miR-212 mediates counter-regulation on CRH expression and HPA axis activity in male mice

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Abstract

The mechanisms of hypothalamic–pituitary–adrenal (HPA) axis regulation have been studied persistently but still are not elucidated. Considering the emerging roles of microRNA in stress response, we conducted a microRNA microarray in mice hypothalamus to identify the potential role of microRNAs in regulating the HPA axis. In total, 41 microRNAs changed during heat stress in which we found that miR-212 contains a binding sequence with corticotropin-releasing hormone (Crh) 3′UTR according to a sequence analysis. We observed that miR-212 expression in the hypothalamus was escalated by repeated heat and restraint stress. By overexpression or inhibition of miR-212 and the dual-luciferase reporter assay, we proved that miR-212 could bind with Crh 3′UTR to regulate its expression in mice hypothalamus primary cells and in the hippocampus neuron cell line HT-22. In addition, we injected miR-212 agomir or antagomir in mice hypothalamus to overexpress or inhibit miR-212, which leads to alterations of CRH expression and HPA axis activity in vivo. Furthermore, miR-212 and CRH were both transcribed by the cAMP response element-binding protein (CREB). Overexpression and inhibition of miR-212 affect CREB-dependent CRH expression. Taken together, our results suggest an inhibitory role of miR-212 on the HPA axis, which acts in a counter-regulatory manner.

Introduction

The hypothalamic–pituitary–adrenal (HPA) axis plays a pivotal role in prompting management, adaptation and recovery from stress (Sapolsky et al. 2000, de Kloet et al. 2005, McEwen 2007). It is well documented, however, that overactivity of the HPA axis is accompanied by impaired physical functions, including growth, metabolism, circulation, reproduction, inflammation and immunity (Charmandari et al. 2005, Chrousos & Kino 2007, Nicolaides et al. 2015). The mechanisms of the HPA axis regulation continue to intrigue researchers (McEwen 1998, 2008, Glaser & Kiecolt-Glaser 2005, Reynolds 2013). As the starting point of the HPA axis, corticotropin-releasing hormone (CRH) is a key element in managing HPA axis activity, and numerous researchers have studied its regulation extensively (Kovacs 2013). The dominant way by which CRH is regulated is through the negative feedback of glucocorticoids (GC) (Herman et al. 2016). Other factors also seem to be involved, however, as
treatment with GC in adrenalectomized rats does not prevent an increase in stress-induced CRH hnRNA (Kageyama & Suda 2009). In addition, a decline in CRH after stress exposure is independent of circulating GC because adrenalectomized rats, which lack GC, display an identical pattern (Shepard et al. 2005). Aside from GC, many negative regulating factors of CRH have been identified so far, including GABAergic neurons (Gunn et al. 2015), endocannabinoid signaling (Hill & Tasker 2012) and inflammatory cytokines (Felger & Lotrich 2013). The network of transcription factors and co-regulators of regulation of CRH expression, however, remain to be explored (Kovacs 2013).

Since their discovery, microRNAs have been found to be involved in various biological processes and usually function as negative regulators through post-transcription regulation by binding target mRNA to inhibit mRNA translation or facilitate mRNA degradation (Zeng et al. 2002, Bartel 2004). Recently, it has been indicated that microRNAs participate in stress response (Leung & Sharp 2010, Hollins & Cairns 2016). A study reported that adult male rats subjected to both acute and chronic restraint stresses show altered expressions of numerous miRNAs in the brain (Meerson et al. 2010). More specifically, Rinaldi et al. found that expressions of let-7a, miR-9 and miR-26a/b increase in the frontal cortex in acute-restraint stress mice (Rinaldi et al. 2010). Furthermore, several studies have reported that alterations of microRNA expression, induced by stress, indirectly affect regulation of HPA axis activity. An in vitro study demonstrates that miR-34c reduces the responsiveness of cells to CRH by regulating corticotrophin-releasing hormone receptor 1 (CRHR1) (Haramati et al. 2011). Additionally, miR-449a contributes to CRHR1 downregulation induced by GC in the pituitary during stress (Nemoto et al. 2013). Another proof is disclosed by the finding that the GC receptor is regulated by miR-18 and miR-124 in the brain (Vreugdenhil et al. 2009). Nevertheless, direct connections between microRNAs and regulation of the HPA axis are absent. Whether the CRH expression is regulated by microRNAs in the hypothalamus remains unknown.

