# The Effect of miR-132, miR-146a, and miR-155 on MRP8/TLR4-Induced Astrocyte-Related Inflammation

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Abstract Astrocyte activation, associated with the release of pro-inflammatory cytokines interleukin 1-β (IL-1β), interleukin-6 (IL-6), and tumor necrosis factor alpha (TNF- $\alpha$ ), is a hallmark of multiple brain diseases, including mesial temporal lobe epilepsy. In recent years, several microRNAs have emerged as important controllers of Tolllike receptor (TLR) signaling. In this study, we investigated the effect of miR-132, miR-146a, and miR-155 on myeloidrelated protein-8 (MRP8) induced astrocyte-related inflammation. Using quantitative polymerase chain reaction (qPCR) and western blot, we found clear upregulation of TLR4 and downstream inflammatory cytokines, along with dysregulation of miR-132, miR-146a, and miR-155 in in vitro astrocytes after exposing them to different concentrations of MRP8. In addition, we focused on the effect of miR-132 on astrocyte-related inflammation induced by MRP8 via lentiviral infection then evaluated the expression of its possible target genes: acetylcholinesterase (AChE) and interleukin-1 receptor-associated kinase (IRAK4). Our results show that miR-132 is a negative feedback regulator of IL-1 $\beta$  and IL-6, but not TNF- $\alpha$ , by targeting IRAK4. Together, our findings demonstrate the novel role of TLR4-related microRNAs, especially miR-132, in the regulation of MRP8-induced

 $\boxtimes$  Jing Peng pengjing4346@163.com astrocyte activation and highlight the importance of miR-132 in the modulation of innate immune response induced by endogenous ligands in neurological diseases.

Keywords Astrocytes . MicroRNA .Inflammation . MRP8 . TLR4

#### Introduction

Astrocytes, constituting the major glial cell population in the central nervous system (CNS), play a crucial role in the regulation of immune response in many human CNS diseases (De Keyser et al. [2008](#page-7-0); Seifert et al. [2006\)](#page-8-0). They become activated under a diversity of insults, with changes in morphology, proliferation, and molecular expression (Hamby and Sofroniew [2010;](#page-8-0) Sofroniew [2009\)](#page-8-0). This reactive astrogliosis, associated with the release of pro-inflammatory cytokines interleukin 1-β (IL-1β), interleukin-6 (IL-6), and tumor necrosis factor alpha (TNF- $\alpha$ ), is a hallmark of multiple brain diseases, including mesial temporal lobe epilepsy (MTLE), migraines, brain edema, and neurodegenerative disorders (Carpentier et al. [2005](#page-7-0); Dong and Benveniste [2001;](#page-8-0) Li et al. [2011;](#page-8-0) Vezzani et al. [2008\)](#page-9-0).

Toll-like receptors (TLRs) are a family of transmembrane proteins of mammalian cells. They are widely expressed in many central nervous system cells and play key roles in the response of innate immunity cells to pathological stimuli (Brown et al. [2011;](#page-7-0) Bsibsi et al. [2002\)](#page-7-0). Besides recognition of bacterial and viral components, TLRs can also play a part in the recognition of several endogenous ligands, including myeloid-related protein-8 (MRP8) (Gill et al. [2010](#page-8-0)).

MicroRNAs (miRNAs) are a class of gene regulators that block subsequent protein production either by inhibiting

