

FORUM REVIEW ARTICLE

The Use of microRNAs to Modulate Redox and Immune Response to Stroke

Yi-Bing Ouyang, Creed M. Stary, Robin E. White, and Rona G. Giffard

Abstract

Significance: Cerebral ischemia is a major cause of death and disability throughout the world, yet therapeutic options remain limited. The interplay between the cellular redox state and the immune response plays a critical role in determining the extent of neural cell injury after ischemia and reperfusion. Excessive amounts of reactive oxygen species (ROS) generated by mitochondria and other sources act both as triggers and effectors of inflammation. This review will focus on the interplay between these two mechanisms. **Recent Advances:** MicroRNAs (miRNAs) are important post-transcriptional regulators that interact with multiple target messenger RNAs coordinately regulating target genes, including those involved in controlling mitochondrial function, redox state, and inflammatory pathways. This review will focus on the regulation of mitochondria, ROS, and inflammation by miRNAs in the chain of deleterious intra- and intercellular events that lead to brain cell death after cerebral ischemia. **Critical Issues:** Although pretreatment using miRNAs was effective in cerebral ischemia in rodents, testing treatment after the onset of ischemia is an essential next step in the development of acute stroke treatment. In addition, miRNA formulation and delivery into the CNS remain a challenge in the clinical translation of miRNA therapy. **Future Directions:** Future research should focus on post-treatment and potential clinical use of miRNAs. *Antioxid. Redox Signal.* 22, 187–202.

Introduction

STROKE IS ONE of the leading causes of death worldwide and the most prominent cause of long-term disability (105). Although many clinical stroke trials have been completed, the only efficacious treatment identified to date is early (<4.5 h) thrombolysis (17). One reason for the widespread failure to translate promising findings in animal studies to successful human clinical trials likely resides in the complex interplay between signaling pathways and the potentially short therapeutic window for acute neuroprotection. Recent evidence increasingly supports a role for microRNAs (miRNAs) in the response to cerebral ischemia, as we have reviewed recently (131). The faster post-transcriptional effect of miRNAs, and their ability to simultaneously regulate many target genes, suggests that miRNAs may have a greater therapeutic potential as candidates for the treatment of stroke than therapies targeting a single gene by direct transcriptional control. Further increasing their potential for translation, several miRNAs are already in clinical trials, suggesting that

formulation and administration will be straightforward in a new disease setting or for a new miRNA target.

In ischemic stroke, the damage is most rapid and severe in the center of the ischemic territory (ischemic core) where neurons are destined to become necrotic and die within hours after the onset of stroke (78). However, the fate of neurons in the adjacent peri-ischemic (penumbral) area is less certain; they may either maintain metabolic homeostasis, re-establish protein synthesis, and survive *via* induction of prosurvival and antiapoptotic signaling pathways, or will die at a later period of reperfusion *via* initiation of proapoptotic pathways (44). This vulnerable region of brain therefore represents a significant target for therapeutic strategies in the poststroke period, which seek to improve clinical outcome by ultimately minimizing the total volume of infarct. Oxidative stress and inflammation are two widely accepted mechanisms of penumbral cell death after cerebral ischemia, which have been reviewed recently (71, 78). The present review will focus on the interplay of these two mechanisms, emphasizing regulation by miRNAs and the

central role of mitochondria in regulation of reactive oxygen species (ROS) and inflammation.

Redox in Stroke

Cellular redox homeostasis is crucial for many biological processes. Whereas ROS have key signaling roles in the cell, excess levels can damage essentially all the constituents of the cell. Oxidative stress is defined as an excess production of ROS relative to antioxidant defense. Oxidative stress disrupts essential cellular functions and is implicated in diseases, including stroke, head trauma, and chronic neurodegenerative diseases, as well as aging.

ROS and antioxidants

ROS are highly reactive and generally short-lived molecules that are O_2 -derived free radicals and reactive nonradical species, of which superoxide anion ($O_2^{\bullet-}$), hydroxyl radical ($\bullet OH$), and the nonradical species hydrogen peroxide (H_2O_2), plus some of their reaction products, including peroxynitrite, are most common (Fig. 1). Mitochondria are thought to be the major intracellular source of ROS in most mammalian cells. The respiratory chain is localized in the inner membrane of the mitochondrion and is the main source of superoxide anion in many settings. Among components of the respiratory chain, complex I and III are the main sites of superoxide anion production (42, 90, 95, 117). During respiration, an estimated 1%–2% of the O_2 consumed gains an extra electron and is reduced to $O_2^{\bullet-}$ (22), which can subsequently be converted to H_2O_2 (20). $\bullet OH$, a highly ROS, is

produced from H_2O_2 through the Fenton or Haber-Weiss reactions. In addition to mitochondrial sources, ROS can be produced by other pathways, including the endoplasmic reticulum (ER), where ROS are generated concomitant with oxidative protein folding (110), the NADPH oxidases (15), xanthine oxidase (60), and other oxidases. ROS cause cell injury through oxidation of lipids, protein, DNA, and RNA.

Under physiologic conditions, production of ROS is not harmful to cells, as antioxidant systems exist intracellularly and extracellularly to detoxify ROS and protect cells from oxidative damage. Antioxidant defense systems include both enzymatic and nonenzymatic antioxidants. Enzymatic antioxidants include superoxide dismutases (SODs), glutathione peroxidase (GSHPx), catalases (CATs), and peroxiredoxins (PRDXs) (99). SODs comprise a family of metal-containing proteins that catalyze dismutation of $O_2^{\bullet-}$ to form H_2O_2 and O_2 (5, 76, 99). Among the SOD family members, SOD1/CuZn-SOD is a copper- and zinc-containing homodimer, primarily localized in the cytoplasm; SOD2/MnSOD is a manganese-containing enzyme exclusively localized in mitochondria; and SOD3/ECSOD is a copper- and zinc-containing tetramer, present largely in the extracellular space (204). H_2O_2 produced by SODs is also harmful to cells, and is converted to the end product water mainly by GSHPx, CATs, or PRDXs (76, 99). GSHPx-1, present in the cytoplasm and mitochondria of most cells, inactivates peroxides using glutathione as a source of reducing equivalents. In addition to antioxidant enzymes, nonenzymatic antioxidants such as glutathione, NAD(P)H, vitamin C, vitamin E, uric acid, and bilirubin play important roles in the scavenging of ROS.

