

# An enriched environment reduces hippocampal inflammatory response and improves cognitive function in a mouse model of stroke

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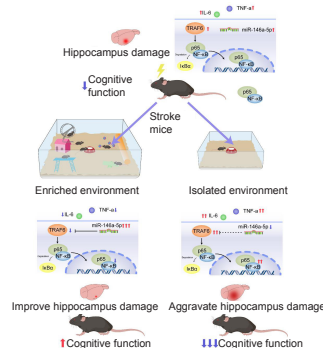
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Hong-Yu Zhou<sup>1, #</sup>, Ya-Ping Huai<sup>2, #</sup>, Xing Jin<sup>1</sup>, Ping Yan<sup>3</sup>, Xiao-Jia Tang<sup>1</sup>, Jun-Ya Wang<sup>1</sup>, Nan Shi<sup>3</sup>, Meng Niu<sup>4</sup>, Zhao-Xiang Meng<sup>1, \*</sup>, Xin Wang<sup>1, \*</sup>

## From the Contents

Introduction	2497
Materials and Methods	2498
Results	2499
Discussion	2499

**Graphical Abstract** Enriched and isolated environments can regulate the TRAF6/NF-κB/p53 signaling pathway in the hippocampus through miR-146a-5p and affect cognitive function in a stroke mouse model



## Abstract

An enriched environment is used as a behavioral intervention therapy that applies sensory, motor, and social stimulation, and has been used in basic and clinical research of various neurological diseases. In this study, we established mouse models of photothrombotic stroke and, 24 hours later, raised them in a standard, enriched, or isolated environment for 4 weeks. Compared with the mice raised in a standard environment, the cognitive function of mice raised in an enriched environment was better and the pathological damage in the hippocampal CA1 region was remarkably alleviated. Furthermore, protein expression levels of tumor necrosis factor receptor-associated factor 6, nuclear factor κB p65, interleukin-6, and tumor necrosis factor α, and the mRNA expression level of tumor necrosis factor receptor-associated factor 6 were greatly lower, while the expression level of miR-146a-5p was higher. Compared with the mice raised in a standard environment, changes in these indices in mice raised in an isolated environment were opposite to mice raised in an enriched environment. These findings suggest that different living environments affect the hippocampal inflammatory response and cognitive function in a mouse model of stroke. An enriched environment can improve cognitive function following stroke through up-regulation of miR-146a-5p expression and a reduction in the inflammatory response.

**Key Words:** cognitive function; enriched environment; isolated environment; miR-146a-5p; neuroinflammation; nuclear factor κB p65; photothrombotic model; stroke; tumor necrosis factor receptor-associated factor 6

## Introduction

Stroke, the second leading cause of death in the world, is a common acute cerebrovascular disease (Xie et al., 2019), and approximately 80% of cases of stroke are ischemic (Faralli et al., 2013). Studies have found that approximately 50% of patients with stroke have varying degrees of cognitive dysfunction (Sachdev et al., 2006; Mijajlović et al., 2017; Zhang and Bi, 2020), which severely affects patients' quality of life and survival time. In clinical practice, most patients with stroke do not like to talk to others, lack subjective initiative, and spend most of their time alone, all of which seriously affect the recovery of neurocognitive function. One study has shown that isolated housing can lead to poor recovery and microRNA (miRNA) imbalance, and decrease hippocampal cell proliferation in older female mice models of stroke (Holmes et al., 2020). Therefore, interventions related to the cognitive function of patients with stroke have become a research hot spot.

An enriched environment (EE) is a special environment that can enhance sports ability, cognition, perception, and social interaction (Will et al., 2004). Animal

studies have shown that an EE not only improves learning, cognitive, and sports abilities in normal animals, but also improves the cognitive and sports abilities of rats with various central nervous system diseases (Hockly et al., 2002; Bezdard et al., 2003; Restivo et al., 2005; Kovsesi et al., 2011). EE is currently used in the clinical rehabilitation of patients with stroke (White et al., 2015), but the specific mechanism underlying its positive effect remains unclear. Our previous study found that an EE can improve post-stroke cognitive impairment (PSCI) by regulating acetylation homeostasis in the cholinergic circuit in mouse models of stroke (Wang et al., 2016). The occurrence of PSCI is closely related to factors such as the inflammatory response (Narasimhalu et al., 2015). As an important immune-related molecule, miR-146a plays a key role in both innate immunity and neuroimmunity, and can inhibit the levels of inflammatory factors such as interleukin 6 (IL-6), IL-8, IL-1β, and tumor necrosis factor-α (TNF-α) by down-regulating tumor necrosis factor receptor-associated factor 6 (TRAF6) expression (Lukiw et al., 2008; Aronica et al., 2010).

Therefore, in this study, photothrombotic stroke mouse models were rehabilitated in either EE or isolated environments. Due to the mutual

<sup>1</sup>Department of Rehabilitation Medicine, Northern Jiangsu People's Hospital Affiliated to Yangzhou University (Clinical Medical College, Yangzhou University), Yangzhou, Jiangsu Province, China; <sup>2</sup>Department of Rehabilitation Medicine, Shenzhen Longhua District Central Hospital, Shenzhen, Guangdong Province, China; <sup>3</sup>School of Nursing, Yangzhou University, Yangzhou, Jiangsu Province, China; <sup>4</sup>Dalian Medical University, Dalian, Liaoning Province, China

\*Correspondence to: Xin Wang, PhD, wx000805qm@yeah.net; Zhao-Xiang Meng, PhD, yzmzx001@163.com.

<https://orcid.org/0000-0003-1961-9615> (Xin Wang); <https://orcid.org/0000-0001-9624-2829> (Zhao-Xing Meng)

#Both authors contributed equally to this article.