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translation or promoting RNA degradation at the posttranscriptional level (Filipowicz et al. [2008](#page-8-0)). In recent years, several miRNAs have emerged as important controllers of TLR signaling, which is being extensively researched (O'Neill et al. [2011](#page-8-0)). Indeed, they may contribute to the pathogenesis of endotoxin tolerance and major age-related diseases, such as cardiovascular diseases, diabetes, Alzheimer's disease (AD), and cancers (Nahid et al. [2011a;](#page-8-0) Olivieri et al. [2013\)](#page-8-0). Although there is a perception that miR-146a, miR-155, and miR-21 are key regulators of TLR signaling (Quinn and O'Neill [2011\)](#page-8-0), miR-132 has been shown to be upregulated in response to several TLRs in multiple monocytic cells (Nahid et al. [2011a](#page-8-0), [2013\)](#page-8-0). miR-132 is a cyclic AMPresponsive element binding (CREB)-regulated miRNA (Cheng et al.  $2007$ ). It was classified as a "neurimmiR" that functions in the "cross-talk" between neuronal and immune systems (Soreq and Wolf [2011\)](#page-8-0). Currently, most studies are focused on its neuronal functions, such as the regulation of neurite outgrowth, spine morphology, and cortical plasticity (Bicker et al. [2014;](#page-7-0) Hancock et al. [2014;](#page-8-0) Scott et al. [2012\)](#page-8-0). However, the immune functions of this miRNA in the CNS have not been completely illustrated. Soreq and his colleagues have reported that miR-132 develops an anti-inflammatory effects by suppressing acetylcholinesterase (AChE) (Shaked et al. [2009](#page-8-0)). This enzyme limits the level of acetylcholine (ACh), an important inhibitor of peripheral inflammation and one of the characterized mediators of "cholinergic antiinflammatory pathway" (Tracey [2007](#page-8-0)). In addition, Soreq showed that excess AChE in transgenic mice induces astrocytic activation (Sternfeld et al. [2000](#page-8-0)). These implied that AChE may play a role in the regulation of astrocytic inflammation. Another study demonstrated that miR-132 plays a crucial role in regulating TLR2-mediated tolerance and cross-tolerance through targeting interleukin-1 receptor-associated kinase (IRAK4) (Nahid et al. [2013](#page-8-0)).

In this study, we first detected the changes of TLR4 and downstream signaling in the MRP8/TLR4 pathway, including IL-1β, IL-6, and TNF-α, in astrocytes with different concentrations of MRP8 stimulation. The expression of miR-132, miR-146a, and miR-155 in astrocytes was also evaluated by quantitative polymerase chain reaction (qPCR). We focused on the effect of miR-132 modulation on MRP8-induced astrocyte-related inflammation via lentiviral infection, and then evaluated the expression of its possible target genes: AChE and IRAK4.

#### Materials and Methods

## Cell Cultures

The U251 human astrocytoma cell line was obtained from the Department of Cell Biology in Xiangya Medical College of Central South University. Cells were cultured in high glucose of Dulbecco's modified Eagle's medium (DMEM; Hyclone, USA) supplemented with 10 % fatal bovine serum (FBS), 100 units/ml penicillin, and 100 μg/ml streptomycin and were kept at 37 °C in humid 5 %  $CO<sub>2</sub>/95$  % air.

## Cell Treatments

Prepared U251 cells were cultured without serum DMEM for 24 h. Then cells were stimulated with increasing concentrations (0.125 μg/ml, 0.25 μg/ml, 0.5 μg/ml, 0.75 μg/ml, 1.0 μg/ml) of purified MRP8 protein (Abcam, Hong Kong) for 24 h. Or, cells were cultured with no serum medium for 24 h after lentivirus transfection, then stimulated with 0.75 μg/ml MRP8 for 24 h. Stimulated cells were used for RNA and protein extraction.

#### RNA Extraction

For RNA isolation, prepared human U251 cells  $(1 \times 10^6)$  from three different experimental sets were homogenized in 1 ml Trizol Reagent (Invitrogen, USA). After adding 0.2 ml of chloroform, mixed vigorously for 15 s, the aqueous phase was isolated by centrifuging at  $4^{\circ}$ C at a speed of 12. 000 rpm for 15 min. RNA was precipitated with 0.5 ml isopropyl alcohol, washed twice with 75 % ethanol by centrifugation at 4 °C at a speed of 7500 rpm for 5 min, then dissolved in 20–50 μl nuclease-free water. The concentration and purity of RNA were determined at 260/280 nm using a Nanodrop spectrophotometer (Thermo, USA).