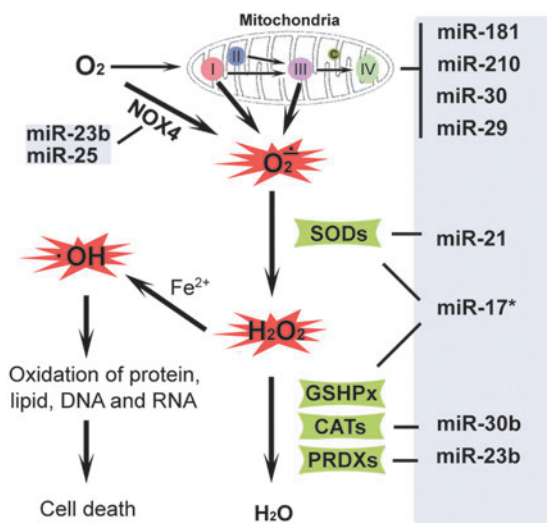


FIG. 1. Reactive oxygen species (ROS) metabolism and regulation by miRNA. Excessive amounts of superoxide anion ($O_2^{\bullet-}$) are produced in mitochondria, mainly through complex I and III, during ischemia–reperfusion. Superoxide dismutase (SOD) detoxifies $O_2^{\bullet-}$ to hydrogen peroxide (H_2O_2), which is converted to water (H_2O) by catalase (CATs) or glutathione peroxidase (GSHPx). Hydroxyl radicals ($\bullet OH$), produced from H_2O_2 through the Fenton or Haber-Weiss reactions, cause cell injury through oxidized lipid, protein, DNA, and RNA. On the right side, miRNAs reported to target mitochondrial protective proteins and antioxidative enzymes are indicated. To see this illustration in color, the reader is referred to the web version of this article at www.liebertpub.com/ars

Immediate increase of ROS after stroke

During brain ischemia–reperfusion, multiple detrimental processes occur concurrently, including overproduction of oxidants, inactivation of detoxification systems, and consumption of antioxidants. These changes disrupt the brain's normal antioxidant defenses (27, 32). Although many ROS have very short half-lives and are difficult to measure directly in the intact brain, several useful techniques have been developed. Electron paramagnetic resonance spectroscopy and hydroxyl radical trapping with salicylate and subsequent analysis by high performance liquid chromatography and electrochemical detection have shown that a rapid increase in ROS occurs during and following ischemia. Hydroxyl radical production was detected in the brain during occlusion and following reperfusion (24, 141, 200). These researchers further demonstrated that mitochondria are an important source of these hydroxyl radicals (141). Oxidative stress has also been demonstrated in cerebral ischemia using hydroethidine (HET), or by measuring the oxidized products of nucleic acid, lipids, or protein (32). Using HET and live cell imaging, we found that ROS increased immediately after ischemia-like stress in cultured primary neural cells (126). ROS generation was readily detected using HET after both focal and global cerebral ischemia (79, 115, 194).

In addition to increased production of ROS, cerebral ischemia also impairs scavenging. Endogenous MnSOD generation was shown to be reduced after ischemia, further aggravating oxidative brain damage (77). SODs have been demonstrated to protect against cerebral ischemic injury (26, 83, 89, 115). Overexpression of SOD1 was protective in *in vivo* cerebral ischemia models (28, 89, 199). Several

laboratories, including ours, have found that overexpression of SOD2 also protects and reduces brain infarction volume after focal ischemia (80) and CA1 delayed neuronal death after global cerebral ischemia (194). Astrocytes have a central role in scavenging ROS because they contain high levels of antioxidants and can initially maintain adenosine triphosphate levels *via* glycolysis (4, 165). Astrocyte cultures from transgenic mice overexpressing SOD1 show increased resistance to xanthine oxidase/hypoxanthine and the superoxide generator, menadione (33). We found earlier that vulnerability to glucose deprivation injury correlates with glutathione levels (137) and vulnerability to oxidative injury increases with age in astrocytes (138).

Immune response to stroke

Cerebral ischemia engages both innate and adaptive immunity, the two main branches of the vertebrate immune system (1). The innate immune system responds quickly to specific molecular patterns and prepares the adaptive immune response by initiating the inflammatory process. The adaptive immune response leads to generation of antigen-specific lymphocytes, which respond to, and retain over time, long-lasting immunity against specific antigens. Cerebral ischemia induces a rapid, localized innate inflammatory response, which contributes to the early phase of irreversible infarction, and which also includes induction of early immunodepression in the days after a stroke, as well as some signs of long-term proinflammatory activation in the brain [for reviews, see Refs. (8, 14, 40, 166, 189)]. Given both the immediate/innate and sustained/adaptive nature of the immune response to stroke, modulation of different immune mediators may represent a therapeutic strategy targeting the early (necrotic) phase, the later (apoptotic) phase of neuronal cell death following cerebral ischemia–reperfusion, and the longer term recovery phase. However, much remains to be learned about the immune response to stroke.

The immune response is an important element contributing to the fate of the ischemic brain, both early and during long-term recovery. The absence of T cells has been shown by several groups to reduce ischemic injury, although the extent of reperfusion may be important to this effect (193). Paradoxically, poststroke immune suppression is known to render stroke patients vulnerable to infections, including pneumonia and sepsis, acting, in part, by activation of the $\alpha 7$ nicotinic acetylcholine receptor to inhibit neutrophil and macrophage accumulation and function (91). Increased sympathetic activation and impairment of the hypothalamic/pituitary/adrenal axis lead to a reduction in T and B lymphocytes, thereby increasing the risk of diminished neurological outcome and death (78). The immune response to stroke has been extensively reviewed (14, 71, 78), so only those factors directly related to oxidative stress, mitochondria, and miRNAs will be considered in this study. In response to cerebral ischemia, immune-responsive cells within the brain (microglia, endothelial cells, astrocytes, and neurons) act immediately to increase the levels of proinflammatory cytokines (8, 38, 45).

Innate immune response after stroke— cytokines and nuclear factor-kappa B

Most notably, tumor necrosis factor alpha (TNF- α), interleukin-1 beta (IL-1 β), and IL-6 appear to be produced by

resident microglia and have been shown to be key inflammatory mediators contributing to tissue injury in both human and experimental models of stroke (92) (Fig. 2). TNF- α mediates many physiological and pathological cellular processes, including acute and chronic inflammation, infection, and apoptosis (171), whereas IL-6 has been shown to be a strong predictor of early neurological deterioration after stroke and final volume of infarct (25). These cytokines also inhibit mitochondrial function (16, 161), contributing to the impairment of mitochondrial function and increase in oxidative stress following ischemia. These inflammatory cytokines increase within the therapeutic window (<4.5 h) after the onset of experimental stroke (187), but remain elevated for up to 72 h, likely due to persistent activation of microglia (8). A key element of microglial-mediated inflammation is activation of the master inflammatory transcription factor nuclear factor-kappa B (NF- κ B), which also plays a role in the control of apoptosis (59, 66) (Fig. 2).