To this end, our study investigates the potential role of microRNAs in regulating CRH and HPA axis activity. By using a microRNA microarray in the hypothalamus and conducting subsequent validation experiments, we prove that miR-212 can bind with Crh 3′ UTR to regulate its expression in a counter-regulatory manner in vitro and can further affect HPA axis activity in vivo. On the basis of our findings, we propose a new perspective of HPA axis regulation, which may be helpful for developing gene therapy interventions for patients with HPA axis overactivity diseases.

**Materials and methods**

**Animals**

We purchased male C57BL/6 (8 weeks old) mice from Slac Laboratory Animal (Shanghai, China) and maintained at 22±2°C, 12 h light/12 h dark cycle (07:00 light on/19:00 light off) with food and water freely available. We conducted all animal experiments in accordance with the ‘Guide for the Care and Use of Laboratory Animals’, and with the approval of the Second Military Medical University Institutional Animal Care and Use Committees.

**Repeated stress process**

After being acclimated for 1 week, 40 mice weighing approximately 22±2g were divided randomly into five groups (n=8) for repeated heat stress, including day 0 (without exposure), day 1 (exposed 1 time), day 3 (exposed 3 times), day 7 (exposed 7 times) and day 14 (exposed 14 times). We also randomly divided another 40 mice in the same batch into five groups for repeated restraint stress with an identical set of groups. Details of the stress procedures are as follows: (1) Heat stimulus: mice were placed in an artificial climate cabin with a temperature of 40°C and relative humidity of 60% for 1h; (2) immobilization: mice were placed in a 50-mL centrifuge tube (28mm diameter×105mm long) with a punching hole for 1h. All experiments were conducted between 09:00h and 10:00h every day. We decapitated the mice at the end of exposure, and then we immediately collected the blood and hypothalamus. We centrifuged the blood at 3000g for 20min to obtain serum for adrenocorticotropic hormone (ACTH) and corticosterone (CORT) detection. We used the hypothalamus to extract RNA and protein for real-time polymerase chain reaction (PCR) and Western blot.

**MicroRNA microarray and data analysis**

We obtained the hypothalamus from another 15 decapitated mice at day 0, day 1 and day 7 (five mice in each group). We abstracted a total of 15 RNA samples by using Trizol reagent (Catalog #15596-026, Invitrogen), which we processed in an Affymetrix GeneChip miRNA3.0 (Catalog #902017, Invitrogen) to profile the patterns of microRNA...
expression. The random-variance model (RVM, which is commonly used for comparison of more than two groups) F-test was applied to filter the differentially expressed microRNAs for the three groups because the RVM F-test can raise degrees of freedom effectively in small samples. After conducting analyses to determine significance and the false discovery rate, we selected the differentially expressed microRNAs according to the P value threshold (Wright & Simon 2003, Clarke et al. 2008).

**Injection of miR-212 agomir and antagonim in mice hypothalamus**

We injected microRNAs agomir and antagonim to the local site for functional research (Hou et al. 2011). We divided the 45 mice weighing between 26g and 28g into five groups (day 0, 1, 3, 7 and 14), and each group had three subgroups (n=3), which we injected with 2μL negative control, miR-212 agomir and miR-212 antagonim (Genepharma, Shanghai, China) at a concentration of 1 OD/μL (~2.5 nmol/μL) in the paraventricular nucleus PVN, respectively. We completed the injection by mouse brain stereotaxic apparatus. The injection coordinates were 0.82 mm caudal and 0.1 mm lateral from Bregma and 4.75 mm ventral from the surface of the skull at Bregma, according to Paxinos & Franklin (2003).

**Determination of serum hormone concentrations**

We measured serum ACTH and CORT by radioimmunoassay kits (Catalog #D14DJB and Catalog # D10PJB, North Institute of Biological Technology Co. Beijing, China) following the manual protocol.