#### Western Blot Analysis

The U251 human astrocytoma cells were washed with PBS before collecting for total protein extraction on ice. After adding NP-40 lysis solution, the homogenate was centrifuged at 12,000 rpm for 30 min at 4 °C. The supernate was collected, and the protein concentration was determined by a bicinchoninic acid (BCA) protein assay kit. Equal amounts of protein (50 μg) were separated by a 10–15 % SDS-PAGE gel and transferred onto a PVDF membrane. The membrane was blocked with 5 % nonfat milk in TBST for 1 h at room temperature. The proteins were detected with specific primary antibodies (TLR4 (1:200; Abcam), IL-1β (1:500; Novus Biologicals), IL-6 (1:1000; Abcam), TNF-α (1:1000; R&D), and IRAK4 (1:1000; Cell Signaling)) with gentle shaking at 4 °C overnight. The expression of β-actin (1:10,000; Sigma) was used as an internal reference. Anti-mouse/rabbit IgG (1:7500; Jackson Immuno Research) peroxidase reactions were used for immunostaining. The membranes were developed using an enhanced chemiluminescence (ECL) kit (Millipore) and exposed to X-ray film. Image J software (Nation Institutes of Health) was used to quantitatively analyze protein expression levels.

## Lentivirus Transfection

Packaging and production of lentivirus, which carry the hsa-pri-miR-132-3p precursor, hsa-anti-miR-132-3p, and their controls were obtained from Shanghai GeneChem Biotech Co. (Shanghai, China). The lentiviral transduction was carried out according to the manufacturer's instructions (GeneChem). Astrocytoma cells were cultured in six-well uncoated plastic plates at a density of  $5 \times 10^5$ cells/well and divided into five groups: blank control group (without lentivirus vector (Con)), miR-132 over-expression group (miR-132-up) and its negative control group (miR-132up-con), and the down-expression group (miR-132-down) and its negative control group (miR-132down-con). Cells were infected with a multiplicity of infection (MOI) of 50 for 10 h at 37  $\degree$ C, followed by addition of fresh medium. Three days later, cells infected with lentiviral vectors were selected using PURO at a concentration of 0.25 μg/ml for 48 h. The transfection efficiency was evaluated by enhanced green fluorescent protein (GFP) and validated by qPCR. Cells were harvested for RNA 5 days after infection or stimulated with MRP8 for further experiments.

# TLR4, IL-1β, IL-6, TNF-α, AChE, and IRAK4 Expression Evaluated by qPCR

We used the following primers: TLR4 (forward: atc atc cag gaa ggc ttc ca, reverse: gct gcc tca gca agg act tct),  $IL-1\beta$ (forward: gcc aac aag tgg tat tct cca, reverse: tgc cgt ctt tca tca cac ag), IL-6 (forward: gtc aac tcc atc tgc cct tc, reverse: tgt ggg tgg tat cct ctg tg), TNF- $\alpha$  (forward: aag gag gag aag ttc cca aa, reverse: tct ttg aga tcc atg cca tt), AChE (forwad: ggg gct cag cag tac gtt ag, reverse: gtc gag cgt gtc ggt gg), IRAK4 (forward: cga gcg aca gtg aca acc t, reverse: atg tgc cag gaa agt ggt g), and β-actin (forward: ccc atc tat gag ggt tac gc, reverse: ttt aat gtc acg cac gat ttc). Complementary DNA (cDNA) was synthesized from 500 pg of total RNA using a Prime Script RT Reagent Kit (TAKARA, Dalian, China). RNase-free  $dH_2O$ was added to make the total reaction volume 10 μl. TLR4, IL-1β, IL-6, TNF-α, AChE, and IRAK4 expressions were analyzed using SYBR® Premix ExTaq<sup>TM</sup> II (TAKARA, Dalian, China), which was run on the BioRad CFX384 Touch Real-Time PCR detection system. All procedures were performed according to the manufacturer's instructions. All assays were performed in triplicate. Data analysis was performed using the  $2^{-(A \Delta C)}$  method to determine the relative quantitative level and was expressed as a fold-difference to the relevant control (recognized as  $1±0.00$ ). β-actin expression was used as an internal reference.

