Inducible microRNA-155 Feedback Promotes Type I IFN Signaling in Antiviral Innate Immunity by Targeting Suppressor of Cytokine Signaling 1

Pin Wang, Jin Hou, Li Lin, Chunmei Wang, Xingguang Liu, Dong Li, Feng Ma, Zhugang Wang and Xuetao Cao

*J Immunol* published online 11 October 2010
http://www.jimmunol.org/content/early/2010/10/11/jimmunol.1000491

Supplementary Material
http://www.jimmunol.org/content/suppl/2010/10/12/jimmunol.1000491.DC1

Subscription
Information about subscribing to *The Journal of Immunology* is online at:
http://jimmunol.org/subscription

Permissions
Submit copyright permission requests at:
http://www.aai.org/About/Publications/JI/copyright.html

Email Alerts
Receive free email-alerts when new articles cite this article. Sign up at:
http://jimmunol.org/alerts
Inducible microRNA-155 Feedback Promotes Type I IFN Signaling in Antiviral Innate Immunity by Targeting Suppressor of Cytokine Signaling 1

Pin Wang,*1† Jin Hou,*1† Li Lin,‡ Chunmei Wang,* Xingguang Liu,* Dong Li,† Feng Ma,† Zhugang Wang,‡ and Xuetao Cao,*1†

Effective recognition of viral infection and subsequent triggering of antiviral innate immune responses are essential for the host antiviral defense, which is tightly regulated by multiple regulators, including microRNAs. Our previous study showed that a panel of microRNAs, including miR-155, was markedly upregulated in macrophages upon vesicular stomatitis virus infection; however, the biological function of miR-155 during viral infection remains unknown. In this paper, we show that RNA virus infection induces miR-155 expression in macrophages via TLR/MyD88-independent but retinoic acid-inducible gene I/JNK/NF-κB-dependent pathway. And the inducible miR-155 feedback promotes type I IFN signaling, thus suppressing viral replication. Furthermore, suppressor of cytokine signaling 1 (SOCS1), a canonical negative regulator of type I IFN signaling, is targeted by miR-155 in macrophages, and SOCS1 knockdown mediates the enhancing effect of miR-155 on type I IFN-mediated antiviral response. Therefore, we demonstrate that inducible miR-155 feedback positively regulates antiviral innate immune response by promoting type I IFN signaling via targeting SOCS1. The Journal of Immunology, 2010, 185: 000–000.

Upon viral infection, host innate immunity is the first line of antiviral defense, designed to recognize viral components and produce proinflammatory cytokines and type I IFN (1–3). Type I IFN plays critical roles in antiviral immune response mainly through induction of cellular resistance to viral infection and apoptosis of virus-infected cells. Hence, type I IFN is extensively applied to the therapy of viral infection. However, the outcome of IFN therapy varies with different individuals depending on different disease stages and the factors influencing host responses to IFN. Although IFN signaling pathways have been investigated extensively so far, the underlying mechanisms for the regulation of this pathway are still not fully characterized. JAK/STAT cascade, the well-established cardinal pathway transmitting IFN signals, was found to be tightly regulated by several mechanisms. Among them, some molecules, such as suppressor of cytokine signaling (SOCS) family members, can negatively regulate type I IFN signaling (4, 5). However, there are few reports about the regulation of type I IFN signaling and subsequent antiviral innate immunity by microRNAs (miRNAs) to date.

miRNAs are an abundant class of highly conserved small noncoding RNAs. They function mainly through suppressing target genes expression by binding to the 3′-untranslational region (UTR) of target mRNAs to induce degradation or suppress translation. It has been demonstrated that miRNAs participate in various biological processes, including innate and adaptive immune responses (6–8). Using genetic approaches, miR-155 has been demonstrated to have an indispensable role in humoral and cellular immunity (9–15). Regarding innate immunity and inflammatory response, miR-155 expression is induced by TLR signals, such as TLR2, TLR3, TLR4, and TLR9, or stimulations from cytokines, such as IL-1, TNF-α, and IFN-β, indicating the participation of miR-155 in these immune responses (13–15). Although the fact that miR-155 expression is induced by stimulation of poly(I:C) or IFN-β implies the involvement of miR-155 in antiviral responses, there is no report by now about the regulation and underlying mechanism of type I IFN signaling and subsequent type I IFN-mediated antiviral innate immunity by the inducible miR-155.