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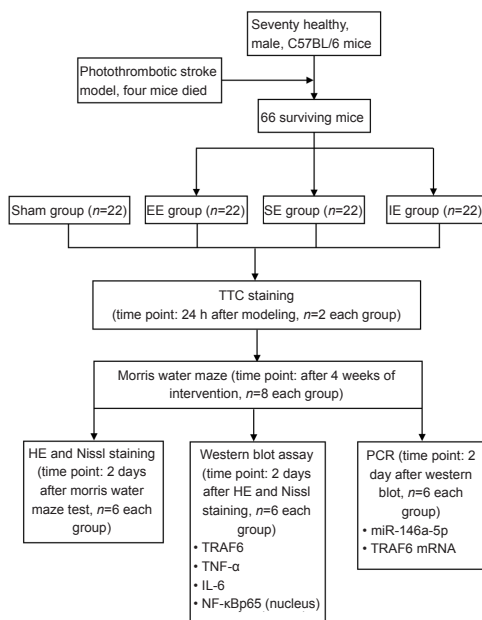
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interaction between miR-146a-5p and neuroinflammation, as well as their association with cognitive function, we examined the efficacy of an EE in improving cognitive function after stroke, as well as the mechanism underlying this effect, at the levels of miRNA and neuroinflammation.

## Materials and Methods

### Photothrombotic stroke models and interventions

The animal experiment was approved by the Animal Ethics Committee of Yangzhou University, China (approval No. 20170312001) in March 2017. We used 92 healthy, male, clean-grade C57BL/6 mice aged 2 months (provided by the Animal Experiment Center of Medical College of Yangzhou University, China; license No. SYXX (Su) 2017-0044). Among them, 70 mice were subjected to photothrombotic stroke. Briefly, after anesthesia (intraperitoneal injection of 1% sodium pentobarbital solution, 0.1 mL/10 g, Cat# P-010, Sigma-Aldrich, St. Louis, MO, USA), Rose Bengal (1%, 1 mg/10 g, Cat# B7767, APExBIO, Houston, TX, USA) was injected intraperitoneally. The mouse was placed in the prone position, the tops of their heads were shaved, and the scalp was cut along the midline to fully expose the bregma (Watson et al., 1985; Labat-gest and Tomasi, 2013). The cold light source probe (Cat# ULP-L20-S, Bete Jia, Suzhou, China) was placed approximately 2 mm below the left of the bregma. After 5 minutes of Rose Bengal injection, the cold light source was turned on and irradiation was continued for 15 minutes (Uzdensky, 2018). Four mice died during the modeling process; the 66 surviving mice were divided into the stroke + standard environment (SE) group, stroke + EE group, and stroke + isolated environment (IE) group using a random number table method. Another 22 mice were selected as the sham operation group. In this sham group, 0.9% normal saline (0.1 mL/10 g) was injected intraperitoneally with the same amount of Rose Bengal without light, and the remaining steps were the same as for stroke model mice. Sham group mice ( $n = 22$ ) were placed in an SE cage for 4 weeks. SE group mice ( $n = 22$ ) group were also placed in another SE cage for 4 weeks. EE group mice ( $n = 22$ ) were placed in an EE cage for 4 weeks. IE group mice were individually caged for 4 weeks. The flow chart of this study design is shown in **Figure 1**.



**Figure 1** | Flow chart of this study.

SE group: Stroke + standard environment group; EE group: enriched environment group; IE group: stroke + isolated environment group; HE: hematoxylin-eosin; TRAF6: factor receptor-associated factor 6; TNF- $\alpha$ : tumor necrosis factor- $\alpha$ ; IL-6: interleukin 6; NF- $\kappa$ Bp65: nuclear factor kappa-Bp65; TTC: triphenyl tetrazolium chloride; RT-qPCR: real time quantitative polymerase chain reaction.

### Construction of mouse cages in different environments

According to our previous research (Wang et al., 2016), the EE cage was improved to comprise a 1.2-m<sup>2</sup> three-layer plexiglass cage. Each floor was connected by a plastic corridor. Inside the EE cage, there were three spiral staircases (each staircase entrance was equipped with rough carpet), three tunnels of different styles, two walking wheel pipes, two turntables, two swings, toy building blocks, a cabin, a bell sound, and color light stimulation. The EE group mice were held in researchers' palms and vigorously brushed from head to tail with a soft brush once a day, and the environment was changed once every 3 days to update the stimulation until the 4<sup>th</sup> week (**Figure 2A and B**). In contrast, the SE cage was 75 × 55 × 35 cm<sup>3</sup>, with mouse food, water, and padding (**Figure 2C and D**), and the IE cage was 29 × 18 × 16 cm<sup>3</sup>, with mouse food, water, and padding (**Figure 2E and F**).

### Triphenyl tetrazolium chloride staining

At 24 hours after modeling, two mice from each group were selected using

the random number table method for mouse brain triphenyl tetrazolium chloride (TTC) staining. The mice were sacrificed under 10% (lethal dose) sodium pentobarbital deep anesthesia. The mice brains were removed and quickly frozen at -20°C for 20 minutes, restored at room temperature for 10 minutes, and then cut into five 2-mm continuous coronal brain slices from the starting point of the optic chiasm toward the caudal side. Following slicing, a newly prepared 2% TTC solution (Servicebio, Wuhan, Hubei Province, China, Cat# G1017) was added, slices were incubated at room temperature for 30 minutes in the dark, and then fixed in a phosphate buffer containing 4% paraformaldehyde overnight. The color of the frontal part of the coronal section of the mouse brain was observed to determine whether the mouse had indeed undergone stroke.

### Morris water maze

After 4 weeks of intervention, eight mice in each group were selected for inclusion in the Morris water maze experiment (Shanghai Xinruan Information Technology Co., Ltd., Shanghai, China). The mice were trained from day 1 to day 4 and tested on days 5 and 6. During training and testing, the water temperature was maintained at 20–22°C, and a platform was placed 2 cm below the water level in one of the four quadrants. During training and testing, each group of mice was put into the water from the four quadrant water inlet points. If the mice did not reach the platform within 60 seconds, they were guided to the platform and stayed there for 30 seconds. Additionally, the escape latency of each group was recorded. On day 6, the platform was removed from the pool, and mice were allowed to swim freely for 60 seconds. The video analysis system automatically recorded the number of times mice crossed the platform zone. After the daily tests, mice were returned to their respective environments.

### Histological observation

Two days after completion of the Morris water maze test, six mice in each group were deeply anesthetized by intraperitoneal injection of 10% sodium pentobarbital, and brains were removed after cardiac perfusion. The fresh brain tissue was immediately put on ice, and then dehydrated gradually in 15%, 20%, and 30% sucrose solution until the specimen sunk to the bottom. The specimen was then removed from the solution, embedded with optimal cutting temperature embedding agent (Servicebio, Cat# G6059), and placed in a freezing microtome (Dakewe Biotech, Shenzhen, China, Cat# 3000A). When the brain block had frozen solid, it was fixed on a freezing microtome and sliced. Starting from the optic chiasm, a serial section of the coronal position was obtained, with a section thickness of 4  $\mu$ m. When the hippocampus appeared, the coronal slices of the hippocampi at the same level were selected for hematoxylin-eosin and Nissl staining in each group.