# miR-132, miR-146a, and miR-155 Expression Evaluated by qPCR

miRNA primer was purchased from GeneCopoeia. The catalog of each primer is as follows. Hsa-miR-132-3p: HmiRQP0161. Hsa-miR-146a-5p: HmiRQP0196. Has-miR-155-5p: HmiRQP0221. Homo sapiens snRNA U6: HmiRQP9001. cDNA synthesis was performed using the One Step PrimeScript® miRNA cDNA Synthesis Kit (TAKARA, RR716) according to the manufacturer's instructions. Total RNA was 500 pg, and total reaction volume was 20 μl. The qPCR reaction was performed using the SYBR® Premix Ex Taq™ II (TAKARA, RR716) kit. Data analysis was performed using the  $2^{-(A \Delta C)}$  method to determine the relative quantitative level and was expressed as a fold-difference to the relevant control (recognized as  $1 \pm 0.00$ ). The expression of the U6 small nuclear RNA gene was used as an internal reference.

#### Statistical Analysis

Data are presented as the mean±standard deviation for at least three independent experiments. We performed a Student's  $t$ test to determine significant differences between two groups. One-way analysis of variance was utilized to determine significant differences among multiple groups. A  $p$  value of less than 0.05 was considered statistically significant.

## Results

# The Effects of MRP8 Treatment on the Expression of TLR4, IL-1 $\beta$ , IL-6, and TNF- $\alpha$

qPCR and western bolt was performed to examine the expression of TLR4, IL-1 $\beta$ , IL-6, and TNF- $\alpha$  in U251 human astrocytoma cells after exposure to different concentrations of MRP8. Our qPCR results showed that the gene expression of TLR4, IL-1β, and IL-6 had a similar tendency. All of them increased significantly after MRP8 stimulation at a concentration of 0.125 μg/ml and reached the highest point at a concentration of 0.75 μg/ml (Fig. [1a](#page-3-0)–c). Expression changes of TNF-α were not as obvious as with IL-1β or IL-6. TNF-α expression began to rise significantly at a concentration of 0.125 μg/ml, and increased the most at 0.5 μg/ml (Fig. [1d\)](#page-3-0). Western blot results showed the same tendency with gene expressions (Fig. [1e, f](#page-3-0)).

# The Effects of MRP8 Treatment on the Expression of miR-132, miR-146a, and miR-155

To verify that miR-132, miR-146a, and miR-155 participate in MRP8-induced inflammation, we exposed U251 human astrocytoma cells to different concentrations of MRP8 for 24 h.

<span id="page-3-0"></span>Fig. 1 Expression of TLR4, IL-1β, IL-6, and TNF-α after stimulation with MRP8. U251 human astrocytoma cells were left untreated or were treated for 24 h with the indicated additions.  $a$ –c TLR4, IL-1 $\beta$ , and IL-6 mRNA increased significantly at 0.125 μg/ml MRP8 and reached the highest point after exposure to 0.75 μg/ml MRP8. d Expression of TNF-α mRNA increased significantly after exposure to 0.125 μg/ml MRP8, reaching the highest point at 0.5 μg/ml MRP8. e, f Western blot results showed the same tendency with gene expressions ( $p<0.05$ )



As shown in Fig. [2a, b](#page-4-0), the expression of miR-132 and miR-146a began to increase significantly compared with controls after exposure to 0.5 μg/ml MRP8. As the concentration of MRP8 increased, the expression of miR-132 also increased. The expression of miR-146a reached its top point at a concentration of 0.75 μg/ml MRP8, then declined from that point on. The general trend of miR-155 expression was similar to miR-146a, except that it augmented significantly with a concentration level of 0.125 μg/ml and gradually reached its peak at  $0.75 \mu$ g/ml (Fig. [2c\)](#page-4-0).

