**Mitochondrial-targeted methionine sulfoxide reductase overexpression increases production of oxidative stress in mitochondria from skeletal muscle.**

Running title: Methionine sulfoxide reductase increases mitochondrial oxidative stress

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**Abstract**

**Objective:** Mitochondrial dysfunction is part of the etiology of myriad health issues particularly those that occur with advancing age. Methionine sulfoxide reductase A (MsrA) is a ubiquitous protein oxidation repair enzyme that specifically catalytically reduces a specific epimer of oxidized methionine, methionine sulfoxide. In this study, we tested how mitochondrial bioenergetic functions are affected by increasing MsrA expression in different cellular compartments. **Methods:** In this study, we tested the function, including free radical generation, ATP production and respiration, of isolated mitochondria from the skeletal muscle of two lines of transgenic mice with increased MsrA expression: mitochondria-targeted MsrA overexpression or cytosol-targeted MsrA overexpression. **Results:** Surprisingly, in samples from mice with mitochondrial-targeted MsrA overexpression we found dramatically increased free radical production though no specific defect in respiration, ATP production or membrane potential. Among the electron transport chain complexes, we found the activity of complex I specifically was reduced in mitochondrial MsrA transgenic mice. In mice with cytosolic-targeted MsrA overexpression, we found no significant alteration to any of these parameters of mitochondrial energetics. **Conclusions:** There is also growing evidence that MsrA is a functional requirement for sustaining optimal mitochondrial respiration and free radical generation. MsrA is knonw to play a partial role in maintaining normal protein homeostasis by specifically repairing oxidized proteins. Our studies highlight a potential novel role for MsrA in regulating the activity of mitochondrial function through interaction with the mitochondrial proteome.

**Keywords.** Superoxide, oxidative stress, mitochondria, protein homeostasis, electron transport chain

**Introduction**

Mitochondrial dysfunction is a causative factor for numerous diseases and pathology and may be a potential primary driver of the aging process itself. One cause of mitochondrial dysfunction *in vivo* is loss of mitochondrial protein homeostasis (mito-proteostasis), the tightly regulated balance of protein translation, protein quality control and protein degradation. In the case of mitochondria this is complicated by two significant factors. First, greater than 90 percent of the mitochondrial proteome is translated in the cytosol and imported to the mitochondria in an unfolded state in which they are highly susceptible to oxidation [1]. Second, relative to the cytosolic proteome, the mitochondrial proteome is highly enriched in methionine which is one of the most readily oxidized amino acids due to its side-chain sulfur atom [2-3]. The sequence of some of the proteins that make up the electron transport chain complexes have been reported to be 8 to 13 percent methionine in contrast to an average usage rate of 2.2 to 2.8 percent among all cellular proteins[2]. Thus, there is a conundrum on why the highly oxidative environment of mitochondria would contain such a high amount of easily oxidized proteins.

Among the eukaryotic antioxidant defenses, methionine sulfoxide reductase A (MsrA) plays a unique role in the oxidative repair, and potentially redox regulation, of proteins in the cells. MsrA was classically defined as a repair enzyme capable of catalytic reduction of oxidized methionine, or methionine sulfoxides ([4](#_ENREF_4)). Subsequent discovery of other methionine sulfoxide reductases also pointed out that there is stereo-specificity among these enzymes with MsrA capable of reduction of primarily the S-epimer of methionine sulfoxide. However, there is growing evidence that MsrA plays a larger role in the regulation of cellular homeostasis. For example, MsrA has also been shown to have stereo-specific *oxidase* activity targeted to methionine[5]. MsrA may thus be capable of regulating protein function through redox regulation of methionine residues[6]. In addition, MsrA has been shown to play protein chaperone-like role in folding proteins; MsrA preferentially repairs oxidized methionine in unfolded proteins and protects these proteins from oxidative protein misfolding [7]. Lastly, MsrA may assist in targeting excessively damaged proteins for proteasome-mediated degradation through ubiquitin-like protein modifications that are distinct from its catalytic modification function [8].