On the basis of our previous observation that a panel of miRNAs including miR-146a and miR-155 were upregulated in murine peritoneal macrophages upon vesicular stomatitis virus (VSV) challenge (16), in this study, we found that the induction of miR-155 by VSV infection was through a TLR/MyD88-independent but retinoic acid-inducible gene I (RIG-I)/JNK/NIK-xB–dependent mechanism. Upregulated miR-155 suppressed SOCS1 expression in macrophages and subsequently enhanced type I IFN effector gene expression and type I IFN-mediated antiviral response, thus suppressing viral replication. We for the first time, to our knowledge, demonstrate that the inducible miR-155, upregulated upon RNA virus infection, acts as a feedback positive regulator of type I IFN signaling in antiviral immunity by targeting SOCS1.
Materials and Methods
Mice and reagents
C57BL/6 mice (6–8 wk) were purchased from Joint Ventures Sipper BK Experimental Animal Company (Shanghai, China). TLR4 knockout mice were described previously (16). TLR4, TLR9, and MyD88 knockout mice were provided by Prof. S. Akira (Osaka University, Osaka, Japan). RIG-I knockout mice were generated as described previously (17). All animal experiments were performed in accordance with the National Institutes of Health Guide for the Care and Use of Laboratory Animals, with the approval of the Scientific Investigation Board of Second Military Medical University (Shanghai, China). VSV was a gift from Prof. W. Pan (Second Military Medical University, Shanghai, China), and Sendai virus (SeV) was from Prof. B. Sun (Chinese Academy of Sciences, Shanghai, China). Pyrrolidinedicarboxylic acid, an inhibitor of NF-κB, SB203580, an inhibitor of p38, PD98059, an MEK/ERK inhibitor, and SP600125, a JNK inhibitor, were from Calbiochem (San Diego, CA). Murine rIFN-β was described previously (16). Abs specific to SOCS1 and phosphorylated STAT2 were from Abcam (Cambridge, U.K.). Anti–STAT1, JAK1, phosphorylated STAT1, and phosphorylated JAK1 were from Cell Signaling Technology (Danvers, MA). Abs specific to STAT2 and phosphorylated STAT2 were from Abcam (Cambridge, U.K.). Abs specific to β-actin was from Sigma-Aldrich (St. Louis, MO).

Cell culture and transfection
Murine macrophage cell line RAW264.7 was obtained from the American Type Culture Collection (Manassas, VA) and cultured as described previously (18). Thyglocylate-elicted murine peritoneal macrophages were prepared and cultured as described previously (19, 20). A total of 0.5 ml 2 × 10^5 cells were seeded into each well of 24-well plates, or a total of 3 ml 1 × 10^6 cells were seeded into each well of 6-well plates and incubated overnight and then transfected as described previously (16). Bone marrow-derived dendritic cells (BMDCs) and splenocytes were generated as described previously (21). SOCS1 stably overexpressed RAW264.7 cell clones were selected in 600 µg/ml G418 for 3–4 wk and then confirmed with Western blot analysis for the expression of SOCS1.

Prediction of miR-155 targeting sites in VSV RNA in silico
RNA22 miRNA target (http://chcsrv.watson.ibm.com/rna22 Targets.html) detection (22) was used to predict miR-155 target site in VSV RNA sequences with settings as follows. Maximum number of allowed unpaired bases: 0 in seed/nucleus of 6 nt; minimum number of paired-up bases in heteroduplex: 12; and maximum folding energy for heteroduplex (Kcal/mol): 25.

miR-155 mimic and inhibitor
miR-155 mimic (dsRNA oligonucleotides) and miR-155 inhibitor (single-stranded chemically modified oligonucleotides) from GenePharma (Shanghai, China) were used for the overexpression and inhibition of miR-155 in murine macrophages, respectively. Macrophages described above were transfected as previously described (16) at a final concentration of 10 nM. Negative control mimic or inhibitor (GenePharma) was transfected as their matched controls.

RNA interference
The SOCS1-specific small interfering RNA (siRNA) (siSOCS1) was 5′-CUA CCC GAG UUC UCC CCC CTT-3′ (sense) and 5′-GGG GAA GGA ACU CAG GUA GUA GTT-3′ (antisense). The scrambled control RNA sequences were described previously (16). siRNA duplexes were transfected into murine peritoneal macrophages at a final concentration of 10 nM as described previously (18).

