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Shuwei Qiu,*+ Yimin Feng,† Gene Le Sage,† Ying Zhang,‡ Charles Stuart,† Lei He,* Yi Li,* Yi Caudle,† Ying Peng,* and Deling Yin†

Opioids have been widely applied in clinics as one of the most potent pain relievers for centuries, but their abuse has deleterious physiological effects including immunosuppression. However, the mechanisms are unclear. TLRs and acetylcholine are widely expressed in the immune and nervous systems, and play critical roles in immune responses. In this article, we show that morphine suppresses the innate immunity in microglia and bone marrow–derived macrophages through differential regulation of TLRs and acetylcholinesterase. Either morphine or inhibition of acetylcholine significantly promotes upregulation of microRNA-124 (miR-124) in microglia, bone marrow–derived macrophages, and the mouse brain, where miR-124 mediates morphine inhibition of the innate immunity by directly targeting a subunit of NF-κB p65 and TNFR-associated factor 6 (TRAF6). Furthermore, transcription factors AP-1 and CREB inhibited miR-124, whereas p65 bound directly to promoters of miR-124, thereby enhancing miR-124 transcription. Moreover, acute morphine treatment transiently upregulated the expression of p65 and phospho-p65 in both nucleus and cytoplasm priming the expression of miR-124, whereas long exposure of morphine maintained miR-124 expression, which inhibited p65- and TRAF6-dependent TLR signaling. These data suggest that modulation of miRs is capable of preventing opioid-induced damage to microglia. The Journal of Immunology, 2015, 194: 1021–1030.
morphone. In this article, we reveal that morphone represses the innate immune function through upregulation of miR-124. Furthermore, acute morphone treatment transiently upregulated the expression of p65 and phospho-p65 in both nucleus and cytoplasm priming the expression of miR-124, whereas long exposure of morphone maintains miR-124 expression, which inhibits p65- and TRAF6-dependent TLR signaling. These findings suggest that modulation of miRs is capable of preventing opioid-induced damage to microglia.

Materials and Methods

Cell lines and cell cultures

HEK 293T cell line was from American Type Culture Collection. Mouse BV2 microglial cell line was kindly provided by Dr. Gary Landreth (Case Western Reserve University School of Medicine). All cell lines were cultured in DMEM (Invitrogen, Carlsbad, CA) supplemented with 10% FBS in a humidified atmosphere containing 5% CO₂ at 37°C without antibiotics.

Primary microglial cells culture

Mouse primary microglial (PM) cells were isolated from mixed glial cultures as described in our previous studies (5). In brief, primary mixed glial cells were from postnatal day 1–2 BALB/c mice. PM cells were cocultured with astrocytes in DMEM/F12, HEPES medium supplemented with 10% FBS and 1% penicillin/streptomycin (all from Invitrogen). After 24 h, the growth medium was changed with fresh medium. On days 12–14, PM cells were harvested by shaking the cultures (180 rpm, 40–60 min) and collecting the floating cells. The cells were harvested at 37°C and 5% CO₂ for 1–2 d to achieve microglia in a quiescent state. PM cells from the first and the second passage were used (>95% purity).

Bone marrow–derived macrophages culture

Bone marrow–derived macrophages (BMMs) were isolated and cultured as follows (26). In brief, bone marrow was isolated from long bones of 4–to 6-week-old BALB/c mice and incubated with M-CSF (10 ng/ml; Sigma-Aldrich) in RPMI 1640 medium (Life Technologies) supplemented with 10% FBS and 1% penicillin/streptomycin for 3 d. The medium was changed every 2 or 3 d. One week later, macrophages were differentiated for assays. BMM cells were used from the first and second passage.

Morphine and TLR agonists treatment on PM and BMM cells

PM and BMM cells were incubated with TLR2 agonist Pam3csk4, TLR4 agonist LPS, TLR5 agonist flagellin, or TLR8 agonist Resiquimod at 10 μM for 2 h and then treated with morphine at 10 μM for another 22 h.