### Hematoxylin-eosin staining

The hippocampal sections were laid flat on a glass slide, fixed for 0.5–1 minute, stained with hematoxylin (Servicebio, Cat# G1005) for 3–4 minutes, washed with water to remove the dye on the surface, and tap water was applied for 5 minutes, until all slices turned blue. The slices were then rinsed in distilled water for 2 minutes. Then, the slices were dyed with eosin solution (Servicebio, Cat# G1001) for 30 seconds before removing with 75% alcohol for 1–2 minutes, 95% ethanol for 3 minutes, dehydration of two grades of absolute ethanol for 3 minutes, two grades of xylene for 3 minutes, and finally sealed with neutral gum (Servicebio, Cat# WG10004160). The sealed slide was then placed under an optical microscope (Olympus, Tokyo, Japan, Cat# BX53) to observe and collect images.

### Nissl staining

The hippocampal sections in the same location were also laid flat on another glass slide for Nissl staining. Nissl staining solution (Cat# G1036, Servicebio) was added dropwise onto the glass slide, rinsed with distilled water twice after staining for 5 minutes, and shaken to remove excess water. For decolorization, the slides were washed twice with 70% ethanol solution to remove excess color, and the slides were removed from ethanol solution in due course. For dehydration, the slides were transferred to a 95% ethanol solution and dehydrated for 2 minutes; the slides were then switched to a fresh 95% ethanol solution and dehydrated for a further 2 minutes. For transparency, the slides were transferred to fresh xylene solution for 5 minutes. Finally, the slides were sealed with neutral gum. The sealed glass slide was placed under an optical microscope to observe and collect images, and the number of Nissl bodies in the hippocampus CA1 region of the selected mice in each group was counted using ImageJ software version 1.49 (National Institute of Health, Bethesda, MD, USA; Schneider et al., 2012).

### Western blot assay

In the absence of stimulation, nuclear factor kappa-Bp65 (NF- $\kappa$ Bp65) is sequestered in the cytoplasm by nuclear factor-kappa B inhibitor  $\alpha$  (I $\kappa$ B- $\alpha$ ). After stimulation, I $\kappa$ B $\alpha$  is phosphorylated, which leads to dissociation of the NF- $\kappa$ B/I $\kappa$ B $\alpha$  complex and translocation of NF- $\kappa$ B in the nucleus (Oeckinghaus and Ghosh, 2009). Therefore, we analyzed the level of NF- $\kappa$ Bp65 in the hippocampal nucleus of a mouse model of stroke. Six mice were taken from each group and sacrificed under deep anesthesia by intraperitoneal injection of 10% (lethal dose) sodium pentobarbital. Brain tissue from the left hippocampus area was rapidly isolated on ice, and then thoroughly crushed. The hippocampal whole protein and nucleoprotein protein were respectively extracted from hippocampus by a total protein extraction kit (KeyGen Biotech, Nanjing, China, Cat# KGP250) and nucleoprotein extraction kit (KeyGen Biotech, Cat# KGP150), then analyzed using western blot. The protein mixture was centrifuged at 4°C and 12,000 × g for 30 minutes, and

the supernatant was collected. A bicinchoninic acid kit (Cat# KGPBCA, KeyGen Biotech) was used to detect protein concentration. The samples were heated at 100°C for 10 minutes. The protein samples (20 µL) were subjected to 10% sodium dodecyl sulfate-polyacrylamide gel electrophoresis, and then transferred to a polyvinylidene fluoride membrane (Cat# 1620112, Bio-Rad, Shanghai, China). The polyvinylidene fluoride membrane was then transferred to nonfat milk-blocking solution for 1 hour at room temperature. The primary antibodies used were anti-NF-κBp65 (1:1000, rabbit, Abcam, Cat# ab76302, RRID: AB\_1524028), anti-TRAF6 (1:2000, rabbit, Abcam, Cat# ab33915, RRID: AB\_778572), anti-TNF-α (1:1000, rabbit, Abcam, Cat# ab183218, RRID: AB\_2889388), and anti-IL-6 (1:1000, rabbit, Abcam, Cat# ab229381, RRID: AB\_2861234). Anti-glyceraldehyde-3-phosphate dehydrogenase (1:10,000, rabbit, Abcam, Cat# ab181602, RRID: AB\_2630358) and anti-histone H3 (1:1000, rabbit, Abcam, Cat# ab215728, RRID: AB\_2118291) were used as a loading control. The membranes were incubated overnight with primary antibodies at 4°C. Membranes were then washed three times with Trisbuffered saline with Tween-20. The membrane was then incubated with the IgG secondary antibody (1:5000, rabbit, Abcam, Cat# ab205718, RRID: AB\_2819160) for 60 minutes at room temperature. After development, ImageJ software was used to measure the relative optical density of each band.

#### Quantitative reverse transcription-polymerase chain reaction

The left hippocampus tissues of six mice in each group were collected. An RNA extraction kit (Tiangen, Beijing, China, Cat# DP501) was used to extract total RNA from the hippocampus, and the RNA concentration was detected using a microplate reader (Tecan, Shanghai, China, Cat# M1000). The concentration of each sample to be tested was diluted to 200 ng/µL.

#### miRNA detection

A 20 µL reaction solution was prepared on ice, comprising total RNA (8 µL), 2× miRNA RT reaction buffer (10 µL), and miRNA RT enzyme mix (2 µL). The reaction mixture was mixed thoroughly, and reverse transcription of miRNA was performed to obtain complementary deoxyribonucleic acid (cDNA). A real-time quantitative polymerase chain reaction (qPCR) plate was used to prepare 20 µL total reaction solution, as follows: 2× miRcute Plus miRNA Premix (with SYBR&ROX; 10 µL), forward primer (10 µM; 0.4 µL), reverse primer (10 µM; 0.4 µL), 50× ROX Reference Dye (2 µL), ddH<sub>2</sub>O (5.2 µL), and cDNA (2 µL). The sample was then transferred to a fluorescence qPCR machine (Cat# StepOne Plus 4376357, Thermo Fisher Scientific, Waltham, MA, USA), and the qPCR reaction was performed with the following amplification conditions: 95°C, 15 minutes for 1 cycle; 94°C, 20 seconds; 64°C, 30 seconds; 72°C, 34 seconds for 5 cycles; 94°C, 20 seconds; and 60°C, 34 seconds for 45 cycles. All the reagents were from Tiangen.