# The Effects of Modulated miR-132 on the Expression of IL-1 $\beta$ , IL-6, and TNF- $\alpha$

Over 80 % of U251 human astrocytoma cells infected with lentivirus expressed enhanced green fluorescent protein (GFP) (Fig. [3a](#page-4-0)). We also validated that using qPCR method (Fig. [3b\)](#page-4-0). qPCR results showed that the expression of IL-1β, IL-6, and TNF- $\alpha$  increased significantly after MRP8 stimulation compared with controls (Fig. [4\)](#page-5-0). Downregulation of miR-132 before MRP8 stimulation promoted the release of both IL-1β and IL-6, whereas upregulation of miR-132 had the opposite effect (Fig. [4a, b\)](#page-5-0). Pre-downregulation or pre-upregulation of miR-132 before MRP8 stimulation had no effect on the release of TNF- $\alpha$  compared with MRP8 stimulation alone (Fig. [4c](#page-5-0)).

# The Effects of Modulated miR-132 on the Expression of AChE and IRAK4

Our qPCR result showed that the expression of AChE increased conspicuously in U251 human astrocytoma cells after MRP8 stimulation compared with control. But it did not show an inhibited regulatory role with aberrant expression of miR-132 (Fig. [5a\)](#page-5-0). IRAK4 is an important kinase in TLR4 signaling and has been verified as a target of miR-132 (Nahid et al. [2013\)](#page-8-0). Here, both our qPCR and western blot results showed that IRAK4 increased significantly after MRP8 pretreatment compared with control. Greatly upregulated miR-132 through lentivirus transfection could inhibit the expression of IRAK4. And pre-downregulation of miR-132 significantly promoted

<span id="page-4-0"></span>



Fig. 2 Gene expression of miR-132, miR-146a, and miR-155 after exposure to MRP8. a Expression of miR-132 began to increase significantly after exposure to 0.5 μg/ml MRP8. As MRP8 concentration increased, the expression of miR-132 upregulated further. b miR-146a upregulated significantly compared with controls after exposure to 0.5 μg/ml MRP8 and reached its top point after exposure to 0.75 μg/ml MRP8. c The expression of miR-155 augmented significantly at a concentration of 0.125 μg/ml MRP8 and reached its peak after exposure to 0.75  $\mu$ g/ml MRP8 ( $\check{p}$ <0.05)

the expression of IRAK4, whereas upregulation of miR-132 before MRP8 stimulation had the opposite effect (Fig. [5b](#page-5-0)–d).



enhanced green fluorescent protein (GFP)-positive rate of U251 human astrocytoma cells after transfection was more than 80 %. Scale bar in (a), 25 μm. b, c qPCR of miR-132 after lentivirus transfection. miR-132 expression in the miR-132-down group was significantly lower than in its negative control group (miR-132down-con). And in the miR-132-up group, miR-132 expression was significantly higher than in its control group. (\* $p$ <0.05; \*\* $p$ <0.01)

# Discussion

Accumulating experimental evidence suggests that proinflammatory molecules can alter glio-neuronal communication, contributing to the generation of seizures and seizurerelated neuronal damage (Devinsky et al. [2013](#page-7-0); Vezzani et al. [2013](#page-9-0)). Although microglia are an important type of immune cell of the CNS, astrocytes are thought to be both the major source and targets of epileptogenic inflammatory signaling (Aronica et al. [2012\)](#page-7-0). Our previous findings showed that astrocyte-related neuroinflammation induced by MRP8 may play an important role in the development of immature MTLE (Gan et al. [2014\)](#page-8-0). In this study, we now report the dose-dependent relationship of MRP8, an endogenous ligand of TLR4, and inflammation-related miR-132, miR-146a, and miR-155 in U251 human astrocytoma cells. Furthermore, we detected the expression of proinflammatory cytokines IL-1β, IL-6, and TNF- $\alpha$  and found that miR-132 participated in the regulation of IL-1β and IL-6 secretion but not TNF-α, by