NF- κ B is a family of dimeric transcription factors that regulate the transcription of hundreds of genes in a coordinated manner in response to an inducing signal. In resting

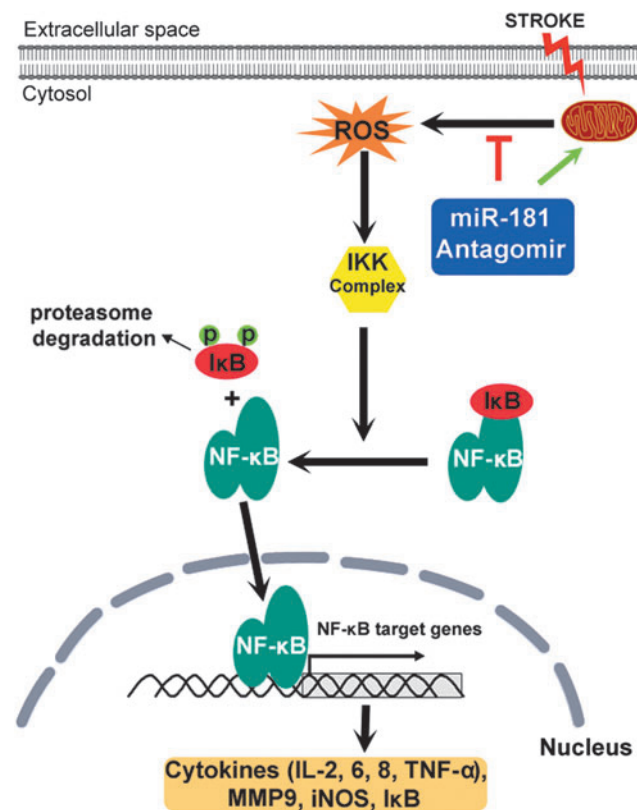


FIG. 2. Nuclear factor-kappa B (NF- κ B) proinflammatory signaling pathway and regulation by miR-181. NF- κ B, a dimer often consisting of p50/p65 subunits, is normally resident in the cytosol and is maintained in an inactive form by its inhibitor I κ B. Stroke stimulates mitochondria to release ROS that activate the I κ B kinase (IKK) complex. The activated IKK complex phosphorylates I κ B and initiates its ubiquitination and degradation, freeing NF- κ B to translocate to the nucleus, and binds the promoters of genes expressing proinflammatory cytokines, I κ B, and other targets. miR-181 interacts with this pathway at multiple points. To see this illustration in color, the reader is referred to the web version of this article at www.liebertpub.com/ars

cells, NF- κ B is found primarily in the cytosol bound to its inhibitor—I κ B proteins. Upon stimulation by cytokines or other inducers, I κ B proteins are targeted for proteasomal degradation by the I κ B kinase. Once I κ B degrades, NF- κ B translocates to the nucleus and binds DNA at κ B sites in the regulatory region of proinflammatory genes and promotes their transcription (49, 61). Its target genes include its own inhibitors and other regulatory proteins that form a complex network that tightly regulates the dynamic response and determines which of the downstream genes are transcriptionally activated. An ordinary differential equation computational model of NF- κ B activation specific for microglia has been developed recently to better understand the regulation of NF- κ B at a systems level in this individual cell type (151).

Adaptive immune response after stroke and the role of cytokines

The adaptive or acquired immune response maintains a sustained response to specific antigens (Fig. 3). Support for involvement of adaptive immunity in stroke outcome is de-

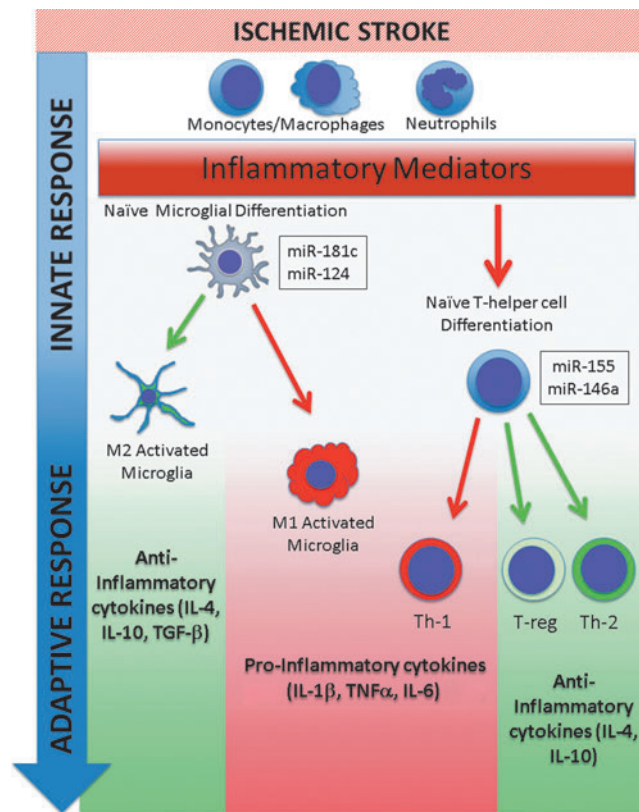


FIG. 3. microRNAs modulate the immune response to stroke. Immediately following stroke, the innate immune system triggers a localized inflammatory response, which then activates the adaptive immune response. The adaptive immune response can promote a proinflammatory state, exacerbating outcome, or can inhibit proinflammatory activation, depending on microglial and T-helper cell subtype differentiation, and local environmental cues. To date, several miRNAs (miR-124, miR-146a, miR-155, and miR-181c) appear to modulate both the innate and adaptive immune responses to stroke and may provide a therapeutic avenue for improving clinical outcome. To see this illustration in color, the reader is referred to the web version of this article at www.liebertpub.com/ars

rived from studies investigating the role of lymphocytes in models of focal cerebral ischemia. Ischemia triggers infiltration of lymphocytes into the ischemic brain, which contribute to injury (48, 52). Lymphocyte-deficient mice are protected from ischemic damage (52, 70, 87). The protection has been attributed to the absence of T cells, as lymphocyte-deficient mice supplemented with reconstituted T cells, but not B cells, are no longer protected from injury. Undifferentiated T-helper lymphocytes have the capacity to differentiate into proinflammatory Th1 or anti-inflammatory Th2 and T-regulatory (T-reg) T-helper phenotypes, and increased Th2 induction appeared protective (64, 188). Recent work suggests that altering the ability to induce Th1 and Th2/T-reg lymphocyte phenotypes plays a large role in the outcome after stroke. The absence of T-regs increased delayed brain damage after stroke and worsened functional outcome (98). Gu *et al.* recently demonstrated that mice with impaired Th1 immunity were protected from experimental cerebral ischemia, while decreased Th2 polarization aggravated brain injury (52, 192). This effect appears to be due to alterations in the expression profile of an array of anti-inflammatory mediators associated with the Th2/T-reg response, including IL-4, IL-10, and transforming growth factor beta (TGF- β), a pleiotropic growth factor found in activated microglia and macrophages (63, 98, 100).