#### mRNA detection

A 20 µL reaction solution was prepared on ice, comprising 5 × FastKing-RT SuperMix (4 µL), RNase-Free ddH<sub>2</sub>O (14 µL), and total RNA (2 µL). The sample was mixed well, and reverse transcription of mRNA was performed to obtain cDNA. Subsequently, a 20 µL system total reaction solution was prepared with a qPCR plate, as follows: 2× SuperReal PreMix Plus (10 µL), forward primer (10 µM; 0.6 µL), reverse primer (10 µM; 0.6 µL), cDNA (2 µL), 50× ROX Reference Dye (2 µL), and RNase-free ddH<sub>2</sub>O (4.8 µL). The amplification conditions were as follows: 95°C, 15 minutes for 1 cycle; 95°C, 10 seconds; and 63°C, 32 seconds for 40 cycles. All the reagents were from Tiangen.

#### Primer sequence

miR-146a-5p: forward: 5'-TGC GCT GAG AAC TGA ATT CCA T-3', reverse: 5'-TGG TGT CGT GGA GTC G-3'; internal reference U6: forward: 5'-CTC GCT TCG GCA GCA CAT-3', reverse: 5'-AAC GCT TCA CGA ATT TGC GT-3'; TRAF6: forward: 5'-CCA ATT CCC AGA ATC CAG AAA-3', reverse: 5'-GAC ACA GAG GAC CCA CAG AGA A-3'; internal reference glyceraldehyde-3-phosphate dehydrogenase: forward: 5'-TGA AGG GTG GAG CCA AAA G-3', reverse: 5'-AGT CTT CTG GGT GGC AGT GAT-3'. The 2<sup>-ΔΔCt</sup> method (Schmittgen and Livak, 2008) was used to calculate the relative expression levels of miR-146a-5p and TRAF6 mRNA, where  $\Delta Ct = Ct_{\text{target gene}} - Ct_{\text{reference gene}}$ .

#### Database prediction comparison analysis

By comparing the base sequences of TRAF6 mRNA 3' untranslated region and miR-146a-5p using Targetscan ([http://www.targetscan.org/vert\\_80/](http://www.targetscan.org/vert_80/)) and Human microRNA disease bioinformatics databases (<http://www.cuilab.cn/hmdd/>), we were able to determine whether they have complementary regions of base pairs.

#### Statistical analysis

No statistical methods were used to predetermine sample sizes; however, our sample sizes are similar to those reported in a previous publication (Wang et al., 2016). No animals or data points were excluded from the analysis. The evaluator was blind to the grouping. All data were analyzed using SPSS 23.0 (IBM, Armonk, NY, USA) and GraphPad Prism 8.0 (GraphPad Software Inc., San Diego, CA, USA) statistical software, and the measurement data are expressed as mean ± standard deviation (SD). The Morris water maze data and western blotting data conformed to a normal distribution, so one-way analysis of variance was used for comparisons between multiple groups, and the least significant difference test was used for pairwise comparisons. The qPCR data did not conform to a normal distribution, so nonparametric tests were used (the Kruskal-Wallis test was used for comparisons between multiple groups, and the Mann-Whitney *U* test was used for pairwise comparisons). A *P*-value < 0.05 was taken to indicate statistical significance.

## Results

### Successful establishment of stroke model

As shown in **Figure 3**, the brain tissue of mice in the sham group was normal with red coloring, while the left cortex and subcortex in mice with photothrombotic stroke were white under TTC staining, which indicates ischemic infarction.

### EE improves learning and memory in a mouse model of stroke

The Morris water maze results are shown in **Figure 4**. Compared with the sham group, the escape latency was significantly longer in the SE group from day 3 (*P* < 0.05). Moreover, the escape latency in the EE group was shorter than that of the SE group on days 3–5 (*P* < 0.05). The escape latency was significantly longer in the IE group than in the SE group (*P* < 0.05) on days 4 and 5. On day 6, the SE group made fewer crossings of the platform zone than the sham group (*P* < 0.05). The times of crossing the platform zone in the EE group was higher than that in the SE group (*P* < 0.05), while the number of platform zone crossings in the IE group was less than that in the SE group (*P* < 0.05). The swimming trajectories of each group are shown in **Figure 5**. The results indicated a significant decrease in the learning and memory ability of post-stroke mice in the SE group. The EE could improve the learning and memory ability of mice after stroke, while the IE aggravated the learning and memory impairments of mice after stroke.

### EE limits cell damage in the hippocampal CA1 region of a mouse model of stroke

The hematoxylin-eosin and Nissl staining results are shown in **Figure 6**. In the hippocampal CA1 region in the sham group, the nerve cells were neatly arranged, with full cytoplasm, normal morphology, and large, round nuclei that were clearly visible and evenly distributed, and there were abundant Nissl bodies. In the SE group, the cell arrangement was disordered, the intercellular density was decreased and the intercellular space increased, the morphology was abnormal, the cell membrane was ruptured, the nucleus was irregular or pyknotic, there was evidence of neuronal degeneration, and inflammatory cells were infiltrated, and the number of Nissl bodies was less than that in the sham group (*P* < 0.05). The morphology and structure of CA1 cells in the EE group were more complete and clearer, the arrangement was relatively regular, and there were more Nissl bodies than in the SE group (*P* < 0.05). In the IE group, the hippocampal CA1 cells were seriously damaged, with unclear cell structure, deep pyknosis, unclear nucleoli, significantly decreased cell density, and an increase in the number of vacuoles and inflammatory cell infiltration, and the number of Nissl bodies was significantly reduced compared with the SE group (*P* < 0.05). Under the SE condition, hippocampal neurons were damaged after stroke in mice, EE protected hippocampal neurons in mice after stroke, while IE aggravated cell damage in the hippocampal tissue of a mouse model of stroke.

