lifespan compared with their genetically matched controls (GAL4-driver/w1118) is displayed in column 5. Maximum lifespan and percent change of the maximum lifespan are shown in columns 6 and 7, respectively. Comparison of two types (transgenic and control) of survivor curves (three curves in each group, 210 flies for panels B and D and 105 flies for other panels) was performed with SAS software (see Section 2.12). Statistics of non-parametrical log rank test (χ²) is shown in column 8; p-value in column 9.
flies, their corresponding driver line control da-GAL4/w1118 and responder line controls w1118/dMsrB and w1118/mMsrB2. Proteins in homogenate were precipitated by trichloroacetic acid and methionine content in a protein-free form was measured (Figure 6A). The pellet was subjected to hydrolysis with potassium-sulfonic acid followed by analysis of Met and MetO content (Figure 6B). Significant reduction of free Met during aging reduction of free methionine during aging (up to 35% decline, Figure 6A) was observed for both experimental and control flies. Our data are in agreement with the previously reported age-related decline of Met content (Rebrin et al., 2004). Remarkably, 17-day-old flies expressing Drosophila MsrB showed approximately 30% increase in Met content in comparison with both control flies. Mice MsrB2 expressing flies had the same content of free Met as control flies (within error).

Analysis of methionine sulfoxide content in hydrolyzed proteins revealed the presence of both diastereoisomers in equimolar ratio ([Met-RO]/[Met-SO] = 1.11 ± 0.04). We explain this finding by racemization of methionine sulfoxide during hydrolysis that was performed at 110 °C for 22 h. However, our experimental flies had a decreased methionine sulfoxide/methionine ratio in comparison with both types of controls (Figure 6B) suggesting the expression of functional MsrB. We observed an almost 40% increase in the MetO/Met ratio during aging for the flies with the same genotype. However, it should be noted that MetO in proteins still stays at low levels even in 17-day-old flies. The MetO/Met ratio in hydrolyzed protein samples was almost 50% higher in 17-day-old flies than in 6-day-old flies with the same genotype (Figure 6B). This finding is consistent with the idea that Met residues in proteins become more oxidized during aging.

3.6. MsrB-expressing flies have the same stress resistance as controls
Drosophila longevity, when influenced by genetic interventions, DR, and selection for lines with postponed senescence, often positively correlates with enhanced resistance of animals to different stresses (e.g., oxidative stress, starvation, desiccation, heat) (Parkes et al., 1998; Ruan et al., 2002; Lin et al., 1998; Ott et al., 2005; Mockett et al., 2001; Arking et al., 1991; Vermeulen and Loeschke, 2007). However, molecular mechanisms for such correlation remain elusive and there were several examples when oxidative stress response was not involved directly in aging (Bayne et al., 2005; Vermeulen and Loeschke, 2007). For example, the lifespan of mitochondrial Mn-SOD/catalase transgenic flies was decreased up to 43%, but their resistance to oxidative stress caused by H2O2 treatment or exposure to 100% oxygen was elevated (Bayne et al., 2005). Similarly, although MsrB expression had no influence on lifespan, this is an important antioxidant enzyme and its protein repair function could presumably be uncoupled from its influence on lifespan. Thus, we examined resistance of transgenic MsrB flies to oxidative stress induced by dietary paraquat, which upon intake generates superoxide radicals (Arking et al., 1991) that oxidize Met to MetO (Ruan et al., 2002).

17-day-old males overexpressing MsrBs in the nervous system were fed with 5% sucrose and 20 mM paraquat (Figure 7A) or were starved for 6 h to minimize the variations in paraquat intake and then fed with 5% sucrose and 30 mM paraquat (Figure 7B). No statistically significant difference in survivorship between experimental (elav-GAL4/mMsrB22A and elav-GAL4/dMsrB2B) and control (elav-GAL4/w1118) flies were observed on 20 mM paraquat (Figure 7A). The 17 h exposure to 30 mM paraquat killed 80% of experimental (mMsrB2/elav-GAL4 and dMsrB/elav-GAL4) and control males (w1118/UAS-MsrBs); only 50% of other control flies (elav-GAL4/w1118) were dead at these conditions (Figure 7B). These data demonstrate no protective effect of MsrB overexpression against oxidative stress induced by paraquat. All control animals (elavGAL4/w1118) fed with the diet containing 5% sucrose in the absence of paraquat were alive after 6 days.

Although we have shown that both types of MsrB-expressing flies have low concentration of MetO in protein-bound form and Drosophila MsrB-expressing flies have a lower decline of free Met, the protective effect of Met was not detected in assay with paraquat. The exact mechanism of paraquat in vivo toxicity is not known, even if it is evident that paraquat generates superoxide radicals. Probably, maintaining higher Met level in MsrB-overexpressing flies is not sufficient to overcome consequences of superoxide radical formation upon paraquat-induced oxidative stress.