Animals and chronic morphine administration in mice

C57BL/6 mice were obtained from The Jackson Laboratory (Bar Harbor, ME) and were maintained in the Division of Laboratory Animal Resources at East Tennessee State University, a facility accredited by the Association for the Assessment and Accreditation of Laboratory Animal Care International. All animal studies were approved by the East Tennessee State University Committee on Animal Care. We followed an established procedure to induce morphine abuse described by us and others (27–30). In brief, 8- to 10-week-old C57BL/6 male mice received twice-daily injections of an escalating dose of morphine sulfate (Sigma-Aldrich, St. Louis, MO) over 8 d (10, 20, 40, 80, 100, 120, 140, 140 ng/day i.p.). Age-matched control male mice were treated twice daily with PBS. Twenty-four hours after the last injection, the prefrontal cortex and hippocampus were harvested and kept at −80°C.

Transfection and injection of miR-124 mimics, miR-124 inhibitor, and small interfering RNA

BV2 cells were transfected with miRNA miR-124 mimics, negative control (NC) mimics, and miR-124 inhibitors (Ambion, Carlsbad, CA) with the final concentration of 10 nM using the transfection reagent HiPerfect (Qiagen, Germantown, MD). BV2 cells were transfected with siRNA p65 and siRNA CREB (Santa Cruz Biotechnology, Santa Cruz, CA) with the working concentration of 100 nM using Lipofectamine 2000 (Invitrogen). Both miRNA in vivo ready miR-124 mimic and inhibitor (Ambion) were complexed with Invitrofectamine 2.0 (Invitrogen) reagent and injected through the tail vein of male C57BL/6 mice on 3 consecutive days at the dose of 7 mg/kg. The mice were treated with miR-124 inhibitor on the last 3 days after morphine treatment. At 24 h after the last injection, the prefrontal cortex and hippocampus were harvested.

Construction and transfection of plasmids

The wild type (wt) 3′-untranslated region (3′-UTR) plasmids of p65 and TRAF6 were cloned using primers (Supplemental Table I) and inserted into the 3′-UTR of the Renilla luciferase gene of the psiCHECK2 vector (Promega, Madison, WI). The mutant type (mut) 3′-UTR plasmids of p65 and TRAF6 were produced by means of site-directed mutagenesis, using primers (see Supplemental Table I for all primers used in the study). There were three binding sites between miR-124 and TRAF6 3′-UTR, whereas the mut1 plasmid was mutant at binding site 1, mut2 at sites 1 and 2, and mut3 at all three binding sites. The putative promoters of miR-124-1-and miR-124-3 on genome loci were cloned using primers in Supplemental Table I and cloned into upstream of luciferase gene in the pGL3-Basic vector (Promega), namely, pGL3-124-1 and pGL3-124-3. The authenticity of DNA sequences was confirmed by sequencing. BV2 or HEK293T cells were transfected with these plasmids (including p65, p50, and c-fos overexpression plasmids [Addgene, Cambridge, MA]) using Lipofectamine 2000 at 0.5–1.5 μg/ml. Cotransfections for miR-124 mimics and p65 overexpression plasmids were performed by using Lipofectamine 2000.

Western blot

Total proteins were extracted using radioimmunoprecipitation assay lysis buffer (Pierce, Rockford, IL). Nuclear and cytoplasmic proteins were extracted separately using NE-PER Nuclear and Cytoplasmic Extraction Reagents (Thermo). Protein lysates were separated by 8% SDS-PAGE and then electrophoretically transferred to polyvinyl difluoride membrane (Millipore). The membrane was incubated with either rabbit anti-mouse p65, phospho-p65, p105, and phospho-p105 (1:1000; Cell Signaling Technology, Beverly, MA), mouse anti-mouse TRAF6 (1:2000; Abcam, Cambridge, MA), rabbit anti-mouse Lamin B1 (1:2000; Cell Signaling Technology), or rabbit anti-mouse GAPDH Ab (1:2000; Cell Signaling Technology) followed by HRP-labeled goat anti-mouse or goat anti-rabbit IgG (1:5000; Cell Signaling Technology). Protein levels were detected using enhanced chemiluminescence detection solution (Pierce) and visualized on x-ray film (Kodak).

ELISA for cytokines

The levels of proinflammatory cytokines TNF-α, IL-1β, and IL-6 were analyzed with mouse Quantikine ELISA immunoassay kits (R&D Systems, Minneapolis, MN) according to the manufacturer’s instructions.