### EE decreases the protein expression levels of TRAF6, NF-κBp65 (nuclear), TNF-α, and IL-6 in the injured hippocampus of a mouse model of stroke

Western blot results are shown in **Figure 7**. Compared with the sham group, the protein expression levels of TRAF6, NF-κBp65 (nuclear), TNF-α, and IL-6 in the left hippocampus of the SE group were increased (*P* < 0.05). The protein expression levels of TRAF6, NF-κBp65 (nuclear), TNF-α, and IL-6 in the left hippocampus of the EE group were lower than those in the SE group (*P* < 0.05). The protein expression levels of TRAF6, NF-κBp65 (nuclear), TNF-α, and IL-6 in the hippocampus of the IE group were higher than those in the SE group (*P* < 0.05).

### EE affects the expression levels of miR-146a-5p and TRAF6 mRNA in injured hippocampus of a mouse model of stroke

The relative expression levels of miR-146a-5p are shown in **Figure 8**. Compared with the sham group, the expression of miR-146a-5p in the hippocampus of the SE group was increased (*P* < 0.05). Compared with the SE group, the expression of miR-146a-5p in the hippocampus of the EE group was increased (*P* < 0.05), and the expression of miR-146a-5p in the hippocampus of the IE group was decreased (*P* < 0.05).

The relative expression levels of TRAF6 mRNA are shown in **Figure 8**. Compared with the sham group, the expression of TRAF6 mRNA in the hippocampus of the SE group was significantly increased (*P* < 0.05). Compared with the SE group, the TRAF6 mRNA expression in the hippocampus of the EE group was significantly reduced (*P* < 0.05), and the expression of TRAF6 mRNA in the hippocampus of the IE group was significantly increased (*P* < 0.05).

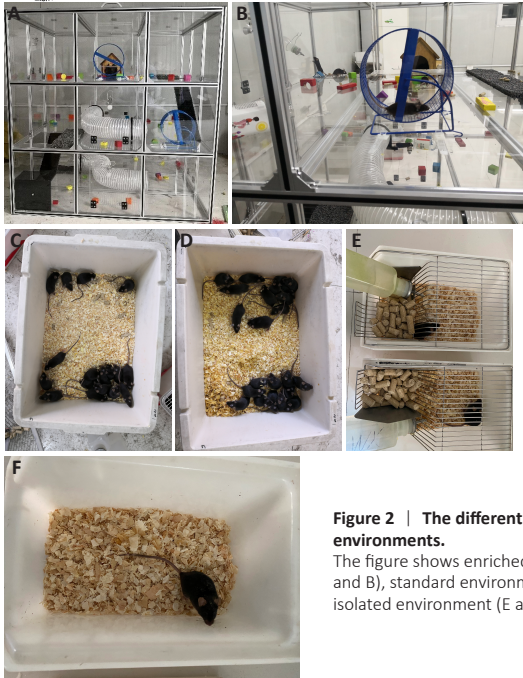
### miR-146a-5p targets and regulates TRAF6 mRNA

According to the database prediction comparison analysis, we found that miR-146a-5p targeted TRAF6 mRNA. Multiple sites in the 3' untranslated region of TRAF6 mRNA that can bind to miR-146a-5p were identified (**Figure 9**).

## Discussion

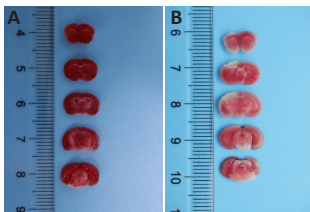
PSCI is a complication of ischemic stroke, and usually manifests as dysfunction of memory, attention, execution, direction, and language (Sun et al., 2014). In addition to the application of drug therapy and traditional cognitive rehabilitation training, the potential of new multi-modal training rehabilitation methods is constantly being explored (Park et al., 2014; Ngandu et al., 2015; Teo et al., 2016; Maresova et al., 2018). Our results demonstrated that EEs and IEs can regulate the TRAF6/NF-κBp65 signaling pathway in the hippocampus of a mouse model of stroke through miR-146a-5p, and affect the morphology and inflammation level of the hippocampus, as well as cognitive function in mice.



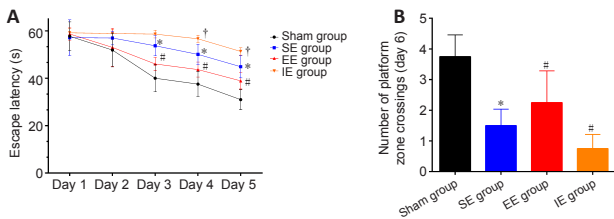


**Figure 2 | The different cage environments.**

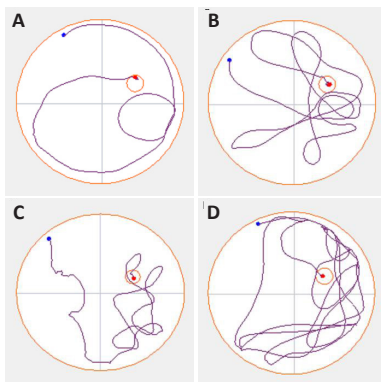
The figure shows enriched environment (A and B), standard environment (C and D), and isolated environment (E and F) cages.



**Figure 3 | Triphenyl tetrazolium chloride staining of the brain in control mice (A) and photothrombotic stroke model mice (B).** The non-ischemic necrosis area was red, and the avascular necrosis area was white. The brain tissue of mice in the sham mice was normal with red color (A), while the left cortex and subcortex in mice with photothrombotic stroke were white (B) under triphenyl tetrazolium chloride staining, which suggests ischemic infarction.

