Emerging Role of LncRNAs in Ischemic Stroke—Novel Insights into the Regulation of Inflammation

Yongli Pan 1,2,*
Qingzheng Jiao 2,3,*
Wei Wei 3,4,*
Tianyang Zheng 4,5,*
Xinyu Yang 5
Wenqiang Xin 6,5

1Department of Neurology, Weifang Medical University, Weifang, Shandong, People’s Republic of China; 2Second Department of Internal Medicine, Gucheng County Hospital, Gucheng, Hebei, People’s Republic of China; 3Department of Neurology, Manyang Central Hospital, Manyang, Sichuan, People’s Republic of China; 4Department of Neurosurgery, The First Hospital of Jinlin University, Changchun, Jinlin, People’s Republic of China; 5Department of Neurosurgery, Tianjin Medical University General Hospital, Tianjin, People’s Republic of China

*These authors contributed equally to this work

Abstract: As a crucial kind of pervasive gene, long noncoding RNAs (lncRNAs) are abundant and key players in brain function as well as numerous neurological disorders, especially ischemic stroke. The mechanisms underlying ischemic stroke include angiogenesis, autophagy, apoptosis, cell death, and neuroinflammation. Inflammation plays a vital role in the pathological process of ischemic stroke, and systemic inflammation affects the patient’s prognosis. Although a great deal of research has illustrated that various lncRNAs are closely relevant to regulate neuroinflammation and microglial activation in ischemic stroke, the specific interactional relationships and mechanisms between lncRNAs and neuroinflammation have not been described clearly. This review aimed to summarize the therapeutic effects and action mechanisms of lncRNAs on ischemia by regulating inflammation and microglial activation. In addition, we emphasize that lncRNAs have the potential to modulate inflammation by inhibiting and activating various signaling pathways, such as microRNAs, NF-κB, and ERK.

Keywords: ischemic stroke, long noncoding RNA, microglia, neuroinflammation

Introduction

Approximately 16.67% of people worldwide may experience an ischemic stroke in their lifetime, and such strokes are responsible for almost 6 million deaths and more than 10% of all mortalities each year; moreover, two-thirds of ischemic survivors remain disabled. Despite the thrombectomy and recombinant tissue plasminogen activator (rtPA) being the main accepted treatments, whether neuroinflammation affects the prognosis of ischemic stroke after such treatment remains controversial since stroke-induced inflammation is one of the most vital factors that limits treatment efficiency. Neuroinflammation plays a vital role in the pathological process of stroke, and systemic inflammation affects patient prognosis. Focal cerebral ischemia in animals leads to an inflammatory cascade that includes oxidative stress, excitotoxicity, inflammatory cell activation, and toxic inflammatory mediators, which in turn impair nerve tissue and cells. On the other hand, inflammation contributes greatly to the recovery of damaged tissue and cells by promoting microglia to immediately migrate to the infarction site. In the past one decade, researchers have performed many studies to explore the therapeutic potential of long noncoding RNAs (lncRNAs), which are endogenous ncRNAs >200 nucleotides in length that lack an open reading frame. LncRNAs are considered a key factor in regulating the expression and function of protein-coding genes, and they are involved in different signaling pathways of cellular processes.
such as cell apoptosis, inflammation angiogenesis and autophagy, thereby regulating stroke prognosis. Previous research indicates that modulating lncRNA expression can inhibit microglial activation and improve neurological functions. To date, the literature investigating the interactional relationship between neuroinflammation and lncRNAs in ischemia is still limited, and the mechanisms have also not been estimated accurately. The purpose of this review is to summarize the potential therapeutic effects and pathways of lncRNAs in stroke based on their ability to regulate inflammation.

**Neuroinflammatory Response and Related Mechanisms in Stroke**

Neuroinflammation is integral to the poststroke pathophysiological process and causes the disruption of tissue homeostasis, including acidosis, excitotoxicity mediated by reactive oxygen species (ROS), increased cytoplasmic Ca$^{2+}$ concentrations, loss of glucose and oxygen, complement activation, destruction of the blood–brain barrier (BBB), mitochondrial damage and secondary messengers by resident central nervous system (CNS) glia and endothelial cells. On the other hand, inflammation combines innate and peripheral immune responses involved in physiological brain development and different pathologic conditions, such as neurodegenerative diseases or stroke. In summary, inflammatory cells are classically involved in innate responses and activated within hours and perfectly situated to sense imbalances in the CNS, including natural killer cells, neutrophils, dendritic cells, macrophages, microglia and astrocytes that participate in the secretion of inflammatory chemokines and the selective recognition and clearance of pathogens and toxic cell debris during infection or tissue injury.