RNA extraction and evaluation of miR levels

RNA was isolated using the miRNA kit or Qiagen RNaseasy kit (Qiagen). Samples after lysis were incubated with DNAse digestion kit (Qiagen) to degrade genome DNA. RNA (10 ng) was converted into cDNA with TaqMan MicroRNA Assay and TaqMan MicroRNA Reverse Transcription kit (Applied Biosystems, Foster, CA). Real-time PCRs were performed with specific primers (TaqMan MicroRNA Assay) and TaqMan Universal PCR Master Mix (Applied Biosystems) on Bio-Rad PCR instrument. PCR conditions were performed according to the standard protocol with the 50°C preincubation for 2 min and 95°C incubation for 10 min, followed by 40 cycles of 95°C for 15 s and 60°C for 1 min. U6 small nuclear ribonucleoprotein was used as an endogenous control.

Evaluation of mRNA levels

Total RNA was reverse-transcribed using reverse transcription system (Promega). Real-time PCR was performed using SYBR GreenER Invitrogen on the Bio-Rad PCR instrument. PCR was performed according to the standard protocol with the 50°C preincubation for 2 min and 95°C incubation for 10 min, followed by 40 cycles of 95°C for 15 s and 60°C for 1min. GAPDH was included as an endogenous control. All real-time PCRs were performed in triplicate, and relative quantifications were calculated using the relative fold changes of cycle threshold method (95% CI). All primer sets were subjected to a dissociation curve analysis and produced single peaks on a derivative plot of raw fluorescence.

Dual-luciferase reporter assay

Validation of miR-124 binding to 3′-UTR was performed using dual-luciferase reporter assays. miRs and p65/TRAF6 wt/mut 3′-UTR plasmids were cotransfected in HEK293T cells for 48 h; then luciferase assays were performed on the Modulus microplate (Turner Biosystem) using the dual-luciferase reporter assay system (Promega). These experiments were repeated at least three times in triplicates. The relative luciferase activities were determined by calculating the ratio of Renilla luciferase activities over firefly luciferase activities. Validation of the transcriptional factor p65 binding to putative promoters of miR-124 was carried out with the dual-

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luciferase reporter assay. The p65 overexpression plasmids (Addgene, Cambridge, MA), miR-124 promoter vectors (pGL3-124-1 and pGL3-124-3), and pK-L-TK Renilla (Promega) were cotransfected into HEK293T cells. After 48 h posttransfection, the cells were lysed for measurement with the Dual-Luciferase reporter assay system (Promega) in the modulator microplate (Turner Biosystem). All experiments were repeated three times in triplicates. The relative luciferase activities were determined by calculating the ratio of firefly luciferase activities over Renilla luciferase activities.

**Chromatin immunoprecipitation assay**

BV2 cells were transfected with p65 plasmid for 48 h. Chromatin immunoprecipitation (ChIP) assay was performed using an EZ-ChIP assay kit (Millipore, Billerica, MA). In brief, cells were grown to 90% confluence and 1% formaldehyde was added followed by incubation at room temperature for 10 min. The cross-link reaction was quenched with 0.125 M glycine for 5 min at room temperature. Cells were then washed, scraped, and resuspended. DNA was digested into around 300-bp fragments on ice for 30 min by EZ-Zyme chromatin prep kit (Millipore). Supernatants were recovered by centrifugation and preclared for 1 h at 4°C with 60 μl protein G-agarose. Then 10 μl (1%) supernatant was removed as input. Immunoprecipitations were performed overnight with p65 Ab (ChIP Grade, 6 μg; Cell Signaling Technology) or IgG control Ab (provided in kit, 1 μg). The immune complexes were captured by incubation with 60 μl protein G-agarose for 2 h at 4°C. The immunoprecipitates were eluted from the protein G-agarose by incubating with elution buffer (1% SDS, 100 mM NaHCO3). DNA–protein complexes were reversely cross-linked by a high-salt solution at 65°C for 5 h. RNA and protein were eliminated by treating with 10 μg RNase A at 37°C for 30 min and then with protease K for 2 h at 45°C. Finally, DNA was purified by the spin column provided in the ChIP kit and eluted with 50 μl elution buffer. Real-time PCR was performed by using the SYBR GreenERqPCRsupermix (Invitrogen) on the Bio-Rad real-time PCR system instrument. The primer pairs used for PCR analysis are shown in Supplemental Table I. All data were normalized to NCs.