MsrA is expressed ubiquitously in mammals and at the sub-cellular level is located natively in both the cytosol and the mitochondria. In yeast, deletion of MsrA significantly increases production of reactive oxygen species (ROS) and reduces mitochondrial efficiency when yeast are grown on substrates of the electron transport chain (ETC) [9]. These defects are not ascribed to reduced mitochondrial number but rather a reduced number of competent mitochondria in MsrA-deleted yeast. In mammalian retinal pigment epithelial (RPE) cells, knockdown of MsrA reduced mitochondrial ATP content and the activity of ETC complex IV [10]. Conversely, adenoviral overexpression of MsrA in RPE cells increased mitochondrial ATP and boosted ETC complex IV activity. Mitochondria isolated from a mouse model of Alzheimer’s disease also lacking MsrA similarly showed reduced oxygen consumption and ETC complex IV activity [11]. Mice lacking MsrA have also shown increased mitochondrial fragmentation and damage following exposure to the DNA damaging agent cisplatin [12]. Collectively, these findings suggest a role for MsrA, and regulation of methionine oxidation indirectly, in preserving normal mitochondrial energetic function.

In this study, we used two murine models of increased expression of MsrA that are targeted primarily either to the mitochondria or to the cytosol. Endogenously, the sub-cellular localization of MsrA is determined by the alternative translation start sites that include (or not) an N-terminal mitochondrial targeting sequence on the native translated protein. While the native distribution of MsrA is ~3:1 cytosolic to mitochondrial, here, we used two different transgenic MsrA mouse strains to test whether increasing MsrA in either subcellular compartment would alter mitochondrial bioenergetics or function. We and others have reported that TgCyto MsrA mice have increased levels of cytosolic MsrA due to a deletion of the endogenous mitochondrial targeting sequence of MsrA in the overexpressed transgene [13-15]. Conversely, TgMito MsrA have preferential overexpression of mitochondrial-targeted MsrA due to preferential expression of the endogenous mitochondrial targeting sequence of MsrA in the transgene [13-14, 16]. In this study, we tested the energetic and oxidative stress characteristics of mitochondria isolated from the skeletal muscle of these mice to address the potential role of MsrA on murine mitochondrial function.

**Methods**

**Animals**

All studies in this research were reviewed and approved by the UT Health San Antonio (UTHSA) Institutional Animal Care and Use Committee (IACUC) that is responsible for monitoring housing and animal condition regularly to ensure all guidelines are met for the safety and health of the animals. All experiments were conducted in compliance with the US Public Health Service's Policy on Humane Care and Use of Laboratory Animals and the Guide for the Care and Use of Laboratory Animals. We have previously reported on the generation and breeding of TgCyto MsrA and TgMito MsrA mice [13-14, 16]. For young mice (5-7 mo of age) were used and mice were maintained on normal animal chow (NIA-31) for their life. Animals were sacrificed by CO2 and muscle and other tissues were collected.