RNA quantification
Total RNA, containing miRNA, was extracted, reverse-transcribed, and real-time PCR amplified as described previously (16). For miRNA analysis, reverse transcription primers for miR-155 were 5′-GTC GTA TCC AGT GCA GGG TCC GAG GTA TTC GCA CTG ACG ACC CCC TA-3′. Quantitative PCR primers were 5′-CTC GTG ATG ATT GCT AAT TGT GA-3′ (forward) and 5′-GTC GAG GGT CCY TGG T-3′ (reverse). The relative expression level of miRNA was obtained as described previously (16). For murine β-actin, IFN-β, and IFN-4 mRNA expression, the primers were described previously (19, 20); for murine SOCS1, the primers were 5′-CTG CGG CTT CTA TTG GGG AGC-3′ (forward) and 5′-AAA AAA CGG CAG TCG AAG GTC TCG-3′ (reverse); for murine inflammatory protein 10 (IP-10), the primers were 5′-CCA AGT GCT GCC GTC ATT TTC-3′ (forward) and 5′-GGC CGC TCG GGA ACA CAA-3′ (reverse); for murine IFN-stimulated gene 15 (ISG15), the primers were 5′-GTT GTC GTG CGT GAC TAA TTC CAT-3′ (forward) and 5′-TGG AAA AAA GGA TAA GAC GCT CCT-3′ (reverse); for VSV Indiana serotype, the primers were described previously (16). Data were normalized to the level of β-actin expression in each sample.

ELISA
A total of 2 × 10^5 cells in 0.5 ml culture medium were seeded into each well of 24-well plates and incubated overnight and then transfected as described above. After 48 h, the cells were infected with VSV or SeV for the indicated time periods. The concentration of IFN-β in culture supernatants was measured as described previously (16).

Western blot analysis
The cells were washed twice with cold PBS and lysed with cell lysis buffer (Cell Signaling Technology) supplemented with protease inhibitor mixture (Calbiochem). Protein concentrations of the cell lysis extracts were measured with BCA assay (Pierce, Rockford, IL) and equalized with the extraction reagent. Equal amount of the extracts were loaded and subjected to SDS-PAGE, transferred onto nitrocellulose membranes, and then blotted as described previously (19, 20).

VSV yield qualification
Macrophages were transfected as described above and infected by VSV as indicated. A total of 0.1 ml cultural supernatants were serially diluted on the monolayer of BHK21 cells, which were obtained from the American Type Culture Collection, and 1 × 10^4 cells were seeded into 96-well plates a day before measurement. Fifty percent tissue culture infectious dose (TCID50) was measured 3 d later as described previously (16).

**FIGURE 1.** RNA virus infection induces significant upregulation of miR-155 in murine macrophages and dendritic cells. A and B, Murine peritoneal macrophages were infected with VSV at MOI 1 (A) or SeV at MOI 10 (B) for indicated time. Expressions of miR-155 was measured by quantitative RT-PCR and normalized to that of U6 in each sample. C and D, Murine peritoneal macrophages were infected with VSV (C) or SeV (D) at indicated MOI for 36 h. Expression of miR-155 was measured as in A. E, Murine splenocytes (left panel) and BMDCs (right panel) were infected with VSV at MOI 1 for indicated time, and miR-155 expression was measured as described in A. Data are shown as mean ± SD (n = 3) of one representative experiment. Similar results were obtained in three independent experiments. MOI, multiplicity of infection.
Results

RNA virus infection upregulates miR-155 expression in macrophages and dendritic cells

We previously reported that a panel of miRNAs was markedly upregulated upon VSV infection in macrophages, and miR-155 was one of the mostly upregulated (16). However, the role of inducible miR-155 expression in antiviral immune response is still not known. The kinetic induction of mature miR-155 following VSV challenge indicated that miR-155 was a VSV infection responsive gene in macrophages, and its induction reached the peak at ~24 h after VSV challenge (Fig. 1A). SeV, another RNA virus, also induced miR-155 expression in macrophages with similar kinetics (Fig. 1B). Furthermore, these RNA viruses both induced miR-155 expression in a dose-dependent manner (Fig. 1C, 1D). Also, miR-155 expression was upregulated by VSV infection in murine splenocytes and BMDCs (Fig. 1E). So, expression of miR-155 can be upregulated in APCs in response to RNA virus infection.