**Statistical analysis**

Quantitative data were presented as mean ± SEM. Statistical analysis was performed with the SPSS13.0 software (version 13.0; SPSS) using two-tailed Student t test or one-way ANOVA for experiments with more than two subgroups followed by Bonferroni’s post hoc test, and graphs were generated by GraphPad Prism (version 5.04; GraphPad Software). A p value <0.05 was considered significant.

**Results**

**Morphine suppresses microglia-mediated innate immunity**

To define the mechanisms by which morphine modulates the innate immunity, we treated primary mouse microglia (PM) cells with morphine with different doses and different times. We found that morphine inhibited the production of proinflammatory cytokines TNF-α, IL-1β, and IL-6, which was increased by overexpression of miR-124 inhibitors (Fig. 2G). Like in BV2 cells, these proinflammatory cytokines were decreased in PM cells (Fig. 2H). To define whether miR-124 participated in morphine-elicted downregulation of TNF-α, BV2 and PM cells were treated with miR-124 inhibitors and morphine. We found that morphine counteracted miR-124 inhibitor-induced TNF-α production in BV2 (Fig. 2I) and the expression of IL-1β in PM cells (Fig. 2J). Collectively, our results suggest that morphine-induced upregulation of miR-124 inhibits the production of proinflammatory cytokines.

We then assessed the effect of ACh on miR expression using ACh receptor antagonist atropine. We showed that either short- or long-time atropine treatment did not alter the expression of miR-124 or miR-132 in PM cells, but short-time atropine promoted upregulation of miR-124 in PM cells and long-time atropine significantly downregulated miR-132 in BMM cells (Supplemental Fig. 2B, 2C).

**miR-124 suppresses microglial immune function by targeting p65 and TRAF6**

miRs function by inhibiting the expression level of targeting genes. To search for potential targets of miR-124 with TargetScanMouse algorithm, we found that p65 and TRAF6 are potential targets of miR-124 (Fig. 3A). To verify whether p65 and TRAF6 are indeed targets of miR-124, we determined luciferase activity by dual-luciferase reporter assay in HEK293T cells transfected with wt and mut 3’-UTR plasmids. We showed that miR-124 reduced the luciferase activity of p65 wt-UTR by ∼40% in comparison with that of NC, whereas miR-124 did not alter the luciferase activity of p65 mut UTR, indicating that miR-124 directly bound to the putative binding site of p65 3’-UTR (Fig. 3B). Compared with NC, miR-124 decreased almost 50% of luciferase activity of TRAF6 wt-UTR, suggesting a direct interaction between miR-124 and 3’-UTR of TRAF6. Interestingly, both luciferase activities of TRAF6 mut1-UTR and mut2-UTR were restored to ∼70%, suggesting miR-124 bound to site 1 rather than site 2 (Fig. 3B).

Meanwhile, luciferase activities of TRAF6 mut3-UTR were re-
covered completely, indicating that miR-124 also bound to site 3. Furthermore, we showed that overexpression of miR-124 downregulated expression of both p65 and TRAF6 at gene and protein levels in PM (Fig. 3C) and BV2 cells (Fig. 3D), whereas knockdown of miR-124 upregulated these two proteins (Fig. 3D). In agreement with these in vitro data, the expression of both p65 and TRAF6 in prefrontal cortex and hippocampus was reduced in mice injected with miR-124 mimics, compared with that of the NC group (Fig. 3E). Taken together, these data suggest that both p65 and TRAF6 are direct targets of miR-124.

**Morphine inhibits p65 and TRAF6 through miR-124**

We next determined the molecular mechanism by which morphine modulates p65 and TRAF6. We showed that morphine reduced the expression of p65 and TRAF6 in a dose-dependent manner (Fig. 4A) and downregulated TRAF6 level in a time-dependent manner (Fig. 4B). Moreover, morphine decreased levels of both p65 and TRAF6 in PM cells (Fig. 4C). LPS significantly activated the expression of phospho-p65 and p65 in nucleus rapidly increased and peaked at ~1 h after morphine treatment, although there seemed to be no significant change with phospho-p105 and p105 (Fig. 5C). The expression of p65 both in nucleus and in cytoplasm increased after short-time morphine treatment (Fig. 5B, Supplemental Fig. 2D). Similarly, expression of phospho-p65 and p65 in nucleus rapidly increased as well and peaked at ~1 h after morphine treatment, although there seemed to be no significant change with phospho-p105 and p105 (Fig. 5C). The expression of p65 both in nucleus and in cytoplasm increased after short-time morphine treatment (Fig. 5B, 5C). Conversely, with acute administration of morphine, transcription of p65 increased and peaked at 3 h in BMM cells, which corresponded with the changes of IL-6 and TRAF6 (Fig. 5B, 5C). In agreement with the results that morphine downregulated p65 in BV2 and PM cells, transcription of p65 in PM and BMM cells and translation of p65 in BV2 cells were also significantly reduced with various time periods (Fig. 5B, 5C). Morphone dynamically modulates expression of the transcriptional factor p65.