As in the case of MsrA-overexpressing flies, MsrB overexpression did not protect against starvation (Figure 7C and D). The median lifespan was approximately 60 h for MsrBs-expressing and control flies. The observation of no influence of MsrA and MsrB overexpression on starvation seems logical, as both types of enzymes are unlikely to have direct influence on metabolic pathways linked to resistance against starvation (e.g., increase in lipid content).

3.7. MsrB-expressing flies show no changes in reproduction and physical activity compared to controls
Aging in many species is associated with decline in physical activity and fertility. The long-lived MsrA-overexpressing flies with transgene expression predominantly in the nervous system
had a markedly delayed age-related decline in general activity and reproduction (Ruan et al., 2002). In contrast, we found that MsrB-expressing flies had similar physical characteristics and showed no changes in the number of developed pupa.

Timing of development of transgenic flies expressing MsrB from eggs to hatching was the same as in the parental and heterozygous control flies that did not express MsrB transgenes (9–10 days at 25 °C). Qualitative observation of flight, courtship, and feeding behavior revealed no significant differences between transgenic MsrB flies and their controls in early life. The average body weight of 10-day-old males expressing MsrBs in the nervous system (elav-GAL4/mMsrB2 and elav-GAL4/dMsrB2) was indistinguishable from the body weight of controls (elav-GAL4/w1118 and w1118/UAS-MsrBs); animals weighted 0.89 ± 0.02 mg (Supplementary Table S1). The average locomotor activity (mean ± S.E.) of 8-day-old males expressing MsrBs in whole body was similar with controls (Supplementary Figure S1).

In a further experiment characterizing overall reproductive vigor, we counted the number of pupa that developed from eggs laid by one female over 24 h (Figure 8). We used female animals expressing MsrBs in the nervous system (elav-GAL4/mMsrB2 and elav-GAL4/dMsrB2) and the offspring of a cross between elav-GALA and white flies (elav-GAL4/w1118) as a control. Pupal progeny developed into adult flies in more than 95% cases. No changes in the number of developed pupa were observed (Figure 8).

4. Discussion

Expression of GFP-fused bovine MsrA in the adult nervous system of fruit flies resulted in a greatly increased median lifespan (~70%) (Ruan et al., 2002). To explain this finding, it was proposed that Drosophila has high levels of ROS and/or low levels of endogenous MsrA in the adult neurons, and that MsrA function might be a factor that limits the lifespan of flies (Ruan et al., 2002). Other studies reported the low level of Cu,Zn-SOD in adult nervous system of fruit flies (Klichko et al., 1999); and overexpression of human Cu,Zn-SOD in adult motoneurons using GAL4-UAS system extended the mean lifespan of fruit flies up to 40% (Parkes et al., 1998). An attempt to reproduce this result using elav-GAL4 driver failed (Ruan et al., 2002). Based on this observation and on a greater life-prolonging effect of MsrA overexpression (70% against published 40% for Cu,Zn-SOD), it was suggested that the antioxidant mechanism involving MsrA-dependent reduction of oxidized Met residues in cellular proteins may be more robust than the SOD/catalase system with regard to lifespan (Ruan et al., 2002). Since MsrA is specific for Met-RO, whereas Met-RO is reduced by MsrB, the analysis of fruit flies overexpressing MsrB provided an opportunity to better understand the unique role of MsrA and/or MetRO reduction in influencing animal lifespan. In addition, since MsrA and MsrB catalyze the same reaction (but with different diastereomers of MetO), one would expect that the lifespan extension
due to MsrA overexpression would be reproduced in flies over-expressing MsrB.

However, we found that overexpression of either mouse mitochondrial MsrB2 or Drosophila cytosolic MsrB in neurons of fruit flies had no dramatic and consistent lifespan-prolonging influence in these animals. Our transgenic flies expressed high levels of catalytically active enzymes, and these animals were examined with four different GAL4-activator lines and on two different diets. None of the conditions showed clear lifespan extension. Since both MsrA and MsrB catalyze the reduction of MetO residues in proteins, it is puzzling how one enzyme could provide such a dramatic effect on lifespan by reducing half of MetO residues, and the other enzyme that reduces the other half of MetO residues could be ineffective under all conditions tested.