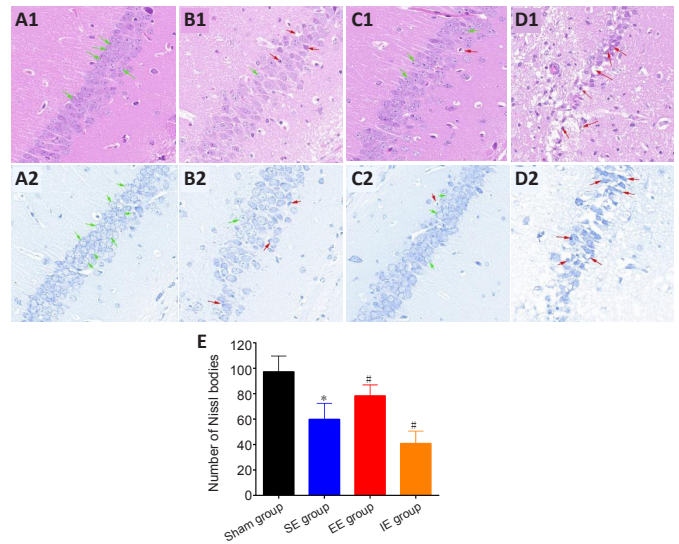


**Figure 4 | The enriched environment improved learning and memory of a mouse model of stroke in the Morris water maze.** (A) Average escape latency on days 1–5. (B) The number of platform zone crossings on day 6. Data are expressed as the mean  $\pm$  SD ( $n = 8$ ). \* $P < 0.05$ , vs. sham group; # $P < 0.05$ , vs. SE group; † $P < 0.05$ , vs. SE group (one-way analysis of variance followed by least significant difference test). EE group: stroke + enriched environment group; IE group: stroke + isolated environment group; SE group: stroke + standard environment group.



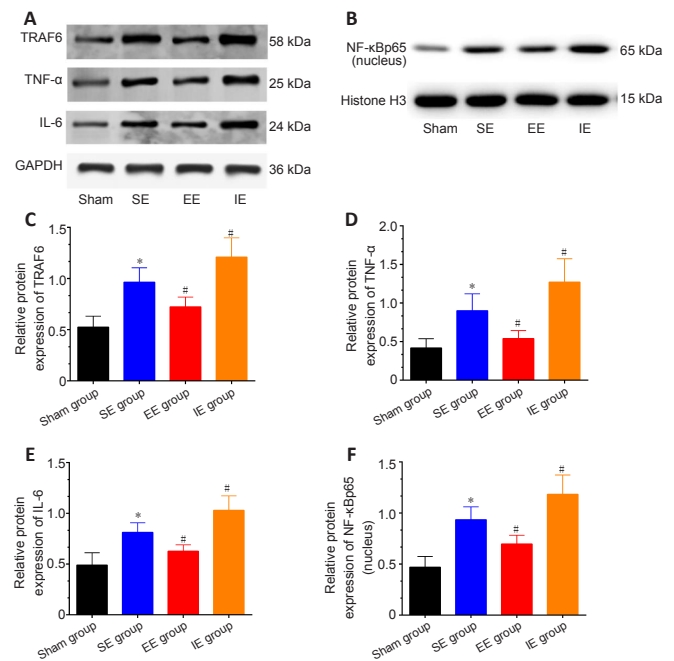
**Figure 5 | Effects of the enriched environment on the swimming trajectory of a mouse model of stroke on day 5 of the Morris water maze test.**

(A) Sham group. (B) SE group. (C) EE group. (D) IE group. After stroke, the swimming trajectory of the mice looking for the platform was extended. The enriched environment shortened the swimming trajectory of mice, and the isolated environment further extended the swimming trajectory of mice. The blue dot indicates the point at which mice were placed into the water; the red dot indicates the end of the swimming track; the big red circle indicates the edge of the pool; the small red circle indicates the platform. EE group: stroke + enriched environment group; IE group: stroke + isolated environment group; SE group: stroke + standard environment group.



**Figure 6 | Effects of the enriched environment on the histopathology in the hippocampal CA1 region of a mouse model of stroke.**

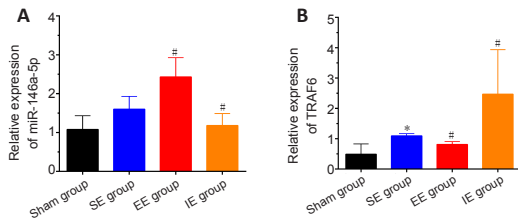
(A–D) Hematoxylin-eosin (A1, B1, C1, D1) and Nissl (A2, B2, C2, D2) staining in the hippocampal CA1 region in the sham (A), SE (B), EE (C), and IE (D) groups (original magnification 400 $\times$ ). Red arrows indicate nerve cells that were obviously irregular, with nuclear pyknosis and vacuoles; and green arrows indicate normal nerve cells. The morphology of hippocampal CA1 cells in the sham group was normal, hippocampal CA1 cells in the SE group were damaged, the morphology of CA1 cells in the EE group was improved compared to SE, and hippocampal CA1 cells in the IE group were more damaged compared to SE. (E) Number of Nissl bodies in the hippocampal CA1 region (per 400-fold field). Data are expressed as the mean  $\pm$  SD ( $n = 6$ ). \* $P < 0.05$ , vs. sham group; # $P < 0.05$ , vs. SE group (one-way analysis of variance followed by least significant difference test). EE group: stroke + enriched environment group; IE group: stroke + isolated environment group; SE group: stroke + standard environment group.



**Figure 7 | Effects of the enriched environment on the protein expression levels of TRAF6, NF-κBp65 (nucleus), TNF-α, and IL-6 in the hippocampus of a mouse model of stroke using Western blot assay.**

(A) Bands of TRAF6, TNF-α, and IL-6 protein. (B) Bands of NF-κBp65 (nucleus) protein. (C–F) Quantitative results of TRAF6, TNF-α, IL-6, and NF-κBp65 (nucleus) protein expression. The expression of TRAF6, TNF-α, and IL-6 protein was normalized against GAPDH, and the expression of NF-κBp65 (nucleus) protein was normalized against Histone H3. Data are expressed as the mean  $\pm$  SD ( $n = 6$ ). \* $P < 0.05$ , vs. sham group; # $P < 0.05$ , vs. SE group (one-way analysis of variance followed by least significant difference test). EE group: stroke + enriched environment group; GAPDH: glyceraldehyde-3-phosphate dehydrogenase; IE group: stroke + isolated environment group; IL-6: interleukin 6; NF-κBp65: nuclear factor kappa-Bp65; SE group: stroke + standard environment group; TNF-α: tumor necrosis factor-α; TRAF6: factor receptor-associated factor 6.