RNA virus infection upregulates miR-155 expression via RIG-I/JNK/NF-κB but not TLR/MyD88 pathway

We next investigated the underlying mechanism by which miR-155 was induced. As it was reported that signals from TLR2, TLR3, TLR4, and TLR9 induced miR-155 expression through MyD88- or TRIF-dependent signaling pathways (13), we exclude the possibility that activation of TLR signals contribute to VSV-induced miR-155 expression. Peritoneal macrophages from TLR3−, TLR4−, TLR9−, or MyD88-deficient mice showed identical induced miR-155 expression following VSV infection as compared with wild-type macrophages (Fig. 2A). However, VSV-induced miR-155 expression was markedly impaired in RIG-I−deficient macrophages and splenocytes (Fig. 2B), suggesting that inducible miR-155 expression was dependent on RIG-I signaling. As control, LPS-induced miR-155 expression was impaired by TLR4 deficiency but not significantly influenced by RIG-I deficiency (Supplemental Fig. 1).

Because induction of miR-155 was reported to be JNK dependent (13), we further investigated the effect of JNK inhibitor on VSV-induced miR-155 expression in macrophages. As shown in Fig. 2C, inhibition of JNK efficiently impaired VSV-induced miR-155 expression. In addition, inhibition of NF-κB also partially impaired VSV-induced miR-155 upregulation, and combined inhibition of JNK and NF-κB suppressed VSV-induced miR-155 expression more significantly. However, inhibition of p38 or ERK had little effect on the induction of miR-155 (Fig. 2D). Taken together, these results suggest that VSV infection upregulates miR-155 expression in macrophages mainly through RIG-I/JNK/NF-κB-dependent pathway.

Statistical analysis

Statistical significance was determined by Student t test, with p < 0.05 considered to be statistically significant.
miR-155 feedback attenuates the viral replication in macrophages

To investigate the biological significance of upregulated miR-155 during viral infection, we further examined the effect of miR-155 on VSV replication in macrophages. By measuring VSV TCID50 in the cultural supernatants of the infected macrophages, we found that inhibition of induced miR-155 facilitated VSV replication, whereas overexpression of miR-155 suppressed VSV replication (Fig. 3A, 3B). Consistent with the data of VSV TCID50 assay in cultural supernatants, intracellular VSV RNA replicates were also increased by miR-155 inhibition and decreased by miR-155 overexpression (Fig. 3C, 3D). Thus, we conclude that induced miR-155 expression in turn, as a positive feedback, attenuates VSV replication in VSV-infected macrophages.

miR-155 attenuates viral propagation mainly through enhancing type I IFN signaling in macrophages

To gain an insight into the mechanism of how miR-155 induction attenuates viral propagation, we analyzed in silico with RNA22 miRNA target detection (22) using both VSV sense and antisense RNA sequences but found no potential target sites in VSV RNA (data not shown). Hence, miR-155 is less likely to target VSV RNA directly, as miR-24 and miR-93 have been shown to do so (23). We next examined type I IFN production in VSV-infected macrophages and found no significant difference in either mRNA or protein level of IFN-β when miR-155 was inhibited or overexpressed (Fig. 4A, 4B), although there was a slight increase in IFN-β production when miR-155 was overexpressed. Similar results were also obtained when IFN-4α mRNA level was examined (Fig. 4C). Finally, we focused on the effect of miR-155 on type I IFN downstream signaling. After type I IFN binds to their receptors, IFN-αβ receptors, JAK/STAT pathway is activated, and the STATs are phosphorylated and translocated into nucleus, resulting in transcription of IFN-stimulated genes. The kinetic phosphorylation of STAT1 was detected after VSV challenge in macrophages transfected with miR-155 mimic or miR-155 inhibitor. As shown in Fig. 4D, VSV-induced STAT1 phosphorylation was promoted by miR-155 overexpression while inhibited by miR-155 inhibition. We also examined expression of IFN-induced immune regulatory genes, such as ISG15 and IP-10. In macrophages treated with rIFN-β, we found that induced expressions of ISG15 and IP-10 were increased by miR-155 overexpression and decreased by miR-155 inhibition (Fig. 4E). These results suggest that inducible miR-155 in response to RNA virus infection promotes type I IFN signaling but does not significantly affect type I IFN production.