**Mice hypothalamic primary cells and HT-22 cells**

We purchased primary cells of mice hypothalamus and HT-22 cells, a kind of mice hippocampus neuron cell line, with identification reports from Zhongqiaoxinzhou Biotech Inc. (Shanghai, China) and cultured the cells in the primary neurons’ culture system (Catalog #PriMed-iCell-005, iCell, Shanghai, China) with precoated poly-1-lysine or in Dulbecco’s Modified Eagle Medium (Catalog #SH30022.01B, HyClone; GE Healthcare) supplemented with 10% fetal bovine serum (Catalog #10099-141, Gibco Laboratories) and 1% antibiotic solution (Catalog #15140-122, Gibco Laboratories) and incubated the cells in a humidified 5% carbon dioxide atmosphere at 37°C.

**Transfection**

For hypothalamic primary cell transfection, we used miR-212 agomir and antagonim (Genepharma) at a concentration of 50nM and 100nM, respectively. For HT-22 transfection, we used miR-212 mimics and inhibitors (Genepharma) at a concentration of 50nM and 100nM, respectively. We transfected plasmids for cAMP response element-binding protein (CREB; Genepharma) at a concentration of 3μg/mL. We performed all transfections by using micropoly-transfecter cell reagent (Catalog #MT115, Micropoly, NanTong, China), and extracted RNA and protein 48h after the transfection for downstream experiments.

**Dual-Luciferase reporter assay**

We grew HT-22 cells on 96-well plates to approximately 50% confluence and co-transfected plasmids of GP-miRGLO (Genepharma) containing either the wild-type or mutated Crh 3’UTR with miR-212 mimics or negative control. Forty-eight hours after transfection, the cells underwent lysis for luciferase activity with a Dual-Luciferase Reporter Assay System (Catalog #E1910, Promega). We normalized firefly luciferase activity to Renilla luciferase activity for each cell culture.

**Total RNA and protein extracted from mice hypothalamus and cells**

Because of the small size of mice hypothalamus, we used All-In-One DNA/RNA/Protein Mini-preps Kit (Catalog #B618003, Sangon Biotech, Shanghai, China) to extract RNA and protein simultaneously. In general, after tissue homogenization and lysis, we centrifuged the liquid in an RNA purification column to obtain RNA and added the flow-through with protein precipitation solution to precipitate protein. In cells, we extracted RNA by Trizol reagent (Catalog #15596-026, Invitrogen) and extracted protein using a whole-protein extraction kit (Catalog #KGP250, Keygene, Nanjing, China).

**Real-time quantitative PCR analysis**

We reverse-transcribed 1μg RNA of each sample to cDNA using a Reverse-Transcription Reagent Kit (Catalog #RR036A & #RR037A, Takara Bio). We performed real-time quantitative PCR amplification with the SYBR Green Kit (Catalog #QPK-201, Toyobo Bio Inc., Osaka,
Japan) using the StepOnePlus (Applied Biosystems). We normalized the mRNA expression of the target gene to 18s and normalized miRNA to U6. We used the following primers: 18s-forward, GTCAACCGTGAACCCCATT; 18s-reverse, CCATCAATCGGTAGTGGG; Creb-forward, TCTCACCCTCACCCTGCT; Creb-reverse, AAGCGCAACATTTACCAATTG; CRH-forward, TGCCACTCCAAATTACCAA and Creb-reverse, ACCCCATCGGTACCATGGT. We purchased the primer set for U6 and miR-212 from Genepharma.

Western blot

We separated 30 μg denatured proteins by electrophoresis in SDS-page gel and transferred the proteins to the polyvinylidene difluoride membrane (Catalog #BSP0161, PALL Life Science, Port Washington, NY, USA) using the Bio-Rad system. We purchased the following antibodies against CREB antibody (Catalog #ab32515), anti-CREB (Phospho-S133, Catalog #ab32096) and anti-β-actin (Catalog #D110001, Sangon Biotech, Shanghai, China). We normalized grayscales of target protein, measured by GeneSnap from SynGene software package, to β-actin.