**Mitochondrial function assays**

Mitochondria were isolated from freshly collected hind-limb skeletal muscle (gastrocnemius, tibialis & soleus) using the methods previously described [17]. Briefly, muscle tissues were homogenized with protease and mitochondria were purified through differential centrifugation. H2O2 release from mitochondria under specified conditions was assessed using the Amplex Red method described elsewhere [18]. Mitochondrial substrates were added at the following concentrations: glutamate (2.5 mM), malate (2.5 mM), succinate (5 mM), rotenone (0.5 µM) and antimycin A (0.5 µM). The same concentrations were used for ATP production, membrane potential and mitochondrial respiration. Superoxide release was measured using electron paramagnetic resonance (EPR) with the use of spin trap 5-diisopropoxyphosphoryl-5-methyl-1-pyrroline-N-oxide (DIPPMPO) as previously described [17]. EPR data are expressed as relative intensity per 20 µg mitochondrial protein then normalized to values generated from control mice. ATP synthesis was measured using the luciferin/luciferase assay from Roche according to manufacturers’ instructions. Slope of kinetic curve generated was converted to ATP measurements using the standards provided in the kit. Membrane potential was measured by the fluorescence of the quench-dye Safarin O as previously described [18]. Respiratory control ratio (RCR) was measured as the ratio of mitochondrial State 3/State 4 respiration rates as measured by Clark electrode as described previously [17-18]. Briefly, State 3 respiration was measured in the presence of 0.3 mM ADP; State 4 respiration was measured as oxygen consumption following the expenditure of ADP. Aconitase catalyzes the reversible isomerization of citrate to isocitrate. In most tissues, aconitase is usually present in both the mitochondrial matrix and the cytoplasm. However, in skeletal muscle, only mitochondrial matrix aconitase is present. Aconitase activity was assayed (in Triton-X-100-treated samples) by measuring NADP+ reduction by citrate in the presence of isocitrate dehydrogenase using a fluorometric method (excitation at 355 nm and emission at 460 nm). Skeletal muscle homogenates (∼1.0 mg of protein/ml) were aliquoted in 96-well plates (100 μl of pH 7.44, 125 mm KCl, 10 mm HEPES, 5 mm MgCl2, 2 mm K2HPO4) and incubated at 30° C up to 40 min. After incubation, aconitase activity measurements were begun by the addition of 1 volume (100 μl) of 50 mm Tris, 0.6 mm MnCl2, 60 mm citrate, 0.2% Triton X-100, 100 μm NADP+, and 1 unit of isocitrate dehydrogenase (Sigma). Fluorometric measurements were then started immediately (Fluoroskan-FL Ascent type 374 microplate reader). Negative blank to measure aconitase-independent NADP+ reduction consisted of the same buffer minus the isocitrate dehydrogenase with the slope of NADPH fluorescence used as assessment of aconitase activity.

**Mitochondrial complex assays.**

Activity of ETC complexes were measured as previously described [17]. In brief, mitochondrial protein was assessed from complex I activity by monitoring the oxidation of nicotinomide adenine dinucleotide (NADH) with ubiquinone-2 as the electron acceptor in the presence of diclorophenolindophenol (DCIP). Complex II activity was assessed by measuring succinate-dependent reduction of DCIP using ubiquinone-2 as the electron receptor. Complex III activity was measured by the reduction of cytochrome c3+ at 550 nm using D-ubiquinol-2 as an electron acceptor. Complex IV as measured by monitoring the oxidation of cytochrome c2+. All assays were measured by spectrophotometry and they are described in greater details elsewhere [17]. The final rates for all activities were normalized to average values obtained from wild type (control) animals.

**Statistical analysis**

All data were analyzed by 1 way ANOVA or Student’s t-test as appropriate. Statistical significance was given to those data where p < 0.05. Post-hoc analysis of ANOVA were performed using the method of Holm-Sidak.

**Results**

Based on reports suggesting the lack of MsrA causes mitochondrial dysfunction, we tested whether isolated mitochondria from mice with elevated MsrA levels, either primarily in the cytosol or primarily in the mitochondria, would differ from those of control mice. We first addressed rates of H2O2 production as marker of mitochondrial-derived reactive oxygen species (ROS) production. Under basal respiration, *i.e.,* no mitochondrial substrates provided, H2O2 production was low and did not differ among genotypes (**Figure 1A**). When provided glutamate and malate (substrates for ETC complex I), H2O2 production is significantly elevated; interestingly, under these conditions H2O2 production is nearly four-times greater in TgMito MsrA mitochondria than for control or TgCyto MsrA mitochondria (**Figure 1B**). When provided glutamate, malate and rotenone, an inhibitor of ETC complex I, we found that mitochondria from all three genotypes showed similar high rates of H2O2 production (**Figure 1C**). When provided succinate, a substrate for ETC complex II which then bypasses ETC complex I, H2O2 production was still significantly elevated in TgMito MsrA compared to control and TgCyto MsrA mitochondria (**Figure 1D**). With addition of antimycin A, an inhibitor of ETC complex III, we found a similar difference between TgMito MsrA and control ROS production though this did not reach statistical significance (**Figure 1E**). For all assays, we found no difference in ROS production between mitochondria from TgCyto MsrA and control mice.