**Figure 8 | Effects of the enriched environment on the expression levels of miR-146a-5p (A) and TRAF6 mRNA (B) in the hippocampus of a mouse model of stroke using quantitative reverse transcription-polymerase chain reaction.**

Data are expressed as the mean ± SD (n = 6), and were analyzed using nonparametric tests. \*P < 0.05, vs. sham group; #P < 0.05, vs. SE group (Kruskal-Wallis test followed by Mann-Whitney U test). EE group: stroke + enriched environment group; IE group: stroke + isolated environment group; SE group: stroke + standard environment group; TRAF6: tumor necrosis factor receptor-associated factor 6.



**Figure 9 | TRAF6 as a target gene of miR-146a-5p according to the database prediction comparison analysis.**

There were three potential binding sites of the TRAF6 mRNA 3' untranslated region to miR-146a-5p according to the principle of base complementary pairing (A=T, C=G). TRAF6: Tumor necrosis factor receptor-associated factor 6.

The EE is an effective rehabilitation therapy. Compared with SEs, EEs provide animals with more space equipped with a variety of toys, and offer more sensations, movement, and social stimulation (Zhang et al., 2021). Social stimulation is recognized as a key factor affecting functional recovery and mortality after stroke (Morris et al., 1990; Hinojosa et al., 2011; Steptoe et al., 2013). Compared with age-matched healthy individuals, stroke survivors experience increased social isolation (Ebrahim et al., 1986). Studies have shown that EE treatment has a neuroprotective effect on animal models of cerebral ischemia (Li et al., 2016) and can improve the learning and memory dysfunction of mice after stroke by promoting plasticity of neuronal circuits (Nithianantharajah and Hannan, 2006) and hippocampal dentate gyrus neurogenesis (Brown et al., 2003). Alternatively, long-term social isolation can increase the risk of vascular and nervous system diseases (Friedler et al., 2015), accelerate the rate of memory decline in older adult people (Bassuk et al., 1999; Ertel et al., 2008), and reduce synaptic plasticity, hippocampal neurogenesis, and spatial cognition (Quan et al., 2010; Kamal et al., 2014; Almeida et al., 2020). In this study, the Morris water maze test was used to detect the effects of different living environments on learning and memory abilities of a mouse model of stroke. We found that in the SE, the post-stroke cognitive function of mice decreased. The EE significantly improved the learning and memory ability of a mouse model of stroke, while the IE aggravates the PSCI of mice.

The hippocampus, located in the temporal lobe of the brain, plays an important role in the formation of normal learning and memory. Previous studies have shown that the hippocampal microstructure of rats will be damaged to varying degrees after stroke (Bettio et al., 2017; Hu et al., 2020). To study the mechanism of the effect of an EE and IE on the behavior of a mouse model of stroke, we first used hematoxylin-eosin and Nissl staining to analyze the pathological morphology of the hippocampal CA1 region of mice in each group, and observed the hippocampal CA1 region with light microscopy. We found that inflammatory damage of neurons appeared in hippocampal CA1 region after stroke in a SE, which led to the decline of learning and memory function. In the EE group, the damaged and inflammatory state of neurons in the hippocampal CA1 region were alleviated, the number of Nissl bodies was restored, and learning and memory ability was improved, which indicates that the EE improves the cognitive function of mice by improving the pathological state of neurons in the hippocampal area. In the IE group, the hippocampal CA1 cells were severely damaged and their structure was unclear; moreover, the number of Nissl bodies was significantly reduced, which indicates that the IE aggravated the pathological damage in the hippocampus of mice after stroke, resulting in more severe cognitive impairment.

Neuroinflammation, especially inflammation in the hippocampus, can lead to cognitive dysfunction (Sun et al., 2017), and is an important pathological mechanism underlying PSCI (Zhang et al., 2021). In recent work, AIM2 inflammasome-mediated inflammation and pyroptosis were found to aggravate PSCI; therefore, it was possible to treat PSCI by targeting and inhibiting inflammation (Kim et al., 2020). The pro-inflammatory cytokines IL-1 $\beta$ , IL-6, and TNF- $\alpha$  are closely associated with learning and memory disorders (Wu et al., 2012), and can lead to cognitive dysfunction by activating different cell signal transduction pathways and interfering with synaptic plasticity and long-term potentiation (Barrientos et al., 2012). TRAF6 is a key binding protein in the inflammatory signaling pathway. Activated by upstream inflammatory stimulation, TRAF6 can interact with IRAK1, promote the nuclear localization and transcriptional activity of NF- $\kappa$ Bp65 (Swantek et al., 2000; Flannery and Bowie, 2010; Lee et al., 2016), and further upregulate

pro-inflammatory cytokines (such as IL-6 and TNF- $\alpha$ ) (Taganov et al., 2006). The present study found that the expression of TRAF6 in the hippocampus of mice in the SE group was upregulated, nuclear NF- $\kappa$ Bp65 was increased, the nuclear translocation of NF- $\kappa$ Bp65 was significantly increased, and the expression of pro-inflammatory factors (IL-6 and TNF- $\alpha$ ) was upregulated, which indicates that the TRAF6/NF- $\kappa$ Bp65 signaling pathway is activated and the neuroinflammatory response is enhanced in the hippocampus of mice after stroke. These results are consistent with the above research conclusions.

Studies have shown that EE treatment can reverse hippocampal neuroinflammation (Jurgens and Johnson, 2012) and reduce inflammation after stroke (Gonçalves et al., 2018). In contrast, previous work has reported glial cell activation and increased IL-1 $\beta$ , IL-6, and TNF- $\alpha$  levels in the prefrontal cortex and hippocampus of IE mice (Wang et al., 2018; Alshammari et al., 2020). We found that after EE intervention, the expression of TRAF6 and pro-inflammatory factors (IL-6 and TNF- $\alpha$ ) in the hippocampus of a mouse model of stroke was reduced, NF- $\kappa$ Bp65 nuclear transport was reduced, and hippocampal neuroinflammation was reversed; however, IE increased the expression of TRAF6/NF- $\kappa$ Bp65 signaling pathway proteins in the hippocampus of a mouse model of stroke and aggravated the neuroinflammatory response in the hippocampus. Our results highlight the therapeutic effect of the EE on hippocampal neuroinflammation in a mouse model of stroke, and the IE-induced inflammatory damage to the hippocampus in a mouse model of stroke.