During the early phase of stroke, the peripheral immune responses of inflammation initiate immediately at a second massive cascade of inflammation, and different damage-associated molecular patterns (DAMPs), such as high mobility group box 1, heat shock proteins, interleukin-33, purines (ATP and UTP), mitochondrial-derived N-formyl peptides and peroxiredoxins, can gain access to the systemic circulation. These molecules activate pattern recognition receptors on microglia and astrocytes and on brain resident immune cells, and subsequently, the activation of endothelial cells aggravates BBB breakdown, thus allowing peripheral leukocytes to arrive in the injured area. Due to the disruption of the BBB, DAMPs and cytokines induce a response of the immune system in primary and secondary lymphoid organs, which leads to systemic inflammatory response syndrome and activates some inflammatory pathways, such as mitogen-activated protein kinase (MAPK) and nuclear factor kappa-light-chain-enhancer of activated B cells (NF-kB). All these factors can greatly affect the prognosis of patients. Thus, exposing the role and mechanism of inflammation and identifying a treatment for the recovery of stroke have been driving forces for extensive studies in recent decades.

**Significant Role of Long Noncoding RNAs in Cerebral Ischemia**

**Essential Characteristics and Associated Functions of LncRNAs**

LncRNAs are a type of RNA defined as transcripts with a length of >200 nucleotides that are not directly translated into proteins. These transcripts regulate the expression of genes through affecting epigenetics, transcription, and translation, playing important physiological and pathological roles, and participating in various signaling pathways underlying multiple diseases. LncRNAs are located in the nucleus or cytoplasm and regulate the expression of genes at the transcriptional or posttranscriptional level. LncRNAs in the nucleus regulate gene expression in various modes, such as isolating transcription factor/protein complexes from chromatin and gathering different proteins to form ribonucleoprotein complexes in response to stimuli. However, cytoplasmic lncRNAs stabilize ribonucleoprotein complexes, regulate the stability of mRNA or bind miRNAs as competitive endogenous RNAs (ceRNAs). Transcription or recruitment of chromatin-modifying enzymes to target genes induces chromosomal circulation to increase the association between enhancer and promoter regions. Various lncRNAs also regulate gene expression by modifying chromosome and mRNA expression, and lncRNAs even act as ceRNAs and cause RNA degradation.

**LncRNAs and Cerebral Ischemia**

Increasing evidence shows that hundreds of abnormally expressed lncRNAs have been found in ischemic models and play a crucial role in the pathogenesis of stroke. LncRNA profiles have been reported to greatly influence ischemic injury progression in microvascular endothelial cells during ischemia after oxygen-glucose deprivation and reperfusion (OGD/R), rodent focal stroke, and...
some blood samples.\textsuperscript{51,52} Recently, several specific lncRNAs, such as H19, taurine upregulated gene 1 (TUG1), growth arrest-specific 5 (GAS5), CaMK2D-related transcript 1 (C2dat1), small nucleolar RNA host gene 14 (SNHG14), HOXA distal transcript antisense RNA (HOTTIP), and N1LR, have been shown to be increased in ischemia.\textsuperscript{46,47,52–62} LncRNAs have been reported to stimulate apoptosis, angiogenesis, inflammation, and neuronal death after ischemic stroke.\textsuperscript{47,52–55,63} These findings demonstrate that the brain responds to stroke-associated stimuli by altering lncRNA transcriptional profiles. These robust stroke-induced lncRNA aberrations suggest the potential functional roles and predictive value of lncRNAs as new biomarkers for stroke. An overview of how lncRNAs act on neurological recovery is given in Figure 1.

### LncRNAs Regulate Cell Death and Apoptosis in Cerebral Ischemia

Numerous studies have demonstrated that changes in lncRNA levels are related to cell death after ischemic stroke. A previous study indicated that metastasis-associated lung adenocarcinoma transcript 1 (MALAT1) promotes neuronal death via targeting miR-30a in ischemic stroke.\textsuperscript{49} It protects the cerebral microvasculature and parenchyma from cerebral ischemic insults by inhibiting endothelial cell death and

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**Figure 1** Overview of the effects of lncRNAs on neurological recovery. LncRNAs predominantly modulate autophagy, cell death, apoptosis, regeneration and inflammation through various pathways, and microRNAs are key players. Created with Biorender.com.