**Transcription factor p65 promotes miR-124 transcription**

We next determined the regulation of p65, AP-1, or CREB on miR-124. Overexpression of c-Fos in BV2 cells significantly inhibited expression of miR-124 (Fig. 6A), whereas inhibition of CREB dramatically induced miR-124 expression (Fig. 6B). However, overexpression of p65 and p50 significantly upregulated the expression of mature miR-124 (Fig. 6C) and transcription of both pri-miR-124-1 and pri-miR-124-3 other than pri-miR-124-2 (Fig. 6D). Moreover, knockdown of p65 led to a significant reduction of miR-124 by ~80% (Fig. 6E). These data strongly suggest that both AP-1 and CREB negatively, whereas p65 positively, regulate transcription of miR-124.
were then added with MOR at 10 μM for 24 h, and the expression of TNF-

hippocampus tissues were harvested and the expression of miR-124 was examined as in (A). BV2 cells were transfected with either miR-124 mimics or inhibitors for 48 h, and the production of TNF-α, IL-1β, and IL-6 was examined by ELISA. (H) PM cells were transfected with miR-124 mimics for 48 h, and the expression of TNF-α, IL-1β, IL-6, and CD11b was assessed by real-time PCR. (I) BV2 cells were transfected with either miR-124 inhibitors (INHs) or NC at 50 nM using the HiPerfect reagent. At 24 h transfection, the cells were then incubated with MOR at 10 μM for 24 h. TNF-α production was assessed as in (G). (J) PM cells were transfected with either miR-124 INHs or NC at 50 nM using the HiPerfect reagent. After 24 h transfection, the cells were then added with MOR at 10 μM for 24 h, and IL-1β expression was determined as in (A). *p < 0.05, **p < 0.01, ***p < 0.001.

To define how p65 promoted miR-124 transcription, we analyzed via the UCSC Web site (http://genome.ucsc.edu/) the genomic loci that may be affected by miR-124. As shown in Fig. 7A, miR-124-1, miR-124-2, and miR-124-3 are located within three different chromosomes, chr14, chr3, and chr2, respectively. Using the computer program MAPPER, a search engine to identify TF binding sites (32), we examined the ~1.8-kb DNA sequence upstream of the AK044422 start codon (miR-124-1), ~2.0-kb DNA sequence upstream of AK011787 start codon (miR-124-2), and ~2.1-kb DNA sequence upstream of precursor miR-124-3. We observed that there are two binding sites for each miR-124-1 (P1 and P2) and miR-124-3 (P3 and P4), rather than miR-124-2 (Fig. 7A). To confirm whether p65 controls transcription of miR-124-1 and miR-124-3, we performed the ChIP assay using lysates from BV2 cells transfected with p65 or empty vectors. We found that p65 bound to the first putative site (P1 and P3) within the promoter of each miR-124 transcript (Fig. 7B, 7C). To verify whether these two binding sites are authentic and active, we cloned the DNA sequences incorporating the binding sites and inserted them upstream of luciferase genes of pGL3 basic vectors. The luciferase reporter assay showed that luciferase activities were increased nearly 10-fold in BV2 cells transfected with p65 and pGL-124-1 plasmids compared with that of control vehicle, whereas luciferase activities of pGL-124-3 in p65 group increased ~6-fold in comparison with empty vector (Fig. 7D). Taken together, our results reveal that the transcription factor p65 promotes miR-124 transcription.