In addition to altering T-cell polarization, cytokine production has recently been shown to contribute to polarization of macrophages and microglia in the evolution of the inflammatory response after stroke. When stimulated with lipopolysaccharides or interferon- γ , macrophages and microglia undergo transformation to an M1 phenotype characterized by production of proinflammatory cytokines, while stimulation with IL-4 or TGF- β leads to a neuroprotective M2 phenotype. When markers of macrophage/microglial activation were characterized in a model of permanent focal ischemia, expression was shown to vary with time after occlusion, consistent with early M2 polarization and subsequently followed by later M1 polarization and phagocytic morphology (140). A second study investigating polarization of macrophages and microglia after transient middle cerebral artery occlusion (MCAO) documented a similar evolution over time (67).

Anti-inflammatory cytokines appear to protect neurons both directly and indirectly by altering the response of immune cells in the brain and periphery. Male IL-4 knockout mice had a greater Th1/Th2 ratio, larger infarct volume, and worsened neurologic outcome following MCAO compared with wild-type mice (192). Intracerebroventricular administration of exogenous IL-4 reduced injury to that seen with wild-type mice and decreased activation of immune-responsive microglia and astrocytes adjacent to the infarct. A recent study by Engelbertsen *et al.* demonstrated that an increase in the Th2 population and circulating IL-4 levels in humans are independently associated with reduced levels of myocardial infarction and stroke (43). Furthermore, whereas IL-10 reduces the proinflammatory response after ischemic stroke by acting on glia, endothelium, and immune cells, it has also been shown to provide protection to primary cortical neurons in culture by activation of the AKT/PI3K prosurvival pathways (150).

TGF- β has been shown to be neuroprotective both *in vitro* and *in vivo* (65). The spatial and temporal expression of TGF- β in activated microglia and macrophages within the ischemic penumbra suggests that microglial-derived TGF- β

functions both in inhibiting cell death and in promoting neuronal regeneration following focal cerebral ischemia (41, 182). These findings suggest that promoting a Th2/T-reg adaptive response may serve to inhibit a proinflammatory response and augment an anti-inflammatory response, thereby providing neuroprotection after stroke, a theory supported by findings using neuropeptides to induce anti-inflammatory activation in other neuroinflammatory and neurodegenerative models (184). However, the deleterious effect of peripheral immune suppression also needs to be taken into account in developing strategies that could also increase immune suppression following stroke. Despite this, lymphocyte-targeted neuroprotection is still an exciting possibility that might simultaneously target multiple immune-responsive bioactive molecules to improve outcome.

Important Roles of Mitochondria in Stroke

Mitochondria are centrally involved in both ischemic injury and recovery of brain tissue after cerebral ischemia due to their major roles in ROS production, regulation of inflammation and apoptosis, and role in neurogenesis (107, 175). This is reflected in observations that mitochondrial protection is associated with reduced brain injury and improved neurogenesis following cerebral ischemia.

Interplay between mitochondrial ROS and inflammation

Ischemia leads to significant mitochondrial dysfunction (156) (Fig. 4). Unsaturation of cytochrome c oxidase at the terminus of the electron transport chain disrupts mitochondrial respiratory function, including the synthesis of ATP, and leads to overproduction of ROS (128) by complex I and III (Fig. 1). ROS interact with NF- κ B at various places within the signaling pathway, and can even have opposing effects on NF- κ B activation in the cytosol *versus* the nucleus [For reviews, see Morgan and Liu (113) and Siomek (159)]. Conversely, NF- κ B has both pro-oxidant inflammatory targets and antioxidant targets. ROS produced by mitochondria can trigger NF- κ B activation (Fig. 2) and synthesis of target messenger RNAs (mRNAs). These include adhesion molecules that promote localization of circulating leukocytes (neutrophils, lymphocytes, and macrophages) to the ischemic region, induction of iNOS, MMPs, and proinflammatory cytokines, as well as maturation of undifferentiated T-helper lymphocytes into a proinflammatory Th1 subtype (Fig. 3), further contributing to the production of inflammatory cytokines (8).

The inflammation triggered by ROS may lead to disruption of mitochondrial homeostasis (148). Activated microglia appear to induce neuronal death *via* mitochondrial dysfunction both *in vitro* (191) and *in vivo* (69), likely mediated by microglial-derived IL-6, TNF- α , and nitric oxide (57, 142, 147). IL-6 augments production of ROS (16), which impair oxidative phosphorylation *via* oxidation of mitochondrial lipids and respiratory enzymes (56, 177). TNF- α induces mitochondrial damage through suppression of mitochondrial complexes I and IV and pyruvate dehydrogenase (149, 161, 205), while nitric oxide inhibits complex IV (21, 51). All of this may explain the secondary mitochondrial failure with longer reperfusion after cerebral ischemia (157). Taken together, these results support the central role of mitochondria in the cascade of ROS and inflammation-induced neurotoxicity.

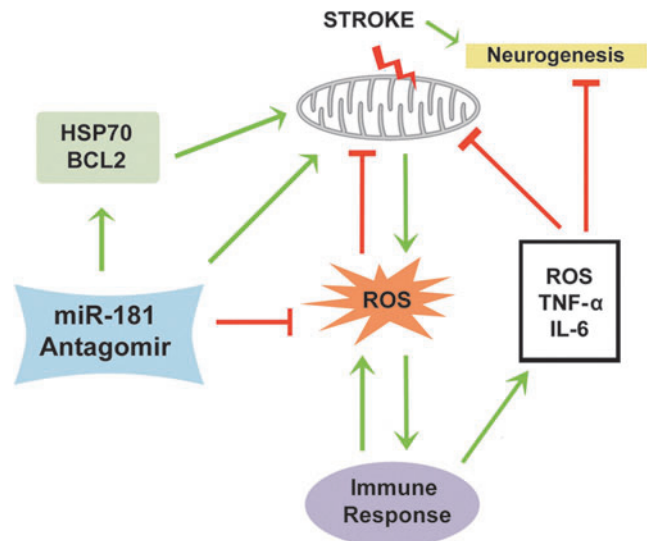


FIG. 4. miR-181 influences immune response, mitochondria, and ROS. Stroke leads to increased proneurogenic signals, but also dysfunction of mitochondria, which inhibits neurogenesis and increases ROS. Overproduction of ROS triggers immune response and the release of inflammatory factors, such as tumor necrosis factor alpha (TNF- α) and IL-6 as well as further increasing ROS, causing additional mitochondrial damage. miR-181 antagomir can increase mitochondrial protective proteins (HSP70 family members and BCL2 family members) to reduce ROS production and inhibit inflammation, thereby efficiently regulating multiple ischemic cell death pathways and facilitating neurogenesis. To see this illustration in color, the reader is referred to the web version of this article at www.liebertpub.com/ars