miRNA, a simple type of non-coding single-stranded small RNA, participates in key biological processes, including cell apoptosis, differentiation, proliferation, metastasis, and metabolism (Mens and Ghanbari, 2018; O'Brien et al., 2018). Multiple studies have shown that regulating the expression of miRNA in the brain can improve the functional recovery of mice with ischemic stroke (Geng et al., 2019; Wang et al., 2019). miR-146a is involved in the regulation of neurological diseases and is closely related to neuroinflammation (Fan et al., 2020; Leontariti et al., 2020). In a study of breast cancer cells, Bhaumik et al. (2008) found that inflammatory factors such as TNF- $\alpha$  can trigger the production of miR-146a through NF- $\kappa$ B-dependent pathways. Another study demonstrated that activation of the NF- $\kappa$ Bp65 signaling pathway promotes the expression of miR-146a-5p to a certain extent (Lu et al., 2015). Additionally, researchers such as Avenoso et al. (2021) found that during the hyaluronic acid 6-mer-induced inflammatory response, the upregulation of miR146a reduced the inflammatory cascade by regulating the activation of NF- $\kappa$ B. The experimental data revealed that the expression of miR-146a in the hippocampus of the SE group was higher than that in the sham group. We believe that, under normal circumstances, the mouse hippocampal NF- $\kappa$ B signaling pathway and miR-146a are in a relatively stable balance. In the SE group, the increased expression of miR-146a in the hippocampus of mice may be caused by activation of the NF- $\kappa$ B signaling pathway induced by stroke, following which the increase in miR-146a negatively regulates the NF- $\kappa$ B signaling pathway through the targeting effect of TRAF6, which controls neuroinflammation of the hippocampus to a certain extent. Taken together, this process may function as a negative feedback regulation mechanism of the body's anti-inflammatory response. However, the increase in miR-146a caused by stroke is insufficient to prevent the cascade effect of neuroinflammation during stroke. Considering that the role of miRNAs in the regulation of neuroinflammation is complex and dynamic, both pro- and anti-inflammatory miRNAs are often activated in parallel (Gaudet et al., 2018). Therefore, the existence of pro-inflammatory miRNAs that promote neuroinflammation remains a possibility.

Interestingly, studies have found that miRNAs can regulate many aspects of social interaction (Bahi, 2016, 2017; Fregeac et al., 2016). A social environment can also directly affect the expression of miRNAs and, in turn, trigger changes in a number of downstream genes (Ferrante and Conti, 2017; Du et al., 2019). Animal experiments have found that an EE can promote neurogenesis in the dentate gyrus of the hippocampus by regulating the levels of miRNAs in the mouse brain (Brenes et al., 2016). EE can also stimulate endogenous mesenchymal stem cells to secrete exosomes miR-146a, preventing cognitive impairment caused by diabetes (Kubota et al., 2018). Moreover, miR-146a is associated with the neuroinflammatory response (Aronica et al., 2010) and can prevent the decline in cognitive function caused by surgical trauma by inhibiting hippocampal neuroinflammation in a mouse model of postoperative cognitive dysfunction (Chen et al., 2019). TRAF6 is a key signaling molecule in the NF- $\kappa$ B signaling pathway. Through a database comparison and literature analysis (Aronica et al., 2010), we determined that TRAF6 is the target gene of miR-146a-5p. In this study, the level of miR-146a-5p in the hippocampus of the EE group was significantly higher than that of the SE group. Meanwhile, the level of TRAF6 mRNA and protein in the EE group was lower than that of the SE group. These results indicate that the EE intervention-induced increase in miR-146a leads to the degradation of TRAF6 mRNA and inhibits the translation of TRAF6 protein by targeting TRAF6 mRNA. This process may effectively control the activation of the hippocampal NF- $\kappa$ B signaling pathway and the progression of neuroinflammation in a mouse model of stroke, and have a significant protective effect on stroke. Furthermore, studies have also reported that isolated feeding can cause miRNA dysregulation in the brain, as well as decreased hippocampal cell proliferation, leading to poor recovery after stroke (Holmes et al., 2020). In this study, the level of miR-146a in the hippocampus of mice in the IE group was significantly lower than that in the SE group, and the levels of TRAF6 mRNA and protein were significantly higher than those in the SE group. It is possible that the IE reduced the promotion of miR-146a expression caused by activation of NF- $\kappa$ B in the hippocampi of a mouse model of stroke. In

that case, the low level of miR-146a would be unable to inhibit the NF- $\kappa$ B signaling pathway and the cascade amplification effect of inflammation in the hippocampus of mice after stroke by targeting TRAF6, thus aggravating the hippocampal neuroinflammation in mice after stroke.

In summary, EE, a behavioral therapy, has been used in the rehabilitation of various nervous system diseases after years of continuous practice and improvement. In this study, we investigated the effects of an EE and an IE on the cognitive function and hippocampal cell morphology of a mouse model of stroke, and explored the underlying molecular mechanisms of these effects. Our data showed that neuroinflammation occurred in the hippocampus of mice after stroke, the TRAF6/NF- $\kappa$ B signaling pathway was activated, miR-146a-5p expression was up-regulated, and cognitive function was decreased. An IE aggravated hippocampal neuroinflammatory response, nerve damage and cognitive impairment in a mouse model of stroke, which may have been caused by a low level of miR-146a-5p in the hippocampus. However, the EE may increase the expression of miR-146a-5p in the hippocampus of a mouse model of stroke, inhibit TRAF6/NF- $\kappa$ B signaling, reduce the neuroinflammatory response in the hippocampus, alleviate the pathological state of hippocampal damaged nerve cells, and improve cognitive impairment of mice. In conclusion, we found that different living environments can affect hippocampal neuroinflammation and cognitive function in a mouse model of stroke by regulating miR-146a-5p. Thus, miR-146a-5p may represent a potential target for treating PSCI. These findings further explore the mechanism underlying EE-induced improvements in PSCI and could help to develop more effective rehabilitation methods.

In future research, we will extend the intervention cycle of a mouse model of stroke, pay more attention to the effects of the EE at different time points, and study the dynamic changes of various observation indicators. We would also like to explore the relationship between peripheral inflammation and neuroinflammation in a mouse model of stroke; lentiviral miR-146a (agonist/inhibitor) could be injected into the hippocampus of mice to further verify the role of this EE-regulated signaling pathway. In terms of clinical research, we hope to design more complete and enriched rehabilitation programs based on EE elements to better reflect the important role of environmental intervention in clinical practice.

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