**Discussion**

Opioid abuse such as chronic morphine administration diminishes immune functions; however, the molecular mechanisms by which opioids affect immune cell functions remain to be elucidated. In this study, we find that chronic administration of morphine damaged the innate immunity and promoted expression of miR-124 in microglia cells and mouse brain tissues. Morphine-induced immune suppression is mediated through upregulation of miR-124, which directly inhibits the TLR downstream p65 and TRAF6. Moreover, acute morphine activated, whereas chronic morphine significantly deactivated, expression of both phospho-p65 and p65, dynamically modulating transcription of miR-124. Morphine may initially prime the expression of miR-124 because of the activation of p65 and later maintain inhibition of TLR signaling through miR-124–dependent inhibition of p65. Our findings therefore provide a novel mechanism for understanding the potential mechanism associated with the immunosuppressive effect of opioids abuse.

Recent studies have shown that miRs play an important role in regulation of genes of the immune system (18), including in macrophages, microglia, dendritic cells, and T cells (19). miRs participate in immune responses through modulation of TLR signaling. First, miRs directly regulate TLRs themselves at transcrip-
p65 and TRAF6 are direct targets of miR-124. (A) Putative binding sites between miR-124 and 3′-UTRs of p65 or TRAF6 were predicted by TargetScanMouse. All the wt and mut 3′-UTR fragments were cloned into psiCHECK2 vectors. The mutant 3′-UTR vectors were produced by the approach of site mutations. TRAF6 mut 1 vectors were mutated at binding site 1, mut 2 vector at binding sites 1 and 2, and mut 3 vector at all three binding sites. (B) Confirmation of miR-124 binding to 3′-UTRs of p65 or TRAF6 was performed by dual-luciferase activity reporter assay. HEK293T cells were cotransfected with miR-124 mimics and either p65 or TRAF6 wt/mut 3′-UTR vectors, with 100 nM for miR-124 mimics and 10 ng/µl for p65 or TRAF6 wt/mut 3′-UTR vectors using the Lipofectamine 2000 reagent. Empty psiCHECK 2 vector was a control of UTR vectors, and NC oligonucleotides were controls of mimic. ***p < 0.001 versus NC. (C) BV2 Cells were transfected with either miR-124 mimics or inhibitors at 10 nM using HiPerfect reagent. NC oligonucleotides were as controls. Expression of p65 and TRAF6 proteins was assessed by immunoblot. ***p < 0.001. (D) PM cells were transfected with miR-124 mimics or NC at 10 nM using HiPerfect reagent. The expression of p65 and TRAF6 was determined by real-time PCR. (E) Eight- to 10-wk-old C57BL/6 male mice (n = 5/group) were treated with in vivo ready miR-124 mimics or NC through tail-vein injection for 3 consecutive days (7 mg/kg body weight). Twelve hours after the last injection, the prefrontal cortex and hippocampus were collected and the expression of p65 and TRAF6 were determined by immunoblot.

It has been confirmed that miR-223 is a regulator of TLR3 and TLR4 (33), miR-105 directly downregulates TLR2 (34), and miR-let-7 family target TLR4 in mouse peritoneal macrophages (35). Second, miRs modulate immune functions via targeting components of TLR signaling. miR-146 negatively regulates the MyD88–NF-κB pathway post bacterial infection through targeting IL-1R–associated kinase-1 and TRAF6 in THP-1 macrophage cells (36). miR-155 involves in inflammation through targeting IL-1R–associated kinase-1 and TRAF6 in THP-1 macrophage cells. This finding is consistent with these earlier miRs, our findings showed that miR-124 is able to inhibit expression of TRAF6 and p65, following with inhibitory production of proinflammatory cytokines in microglia and bone marrow macrophage cells. This finding is consistent with the recent observation that miR-124 promotes microglia quiescence in encephalomyelitis models (44). On the contrary, IkBζ, a member of IκB proteins of NF-κB inhibitors, is another target of miR-124 in liver cancer cells (45). However, the effect of miR-124 on IkBζ was not investigated in this study, because IkBζ is not a typical member of classical IκB proteins (45). Collectively, our findings suggest that miR-124 inhibits microglia immunity by directly targeting TRAF6 and p65.