<span id="page-5-0"></span>Fig. 4 Effect of miR-132 on the MRP8-induced release of IL-1β, IL-6, and TNF- $\alpha$ . **a**–c IL-1 $\beta$ , IL-6, and TNF- $\alpha$  increased significantly after MRP8 stimulation compared with controls. Downregulation of miR-132 before MRP8 stimulation promoted the release of both IL-1β and IL-6, whereas upregulation of miR-132 had the opposite effect. Downregulation or upregulation of miR-132 before MRP8 stimulation had no effect on the release of TNF-α compared with MRP8 stimulation alone. (\* $p$ <0.05;  $\frac{4}{7}$ p>0.05)



targeting IRAK4. This finding highlights the importance of miR-132 in the modulation of the innate immune response induced by endogenous ligands in the CNS.

TLR4 is one of the membrane-bound pattern-recognition receptors profoundly expressed in astrocytes (Bsibsi et al.

[2002\)](#page-7-0). It can sense a variety of microbial-specific motifs or endogenous ligands to trigger an innate immune response. TLR4 activation results in the induction of transcriptional factors such as nuclear factor-κB (NF-κB), which has the ability to trigger various pro-inflammatory genes such as those



Fig. 5 AChE and IRAK4 expression after regulating miR-132 in astrocytes exposed to MRP8. a AChE mRNA increased significantly after MRP8 stimulation in U251 human astrocytoma cells. Modulation miR-132 via lentivirus transfection has no effect on AChE mRNA expression. mRNA expression (b) and protein expression of IRAK4 (c, d) after exposure to MRP8 for 24 h in U251 human astrocytoma cells transfected with anti-miR-132 or pre-miR-132 lentivirus vector (MOI= 50). Greatly upregulated miR-132 could inhibit the expression of IRAK4,

and downregulated miR-132 promotes the expression of IRAK4. IRAK4 increased significantly after MRP8 pretreatment in U251 cells compared with the control group. Pre-downregulation of miR-132 enhanced the effect of MRP8 inducing the expression of IRAK4, whereas upregulation of miR-132 before MRP8 stimulation had the opposite effect (\* $p$ <0.05; \*\* $p$ <0.01; \* $p$ >>0.05). MRP8 myeloid-related protein 8, MOI multiplicity of infection

encoding cytokines, chemokines, proteins of the complement system, cyclooxygenase-2, and inducible nitric oxide. As an endogenous ligand of TLR4, MRP8 participates in the neuroinflammation of multiple CNS diseases, including MTLE, traumatic brain injury, and ischemic and neurodegenerative diseases (Engel et al. [2000;](#page-8-0) Gan et al. [2014](#page-8-0); Sheng et al. [1994;](#page-8-0) Ziegler et al. [2009\)](#page-9-0). Our study is the first to demonstrate the dose-dependent relationship of MRP8 and TLR4 activation in astrocytes in vitro. Although MRP8 always presents as a heterocomplex together with MRP14 (Floris et al. [2004](#page-8-0); Viemann et al. [2007;](#page-9-0) Vogl et al. [2004\)](#page-9-0), it has been argued that MRP8 is the active component that binds to the receptor site (Vogl et al. [2007;](#page-9-0) Yonekawa et al. [2011](#page-9-0)). The significant activation of TLR4 after MRP8 exposure in our experiments supports that point. Furthermore, we found that the expression of IL-1β, IL-6, and TNF-α, downstream inflammatory cytokines in the MRP8/TLR4 pathway, increased to various degrees. In our previous study, we reported elevated expression of IL-1β along with activation of the MRP8/TLR4/NF-κB pathway in astrocytes (Gan et al. [2014](#page-8-0)). In addition, other research has shown that activation of the TLR4/NF-κB signal pathway results in the transcription of TNF- $\alpha$ , IL-1 $\alpha$  and IL-1β in other immune cells (Vainas et al. [2006](#page-8-0); Vogl et al. [2007](#page-9-0); Ziegler et al. [2009](#page-9-0)). So we speculate that MRP8 may influence the expression of IL-1 $\beta$ , IL-6, and TNF- $\alpha$  in a similar fashion. These findings provide a possible mechanism for how MRP8 contributes to neurological diseases.