**Abbreviations:** MALAT1, metastasis-associated lung adenocarcinoma transcript 1; SNHG12, small nucleolar RNA host gene 12; KCNQ1OT1, potassium voltage-gated channel subfamily Q member 1 opposite strand 1; CHRF, cardiac hypertrophy-related factor; FosDT, Fos downstream transcript; MEG3, maternally expressed gene 3; NKILA, NF-κB interacting lncRNA; C2dat1, CAMK2D-associated transcript 1; GAS5, growth arrest-specific 5; TUG1, taurine-upregulated gene 1; Oprm1, opioid receptor μ1 gene; ANRIL, antisense noncoding RNA in the INK4 locus; NEAT1, nuclear paraspeckle assembly transcript 1; DANC1, differentiation antagonizing nonprotein-coding RNA; FIRRE, functional intergenic repeating RNA element; Macilpl, macrophage containing lymphocyte cytosolic protein 1 factor (LCP1)-related proinflammatory; DAPK1, death-associated protein kinase 1; MAP4K4, mitogen-activated protein kinase 4; SOX6, sex-determining region Y-box 6; NF-κB, nuclear factor kappa B; VEGF, vascular endothelial growth factor.
inflammation and plays roles in the progression of cerebrovascular permeability and BBB integrity after stroke.\textsuperscript{46} In addition, MALAT1 interacted with miR-26b and upregulated ULK2 expression, which in turn suppressed neuronal death.\textsuperscript{47} In addition, N1L1 and maternally expressed 3 (MEG3) also interact with neuronal death after ischemic stroke by inactivating p53.\textsuperscript{36} Knockdown of MEG3 inhibits neuronal death by targeting the miR-21/PDCD4 signaling pathway.\textsuperscript{54} Consistent with these findings, growth arrest-specific 5 (GAS5) inhibits cell death and increases neuronal survival by targeting the miR-137/Notch1 signaling pathway.\textsuperscript{57} Small nucleolar RNA host gene 14 (SNHG) mediated by hypoxia-inducible factor-1α (HIF-1α) and vascular endothelial growth factor (VEGF) signaling acts as a ceRNA for miR-18a, thereby affecting cerebral infarction.\textsuperscript{60} To date, a series of preclinical studies have assessed the effects of lncRNAs on regulating cell death in ischemia models.

Among the various programmed cell death pathways, apoptosis accounts for a large proportion of neuronal death through brain ischemia,\textsuperscript{65} which efficiently removes damaged cells from DNA damage or during development.\textsuperscript{66} Apoptosis plays a pivotal role in the homeostasis of normal tissues, and researchers have recently found that lncRNAs have essential effects on regulating cell apoptosis following stroke.\textsuperscript{67} LncRNA growth arrest-specific 5 (GAS5), a ceRNA for miR137, was upregulated and negatively correlated with miR137 expression in stroke mice and OGD/R-treated primary neurons.\textsuperscript{68} Chen et al.\textsuperscript{69} illustrated that lncRNA TUG1 was significantly upregulated in ischemia in an MCAO model. TUG1 has been proven to interact with miR-9 and decrease Bcl2 protein, which activates bax and ultimately leads to neuronal apoptosis.\textsuperscript{70} Overexpression of lncRNA opioid receptor μ1 gene (Oprm1) attenuated apoptosis-induced cerebral injury via the Oprm1/miR-155/GATA3 axis by reducing cleaved caspase-3 levels.\textsuperscript{71} One study illustrated that lncRNA rhabdomyosarcoma 2-associated transcript (RMST) promoted OGD-induced injury in brain microvascular endothelial cells by regulating the miR204–5p/VCAM1 pathway.\textsuperscript{72} To date, a great number of studies have assessed the effect of lncRNAs on regulating apoptosis in ischemia. The characteristics of some of these studies are summarized in Table 1.