Mitochondria and neurogenesis

Following central nervous system development, the birth of neurons in the adult brain is restricted to two regions, the subventricular zone and the subgranular zone of the hippocampal dentate gyrus (47). Recent studies have suggested that this neurogenesis is important in the consolidation of memories (86), and that disruption of neurogenesis *via* irradiation is detrimental to memory and cognitive function (112, 145). After stroke, although neural progenitor cells proliferate, very few survive to replace the lost neurons (7). Furthermore, increasing neurogenesis using factors such as fibroblast growth factor 2 promotes poststroke functional recovery (55, 94).

Recent studies suggest that mitochondrial function may have a significant direct impact on neurogenesis. Neural progenitor cells from aged brains, which have impaired neuronal production, have decreased mitochondrial proteins and oxygen consumption (162). Notably, mitochondrial DNA damage results in attenuated neurogenesis. Neural progenitor cells lacking 8-oxoguanine glycosylase, a protein needed for repair of mitochondrial DNA damage, have decreased neurogenesis and increased astrogenesis (180), likely due to decreased mitochondrial metabolism (181). In addition, embryonic stem cells with mutations in mitochondrial DNA exhibit impaired neuronal differentiation (84). Multiple studies have found that alterations in Krebs cycle proteins are associated with dysfunctional neurogenesis. Mutations in the electron transfer flavoprotein lead to attenuated neurogenesis *via* the PPARG-ERK pathway (160), and mice lacking either

TABLE 1. miRNA INVOLVED IN REDOX AND IMMUNE RESPONSE AND THEIR TARGETS

miRNAs	Targets	References
miR-1	HSP60	(135)
miR-15b	Arl2, BCL2	(122, 153)
miR-17*	SOD2, GPX2, TrxR2	(197)
miR-17-92	PTEN	(103)
miR-21	SOD3, TNF- α	(208)
miR-23b	PRDX3, NOX4	(62, 72)
miR-24-2	BCL2	(158)
miR-25	MCU, NOX4	(46, 111, 173)
miR-29a	PUMA	(133)
miR-29b	BCL-w, BIM, BMF, HRK, PUMA, BAK	(88, 152)
miR-30a	P53	(96)
miR-30b	Catalase, p53	(58, 96)
miR-30e	UCP2, BCL2	(75, 82)
miR-34a	BCL2	(82)
miR-92a	BIM	(123)
miR-124a	JAG1	(104, 143)
miR-125b	BCL2, MCL1, BAK1	(154, 206)
miR-128	BAX	(3)
miR-141	Slc25a3	(12)
miR-145	Bnip3	(97)
miR-146a	TRAF6, IRAK1	(18, 73, 210)
miR-155	SOCS1	(108, 125, 168)
miR-181a	BCL2, MCL1, GRP78, c-Fos,	(93, 129, 130, 190)
miR-181a-1*	BCL2	(82)
miR-181b	Importin- α 3	(164)
miR-181c	Mt-COX1	(207)
miR-181d	BCL2	(183)
miR-195	BCL2	(158)
miR-210	ISCU1/2, SDHD	(29, 30, 116, 144)
miR-320	HSP20	(146, 186)
miR-338	COXIV, ATP5G1	(9, 10)
miR-365-2	BCL2	(158)
miR-378*	HSP72	(170)
miR-451	BCL2	(119)
miR-484	Fis1	(179)
miR-491-5p	BCL-xL	(53)
miR-497	BCL2, BCL-w	(198, 201)
miR-499	Calcineurin	(178)
miR-711	HSP72	(170)
miR-743	Mdh2	(155)
miR-885-3p	BCL2	(68)

dihydrolipoamide dehydrogenase (Dld) or dihydrolipoyl succinyltransferase (E2k), subunits of the essential mitochondrial enzyme oxoglutarate dehydrogenase complex, have decreased hippocampal neuroblasts compared with wild-type mice (23). Additionally, P19 cells deficient in the mitochondrial protein, frataxin, exhibit increased apoptosis and decreased neuronal differentiation following induction of neurogenesis (136).

ROS and inflammation are detrimental to neurogenesis (112, 145, 175). NeuroD6, a transcription factor that promotes survival of newborn neurons, acts by preserving mitochondrial function after exposure to ROS (172) and increasing mitochondrial mass (13). Several studies have also shown that proinflammatory factors produced by activated microglia, such as IL-6, TNF- α , and nitric oxide, lead to mitochondrial dysfunction in progenitor cells and subsequent inhibition of neurogenesis (175). Our laboratory has directly examined the influence of mitochondrial dysfunction on neurogenesis (176).

Treatment of progenitor cells *in vitro* with antimycin-A, a mitochondrial inhibitor, significantly decreased expression of doublecortin (Dcx) - expressing immature neurons and MAP2-expressing mature neurons. Similarly, conditioned media from activated microglia decrease Dcx-positive cells, while overexpression of the mitochondrial-specific heat-shock protein (HSP) GRP75 partially rescues these cultures, suggesting a significant role of mitochondrial dysfunction in inflammation-induced neurogenesis impairment.