Apparently, MsrA has broader substrate specificity than MsrB. Besides Met-SO residues in proteins, this enzyme has activity for free Met-SO (Lee et al., 2008). In yeast, MsrA transcriptional regulation clusters it with genes involved in methionine metabolism and sulfur acquisition, whereas MsrB does not show this expression pattern (Koc et al., 2004). Moreover, MsrA deletion has a more significant effect on the growth of cells on free MetO than the deletion of MsrB (Kryukov et al., 2002). We hypothesize that the role of MsrA in sulfur or methylation pathways is responsible for the observed role of this enzyme on lifespan extension and methionine metabolism.

Methionine serves as a source of sulfur for cysteine synthesis via the transsulfuration pathway (Stipanuk, 2004). Cysteine may influence cellular redox homeostasis and serves as an intermediate in GSH biosynthesis. The GSH/GSSG ratio determines an intracellular redox potential as GSH is a major antioxidant in the cell. In Drosophila, the GSH/GSSG ratio is decreased during aging (Rebrin et al., 2004; Mockett et al., 1999). Addition of GSH to food significantly increased resistance of fruit flies to oxidative stress induced by paraquat (Bonilla et al., 2006). The importance of glutathione balance for Drosophila aging was previously shown in flies overexpressing glutamate-cysteine ligase, which catalyzes a rate-limiting reaction in GSH biosynthesis. These flies, expressing transgene in the nervous system, had extended mean and maximum lifespans up to 50% (Orr et al., 2005).

Overexpression of MsrA in flies may influence GSH synthesis or methylation pathways by providing cells with an additional source of free Met. Additionally, Drosophila lacks glutathione reductase and GSSG reduction is carried out by the thioredoxin reductase/thioredoxin system (Kanokz et al., 2001) that may be affected during aging. Thus, it is possible that an altered metabolism of sulfur-containing compounds in MsrA-overexpressing flies may be one of the reasons for their delayed aging. Recent data on the role of MsrA in the aging process appear to support this idea. It was found that MsrA and a dietary supplementation of S-methyl-L-cysteine prevent Parkinson’s-like symptoms in a fruit fly model (Wassef et al., 2007). In this model, S-methyl-L-cysteine could enhance MsrA function, presumably through its cyclic oxidation by ROS and reduction by MsrA. MsrB is not efficient for this oxidized substrate. Importance of free Met-RO reduction was demonstrated in human liver carcinoma SK-Hep1 cells expressing yeast free Met-RO reductase (Lee et al., 2008). These cells had an increased resistance against oxidative stress induced by hydrogen peroxide as they had an additional source of Met derived from Met-RO.

An indirect proof of an important role of MsrA in processes other than reduction of Met-SO residues in proteins came from our experiment on the resistance of MsrB-overexpressing flies to oxidative stress induced by paraquat. It was previously shown (Ruan et al., 2002) that long-lived flies expressing MsrA in the nervous system had an enhanced resistance to oxidative stress caused by dietary paraquat. Based on these data, the authors suggested that the lifespan extension is offered by the antioxidant action of MsrA (Ruan et al., 2002). We used the same system for MsrB overexpression and the GAL4-driver with the same genotype as that in the study that examined MsrA overexpression. Our data demonstrated no protective effect of MsrBs overexpression in the fruit fly nervous system against paraquat-generated oxidative stress. We propose that an altered metabolism of sulfur-containing compounds in MsrA-overexpressing flies could provide an additional protection to oxidative stress in comparison with metabolism of MsrBs-overexpressing flies. In any case, our data suggest that further studies are needed to explain how MsrA increases resistance to oxidative stress.

MsrA expression in whole body (Ruan et al., 2002) offered an approximately 40% increase in median lifespan in comparison with homozygous GAL4-activator line Ubi-GAL4 and 80% increase in comparison with homozygous UAS-MsrA responder line. It is possible that the extension effect was caused by a combination of different genetic backgrounds from UAS-MsrA line and Ubi-GAL4. In our study, we used heterozygous lines as controls that combined genetic backgrounds of lines carrying GAL4 and UAS transgenes (GAL4-activator/μ118 and UAS-MsrB/μ118). In the experiments with whole body MsrBs expression, two different drivers (tubP- and da-GAL4) and two different enzymes (mouse MsrB2 and Drosophila MsrB) were studied. No lifespan extension was observed at any conditions tested.

Overall, our study highlights an important difference in the aging process between two enzymes that catalyze the same reaction, MetO reduction, with different stereospecificity. Apparently, MsrA is unique in providing a remarkable lifespan extension, whereas MsrB is more in line with most other antioxidant enzymes in that its overexpression does not significantly influence lifespan in the fruit fly model. Since MsrA can also reduce free Met-SO, it would be important to examine the contribution of this process to Drosophila aging in future studies.

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