### LncRNAs Regulate Angiogenesis in Cerebral Ischemia

During angiogenesis, the blood supply recovers in damaged regions after ischemia, thus alleviating ischemic necrosis by assisting the brain in restoring collateral circulation.\textsuperscript{73} Current studies have indicated that several lncRNAs play a vital role in regulating endothelial cell survival, vascular integrity, and angiogenesis in ischemia. Numerous lncRNAs are associated with angiogenesis after stroke by affecting transcription and translation.\textsuperscript{74} A recent study found that the overexpression of MEG3 suppresses functional recovery after ischemia, the silencing of MEG3 ameliorates brain lesions, and the expression of MEG3 increases angiogenesis after ischemia by promoting endothelial cell migration, proliferation, sprouting, and tube formation by regulating the Notch pathway.\textsuperscript{75} Furthermore, another study demonstrated that lncRNA Aerrie and SNHG12 contribute to DNA signaling and repair mechanisms and relieve endothelial cell injury after ischemic stroke.\textsuperscript{76–78} In addition, another clinical study demonstrated that lncRNA MACC1-AS1 also exerts a protective role after stroke.\textsuperscript{74} To date, a range of preclinical studies have assessed the effect of lncRNAs on regulating neurogenesis and angiogenesis in cerebral ischemia. The characteristics of some of these studies are summarized in Table 2.

### LncRNAs Regulate Autophagy in Cerebral Ischemia

Autophagy is an evolutionarily conserved cellular mechanism that can maintain cellular nerve homeostasis, and it is associated with degraded misfolded or nonfunctional proteins and damaged organelles.\textsuperscript{67,79} Numerous studies confirm that autophagy provides a neuroprotective effect on stroke by promoting the clearance of damaged proteins and organelles, which facilitates energy recycling and cellular defense.\textsuperscript{67} It is widely accepted that various lncRNAs affect cell survival in stroke by regulating autophagy.\textsuperscript{56} MALAT1 is one of the most significantly upregulated lncRNAs in both in vivo and in vitro models of stroke and serves as a competing endogenous RNA by sponging miR-126 to upregulate its target ULK2 under hypoxic injury based on the protective effect of autophagy.\textsuperscript{17} Similarly, lncRNA antisense noncoding RNA in the INK4 locus (ANRIL) and lncRNA FosDT were all elevated by negatively regulating miR-127 expression\textsuperscript{80} and interacting with REST-associated chromatin-modifying proteins separately to protect against ischemic stroke.\textsuperscript{81} In contrast, exogenous overexpression of H19 results in autophagic cell death in cerebral ischemia.\textsuperscript{82} Acting as a competing endogenous RNA of miR-200a, lncRNA
Table 1: Preclinical and Clinical Stroke Studies Assessing the Effect of Different LncRNAs on the Regulation of Apoptosis and Cell Death

