NMR methods. TICAM-1 NTD formed a single, compact domain comprised of eight α-helices (α1: 9–18, α2: 20–31, α3: 38–51, α4: 54–64, α5: 68–76, α6: 92–106, α7: 111–128, and α8: 133–144) and a long loop region between α5 and α6 helices (Fig. 2). In this loop, the region between Ser82 and Glu87 is located that shows low convergence of backbone structure because these residues have no long range NOEs. The overall arrangement of the α-helices in TICAM-1 NTD was found to be novel after an homology search of the previously determined structures using the DALI server (Holm et al. 2008). TICAM-1 NTD can be divided into two segments, a TPR (tetratricopeptide repeat) motif-like region (α1–α5) and a three-helix bundle region (α6–α8). The TPR motif-like region has two sequentially adjacent anti-parallel α-helical pairs (α2–α3 and α4–α5), as is observed in typical TPR proteins. The TPR proteins mediate the protein–protein interactions or inter-domain assembly of multiple domain proteins. The TPR proteins generally present tandem arrays of 3–16 motifs, which form a right-handed super-helical structure and create an amphipathic groove for target recognition. However, the TPR-motif of TICAM-1 NTD does not have sufficient repeats to create a super-helical structure, and moreover, the α1-helix lies on the amphipathic groove (Fig. 2b).

TICAM-1 TIR domain binding site

Recent studies have shown that TICAM-1 NTD is an autorepression domain that directly interacts with the TICAM-1 TIR domain, leading to attenuation of the TIR–TIR interaction (Tatematsu et al. 2010). In a previous paper (Enokizono et al. 2013), we presented the TICAM-1 TIR domain structure and identified two distinct interaction sites required for homotypic and heterotypic TIR oligomerization. A hydrophobic patch that includes the BB loop was important in mediating the homotypic interaction of TICAM-1 TIR, whereas a basic patch on the αE- and αE′-helices was essential for heterotypic interaction with TICAM-2 TIR (Fig. 3b left). An acidic cleft stretched over the TPR motif-like region and three-helix bundle region (Fig. 3a right) that could interact with the basic patch of TICAM-1 TIR domain (Fig. 3b left) was found on the TICAM-1 NTD surface. This suggests the possibility that TICAM-1 NTD blocks the binding between TICAM-1 TIR and TICAM-2 TIR, thus regulating TICAM-1-mediated TLR4 signaling in an autoinhibitory manner. Further studies are required to confirm this hypothesis.

References

Botos I, Segal DM, Davies DR (2011) The structural biology of Toll-like receptors. Structure 19:447–459

Delaglio F, Grzesiek S, Vuister GW, Zhu G, Pfeifer J, Bax A (1995) NMRPipe: a multidimensional spectral processing system based on UNIX pipes. J Biomol NMR 6:277–293

Enokizono Y, Kumeta H, Funami K, Horiuchi M, Sarmiento J, Yamashita K, Standley DM, Matsumoto M, Seya T, Inagaki F (2013) Structures and interface mapping of the TIR domain-containing adaptor molecules involved in interferon signaling. Proc Natl Acad Sci USA 110:19908–19913

Funami K, Sasai M, Ohba Y, Oshiumi H, Seya T, Matsumoto M (2007) Spatiotemporal mobilization of Toll/IL-1 receptor domain-containing adaptor molecule-1 in response to dsRNA. J Immunol 179:6867–6872

Funami K, Sasai M, Oshiumi H, Seya T, Matsumoto M (2008) Homo-oligomerization is essential for Toll/interleukin-1 receptor domain-containing adaptor molecule-1-mediated NF-κB and interferon regulatory factor-3 activation. J Biol Chem 283:18283–18291

Goddard TD, Kneller DG (1997) SPARKY 3, University of California, San Francisco. http://www.cgl.ucsf.edu/home/sparky

Güntert P (2004) Automated NMR structure calculation with CYANA. Methods Mol Biol 278:353–378

Holm L, Kääriäinen S, Rosenström P, Schenkel A (2008) Searching protein structure databases with Dali Lite v. 3. Bioinformatics 24:2780–2781