**FIGURE 4.** miR-155 promotes type I IFN signaling rather than enhances type I IFN production. A and B, A total of 0.5 ml 2 × 10^5 murine peritoneal macrophages were transfected with control mimic or miR-155 mimic (A) or control inhibitor or miR-155 inhibitor (B) as indicated. After 48 h, cells were infected by VSV at MOI 10 for indicated time. IFN-β mRNA expression (left panel) was measured by quantitative RT-PCR and normalized to that of β-actin in each sample. IFN-β in supernatants (right panel) was measured by ELISA. C, Murine peritoneal macrophages were transfected and infected as in A and B, and IFN-4α mRNA expression was measured as in A and B. D, Murine peritoneal macrophages were transfected as in A and B and then infected by VSV at MOI 10. Phosphorylated STAT1 was detected by immunoblot at the indicated time and total STAT1 as an input control. E, Macrophages were transfected as in A and B. After 48 h, recombinant murine IFN-β (100 U/ml) was added for indicated time, and ISG15 and IP-10 mRNA expression were measured as in A and B. Data are shown as mean ± SD (n = 3) of one representative experiment. Similar results were obtained in three independent experiments. **p < 0.01; ▲ p > 0.05.
miR-155 targets SOCS1 in virus-infected macrophages

We next investigated what was the major target of miR-155 that could modulate type I IFN signaling. We found that miR-155 was one of the broadly conserved miRNAs that putatively targets conserved sites of murine SOCS1’s 3’-UTR by computational prediction via TargetScan (www.targetscan.org) (Supplemental Fig. 2). SOCS1 has been identified to negatively regulate various immune responses and signaling pathways, including type I IFN signaling (24). SOCS1 mRNA level accumulates sharply in no more than 24 h after VSV challenge (Fig. 5A), but its protein level hardly changes or even slightly decreases over a time course of 48 h (Fig. 5B), suggesting that the expression of SOCS1 in macrophages is regulated by a posttranscriptional mechanism, presumably miRNA inhibition. Hence, we hypothesized that miR-155 might suppress SOCS1 translation in macrophages after VSV challenge.

Then we examined whether the protein level of SOCS1 in macrophages was targeted and regulated by miR-155. As expected, SOCS1 expression was increased by miR-155 inhibition and decreased by miR-155 overexpression (Fig. 5C). To present direct evidence that inducible miR-155 during VSV infection suppressed SOCS1 protein expression, we examined the kinetic level of SOCS1 protein and mRNA after VSV challenge when inducible miR-155 was inhibited. As shown in Fig. 5D and 5E, miR-155 inhibitor rescued SOCS1 mRNA translation upon VSV challenge, and SOCS1 mRNA kinetic level was not affected significantly. As SOCS1 was reported to be recruited to the JAKs and in turn block JAKs’ tyrosine kinase activity and downstream STAT phosphorylation (25, 26), so we further proved that miR-155 regulated SOCS1 protein expression, we examined the kinetic level of SOCS1 protein and mRNA after VSV challenge when inducible miR-155 was inhibited. As shown in Fig. 5D and 5E, miR-155 inhibitor rescued SOCS1 mRNA translation upon VSV challenge, and SOCS1 mRNA kinetic level was not affected significantly. As SOCS1 was reported to be recruited to the JAKs and in turn block JAKs’ tyrosine kinase activity and downstream STAT phosphorylation (25, 26), so we further proved that miR-155 regulated type I IFN signaling via SOCS1 by examining kinetic phosphorylation of JAK1 and STAT1/2 in response to rmIFN-β. As shown in Fig. 5F, inhibition of inducible miR-155 suppressed STAT1/2 and JAK1 phosphorylation, whereas overexpression of miR-155 enhanced STAT1/2 and JAK1 phosphorylation, which is consistent with the regulatory mechanism of SOCS1 (27, 28). These results were consistent with a recent report showing that miR-155 directly targeted the potential conserved target site in SOCS1 mRNA 3’-UTR through reporter gene assay (29). Taken together, these data show that endogenous SOCS1 is targeted and directly regulated by miR-155 in macrophages.

Antiviral function of miR-155 is mainly through targeting SOCS1

To demonstrate the role of targeting SOCS1 in the antiviral function of miR-155, we carried out experiments of SOCS1 RNA interference knockdown and overexpression. And we confirmed that SOCS1 siRNA effectively inhibited its expression in murine peritoneal macrophages (Fig. 6A), whereas SOCS1-stably overexpressed cell clone of RAW264.7 macrophages, which expressed SOCS1 mRNA without its 3’-UTR sequence, had significantly elevated SOCS1 protein expression (Fig. 6B).