**Figure 1**. Mitochondrial production of H2O2 with no substrates provided (**A; state 1**) or provided with glutamate and malate (**B; Glu/Mal**), glutamate, malate and rotenone (**C; Glu/Mal/Rot**), succinate and rotenone (**D; Suc/Rot**) or succinate, rotenone and antimycin A (**E; Suc/Rot/AA**). Skeletal muscle mitochondria was isolated from wild type (Control),TgMito MsrA (Mito) and TgCyto MsrA (Cyto) mice. Bars represent average values for n=5 for each group ± SEM. Asterisks indicate group differs significantly from others by ANOVA (p < 0.05).

Because mitochondria do not produce H2O2 directly, we also measured superoxide production from isolated mitochondria using electron paramagnetic resonance (EPR). Whether substrates for ETC complex I (glutamate and malate) or for complex II (succinate with rotenone to inhibit complex I) were provided, superoxide generation was higher in mitochondria from TgMito MsrA mice relative to control using this method (**Figure 2A**). We also measured whether superoxide are released into the mitochondria through measurement of aconitase activity which is inhibited in the mitochondrial matrix by interaction with superoxide [19]. The significantly reduced activity of aconitase in TgMito MsrA mitochondria suggested again elevated levels of superoxide with increased mitochondrial MsrA (**Figure 2B**).



**Figure 2**. **A.** Superoxide generation from mitochondria isolated from muscle of wild type (Control) and TgMito MsrA (mito) mice provided glutamate and malate (**Glu/Mal**) or succinate and rotenone (**Suc/Rot**). B. Aconitase activity in isolated mitochondria provided glutamate and malate (**Glu/Mal**) or succinate and rotenone (**Suc/Rot**). Bars represent average values for n=6 for each group ± SEM. Asterisks indicate significant difference as measured by t-test (p < 0.05).

Of the potential sources of mitochondrial superoxide production, we focused on the activity of the ETC complexes, especially ETC complex I and III, as potential mechanisms for these differences. In isolated mitochondria, we found a significant reduction in ETC Complex I activity in TgMito MsrA mitochondria compared to control (**Figure 3**). ETC Complex II, III, and IV were all similar between the two genotypes suggesting this could be the potential source of increased superoxide generation in TgMito MsrA mitochondria.



**Figure 3**. Electron transport chain complex activity in isolated mitochondria from wild type (Control) and TgMito MsrA mice (Mito). Bars represent average values for given complex for n=5 for each group ± SEM. Asterisks indicate significant difference as measured by t-test (p < 0.05).

Despite the increase in free radical production and reduction in ETC Complex I activity, we found little detrimental effect on actual bioenergetics of mitochondria from TgMito MsrA mice. ATP production was not different among the three genotypes of mice when generating ATP from ETC Complex I (glutamate and malate) or complex II (succinate and rotenone to inhibit Complex I). Similarly, increasing MsrA levels had no effect on the respiratory control ratio (RCR) of mitochondria given these substrates or the mitochondrial membrane potential (**Figure 4**).