Protecting mitochondrial function

Two families of well-known cell protective proteins, the HSP70 family of protein chaperones and the antiapoptotic BCL2 protein family, are also related to mitochondrial function. Both have also been shown to protect the brain from ischemia when overexpressed. HSP72, the inducible cytosolic member of the HSP70 family, is known to protect from both necrotic and apoptotic cell death, and affects several different steps in the apoptosis cascade, including reduction of mitochondrion-dependent apoptotic signaling [see Fig. 1 in (50)]. Several studies have shown that overexpression of GRP75/HSP75/mortalin, the mitochondrial-specific member of the HSP70 family, reduces damage in both *in vitro* and *in vivo* models of ischemic stroke (174, 195). The mechanisms of GRP75 protection against ischemia include attenuated oxidative stress, preservation of mitochondrial function, inhibition of apoptosis, and enhanced neurogenesis. For more detailed information on the protective effect of GRP75 on ischemic brain injury and the mechanisms involved, the reader is referred to a recent book chapter (185). GRP78/HSP78/BIP, another member of the HSP70 family, is largely localized to the ER and is a master regulator of the unfolded protein response. Overexpressing GRP78 protects neural cells against ischemic injury, preserves the respiratory activity and mitochondrial membrane potential, and reduces ROS production after ischemia-like stress (132). Interestingly, GRP78 relocates from ER to mitochondria shortly after stress (134, 163). It is increasingly accepted that the HSP70 family members, together with other molecular chaperones, are organized in a chaperoning network serving as a basic regulatory mechanism in diverse cellular functions [for a recent review, see Ouyang and Giffard (134)].

The BCL2 protein family (2) is a principal regulator of apoptosis through mitochondrial membrane integrity, function, and apoptotic signaling (139). The BCL2 protein family consists of three subgroups: the prosurvival proteins (BCL2, BCLxL, BCLw, MCL1, and A1), the multidomain proapoptotic proteins (BAX and BAK), and the BH3 domain-only proapoptotic proteins (BIM, PUMA, BID, BAD, BIK, BMF, HRK, and NOXA). In response to stress, the decision whether or not to undergo apoptosis is determined by interactions between these three groups. BH3-only proteins are upregulated in response to apoptotic stimuli and transduce the damage signal. In addition, they inhibit antiapoptotic proteins and activate proapoptotic proteins resulting in mitochondrial outer membrane permeabilization, cytochrome c release, and activation of caspases to initiate apoptosis (202). Overexpressing prosurvival BCL2 family members protects against cerebral ischemia *in vivo* (85, 209) and *in vitro* (126). Together, these results show that maintaining mitochondrial function is integral for neuroprotection [for review, see Ouyang and Giffard (127)].

Interestingly, HSP72 and BCL2 share a close relationship. HSP72 overexpression increases the expression of BCL2 *in vitro* and *in vivo* (81). The HSP70 family members and the BCL2 family members coexist in the mitochondrion-associated ER membrane, and affect ER and mitochondrial calcium homeostasis after cerebral ischemia [(134) and Fig. 2 in (131)].

miRNAs in Stroke

Multitarget therapeutic strategies offer a potential solution to the translational barrier that has burdened research in the treatment of stroke. Given that a single miRNA can theoretically bind to and inhibit a large number of related targets, the potential for miRNA modulation in cerebral ischemia is promising. miRNAs are small (~22 nucleotides) noncoding RNAs that participate in mRNA translational regulation. Despite their relatively recent discovery, it is already known that miRNAs play important roles in ischemic disease. Changes in miRNAs with ischemic brain injury have been identified using miRNA profiling techniques in a rat focal cerebral ischemia model (39, 74, 102), in forebrain ischemia (203), and in stroke patients (167). Recently, a few studies have evaluated the significance of individual miRNAs and their regional expression in ischemic brain damage [for a recent review, see Ouyang *et al.* (131)]. This section will focus on miRNA modulation of ROS, inflammation, and mitochondrial function.

miRNAs modulate cellular redox state

miRNAs have recently been found to be critical regulatory molecules in cellular redox regulation (Fig. 1). Mitochondria are the main site of ROS production and Shi and Gibson (155) reported that post-transcriptional upregulation of the mitochondrial enzyme malate dehydrogenase by oxidative stress in a neuronal cell line is mediated by miRNA-743a, providing insight into possible roles of miRNAs in oxidative stress. miR-338 regulates multiple mitochondrial mRNAs that encode subunits of the oxidative phosphorylation machinery (9). miR-145 protects cardiomyocytes against H₂O₂-induced apoptosis through targeting the mitochondrial apoptotic pathway (97). In addition to regulation of mitochondrial targets, there are already a few studies noting that miRNAs regulate other sources of ROS. Type 4 NADPH oxidase (NOX4) is a direct target of miR-23b in the spinal cord (72) and of miR-25 in the heart and kidney (46, 173). miRNAs also influence the ROS defense system. miR-21 inhibits the metabolism of superoxide to H₂O₂ by directing attenuating SOD3 or by indirectly reducing SOD2 levels (208). In an epithelial cell line, miR-30b regulates ROS levels by targeting CATs (58). miR-17* suppresses tumorigenicity of prostate cancer by inhibiting mitochondrial antioxidant enzymes such as MnSOD and GSHPx (197). In addition, miR-23b downregulates PRDX3 in human prostate cancer (62). miR-210, nicknamed “the hypoximir,” is strongly induced in response to hypoxia and represses mitochondrial respiration, in addition to several other important effects (30).

Oxidative stress can also alter the miRNA expression profile (196). This suggests they can be part of a feedback mechanism on overall ROS regulation. Possible feedback between miRNA and ROS has recently been reviewed (109). Nelson *et al.* reviewed accumulating evidence for the roles of

miRNAs and discussed a possible involvement of miRNA oxidation in the pathogenesis of neurodegenerative disorders (120). It has been hypothesized that RNA oxidation causes aberrant expression of miRNAs and proteins, subsequently initiating inappropriate cell fate choices (124).

Direct roles for miRNAs in neurogenesis

Several recent articles have highlighted potential ways in which miRNA manipulation may influence neurogenesis. During normal development, a specific miRNA profile is expressed in the cerebral cortex, suggesting a role for miRNAs in brain maturation (121). The function of miRNAs in poststroke neurogenesis has also been examined. Following focal cerebral ischemia in rats, progenitor cells in the subventricular zone express decreased levels of miR-124a (104). The same study showed that, *in vitro*, overexpression of miR-124a in progenitor cells decreases expression of the Notch ligand JAG1 and subsequently decreases proliferation and increases neuronal differentiation. The miR-17-92 cluster is also overexpressed in adult mouse neural progenitor cells after stroke, which increases proliferation *in vitro* (103). Interestingly, the miR-17-92 cluster targets phosphatase and tensin homolog (PTEN), and is increased by the neural patterning protein Sonic hedgehog (103).