The discovery of miRNAs represents a tremendous revolution in the regulation of transcription and translation. Activation of mammalian immune response needs exquisite manipulation. The capability of miRNAs to fine-tune gene expression naturally lends itself to the regulation of the immune system (Virtue et al. [2012\)](#page-9-0). Therefore, this study focused on the relationship between TLR4-related miR-132, miR-146a, and miR-155 and MRP8-induced inflammation in astrocytes.

The dysregulation of miR-132 is associated with several neurological disorders, such as Toxoplasma gondii infection, MTLE, primary glioblastoma multiforme, schizophrenia, AD, and Parkinson's disease (Parker et al. [2013;](#page-8-0) Peng et al. [2013](#page-8-0); Tognini and Pizzorusso [2012](#page-8-0); Xiao et al. [2014\)](#page-9-0). However, the underlying molecular mechanisms are still incompletely illustrated. In this study, we report a dose-dependent reaction between miR-132 upregulation and MRP8 stimulation in astrocytes. To further evaluate the function of miR-132 in response to MRP8 stimulation, we investigated the effect of miR-132 on IL-1 $\beta$ , IL-6, and TNF- $\alpha$ , three major inflammatory cytokines related to neuroinflammation and epilepsy (Li et al. [2011](#page-8-0); Shimada et al. [2014](#page-8-0); Vezzani et al. [2013](#page-9-0)). Our results show that upregulation of miR-132 reduced IL-1β and IL-6 gene levels in cultures stimulated with MRP8, while downregulation of miR-132 had the opposite effect. This finding testifies to the fact that miR-132 is a negative feedback regulator of IL-β and IL-6 expression in activated astroctyes. Combined with our previous in vivo studies (Gan et al. [2014;](#page-8-0) Peng et al. [2013](#page-8-0)), increased miR-132 probably protects the immature brain by suppressing the neuroinflammation that would facilitate seizures. miR-132 can also modulate antiviral innate immunity induced by Kaposi's sarcoma-associated herpesvirus (KSHV) infection through suppression of the p-300 transcriptional co-activator (Lagos et al. [2010](#page-8-0)). Due to the homologous sequence, each miRNA has the potential to regulate the translation of hundreds of genes (Selbach et al. [2008\)](#page-8-0). Coinciding with previous study (Nahid et al. [2013\)](#page-8-0), we found that miR-132 might influence the MRP8-induced activation of astrocytes by targeting IRAK4, a pivotal adaptor kinase. As illustrated in Fig. 6, IRAK4 is recruited to MyD88 after TLR4 activation, forming a helical assembly of the Myd88-IRAK4-IRAK2/1 complex that further activates TNFR-associated factor 6 (TRAF6) and eventually leads to gene transcription and inflammation (Nahid et al. [2011b\)](#page-8-0). In cultured glia, AChE levels increase in response to dibutyrylcyclic-AMP (Karpel et al. [1996](#page-8-0)). Moreover, AChE activities were found in astrocytoma and glioblastoma tumors (Grisaru et al. [1999](#page-8-0)). Consistently, we found significant upregulation of AChE messenger RNA (mRNA) after MRP8 stimulation in this study. Although miR-132 can attenuate inflammation by suppressing AChE, enhancing the brain's ability to govern inflammation via cholinergic signaling in macrophages (O'Neill [2009](#page-8-0); Shaked et al. [2009\)](#page-8-0). What is more, it may participate in amelioration of the inflammation in human inflammatory bowel disease (Maharshak et al. [2013\)](#page-8-0) and mediate stress-inducible cognitive deficits through



Fig. 6 miR-132 negative regulation on MRP8-induced inflammation in astrocytes. MRP8 binds to TLR4 and activates the MyD88-dependent pathway. This eventually leads to gene transcription with the production of IL-1β, IL-6, and TNF-α. Upregulated miR-132 in turn negatively regulates the release of inflammatory factors by targeting IRAK4