<table>
<thead>
<tr>
<th>Author, Year</th>
<th>LncRNA</th>
<th>Models</th>
<th>Species</th>
<th>Regulation</th>
<th>Targets</th>
<th>Functions</th>
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<tr>
<td><strong>LncRNAs regulate apoptosis in stroke</strong></td>
<td></td>
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<td></td>
<td></td>
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</tr>
<tr>
<td>Xiao et al 2019</td>
<td>H19</td>
<td>MCAO, OGD/R</td>
<td>Human, Rats, Cells</td>
<td>Up</td>
<td>miR-19a</td>
<td>Modulate hypoxia induced neuronal apoptosis</td>
</tr>
<tr>
<td>Wang et al 2020</td>
<td>MEG3</td>
<td>MCAO, OGD/R</td>
<td>Human, Mice, Cells</td>
<td>Up</td>
<td>Bax, cleaved Caspase-3</td>
<td>Promote cell apoptosis and aggravates hypoxia</td>
</tr>
<tr>
<td>Xiang et al.</td>
<td>MEG3</td>
<td>MCAO, OGD/R</td>
<td>Mice, Cells</td>
<td>Up</td>
<td>miR-424-5p, MAPK</td>
<td>Mediate neuronal apoptosis</td>
</tr>
<tr>
<td>Luo et al 2020</td>
<td>GASS</td>
<td>OGD/R</td>
<td>Human, Cells</td>
<td>Up</td>
<td>Bax, Bcl-2, cleaved caspase-3</td>
<td>Regulate neuronal apoptosis and infarction size</td>
</tr>
<tr>
<td>Wu et al 2017</td>
<td>NILR</td>
<td>MCAO, OGD/R</td>
<td>Mice, Cells</td>
<td>Up</td>
<td>P53</td>
<td>Promote neuroprotection</td>
</tr>
<tr>
<td>Zhou et al 2020</td>
<td>SNHG7</td>
<td>MCAO, OGD/R</td>
<td>Mice, Cells</td>
<td>Down</td>
<td>miR-9, SIRT1</td>
<td>Alleviate neuronal injury</td>
</tr>
<tr>
<td>Jing et al 2019</td>
<td>Oprm1</td>
<td>MCAO, OGD/R</td>
<td>Mice, Cells</td>
<td>Up</td>
<td>miR-155, GATA3, Caspase-3</td>
<td>Overexpression alleviates apoptosis</td>
</tr>
<tr>
<td>Cheng et al 2020</td>
<td>RMST</td>
<td>OGD/R</td>
<td>Cells</td>
<td>Up</td>
<td>miR-107, Bcl2, Bax, p53</td>
<td>Promote OGD-induced neuronal apoptosis</td>
</tr>
<tr>
<td>Yao et al 2019</td>
<td>Rian</td>
<td>MCAO, OGD/R</td>
<td>Mice, Cells</td>
<td>Down</td>
<td>miR-144-3p, caspase-3, Bax, Bcl-2</td>
<td>Attenuated cell apoptosis from cerebral I/R injury</td>
</tr>
<tr>
<td>Gao et al</td>
<td>HCP5</td>
<td>OGD/R</td>
<td>Cells</td>
<td>Up</td>
<td>miR-652-3p, LC3, p62</td>
<td>Protect against cerebral I/R injury</td>
</tr>
<tr>
<td>Cao et al 2021</td>
<td>TALNEC2</td>
<td>MCAO, OGD/R</td>
<td>Mice, Cells</td>
<td>Up</td>
<td>miR-650, APAF1</td>
<td>Aggravate apoptosis cerebral I/R injury</td>
</tr>
<tr>
<td><strong>LncRNAs regulate cell death in stroke</strong></td>
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</tr>
<tr>
<td>Yan et al 2016</td>
<td>MEG3</td>
<td>MCAO, OGD/R</td>
<td>Rats, Cells</td>
<td>Up</td>
<td>P53</td>
<td>As a cell death promoter</td>
</tr>
<tr>
<td>Yan et al 2017</td>
<td>MEG3</td>
<td>MCAO, OGD/R</td>
<td>Mice, Cells</td>
<td>Up</td>
<td>miR-21</td>
<td>Target miR-21/PDCD4 signaling pathway</td>
</tr>
<tr>
<td>Deng et al 2019</td>
<td>Nespas</td>
<td>MCAO, OGD/R</td>
<td>Mice, Cells</td>
<td>Up</td>
<td>Bcl-2, Bax</td>
<td>Silence aggravates I/R-induced ischemic damage</td>
</tr>
<tr>
<td>Xu et al 2020</td>
<td>D63785</td>
<td>OGD/R</td>
<td>Cells</td>
<td>Down</td>
<td>miR-422a</td>
<td>Overexpression reverses neuronal cell death</td>
</tr>
<tr>
<td>Guo et al 2017</td>
<td>MALAT1</td>
<td>MCAO, OGD/R</td>
<td>Mice, Cells</td>
<td>Up</td>
<td>miR-30a</td>
<td>Downregulation attenuates neuronal cell death</td>
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<td>Wang et al 2018</td>
<td>NKILA</td>
<td>OGD/R</td>
<td>Cells</td>
<td>Up</td>
<td>miR-103, miR-107</td>
<td>Upregulation mediates neuronal cell death</td>
</tr>
</tbody>
</table>

**Abbreviations:** LncRNA, long non-coding RNA; MCAO, middle cerebral artery occlusion; OGD/R, oxygen glucose deprivation/re-oxygenation; I/R, ischemia and reperfusion; MAPK, Mitogen-activated protein kinases; APAF1, apoptotic peptidase activating factor 1; MEG3, maternally expressed gene 3; PDCD4, programmed cell death 4; MALAT1, metastasis associated lung adenocarcinoma transcript 1; NKILA, NF-kB interacting long non-coding RNA.
KCNQ1OT1 is significantly upregulated in ischemic stroke and increased the infarct volume and neurological impairments in mice induce transient middle cerebral artery occlusion (MCAO). To date, a vast number of studies have assessed the effect of lncRNAs on regulating autophagy in ischemia. The characteristics of some of these studies are summarized in Table 3.

### LncRNAs Regulate Neuroinflammation in Cerebral Ischemia

Data from four electronic databases, PubMed, Cochrane Library, EMBASE, and Web of Science, were retrieved to identify all literature (clinical and preclinical) evaluated the effect of lncRNAs on regulating autophagy in ischemia. The characteristics of some of these studies are summarized in Table 3.