miRNAs modulate the immune response

Recent work has begun to reveal many ways in which miRNAs regulate the immune system, including regulating the development of immune cells as well as modulating the innate and adaptive immune responses (106) (Figs. 2 and 3). Two well-studied miRNAs appear to coordinate both the innate and adaptive arms of the immune response (Fig. 3). miR-155 is rapidly induced in mice treated with the strongly proinflammatory agent lipopolysaccharide, and appears to augment the expression of innate inflammatory cytokines *via* repression of the negative regulators of inflammation, suppressor of cytokine signaling 1 (SOCS1) (6). However, miRNA-155 also promotes an adaptive proinflammatory immune response by coordinating T-cell development (125). A second miRNA, miR-146a, appears necessary in suppressing inflammatory cytokine production, including IL-6, IL-1 β , and TNF- α (18). The miR-146a promoter contains two consensus NF- κ B sites that are essential for the transcriptional activation of the miR-146a gene in response to inflammatory stimuli [for a recent review, see Boldin and Baltimore (19)]. By repressing TNF receptor-associated factor 6 (TRAF6) and IL-1 receptor-associated kinase 1 (IRAK1) molecules, miR-146a acts as a negative regulator of the NF- κ B pathway and an important regulator of toll-like receptor signaling (19). On the other hand, miR-146a-deficient mice display a spectrum of immunoproliferative and autoimmune diseases (18), indicating a regulatory role in lymphocyte proliferation and differentiation, contributions that serve to define the adaptive immune response.

T-helper lymphocytes serve to both activate and suppress inflammatory components of the immune system, and preliminary research suggests that miRNAs play an important role in the development, differentiation, and activation of specific subpopulations of T-helper lymphocytes [for review, see Contreras and Rao (36)]. Early observations from a global knockout of Dicer, a key regulatory enzyme in the processing

of miRNAs, indicated that miRNAs were necessary in T-cell development and differentiation (35, 114). Subsequently, Liston *et al.* demonstrated that specific knockout of anti-inflammatory T-reg cells leads to a lethal and severe autoimmune disease in mice (101). Interestingly, both miR-155 and miR-146a appear to regulate T-reg function. For example, miR-155/T-reg-deficient mice have impaired survival compared with wild-type T-reg mice (108) and miR-146a knockout mice display a hyperinflammatory phenotype (18, 210). These studies highlight the relevance of miRNAs in differentiation of the T-helper lymphocyte lineage, and offer insight into potential neuroprotective therapeutic strategies whereby modulation of specific miRNAs effects systemic immune signaling and inflammation. Involved in redox and immune response, miRNAs and their targets are summarized in Table 1.

In addition to systemic therapeutic strategies, several miRNAs appear to be selectively upregulated in the brain subsequent to inflammation [for review see Thounaojam *et al.* (169)]. The miR-181 family is one of the key regulators of immune response (31). In addition to its established role in T- and B-cell development, miR-181 also affects human natural killer cell development by regulating Notch signaling (34). miR-181a inhibited the secretion of IL-6 and TNF- α , and up-regulated IL-10, an important anti-inflammatory cytokine, targeting c-Fos (190). miR-181b has been identified as an essential regulator of downstream NF- κ B signaling, endothelial cell activation, and vascular inflammation *in vivo* by directly targeting importin- α 3, a protein critical for NF- κ B nuclear translocation (164). miR-181 is also implicated in controlling viral infection (54) and plays an important role in systemic lupus erythematosus pathogenesis (93). The miR-181 family also targets the mitochondrial protective system as discussed below in the miRNAs Regulate Mitochondrial Function section.

miRNAs are thought to have distinct functions in different cell types. As described above, activated microglia play a role in disruption of mitochondrial homeostasis, contributing to neurotoxicity *via* production of proinflammatory cytokines such as TNF- α . Ponomarev *et al.* demonstrated that miR-124 was specifically expressed in quiescent microglia, but not in peripheral monocytes, and was subsequently downregulated in activated microglia (143). They identified a CCAAT enhancer-binding protein thought to play a role in microglial activation as a potential target. Recently, Zhang *et al.* reported TNF- α as a potential target for miR-181c in a model of microglial-mediated neurotoxicity, whereby inhibition of miR-181c decreased neuronal apoptosis induced by TNF- α (207).

Astrocytes contribute to neuroprotection by several mechanisms (11). Tarassishin *et al.* observed a decrease in miR-155 in astrocytes concurrent with suppression of proinflammatory cytokines, suggesting a proinflammatory role for miR-155 (168). More recently, Iyer *et al.* reported that the expression of miR-146a in human astrocytes was significantly upregulated by IL-1 β (73). Interestingly, as noted above, miR-146a and miR-155 are also implicated in the differentiation and maturation of anti-inflammatory T-helper lymphocytes. Moreover, miRNAs are emerging as significant upstream modulators of neuropsychiatric disorders that contain a neuroinflammatory component, such as Alzheimer's disease, Parkinson's disease, Huntington's disease, multiple sclerosis, and traumatic brain injury (36). Exploration of miRNAs in these disorders may yield further

insight into the role miRNAs play in the pathogenesis of immune-mediated inflammation in the CNS after stroke.

miRNAs regulate mitochondrial function

In recent years, multiple studies have shown that miRNAs target a variety of mitochondrial and mitochondrial-associated proteins and may be a useful tool for the manipulation of mitochondrial function (Fig. 4). miR-181c is encoded in the nucleus, assembled in the cytoplasm, translocated into the mitochondria, and targets cytochrome c oxidase subunit 1 (mt-COX1) mRNA (37). It causes electron transport chain complex IV remodeling and influences mitochondrial function. Some other miRNAs, such as the miR-30 family and miR-210, target multiple mitochondrial proteins and could impact mitochondrial functioning using several mechanisms. miR-30a and miR-30b decreases p53 and mitochondrial fission *via* dynamin-related protein-1 (96), while miR-30e targets mitochondrial uncoupling protein 2, contributing to kidney fibrosis (75).

miR-210 has multiple mitochondrial-related targets, such as the iron-sulfur cluster assembly enzyme (116) and succinate dehydrogenase complex subunit D, a component of the electron transport chain (144). miRNAs also target several genes required for ATP production, such as solute carrier family 25 member 3 [miR-141, (12)], COX-IV [miR-338, (10)], and ADP-ribosylation factor-like protein 2 [miR-15b, (122)]. Additional miRNAs decrease production of proteins that affect susceptibility to apoptosis, such as the mitochondrial calcium uniporter [miR-25, (111)], the calcineurin catalytic subunit [miR-499, (178)], and mitochondrial fission Fis1 protein [miR-484, (179)].