<span id="page-7-0"></span>targeting AChE (Shaltiel et al. [2013](#page-8-0)). Nevertheless, the expression of AChE mRNA was not influenced by modulating miR-132 in our study. This may be due to that different circumstances call for different manipulations of the AChE transcript (Shaked et al. [2009](#page-8-0); Berson et al. 2008; Sklan et al. [2004\)](#page-8-0). In addition, the impact of altering a miRNA on a biological process is influenced by several factors, including the expressions level of the miRNA and the mRNA target (Ebert and Sharp [2012\)](#page-8-0). AChE levels are known to be very low in all types of normal glia (Karpel et al. [1996](#page-8-0)).

miR-146a is a NF-κB-dependent miRNA and plays an important role in innate immune regulation (Taganov et al. [2006\)](#page-8-0). It is known to target key elements of the MyD88 signaling pathway (such as IRAK1 and TRAF6), modulating the inflammatory response mediated by several TLR ligands in endotoxin tolerance (Nahid et al. [2011a](#page-8-0)). As observed in the MTLE hippocampal region, miR-146a is mainly localized in activated astrocytes and increases significantly in the acute and latent stages of disease (Aronica et al. 2010; Omran et al. [2012\)](#page-8-0). Our study consistently found that miR-146a increased significantly after exposure to 0.5 μg/ml MRP8, accompanied by an obvious release of IL-1β and IL-6. This specific location and expression pattern could help miR-146a to modulate seizure-related neuroinflammation. Other studies have also indicated that the aberrant expression of miR-146a contributes to the age-associated dysfunction of macrophages (Jiang et al. [2012](#page-8-0)). Specifically, Anand found that miR-146a was a negative feedback regulator of IL-1βinduced inflammation in both primary human astroctyes and the astrocytoma cell line by targeting IRAK1, IRAK2, and TRAF6 (Iyer et al. [2012\)](#page-8-0). All of the above findings indicate that miR-146a may be involved in the regulation of astroctye activation induced by endogenous ligand MRP8 through modification of different target genes together with miR-132.

Although the expression of pro-inflammatory factor TNF- $\alpha$  also increased with MRP8 stimulation, the changes were much weaker compared with IL-1β and IL-6. We speculate that it is due to TNF- $\alpha$  not playing a main role in this inflammatory process. It is worth noting that modulating miR-132 before MRP8 stimulation did not influence the expression of TNF- $\alpha$  in our experiment. Although, they observed dosedependent production of TNF- $\alpha$  in PBMCs and THP-1 monocytes after stimulation with several TLR ligands accompanying the upregulation of several miRNAs (Nahid et al. [2013\)](#page-8-0). It is widely believed that the regulation of TNF- $\alpha$  is associated with miR-155. In our previous report, we found that suppressing TNF- $\alpha$  with its inhibitor resulted in a significant decline of miR-155 (Omran et al. [2013](#page-8-0)). Other reports have also shown a direct relationship between TNF- $\alpha$  and miR-155 in other diseases, such as epilepsy (Ashhab et al. 2013), B cell lymphomas (Pedersen et al. [2009\)](#page-8-0), alcoholic liver disease (Bala et al. 2011), and septic shock (Tili et al. [2007\)](#page-8-0). Therefore, it is very likely that the upregulation of miR-155 after MRP8

stimulation is mainly responsible for the changes in TNF- $\alpha$ in our study.

In summary, we report the activation of MRP8/TLR4 signaling in vitro in astrocytes and the effect on downstream inflammatory cytokines (IL-1β, IL-6 and TNF- $\alpha$ ) accompanying the upregulation of miR-132, miR-146a, and miR-155. Furthermore, we demonstrate that miR-132 modulates the release of IL-1β and IL-6 induced by MRP8 in astrocytes by targeting IRAK4. These findings open up a new perspective on modulating astrocyte-related neuroinflammation in noninfectious CNS diseases.

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Conflict of Interest The authors declare that there are no conflicts of interest.

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