Kang JY, Lee JO (2011) Structural biology of the Toll-like receptor family. Ann Rev Biochem 80:917–941

Matsumoto M, Funami K, Tanabe M, Oshiumi H, Shingai M, Seto Y, Yamamoto A, Seya T (2003) Subcellular localization of Toll-like receptor 3 in human dendritic cells. J Immunol 171:3154–3162

Mobli M, Maciejewski MW, Gryk MR, Hoch J (2007) Automatic maximum entropy spectral reconstruction in NMR. J Biomol NMR 39:133–139

Seya T, Oshiumi H, Sasai M, Akazawa T, Matsumoto M (2005) TICAM-1 and TICAM-2: toll-like receptor adapters that participate in induction of type 1 interferons. Int J Biochem Cell Biol 37:524–529

Shen Y, Delaglio F, Cornilescu G, Bax A (2009) TALOS+: a hybrid method for predicting protein backbone torsion angles from NMR chemical shifts. J Biomol NMR 44:213–223

Tatematsu M, Ishii A, Oshiumi H, Horiuchi M, Inagaki F, Seya T, Matsumoto M (2010) A molecular mechanism for Toll-IL-1 receptor domain-containing adaptor molecule-1-mediated IRF-3 activation. J Biol Chem 285:20128–20136

Published February 14, 2014, doi:10.4049/jimmunol.1301459

IPS-1 Is Essential for Type III IFN Production by Hepatocytes and Dendritic Cells in Response to Hepatitis C Virus Infection

Masaaki Okamoto,* Hiroyuki Oshiumi,* Masahiro Azuma,* Nobuyuki Kato,† Misako Matsumoto,* and Tsukasa Seya*

Hepatitis C virus (HCV) is a major cause of liver disease. The innate immune system is essential for controlling HCV replication, and HCV is recognized by RIG-I and TLR3, which evoke innate immune responses through IPS-1 and TICAM-1 adaptor molecules, respectively. IL-28B is a type III IFN, and genetic polymorphisms upstream of its gene are strongly associated with the efficacy of polyethylene glycol–IFN and ribavirin therapy. As seen with type I IFNs, type III IFNs induce antiviral responses to HCV. Recent studies established the essential role of TLR3–TICAM-1 pathway in type III IFN production in response to HCV infection. Contrary to previous studies, we revealed an essential role of IPS-1 in type III IFN production in response to HCV. First, using IPS-1 knockout mice, we revealed that IPS-1 was essential for type III IFN production by mouse hepatocytes and $CD8^+$ dendritic cells (DCs) in response to cytoplasmic HCV RNA. Second, we demonstrated that type III IFN induced RIG-I but not TLR3 expression in $CD8^+$ DCs and augmented type III IFN production in response to cytoplasmic HCV RNA. Moreover, we showed that type III IFN induced cytoplasmic antiviral protein expression in DCs and hepatocytes but failed to promote DC-mediated NK cell activation or cross-priming. Our study indicated that IPS-1–dependent pathway plays a crucial role in type III IFN production by $CD8^+$ DCs and hepatocytes in response to HCV, leading to cytoplasmic antiviral protein expressions. ***The Journal of Immunology*****, 2014, 192: 000–000.**

Hepatitis C virus (HCV) is a major cause of chronic liver disease (1). The 3′ untranslated region (UTR) of the HCV genome is recognized by a cytoplasmic viral RNA sensor RIG-I (2). HCV RNA induces RIG-I–dependent type I IFN production to promote hepatic immune responses in vivo (2). RIG-I is a member of RIG-I–like receptors (RLRs), which include MDA5 and LGP2. RLRs trigger signal that induces type I IFN and other inflammatory cytokines through the IPS-1 adaptor molecule (3). RLRs are localized in the cytoplasm and recognize cytoplasmic dsRNAs. Another pattern recognition receptor, TLR3, recognizes dsRNAs within early endosomes or on cell surfaces (4). Human monocyte-derived dendritic cells (DCs) require TLR3 to recognize HCV RNA in vitro (5), and TLR3 induces type I IFN production through the TICAM-1 adaptor, also called Toll/IL-1R domain-containing adapter inducing IFN-β (6, 7).