Thus, miRNAs can have a substantial impact on mitochondrial functioning. As mitochondria have multiple essential roles in the cell, these miRNAs may be used to alter cell functioning in both normal and injury/disease states, including brain ischemia. As described below, manipulation of mitochondrial proteins by miRNAs is a promising therapeutic tool to encourage neurogenesis, HSP-induced protection, and antiapoptotic mechanisms in the ischemic brain.

miRNAs and mitochondrial protective proteins

Recent research has shown that several miRNAs that target HSPs may be manipulated to improve the outcome after injury. miR-1, which exacerbates cardiac ischemia-reperfusion injury, decreases expression of HSP60 (135). Cardiac ischemia preconditioning, which protects against ischemic injury, decreases miR-378* and miR-711, both of which target the HSP70 family (170). Overexpression of miR-320 in cardiomyocytes enhances ischemia-reperfusion injury, in part, *via* downregulation of HSP20 (146). Finally, Gefitinib, a drug that decreases HSP72 expression *via* miRNA-mediated mechanisms, exacerbates interstitial lung disease (118).

Research has shown that BCL2 is targeted by multiple miRNAs, including miR-195, miR-24-2, and miR-365-2 (206), miR-125b (154), miR-885-3p (68), miR-181a-1*, miR-30e, and miR-34a (82), miR-451 (119), and miR-181d (183). Chronic exposure of neurons to alcohol increases the levels of miR-497, leading to apoptosis by targeting BCL2 (198). miR-15b, which is upregulated 72 h following MCAO, targets BCL2 as well (153). BCL-xL, another antiapoptotic member of the BCL2 family, is targeted by miR-491-5p (53).

In addition, proapoptotic BAX is targeted by miR-128 (3) and BIM is decreased by miR-92a (153). We found that miR-29a targets BH3-only protein PUMA and reduces neuronal vulnerability to forebrain ischemia (133). In contrast, increasing miR-29b had the effect of promoting neuronal cell death in focal ischemia by inhibiting BCL-w, an antiapoptotic member of the BCL2 protein family (152).

A few miRNAs target multiple members of the BCL2 family. In addition to BCL2 (154), miR-125b decreases both proapoptotic BAK1 along with the antiapoptotic gene MCL1 (206). miR-497 also targets BCL-w in addition to BCL2 in Neuro-2A cells (201). Knockdown of miR-497, which targets both BCL2 and BCL-w (201), is protective against MCAO-induced neuronal death. Our laboratory has focused extensively on miR-181a, which downregulates both BCL2 and MCL1, antiapoptotic members of the BCL2 family. Indeed, overexpression of miR-181a in astrocytes subjected to glucose deprivation decreases mitochondrial membrane potential, increases ROS formation, and increases cell death (129). A group has reported that miR-29b is activated during neuronal maturation and targets several proapoptotic genes, BIM, BMF, HRK, PUMA, and BAK in the BCL2 family (88). In addition to targeting antiapoptotic members of the BCL2 family, miR-181 also targets the ER protein GRP78/HSP78. In our laboratory, we have found that knockdown of miR-181a, which increases in the ischemic core during reperfusion following transient MCAO, increases GRP78 levels in the brain and significantly decreases the infarct size following stroke (130). As miR-181a also targets BCL2 and MCL1 (129), it is likely that the protective phenotype of mice treated with the miR-181a antagomir results from enhanced protein levels of GRP78, BCL2, and MCL1. These data show that miRNAs targeting HSPs and/or BCL2 family members are promising candidates in the treatment of stroke by enhancing the mitochondrial function.

Future Directions

miRNAs may have greater therapeutic potential as candidates for the treatment of stroke than therapies targeting a single gene because of their faster post-transcriptional effect and their ability to simultaneously regulate many target genes. A single miRNA, such as miR-181, can simultaneously regulate target genes affecting ROS, mitochondrial metabolism, apoptosis, and inflammation regulatory pathways, all key players in the mechanisms of cerebral ischemia (Fig. 4). Another exciting possibility with miRNAs is targeting plasticity and recovery after the acute phase of stroke. miRNAs have been shown to be critical in neuronal development, and there is potential that plasticity could be increased following stroke by, for example, encouraging neurite outgrowth using miRNAs such as miR-320 (186). Whereas pretreatment using miR-181a (130) and miR-29a (133) was effective in focal and global cerebral ischemia in rodents, testing treatment after the onset of ischemia is an essential step for the development of acute stroke treatment. Several miRNAs are already in clinical trials in liver diseases, suggesting that formulation and administration will be possible in a new disease setting or for a new miRNA target. However, in this regard, delivery into the CNS is often challenging, and remains part of the challenge in the clinical translation of miRNA therapy.

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Address correspondence to:

Dr. Rona G. Giffard
Department of Anesthesia
Stanford University School of Medicine
300 Pasteur Drive S272A and S290
Stanford, CA 94305-5117

E-mail: rona.giffard@stanford.edu

Dr. Yi-Bing Ouyang
Department of Anesthesia
Stanford University School of Medicine
300 Pasteur Drive S272A and S290
Stanford, CA 94305-5117

E-mail: ybouyang@stanford.edu

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Abbreviations Used

Arl2 = ADP-ribosylation factor-like 2
ATP5G1 = ATP synthase
Bnip3 = Bcl2/adenovirus E1B 19kDa-interacting protein 3
CATs = catalase
COXIV = cytochrome c oxidase IV
Dcx = doublecortin
ER = endoplasmic reticulum
Fis1 = mitochondrial fission protein
GPX2 = glutathione peroxidase-2
GSHPx = glutathione peroxidase
H₂O = water
H₂O₂ = hydrogen peroxide
HEt = hydroethidine
HSP70 = heat shock protein 70
IKK = I κ B kinase
IL = interleukin
IRAK1 = IL-1 receptor-associated kinase 1
JAG1 = Jagged-1, a ligand of Notch
MCAO = middle cerebral artery occlusion
MCU = mitochondrial calcium uniporter
Mdh2 = mitochondrial tricarboxylic acid cycle gene
miRNAs = microRNAs
MnSOD = manganese superoxide dismutase, SOD2,
mRNA = messenger RNA
mt-COX1 = cytochrome c oxidase subunit 1
NF- κ B = nuclear factor-kappa B
NOX4 = NADPH oxidase 4
PRDX3 = peroxiredoxin III
PTEN = phosphatase and tensin homolog
ROS = reactive oxygen species
SDHD = subunit D of succinate dehydrogenase complex
Slc25a3 = mitochondrial phosphate carrier
SOCS1 = suppressor of cytokine signaling 1
TGF- β = transforming growth factor beta
TRAF6 = tumor necrosis factor (TNF) receptor-associated factor 6
T-reg = T-regulatory
TrxR2 = thioredoxin reductase-2
UCP2 = mitochondrial uncoupling protein 2