Statistics

We represented the data as mean ± S.E.M. The statistical difference between the two groups was assessed by an independent T-test. We performed one-way analysis of variance, followed by a Bonferroni test as the post-test, to analyze differences among the three or more groups. Differences were considered significant at the 95% confidence level (#P < 0.001, &P < 0.01, and ***P < 0.001: *P < 0.05, **P < 0.01, and ***P < 0.001: *P < 0.05, **P < 0.01, and ***P < 0.001: *P < 0.05, &P < 0.01, and ***P < 0.001; &P < 0.05, &P < 0.01, and ***P < 0.001; and 5& < 0.05, 5& < 0.01, and 5& & < 0.001).

Results

Hypothalamic miR-212 expression was escalated in mice exposed to repeated stress

To observe changes of hypothalamic microRNAs expression in mice exposed to repeated stress, we used Affymetrix GeneChip miRNA3.0 to investigate the expression pattern of microRNAs in the hypothalamus during heat stress as described in the Materials and methods section. Among all the microRNAs detected, we identified 41 microRNAs with significant changes and a cluster analysis was exhibited in Fig. 1A. Through sequence-matching analysis of these 41 microRNAs, we identified 1136 target genes in three microRNA databases: Targetscan, miRdb and miRanda. The most relevant gene ontology and pathway pertaining to these genes were the DNA-dependent regulation of transcription and the PI3K-Akt signaling pathway, respectively. We did find the direct link between the microRNA and the HPA axis in which miR-212-5p could bind with Creb3UTR at position 284–290 (Fig. 2E) according to Targetscan. The expression of miR-212 increased gradually at day 1 and day 7 compared with day 0 in the microarray.

To elucidate changes of miR-212 expression and HPA axis activity, we conducted two repeated stress processes on mice and added two groups: day 3 and day 14. Results showed that miR-212 expression escalated by the amount of time exposed to stress, whereas Creb expression was enhanced in the mice that were exposed to the stimulus at day 1 and climaxed at around day 3. Subsequently, the Creb expression showed a significant decrease at day 7 and day 14 in both heat and restraint stress models (Fig. 1B and C) as well as protein level (Fig. 1E and F). In addition to the CRH expression in the hypothalamus, the serum content of ACTH and CORT exhibited identical alterations (Fig. 1D and G) in both models, which indicated that the inhibitory mechanisms of HPA axis produced effects at day 7 and day 14.

Because of the inverse relationship between a gradual increase in miR-212 and a subsequent decrease in HPA axis activity in mice subjected to repeated stress, and more meaningfully, considering potential binding site for miR-212 exists in Creb3′UTR, we hypothesized that miR-212 may bind with Creb and could be involved in regulating its expression and HPA axis activity during repeated stress.

miR-212-regulated CRH expression in primary cells of mice hypothalamus and hippocampus cell HT-22

To explore whether miR-212 had a role in regulating the CRH expression, we first observed changes of Creb expression in primary hypothalamic cells after overexpression or inhibition of miR-212. Hypothalamic primary cells extracted from mice were identified by immunofluorescence using the neuron specific enolase antibody. The purity of these primary cells was greater than 95% according to the analysis of immunofluorescence (Fig. 2A). As shown in Fig. 2B, overexpression of miR-212 by miR-212 agomir transfection decreased
miR-212 regulates CRH and HPA axis activity

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We used the cell line HT-22, a kind of hippocampus cell that also expresses CRH, to conduct a dual-luciferase reporter assay to further identify the binding activity of miR-212 and Crh 3′UTR. At first, we proved that transfection with miR-212 mimics could decrease mRNA and the protein expression of CRH and miR-212 inhibitors could increase mRNA and protein expression of CRH (Fig. 2C and D). Next, we constructed GP-miRGLO plasmids that contained either a wild-type or mutated binding site in Crh 3′UTR for miR-212 (Fig. 2E). The result of the dual-luciferase reporter assay showed that co-transfection with wild-type plasmids and miR-212 mimics could significantly reduce the relative luciferase activity (firefly luminescence and Renilla luminescence); however, when the binding site was mutated, the effect of the miR-212 mimics disappeared (Fig. 2F). Taken together, our results showed that miR-212 could bind directly to Crh 3′UTR and could regulate the CRH expression in vitro.