In murine peritoneal macrophages, SOCS1 knockdown attenuated VSV replication, which resembled the effect of miR-155 overexpression (Fig. 6C). And VSV replication increased by miR-155 inhibition was rescued by SOCS1 knockdown (Fig. 6D). Also, rmIFN-β–induced ISG15 expression is reduced by miR-155 inhibition and further rescued by SOCS1 knockdown (Fig. 6E).

FIGURE 5. miR-155 targets murine SOCS1 in VSV-infected macrophages. A and B, Murine peritoneal macrophages were infected with VSV at MOI 10 for indicated time. SOCS1 mRNA expression was measured as in Fig. 4A (A), and SOCS1 protein level and β-actin were detected by immunoblot (B). C, Murine peritoneal macrophages were transfected with control mimic or miR-155 mimic (top panel), or control inhibitor or miR-155 inhibitor (bottom panel) as indicated. After 48 h, SOCS1 was detected by immunoblot as in B, D and E, Murine peritoneal macrophages were transfected with control inhibitor or miR-155 inhibitor as indicated; 12 h after transfection, cells were infected with VSV at MOI 10 for indicated time. SOCS1 mRNA expression was measured as in Fig. 4A (D), and SOCS1 protein level and β-actin were detected by immunoblot (E). F, Macrophages were transfected as in Fig. 4A and 4B. After 48 h, recombinant murine IFN-β (100 U/ml) was added, and SOCS1 and tyrosine phosphorylation of STAT1, STAT2, and JAK1 were detected by immunoblot at indicated time and total STAT1, STAT2, and JAK1 as input controls. Data are shown as mean ± SD (n = 3) of one representative experiment. Similar results were obtained in at least three independent experiments.
Similar results were obtained in at least three independent experiments. Overexpressed RAW264.7 cells or mock control cells transfected with control mimic or miR-155 mimic were infected as in Fig. 3 and intracellular VSV RNA replicates (Fig. 6) both measuring VSV TCID<sub>50</sub> in the cultural supernatants (Fig. 6). In SOCS1-stably overexpressed RAW264.7 cells, documented by that miR-155 overexpression could influence VSV proliferation longer target SOCS1 expression in these cells. We did not find after 48 h, macrophages were treated, infected, and detected as in Fig. 3A. D, Murine peritoneal macrophages were transfected with control inhibitor, miR-155 inhibitor, miR-155 inhibitor combined with control RNA, or miR-155 inhibitor combined with SOCS1 siRNA, respectively, as indicated. After 48 h, macrophages were treated, infected, and detected as in Fig. 3A. E, Murine peritoneal macrophages were transfected as in D. After 48 h, recombinant murine IFN-β (100 U/ml) was added for indicated time, and ISG15 mRNA expression was measured as in Fig. 4A. F and G, SOCS1-stably overexpressed RAW267.4 cells or mock control cells transfected with control mimic or miR-155 mimic were infected as in Fig. 3A. Virus in supernatants (F) and intracellular VSV RNA replicates (G) were detected as in Fig. 3A and 3B. Data are shown as mean ± SD (n = 3) of one representative experiment. Similar results were obtained in at least three independent experiments. *p < 0.01; †p < 0.05; ▲p > 0.05.

These results suggest that SOCS1 knockout phenocopied the antiviral effect of induced miR-155 and counteracted the effect of miR-155 inhibition.

Because the SOCS1-stably overexpressed RAW264.7 cell clones transcribed SOCS1 mRNA without its 3′-UTR, miR-155 should no longer target SOCS1 expression in these cells. We did not find that miR-155 overexpression could influence VSV proliferation in SOCS1-stably overexpressed RAW264.7 cells, documented by both measuring VSV TCID<sub>50</sub> in the cultural supernatants (Fig. 6F) and intracellular VSV RNA replicates (Fig. 6G). So, we concluded that induced miR-155 upon viral infection exhibits its antiviral function mainly through suppressing endogenous SOCS1 expression and subsequently promoting type I IFN signaling.