Intriguingly, in our study, alteration of TLR expression by morphine in microglia varied from majority increased to minority decreased. Moreover, morphine inhibited IL-1β and IL-6 production induced by TLR2 agonist and LPS, whereas synergistically promoting those induced by TLR5 and TLR8 agonists. These suggest different roles of TLRs in morphine induction of immune function in microglia and also that the integrated inhibitory function of morphine on immunity is attributed to suppression of TLR downstream molecules TRAF6 and p65, rather than TLRs themselves. This provides a new explanation for morphine-mediated immune suppression. It is well-known that neuroendocrine reflex takes part in inflammation, with AChE-Ach signaling involved in this process. Soreq’s group (8) demonstrated that upregulation of miR-132 potentiates ACh-mediated anti-inflammation through targeting AChE in LPS-induced inflammation model in vitro and in vivo. In support of this study, downregulation of miR-132 varied inversely with AChE in morphine-induced inflammation model of macrophages. Compared with the LPS model, however, this phenomenon was not observed in the microglia model (Supplemental Fig. 2A), which is consistent with the finding that atropine did not induce significant miR-124 expression and that miR-124 did not target AChE in PM cells (Supplemental Fig. 2B, 2C, 2E). This could be because of the slight and cumulative suppression of immunity by morphine. Although upregulation of miR-124 is not by serum
treatment, we speculated that this could be attributed to starvation-induced effect instead of AChE, which needs further confirmation. In this study, our results suggest that AChE exerted less function in morphine-induced inflammation in microglia than that in macrophage.

In this study, we found that long-term morphine treatment inhibits production of proinflammatory cytokines and the expression of microglial activation marker CD11b. This is supported by the immunoblot result that morphine downregulated proteins TRAF6 and p65 both in vitro and in vivo, suggesting that long-term morphine exposure attenuates the immune function of microglia in the CNS. This is consistent with Franchi's (9) report that morphine exposure downregulated the expression of TLR4 mRNA and protein in RAW264.7 and peritoneal macrophages. Another recent study also found that acute and chronic morphine evoke a differential expression of cytokines in the rodent brain, with chronic

FIGURE 4. Morphine inhibitory effect on p65 and TRAF6 through miR-124. (A) BV2 cells were incubated with various doses of morphine (MOR) for 24 h, and the expression of p65 and TRAF6 were examined by immunoblot. (B) BV2 cells were treated with different times of MOR at 10 μM, and TRAF6 expression was determined as in (A). (C) PM cells were added with MOR at 10 μM for 24 h, and the expression of p65 and TRAF6 were determined by real-time PCR. **p < 0.01. (D) PM cells were incubated with LPS at 10 μM for 2 h and then treated with MOR at 10 μM for 22 h. The expression of p65 and TRAF6 were assessed as in (C). ***p < 0.01 versus PBS, *p < 0.01 versus LPS. (E) BV2 cells were transfected with miR-124 inhibitors (INHs) for 24 h and then treated with MOR at 10 μM for 24 h. The expression of p65 and TRAF6 were determined as in (A) and subsequent analysis of gray values (F). *p < 0.05, **p < 0.01 versus NC + PBS, *p < 0.01 versus INH + PBS. (G) Eight- to 10-wk-old C57BL/6 male mice (n = 5/group) were i.p. injected with MOR or PBS for 8 consecutive days. On days 6, 7, and 8, mice were also injected with miR-124 INHs or NC through tail veins. Twelve hours after the last morphine injection, brain tissues were collected for immunoblot.

FIGURE 5. Morphine (MOR) dynamically modulates the expression of p65 in microglia. (A) BV2 cells were incubated with MOR at 10 μM for different times, and the expression of c-FOS, p-c-FOS, c-JUN, p-CREB, and CREB were examined by immunoblot. (B) PM and BMM cells were incubated with MOR at 10 μM for different times, and expression of p65 was examined by real-time PCR. (C) BV2 cells were treated with MOR at 10 μM for different times, and proteins in nucleus and cytosol were extracted separately. Expression levels of phospho-p65, p65, phospho-p105, and p105 in nucleus and cytosol were evaluated as in (A). Lamin B was the endogenous control, whereas GAPDH was the exogenous control.
morphine significantly lowering expression of IL-1β (46). However, studies from Hutchinson’s group (47–50) showed the opposite result where morphine increased proinflammatory cytokines in macrophages and promoted activation of microglia in spinal cord, and these effects are probably mediated through TLR4. Fukagawa et al. (15) reported that microglia activation induced by morphine is independent of TLR4 in spinal cord using the TLR4 mutation and deletion mice, although CD11b expression was significantly increased after morphine treatment. Despite opioids such as morphine playing important roles in immunosuppression, it is unclear why discrepancies occur among these studies. We speculate that the different concentrations and various treatment periods with morphine are important causes for these differences. For example, the concentration of morphine, 100 μM for cell treatment, in Hutchinson’s study is high enough to induce toxicity rather than physiological function, resulting in cell apoptosis (14), because in their studies, concentrations seem not to elicit significant changes in IL-1β and TLR4 mRNAs. Moreover, the different types of morphine among these studies may also contribute to these discrepancies. However, a similar effect of morphine on TLR-mediated signaling through classic μ opioid receptor was observed in our studies and in Franchi’s report (5, 9).