A counter-regulatory pathway mediated by miR-212 to inhibit CRH expression in vitro

It has been reported that CREB-responsive elements in both miR-212 and CRH promoters are required for pCREB-dependent transcription of miR-212 in primary cortical neurons and THP-1 monocytes (Remenyi et al. 2010, Nahid et al. 2013) and CRH in response to stress (Seasholtz et al. 1991, Kovacs & Sawchenko 1996, Kovacs 2013). This finding inspired our curiosity to determine the underlying mechanism since we observed that miR-212 and CRH displayed different expression patterns in the hypothalamus after stress (Fig. 1). To explore this, we first observed the expression of CREB in the hypothalamus. Results showed that mRNA expression (Fig. 3A), protein expression and phosphorylation level of CREB in both heat stress (Fig. 3B) and restraint stress (Fig. 3C) had the

mRNA expression of Crh, whereas inhibition of miR-212 by miR-212 antagomir transfection increased mRNA expression of Crh.

Figure 1

Hypothalamic miR-212 expression was escalated in mice exposed to repeated stress. (A) Cluster analysis of 41 significantly changed microRNAs in the hypothalamus of heat-exposed mice (n=5 in groups of day 0, 1 and 7). (B) miR-212 and CRH mRNA expressions (n=8) in a 14-day heat stress process. (C) CRH protein expression in a 14-day heat stress. Grayscale of CRH protein bands normalized to β-actin. (D) Serum contents (n=8) of ACTH and CORT in a 14-day heat stress process. (E) miR-212 and CRH mRNA expressions (n=8) in a 14-day restraint stress process. (F) CRH protein expression in a 14-day restraint stress process. (G) Serum contents (n=8) of ACTH and CORT in a 14-day restraint stress process. Data were presented as mean±s.e.m. *P<0.05, **P<0.01, and ***P<0.001 (vs group of day 0); *P<0.05, **P<0.01, and ***P<0.001 (vs group of day 1); *P<0.05, **P<0.01, and ***P<0.001 (vs group of day 3); and *P<0.05, **P<0.01, and ***P<0.001 (vs group of day 7). A full color version of this figure is available at http://dx.doi.org/10.1530/JME-17-0124.
miR-212 regulates CRH and HPA axis activity

The CRH expression, however, increased at first and subsequently decreased under the condition that CREB persistently increased during repeated stress process.

To observe the role of miR-212 in CREB-dependent CRH expression, we used HT-22 cells for transfection and set 5 groups: blank control (C), negative control of CREB plasmids (NC), CREB overexpression plasmids (CR), co-transfection of CREB plasmids and miR-212 mimics (CRM), and co-transfection of CREB plasmids and miR-212 inhibitors (CRI). Transfection with CREB plasmids resulted in an increase in CREB, miR-212 and CRH (Fig. 3D and E; the group of CR), which meant that CREB was a transcriptional activator of miR-212 and CRH gene expressions, which is in accordance with other research works (Remenyi et al. 2010, Kovacs 2013, Nahid et al. 2013). Co-transfection of CREB plasmids and miR-212 mimics reduced the increase in the CRH expression, whereas miR-212 inhibitors amplified the role of CREB overexpression on the CRH expression compared with the group that had only CREB overexpression (Fig. 3D and E; the group of CRM and CRI). Thus, we thought that miR-212 acted in a counter-regulatory way to prevent the overexpression of CRH when CREB was activated during stress.

miR-212-regulated CRH expression and further affected HPA axis activity in vivo

To observe the effects of miR-212 on CRH expression and HPA axis activity in vivo, we overexpressed or inhibited miR-212 in the hypothalamus through injection of miR-212 agomi or antagomi. At first, we observed that injection of miR-212 agomi could significantly increase...
miR-212 regulates CRH and HPA axis activity

Y TANG, X CAI, H ZHANG and others

miR-212 regulates CRH and HPA axis activity

The miR-212 expression in hypothalamus. Meanwhile, CRH expression and HPA axis activity decreased after one-time heat stimulus (data not shown). After that, we conducted a 14-day heat stress process on mice by injecting a negative control, miR-212 agomir or miR-212 antagomir into the hypothalamus. During repeated stress, mice injected with miR-212 agomir or antagomir showed a significant increase or decrease in miR-212 in the hypothalamus (Fig. 4A).