Discussion

miR-155 is generally believed to be a multifunctional miRNA (9, 10). It is transcribed from a noncoding gene named BIC gene, which is highly conserved in many species and broadly expressed in various organs, tissues, and cell types, indicating its versatile functions in various biological processes. It has been demonstrated that miR-155 plays important roles in physiological conditions (e.g., circulation, hematopoiesis, immunity, and inflammation), as well as pathological conditions (e.g., neoplastic diseases and cardiovascular disorders). Up until now, there were only two reports about the roles of miR-155 in viral infection: one was about the miR-155 ortholog named miR-K12-11 encoded by Kaposi’s sarcoma-associated herpes virus (30); the other was the induced miR-155 expression during EBV infection (31). Both of the viruses belong to the herpesvirus family, DNA virus. The induced miR-155 and the viral ortholog miR-K12-11 were both found to participate in the biological process of the indicated herpesvirus infection. In this paper, we show that miR-155, as a positive feedback regulator, participates in antiviral immune responses once induced in murine macrophages upon RNA virus challenge. Our data broaden and deepen the understanding of the roles of miR-155 in the interaction between host and virus.

For IFN-β stimulation-induced downstream signaling, we found that miR-155 could not significantly influence JAK1 phosphorylation at short time points (0, 15, and 30 min poststimulation), but STAT1/2 phosphorylation is influenced by miR-155 expression more obviously (Supplemental Fig. 3). This discrepancy may be due to the expression level of endogenous SOCS1 in peritoneal macrophages. Considering that SOCS1 is expressed at a relative low level in peritoneal macrophages (32) and its expression could be induced upon IFN stimulation in 2 h (Supplemental Fig. 4), it is plausible that lower expression of SOCS1 preferentially inhibits STAT1/2 phosphorylation, whereas the enhanced expression of SOCS1 inhibits both JAK1 and STAT1/2 phosphorylation as detected at longer time points in Fig. 5F. This presumption is consistent with previous reports showing that SOCS1 could inhibit STAT1 activation at a very low protein expression level in vivo (33), phosphorylation of JAKs is required for the binding of SOCS1 (34), and further forced SOCS1 overexpression inhibits both JAKs autophosphorylation and STAT1/2 phosphorylation in...
vito (27, 28). However, the detailed regulatory mechanism mediating this discrepancy remains to be investigated in the future.

Up until now, several genes have been identified as targets of miR-155, through which the function of miR-155 is revealed. However, the target profile of miR-155 does not seem to end so far. The major targets of one specific miRNA always changes in different physical or pathological conditions, or different cell types, to implement different functions accordingly. miR-155 has been suggested to participate in different biological processes by targeting different genes, expression, such as PUMA (11, 35), AID (36, 37), SHIP1 (38), and SMAD5 (39). In this paper, we show that miR-155 directly targets SOCS1 expression in VSV-infected macrophages to strengthen IFN effects, which is consistent with a recent report revealing that miR-155 expression is required for regulatory T cell activity also via targeting SOCS1 expression (29). It seems that the essential roles of miR-155 elucidated by the pathological phenotypes in miR-155 knockout mice or miR-155 overexpression are not confined to regulatory T cells or macrophages. Because SOCS1 is a general regulator of cell signaling downstream lots of cytokines, such as IL-2, IL-4, IL-6, IFN-γ, growth hormone, and erythropoietin, thus modulating various biological functions of immune cells (4), the finding that miR-155 targeting SOCS1 may explain, to some extent, some of the pathological phenotypes in miR-155 knockout mice or miR-155 transgenic mice [e.g., impaired hematopoietic homeostasis (40), lymphoblastic leukemia (41), increased lung airway remodeling (40), and unbalanced cytokine production (12)]. Also, miR-155 targeting SOCS1 may contribute to the pathogenesis of many human hematopoietic tumors with overexpressed miR-155 (42–44). In addition, overexpressed SOCS1 lacking miR-155 suppression in incompetent immunocytes is probably the explanation for immune tolerance or immunodeficiency in patients with poor response to IFN antiviral or antitumor therapy. Predictably, upregulation of miR-155 expression in activated immunocytes may facilitate antitumor responses, whereas, in contrast, enhanced reactivity of immunocytes to proliferative cytokines mediated by miR-155 overexpression may otherwise contribute to the increased risk of suffering hematopoietic tumors. These predictions need to be validated further through extensive experiments in the future.