### LncRNAs Modulate Inflammation and Regulate Microglia Activation in Preclinical Stroke Studies

The inflammatory response is a double-edged sword after ischemia because it not only intensifies secondary injury to the brain but also promotes the recovery of neurological function, thus revealing that inflammation is associated with the pathogenesis and prognosis of ischemia. A large number of studies have illustrated that various lncRNAs are closely associated with the regulation of inflammation and microglial activation in ischemia. Several studies have revealed that knocking down lncRNA MALAT1 reduces inflammatory damage after ischemia by Myd88.
signaling while overexpressing lncRNA MALAT1 is positively associated with higher levels of interleukin (IL-1β), tumor necrosis factor α (TNF-α) and IL-6. H19 is one of the most representative lncRNA genes that can be activated after hypoxia, and it can potentially increase inflammation. Knockdown of lncRNA H19 in the MCAO model promoted cerebral recovery, increased plasma IL-10 levels, and reduced TNF-α and IL-1β levels. Higher lncRNA H19 levels in stroke participants inhibited the recovery of neurological function and were associated with the levels of TNF-α.

Normally, microglia are the main resident immune cells and contain a ramified structure to maintain homeostasis in the area surrounding microglial cells. Microglia in the central nervous system are activated immediately when ischemic stroke occurs. Microglial activation is the first step of the inflammatory response, and then other immune cells, such as neutrophils, T cells, and natural killer cells, are activated in the brain. There are dual subtypes of microglia in the pathological process of stroke, including M1 and M2 microglia. M1 microglia exacerbate brain damage by producing IL-6, IL-1β, nitric oxide (NO), TNF-α, etc., while M2 microglia repair the brain by secreting IL-4, IL-10, and transforming growth factor (TGF-β). A series of studies provided the initial evidence that lncRNA SNHG14 and SNHG4 are highly expressed under ischemic conditions and upregulate the expression of inflammation-related cell pathways, such as signal transducer and activator of transcription (STAT) 6 and AQP4, by regulating miR-145–5p and miR-199b, thus leading to the microglial activation in cerebral infarction. By regulating Kruppel-like factor 4 and protein kinase B (AKT)/STAT3 cell pathway, lncRNA MEG3 and nuclear paraspeckle assembly transcript 1 (NEAT1) affect microglial polarization and the levels of proinflammatory and anti-inflammatory factors. Finally, the inhibition of H19 also can reduce activation of microglia and promote microglial M2 polarization.

### LncRNA Regulation Correlates with the Level of Inflammatory Cytokines in Stroke Patients

In the pathogenesis of ischemic conditions, the inflammatory response is regarded as one of the most

<table>
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<th>Author, Year</th>
<th>LncRNA</th>
<th>Models</th>
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<th>Regulation</th>
<th>Targets</th>
<th>Main Functions</th>
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<tr>
<td>Yu et al 2019</td>
<td>KCNQ1OT1</td>
<td>tMCAO, OGD/R</td>
<td>Human, Mice, Cells</td>
<td>Up</td>
<td>miR-200a, FOXO3, ATG7</td>
<td>Knockdown inhibits autophagy and increase cell viability</td>
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<td>Luo et al 2020</td>
<td>MEG3</td>
<td>MCAO, OGD/R</td>
<td>Mice, Cells</td>
<td>Up</td>
<td>miR-378, Beclin1, LC3</td>
<td>MEG3/miR-378/GAB2 protected against neuronal autophagy</td>
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<td>Yao et al 2019</td>
<td>SNHG12</td>
<td>MCAO, OGD/R</td>
<td>Mice, Cells</td>
<td>Up</td>
<td>Beclin1, LC3, p62</td>
<td>Up-regulation of SNHG12 induce autophagy activation</td>
</tr>
<tr>
<td>Wu et al 2020</td>
<td>SNHG12</td>
<td>OGD/R</td>
<td>Cells</td>
<td>Up</td>
<td>SIRT1, FOXO3α</td>
<td>Knockdown inhibits SIRT1/FOXO3α signaling-mediated autophagy</td>
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<td>Gao et al 2020</td>
<td>LNHG3</td>
<td>tMCAO, OGD/R</td>
<td>Mice, Cells</td>
<td>Up</td>
<td>miR-485, LC3, Beclin1</td>
<td>Knockdown improve brain I/R injury to restrain autophagy</td>
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<td>MALAT1</td>
<td>OGD/R</td>
<td>Mice, Cells</td>
<td>Up</td>
<td>miR-26b, LC-3, p62</td>
<td>MALAT1 promote BMEC autophagy and survival under OGD/R condition</td>
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<td>MALAT1</td>
<td>OGD/R</td>
<td>Cells</td>
<td>Up</td>
<td>miR-300c-3p, p62, LC3</td>
<td>MALAT1 activate autophagy and promoted cell survival under hypoxic condition</td>
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<td>MIAT</td>
<td>MCAO, OGD/R</td>
<td>Rats, Cells</td>
<td>Up</td>
<td>LC3, p62</td>
<td>MIAT promote autophagy of neural cells and aggravate ischemic stroke</td>
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<td>Xu et al 2021</td>
<td>C2dat2</td>
<td>MCAO, OGD/R</td>
<td>Mice, Cells</td>
<td>Up</td>
<td>miR-30d-5p, LC3, Beclin1, p62</td>
<td>C2dat2/miR-30d-5p/DDIT4/mTOR facilitate autophagy</td>
</tr>
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</table>