Discussion

Much is known about CRH regulation to date, and many aspects of the inhibitory mechanisms of CRH have been elucidated, including the following two main aspects: (1) negative feedback, which includes GC negative feedback (Di et al. 2003, Evanson et al. 2010), ACTH negative feedback (Silverman & Sternberg 2012) and negative feedback of other hormone or cytokine (Uchoa et al. 2014); and (2) counter-regulation, including an inhibitory neuron projecting to the PVN (Evanson & Herman 2015), an inhibitory factor inducible cyclic AMP

Figure 3

CREB-mediated CRH expression was regulated by miR-212. (A) Effects of heat–restraint stress on the expression of CREB mRNA (n=8) in a 14-day repeated stress process. (B) Protein expression of CREB and p-CREB in the heat stress process (n=3). (C) Protein expression of CREB and p-CREB in the restraint stress process (n=3). Data were presented as mean±s.e.m. *P<0.05, **P<0.01, and ***P<0.001 (vs group of day 0); #P<0.05, ##P<0.01, and ###P<0.001 (vs group of day 1); aP<0.05, aAP<0.01, and aAAP<0.001 (vs group of day 3); and bP<0.05, bP<0.01, and bAP<0.001 (vs group of day 7). (D) In HT-22 cells, overexpression of CREB (CR) led to an increase in miR-212 and CRH mRNA compared with group of control (C) or negative control (NC), co-transfection of CREB plasmids and miR-212 mimics and miR-212 inhibitors (CRI) amplified the increase in CRH mRNA, whereas co-transfection of CREB plasmids and miR-212 inhibitors (CRI) suppressed the increase in miR-212 mRNA compared with the group of NC. (E) Changes of CREB and CRH protein resulted from co-transfection of CREB plasmids and miR-212 mimics or miR-212 inhibitors in HT-22 cells. Data were presented as mean±s.e.m. *P<0.05, **P<0.01, and ***P<0.001 (vs group of C); #P<0.05, ##P<0.01, and ###P<0.001 (vs group of NC); aP<0.05, aAP<0.01, and aAAP<0.001 (vs group of CR); bP<0.05, bP<0.01, and bAP<0.001 (vs group of CRI). A full color version of this figure is available at http://dx.doi.org/10.1530/JME-17-0124.
miR-212 regulates CRH and HPA axis activity

Effects of overexpression or inhibition of miR-212 on CRH expression and HPA activity in mice exposed to the heat stress process. (A) miR-212 expression in mice hypothalamus. Injection of miR-212 agomir significantly increased the miR-212 expression in the hypothalamus, whereas injection of miR-212 antagonist had an inhibitory effect. (B) Effects of miR-212 agomir and antagonist on the mRNA expression of CRH during the 14-day heat stress process. In mice injected with negative control, level of CRH mRNA increased at beginning and returned to baseline at the end. Compared to group of the negative control, the miR-212 agomir injection group showed a significant decrease in the CRH mRNA expression. At the same time, the miR-212 antagonist injection group showed an increase in the CRH mRNA expression. (D and E) The protein expression of CRH was in accord with the mRNA expression. (C) CREB mRNA expression was escalated during the stress process independent of the miR-212 injection, as well as the protein expression of CREB and p-CREB (D, F and G). (H and I) Effects of miR-212 agomir and antagonist injection on serum contents of ACTH and CORT. Like CRH expression in the hypothalamus, serum contents of ACTH and CORT were also regulated by miR-212. The results show that miR-212 had a role in regulating HPA axis activity by modulating hypothalamic CRH expression. Data were presented as mean ± s.e.m. *P<0.05, **P<0.01, and ***P<0.001 (vs group of NC at each time-point respectively). A full color version of this figure is available at http://dx.doi.org/10.1530/JME-17-0124.