The regulation of p65 by morphine remains to be defined. Some investigations reported that morphine is able to increase p65 activity in various cell types (51–53), whereas others reported the opposite effect (54). Consistent with Börner et al.’s report (55) in neuronal cells, our study showed that morphine exposure tran-

**FIGURE 6.** AP-1 and CREB negatively, but p65 positively, regulate transcription of miR-124. BV2 cells were transfected with c-FOS vector (A), siRNA CREB (B), or p65/p50 vectors (C) for 48 h, and miR-124 expression was determined by real-time PCR. The corresponding empty vector was an NC. (D) BV2 cells were transfected with p65 or p50 vectors as in (C). The genome was first removed before mRNAs were converted into cDNA. Then quantification of three pri-miR-124s was determined as in (A). (E) BV2 cells were transfected with siRNAP65 for 48 h and miR-124 expression was assessed as in (A). **p < 0.01, ***p < 0.001.

**FIGURE 7.** The transcription factor p65 promotes transcription of miR-124. (A) miR-124-1 was located within the fourth exon of the gene AK044422 on chromosome (Chr) 14. There were two p65 binding sites within the ~1.8-kb DNA sequence upstream of the AK044422 start codon, and this sequence was cloned into pGL3 basic vector and designated as pGL3-124-1. miR-124-2 was located between exons 2 and 3 of the gene AK011787 on Chr 3. miR-124-3 was harbored on Chr 2, and the ~2.1-kb DNA sequence upstream of precursor miR-124-3 was predicted as promoter region. There were two binding sites for p65 in this fragment, and it was cloned into pGL3 basic vector and designated as pGL3-124-3. (B) BV2 cells were transfected with p65 overexpression and empty vectors for 48 h before the ChIP assay was performed. The chromatin from BV2 cells was immunoprecipitated by using Abs against p65 protein. Shown are the binding sites of p65 to pGL3-124-1 and pGL3-124-3 detected by real-time PCR analysis. Ab against IgG was included as an NC. (C) Gel graph of real-time PCR result after ChIP assay for putative binding sites P1 and P3 from (B). (D) HEK 293T cells were cotransfected with miR-124 promoter vectors (pGL3-124-1 and pGL3-124-3), p65 overexpression vectors, and pRL-TK Renilla vectors (empty vector) for 48 h, and luciferase activities were measured using the dual-luciferase reporter assay system.
siently increased and then decreased expression of p65 and phospho-p65 in microglia, which provides a basis for the p65 acutely promoting expression of miR-124. We demonstrated that overexpression of p65 drove transcription of pri-miR-124-1 and pri-miR-124-3 other than pri-miR-124-2, in agreement with the prediction that transcriptional binding sites between p65 and miR-124 are located within pri-miR-124-1 and pri-miR-124-3 rather than pri-miR-124-2 promoters on genome loci. However, morphine exposure increased expression levels of all three pri-miR-124 in our study; thus, other transcriptional factors are likely to be involved in the transcription. Even though c-Fos was observed to be persistently increased after morphine treatment, overexpression of c-Fos did not induce miR-124 upregulation, similar to CREB, which are considered main transcription factors of morphine (31). Conclusively, our studies reveal that transcriptional factors p65, Ap-1, and CREB and cholinergic signaling are involved in regulation of miR-124 that exerts a central contribution to morphine inhibitory function on the innate immunity of microglia/macrophage through differential modulation ofTLRs and cholinergic signaling pathway (Supplemental Fig. 3).

In summary, our studies demonstrate that miR-124 plays a critical role in morphine-mediated suppression of microglia immunity, and upregulation of miR-124 is partially mediated by morphine-induced transient upregulation of p65. These findings provide direct molecular evidence for morphine-induced immune suppression.

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Disclosures

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References