**Abbreviations:** LncRNA, long non-coding RNA; MCAO, middle cerebral artery occlusion; tMCAO, transient middle cerebral artery occlusion; OGD/R, oxygen glucose deprivation/re-oxygenation; I/R, ischemia and reperfusion; FOXO3, forkhead box O3; MEG3, maternally expressed gene 3; BMEC, Brain microvascular endothelial cell; CIRI, cerebral ischemia-reperfusion injury.
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<th>Author, Year</th>
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<th>Provenance</th>
<th>Cell</th>
<th>Expression</th>
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<td>Cao et al 2020</td>
<td>MALAT1</td>
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<td>Decrease</td>
<td>miR-181c-5p/ HMGB1</td>
<td>Activation</td>
<td>IL-1β, IL-6, TNF-α, IL-10</td>
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<td>Zhang et al 2017</td>
<td>MALAT1</td>
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<td>Mouse BMECs</td>
<td>Increase</td>
<td>NA</td>
<td>NA</td>
<td>MCP-1, IL-6, and E-selectin</td>
<td>MACO, OGD/R</td>
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<td>Ren et al 2020</td>
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<td>Human</td>
<td>Blood</td>
<td>Decrease</td>
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<td>eMCAO, OGD/R</td>
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<td>Rats, Cells</td>
<td>Microglia</td>
<td>Increase</td>
<td>MyD88/IRAK1/ TRAF6</td>
<td>Activation</td>
<td>IL-1β, IL-6, TNF-α</td>
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Table 4 (Continued).

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LncRNA–microRNA–mRNA Axis is the Key Player in Regulating Inflammation Upon Ischemic Stroke

MiRNAs belong to a subtype of noncoding RNAs of approximately 22 nucleotides that have a stabilizing effect on mRNA, interact with target genes via degradation or suppression of mRNAs, and then inhibit gene translation. MiRNAs can act as mediators in regulating multiple target genes, and one target gene is always modulated by multiple miRNAs. LncRNAs are the widest subtype of noncoding RNAs, and they have direct ‘sponging-like effects’ on miRNAs, which in turn regulates the transcriptional and epigenetic levels of target genes through imperfect complementarity targeting the 3′-UTR of mRNA. Some lncRNAs bind to miRNAs, thereby competing directly with miRNAs. The lncRNA–microRNA–mRNA axis, therefore, contributes to the regulation of disease. Current evidence has shown that the anti- or proinflammatory effects of specific miRNAs are highly regulated by lncRNAs after ischemic stroke. LncRNA SNHG14 modulates microglial activation and achieves its proinflammatory ability by sponging miR-136–5p, miR-145–5p, and miR-199b. Knockdown of lncRNA H19 increased functional recovery after cerebral ischemia by targeting miR-29b and miR-138–5p and promoted microglial M2 polarization due to its stimulative effect on HDAC1. Several studies have shown that miR-145 functions as an inflammatory mediator, while miR-145 overexpression has the potential to suppress inflammatory injury after ischemic stroke. LncRNA TUG1 is able to bind to miR-145a-5p directly.
LncRNAs Regulate Inflammation Through the TRAF, STAT, and NF-κB Pathways Upon Ischemic Stroke