As verified by other research works, the HPA axis is activated when subjected to stressors and partly alleviated in long-term stress (Dallman 1993, Nyhuis et al. 2010a, b, Zimmerman et al. 2015). This study also shows that the HPA axis activity is partially returned to normal level when subjected to stressors for 14 days. By using a microRNA microarray analysis in the hypothalamus of mice subjected to heat stress, we found that miR-212, which is necessary for the proper development, maturation and function of neurons (Wanet et al. 2012), is capable of regulating CRH expression and HPA axis activity both in vitro and in vivo. As a concern, it was reported that dexamethasone treatment has no effect on miR-212 expression in rat adrenal glands (Hu et al. 2013) and level of pCREB and CREB in hypothalamic 4B cells (Evans et al. 2013). In our studies, the trend of corticosterone, which peaks at day 3, and that of miR-212, which rises continuously in 14 days, also suggested that the expression of miR212 is independent of the stress-induced adrenal steroid. In addition, our results show that treatment of CREB-overexpressed cells with miR-212 inhibitors resulted in higher levels of CRH expression compared with the CREB-overexpressed group, whereas the lower level of CRH expression was exhibited in the group treated with miR-212 mimics. These results suggest that miR-212 acts as a counter-regulatory factor in regulating CRH expression and HPA axis activity. Another explanation for the alleviation of HPA axis activity is habituation, which is a whole body response to rebuilding homeostasis during unalleviated repeated stress. Our results showed that miR-212, which escalated during repeated stress, may be a part of
habituation processes since miR-212 could regulate HPA axis activity and level of serum corticosterone, which is important in adaptation and recovery from stress (Sapolsky et al. 2000, de Kloet et al. 2005, McEwen 2007). More important, because of the simultaneously synthesis of CRH and miR-212, we thought that regulation of miR-212 on CRH expression and HPA axis activity was prompt and efficient. Therefore, we proposed that once exposed to stress, a switch is turned on to activate the HPA axis but at the same time, a fuse (which miR-212 seems to be) is triggered to prevent overactivation of HPA axis (Fig. 5). Future studies will continue to explore the relationships among miR-212, HPA axis and habituation.

Currently, increasing numbers of people are threatened by excess HPA axis activity, especially those suffering from chronic physiological or psychological stress. Epidemiological investigations show that high levels of endogenous GCs, or treatment with exogenous GCs, are associated with adverse metabolic profile, increased cardiovascular disease and altered mood and cognitive decline (Reynolds 2013). Additionally, a major depressive disorder is characterized by an increased release of GCs and hyperactivity of the HPA axis (Keller et al. 2017). Other meaningful reports concluded that a decrease in miR-212 was linked with postpartum psychosis (Weigelt et al. 2013), mesial temporal lobe epilepsy (Haenisch et al. 2015) and Alzheimer’s disease (Pichler et al. 2017). More significantly, dysregulation of miR-212 was associated with schizophrenia and bipolar disorders (Kim et al. 2010). Because our study indicates that inhibition of miR-212 leads to an increase in CRH expression and overactivity of the HPA axis both in vitro and in vivo, loss of miR-212 may be one of the reasons resulting in overactivity of the HPA axis and therefore may induce these mental disorders. The relationships among loss of miR-212, overactivity of the HPA axis and relative mental diseases deserve further investigation.

Another concern is that interventions for people who suffer from an overreactive HPA axis are lacking (Reiche et al. 2004, Wingenfeld & Wolf 2011, Doom & Gunnar 2013, Walker et al. 2016, Roelofs & Pasman 2017). As a kind of gene-based therapy, many researchers are intrigued by microRNA therapy, and currently, these therapies are undergoing testing in clinical trials (Kasinski & Slack 2011, Yin et al. 2014, Fernandez-Pineiro et al. 2017, Ji et al. 2017). Therefore, microRNA intervention may be a promising method to help people who suffer from an overreactive HPA axis as our study shows that overexpression of miR-212 could significantly reduce CRH expression and HPA axis activity in vitro and in vivo.

In conclusion, our study illustrates that microRNA participates directly in the regulation of the HPA axis...
and suggests that miR-212 may be the link between overactivity of the HPA axis and relative diseases. Preventive or therapeutic measures based on miR-212 will be helpful for those people who suffer from the adverse effects of an overactive HPA axis.

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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