**Figure 4.** **A.** ATP production from isolated mitochondria provided glutamate and malate (**Glu/Mal**) or succinate and rotenone (**Suc/Rot**). **B.** Respiratory control ratio (RCR) of mitochondria provided glutamate and malate. **C.** Membrane potential of isolated mitochondria provided glutamate and malate (**Glu/Mal**) or succinate and rotenone (**Suc/Rot**). Skeletal muscle mitochondria was isolated from wild type (Control),TgMito MsrA (Mito) and TgCyto MsrA (Cyto) mice. Bars represent average values for n=5 for each group ± SEM. Asterisks indicate group differs significantly from others by ANOVA (p < 0.05).



**Discussion**

Contrary to our initial prediction, our findings suggest that elevated levels of MsrA in the mitochondria leads to increased generation of mitochondrial-derived free radicals without significantly affecting mitochondrial bioenergetics. These outcomes raise interesting questions, the first of which why might increasing mitochondrial MsrA reduce ETC complex I activity? Of note, mammalian complex I is highly enriched in methionine content with up to 4X the quantity of methionine compared to the methionine content of the total cellular proteome [2]. It has been proposed that the high methionine content might act as an antioxidant or “free radical sink” within the highly oxidative environment of the mitochondria [2, 20]. Moreover, the majority of the proteins making up this complex are imported to the mitochondria as unfolded proteins [21]. As MsrA has been shown to preferentially bind unfolded proteins [7], it may be that the overabundance of MsrA in mitochondria from TgMito MsrA mice may be physically bound to these components potentially inhibiting the proper folding of the complex structures. While the levels of MsrA expressed in these mice may be much higher than biological 14, 16], these results raise the intriguing possibility that MsrA plays a protein chaperone-like function in assembly of mitochondrial protein complexes.

We have previously shown that TgMito MsrA are protected against glucose metabolic dysfunction caused by either high fat diet or advanced age [14, 16]. In light of the results presented here, these physiological outcomes are intriguing because there has been some consensus that oxidative stress is associated with, and may be causative for, metabolic dysfunction including insulin resistance [15, 22]. However, there is also growing evidence that H2O2 signaling is required for many normal cellular functions including metabolic function [23-24]. Because our assays were performed using isolated mitochondria, it is still possible that these findings are an artifact of the experimental procedure. It would be of interest to determine *in vivo* free radical production in living TgMito MsrA mice to better define this potential relationship.

More broadly, our data align with an expanding number of findings that seem to refute the oxidative stress theory of aging at least in murine models. While this theory originally received much attention, in part due to its simplicity, the support for this theory has been largely equivocal. Most aging studies conducted in mice with genetically altered enzymatic antioxidants have shown no consistent effect on longevity [25]. Even in transgenic mice with mitochondrial-targeted antioxidant overexpression there has been little consensus to their effect on lifespan [14, 26-27]. On the other hand, aging is a biological process and there is clear interest in understanding how age-related changes in health, and not just lifespan, might be regulated by processes such as mitochondrial oxidative stress [28-29]. In this regard, there is evidence that increased oxidative stress drives multiple health deficits in mouse models of aging [30-31]. We have reported a potential aging benefit of TgMito MsrA mice on metabolic function, while others have shown these mice are not protected from a cardiac ischemia-reperfusion model [14, 32]. It would be of interest to take a more holistic approach towards functional aging assessments toward determining how increasing mitochondrial MsrA alters aging as a whole in these mice.

The actions of MsrA in the mitochondria may be beyond that of catalytic reduction of methionine sulfoxide. There is a developing set of evidence that methionine oxidation can regulate protein function with stereo-specific oxidation and reduction by methionine sulfoxide reductases as a key regulator [5-6, 33]. In addition, the burgeoning clues that MsrA directs protein degradation through ubiquitin-like modifications suggest that MsrA have a far more central role in proteostasis than previously thought [8]. Moreover, the importance of methionine metabolism in regulating cellular homeostasis, for example trans-sulfuration and hydrogen sulfide generation, suggests methionine sulfoxide reductases could be a previously unrecognized pivotal regulatory mode for maintaining normal cellular function and communication [34-35].

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