NF-κB is present in almost all kinds of cells and mainly acts as a transcription factor. It plays a key role in various biological processes, including inflammation, stress response, B cell development and lymphoid organ formation. NF-κB is reported to promote various proinflammatory mediators, and inhibition of NF-κB signaling has beneficial effects in cerebral stroke. LncRNA Snhg8 serves as a competitive endogenous RNA by sponging miR-425–5p, and a bioinformatics analysis showed that this process promotes inflammation by the NF-κB pathway, which was confirmed in microglia. Similarly, Kuai et al illustrated that lncRNA THRIL was negatively correlated with recovery of rat neurological functioning and affected ischemia-reperfusion injury-induced neuronal apoptosis and inflammatory response by regulating NF-κB through miR-24–3p. However, the following question remains: how can these lncRNAs achieve this pro-inflammatory effect through the NF-κB signaling pathway? The STAT pathway is well known to participate in the cell proliferation, apoptosis and immune modulation and plays a crucial role in the signal transduction of a great number of cytokines. M1 microglia are characterized by the induction of STAT1 and NF-κB transcription factors, while the M2 type is related to the transcription factor STAT6. LncRNA SNHG15 increases neuronal damage and microglial inflammation by sponging miR-302a-3p as a competitive endogenous RNA, while this miRNA targets STAT1 and negatively regulates the NF-κB pathway. In addition, Kuai et al and Tian et al revealed that lncRNAs Snhg8 and THRIL regulate inflammation and microglia activation via SIRT1 and neuropilin-1 (NRP1), respectively, by regulating the NF-κB pathway. Thus, lncRNAs might contribute to regulating neuroinflammation and microglia activation by THRIL, NRP1, and STAT1, which further regulate the NF-κB pathway. Information regarding this aspect, however, is scarce.

LncRNAs Regulate Inflammation Through the AKT and ERK Pathways Upon Stroke

Akt includes three subtypes: Akt1, Akt2 and Akt3. Numerous scientists have recently focused on the protective effects of Akt by increasing phosphorylated Akt in...
stroke conditions. The Akt pathway has been shown to participate in neuronal survival and inflammation regulation after ischemic stroke, thus illustrating that pharmacological upregulation of Akt signaling might be a potential target for protecting the injured brain. Gao et al pointed out that lncRNA FAL1 has the potential to protect primary brain microvascular endothelial cells against OGD/R-induced endothelial inflammation by regulating the PAK1/AKT signaling pathway. Phosphorylated PI3K can convert Akt into phosphorylated Akt and activate the key subunit of NF-κB to phosphorylated p65, which leads to the nuclear entry of NF-κB and subsequently causes the genetic transcription of inflammatory factors. Silencing of lncRNA SNHG15 can decrease the levels of proinflammatory cytokines (TNF-α and IL-1β) and apoptosis of N2a cells via sequestering the mir-18a and subsequently activating the extracellular signal-regulated kinase (ERK) signaling pathway. Similarly, lncRNA ANRIL knockdown can suppress mouse mesangial cell proliferation, inflammation and fibrosis via ERK pathways in a diabetic nephropathy model. Akt also participates in inhibiting cell apoptosis and reducing eNOS expression via the ERK pathway in a bilateral common carotid occlusion model.

Conclusion

Neuroinflammation usually results in aberrant expression of numerous lncRNAs that exert important functions in epigenetic and transcriptional regulation of the expression of genes. lncRNAs can modulate inflammation by interacting with different signaling pathways, which offers an exceptional opportunity for adjuvant stroke treatment. A great amount of evidence illustrates that numerous lncRNAs can regulate microglial activation and polarization and modulate the inflammatory response in clinical and preclinical stroke studies. The lncRNA–microRNA–mRNA axis is a key player in regulating inflammation upon ischemic stroke, and the NF-κB and AKT pathways are also essential. Although we have witnessed remarkable progress in our understanding of the vital role of lncRNAs in regulating neuroinflammation, many lncRNAs have not yet been functionally characterized and their molecular mechanisms are poorly known. Further efforts should be made to identify more inflammatory lncRNAs species that function under hypoxia. With a better understanding of the gene regulation modalities of lncRNAs, greater progress in this area can be made.

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Disclosure

Yongli Pan, Qingzheng Jiao, Wei Wei and Tianyang Zheng should be considered co-first authors. The authors declare that they have no competing interests.

References