Induced cytokine production is required for the elimination of pathogen infection; nevertheless, it is clarified that their overproduction or overreaction may result in local or systematic pathology. For instance, solid evidence reveals that host immune responses contribute to the pathogenesis of human seasonal influenza A virus disease (45). Hence, the suppression of SOCS1 by inducible miR-155 strengthens antiviral immunity and elicits more effective immune responses as a positive aspect. In contrast, miR-155 overexpression may also probably initiate excessive antiviral responses and contribute to viral infection-induced tissue damage, which is supported by studies demonstrating that SOCS1 negatively regulates innate immune responses triggered by influenza A virus (46) and SOCS1 protects mice against lethal poxvirus infection (47) and Chlamydia pneumoniae infection (48). Induced miR-155 expression upon viral infection may be a double-edged sword, because it may participate in both physiological antiviral immune response and pathological viral infection-induced tissue damage. And maybe this is the reason why miR-155 is moderately, neither vigorously nor slightly, induced in macrophages and other APCs upon RNA virus challenge, and deregulation of miR-155 probably contributes to the pathogenesis of viral infection-induced pathological responses.

Our previous work documented that miR-146a, upregulated upon VSV challenge, inhibited RIG-I–dependent type I IFN production as a negative feedback regulator in antiviral immunity (16), whereas in this study, the inducible miR-155 promoted type I IFN signaling as a positive feedback regulator. Taking these works together, we further confirmed that antiviral immune response was under accurate and sophisticated regulation by multiple regulators, both negatively and positively, like miR-146a and miR-155. It is probable that we are far from revealing the last miRNA that modulates antiviral immunity. And each miRNA may act as a counterbalance to the other, so the overall effect of all these miRNAs on IFN-mediated antiviral response may be not apparent. This may be the reason why Dicer-deficient macrophages, which leading to deficiency of all miRNAs, showed no obviously altered IFN-mediated antiviral response (23). In addition, besides these significantly induced miRNAs after VSV challenge, we could not exclude the possibility that the less markedly altered miRNAs also influence host antiviral response via the cumulative impact of all or most of them, if single one has little effect.

Host favorable defense against viral infection requires not only appropriate induction of antiviral cytokines but also appropriate cellular responses to them. We show in this study that the inducible miR-155 promotes host cell response to type I IFN in antiviral immunity by targeting SOCS1, further indicating that different host miR-155 expression levels may contribute to different responses to IFN therapy of viral infections among individuals. Hence, miR-155 may be a potential therapeutic target in viral infections or diseases subjected to type I IFN therapy, which needs to be identified in the future.

Acknowledgments
We thank Prof. Shizuo Akira for providing TLR4, TLR9, or MyD88 knockout mice, Prof. Wei Pan for providing VSV, Prof. Bing Sun for providing SeV, Mei Jin and Yan Li for their excellent technical assistance, and Prof. Jiahui Han, Genhong Chen, Dr. Xiaoping Su, Dr. Taoyong Chen, and Dr. Qian Zhang for their helpful discussions.

Disclosures
The authors have no financial conflicts of interest.

References


Supplemental Materials

Figure S1. miR-155 expression in wild-type, RIG-I-deficient, or TLR4-deficient macrophages stimulated with LPS

Peritoneal macrophages from wild-type, RIG-I-deficient, or TLR4-deficient mice were stimulated with 100 ng/ml LPS for 6 hrs, and then miR-155 expression was measured by qRT-PCR. Data are shown as mean ± SD (n = 3) of one representative experiment. Similar results were obtained in three independent experiments. **, P<0.01.

Wang P, et al. Fig.S1
Figure S2. SOCS1 might be molecular target of miR-155

Shown is a sequence alignment of miR-155 and its putative conserved (among the indicated species) target sites in the 3'UTR of SOCS1, which was obtained from TargetScan (http://www.targetscan.org).
Figure S3. The effects of miR-155 mimic or inhibitor on type I IFN signaling in macrophages at short time points.

Macrophages were transfected as in (Fig. 4A, 4B). After 48 hrs, recombinant murine IFN-β (100 U/ml) was added, and phosphorylation of STAT1, STAT2 and JAK1 was detected by immunoblot at indicated time and total STAT1, STAT2 and JAK1 as input controls. Similar results were obtained in at least three independent experiments.

Wang P, et al. Fig.S3
Figure S4. Induction of SOCS1 protein expression in mouse peritoneal macrophages by IFN-β and IFN-γ

Mouse peritoneal macrophages were stimulated with rmIFN-β (100 U/ml) or rmIFN-γ (100 U/ml). SOCS1 was detected by immunoblot 2 hrs post stimulation.