*Department of Microbiology and Immunology, Hokkaido University Graduate School of Medicine, Sapporo 060-8638, Japan; and †Department of Tumor Virology, Okayama University Graduate School of Medicine, Dentistry, and Pharmaceutical Science, Okayama 700-8558, Japan

Received for publication June 3, 2013. Accepted for publication January 13, 2014.

This work was supported in part by a grant-in-aid from the Ministry of Education, Science, and Culture of Japan, the Ministry of Health, Labour, and Welfare of Japan, and the Kato Memorial Bioscience Foundation.

Address correspondence and reprint requests to Dr. Hiroyuki Oshiumi and Dr. Tsukasa Seya, Department of Microbiology and Immunology, Graduate School of Medicine, Hokkaido University, Kita-15, Nishi-7, Kita-ku Sapporo 060-8638, Japan. E-mail addresses: oshiumi@med.hokudai.ac.jp (H.O.) and seya-tu@pop.med.hokudai.ac.jp (T.S.)

The online version of this article contains supplemental material.

Abbreviations used in this article: BM-DC, bone marrow–derived dendritic cell; BM-Mf, bone marrow–derived macrophage; DC, dendritic cell; HCV, hepatitis C virus; KO, knockout; Mf, macrophage; Oc, O cured; RLR, RIG-I–like receptor; UTR, untranslated region.

Copyright © 2014 by The American Association of Immunologists, Inc. 0022-1767/14/$16.00

IL-28B is a type III IFN (also called IFN-λ), which includes IL-28A (IFN-λ2) and IL-29 (IFN-λ1) (8). Type III IFNs interacts with heterodimeric receptors that consist of IL-10Rβ and IL-28Rα subunits (8). Polymorphisms upstream of the IL-28B (IFN-λ3) gene are significantly associated with the responses to polyethylene glycol–IFN and ribavirin in patients with chronic genotype 1 HCV infections (9–12). As seen with type I IFNs, type III IFNs have antiviral activities against HCV (13). Type I IFNs induce the expression of IFN-inducible genes, which have antiviral activities, and can promote cross-priming and NK cell activation (14). However, the roles of type III IFN in cross-priming and NK cell activation are largely unknown, and the functional differences between type I and III IFN are uncertain.

Mouse $CD8^+$ DCs and its human counterpart $BDCA3^+$ DCs are the major producers of type III IFNs in response to polyI:C (15). $CD8^+$ DCs highly express TLR3 and have strong cross-priming capability (16). A recent study showed that TLR3 was important for type III IFN production by $BDCA3^+$ DCs in response to cell-cultured HCV (17). RIG-I efficiently recognizes the 3′ UTR of the HCV RNA genome, and, thus, RIG-I adaptor IPS-1 is essential for type I IFN production (2). However, the role of an IPS-1–dependent pathway in type III IFN production in vivo has been underestimated. In this study, we investigated the role of an IPS-1–dependent pathway in type III IFN production in vivo and in vitro using IPS-1 knockout (KO) mice and established an essential role of IPS-1 in type III IFN production in response to HCV RNA. Our study indicated that not only TICAM-1 but also IPS-1 are essential for type III IFN production in response to HCV.

Materials and Methods

Mice

All mice were backcrossed with C57BL/6 mice more than seven times before use. The generation of TICAM-1 and IPS-1 KO mice was described

Downloaded from http://www.jimmunol.org/ at National Institute of Infectious Disease on February 27, 2014

previously (18). All mice were maintained under specific pathogen-free conditions in the Animal Facility of the Hokkaido University Graduate School of Medicine (Sapporo, Japan). Animal experiments were conducted according to the guidelines established by the Animal Safety Center, Japan.

Cell lines and reagents

Human hepatocyte cell lines O cells and O cured (Oc) cells that contained HCV 1b replicons were provided by N. Kato (Okayama University). Mouse hepatocyte cell line was described previously (19). PolyI:C was purchased from GE Healthcare and dissolved in saline. An OVA ($H2K^b$-SL8) tetramer was purchased from MBL. PE-CD80, -CD86, -NK1.1, FITC-CD8, and allophycocyanin-CD3e Abs were purchased from BioLegend, and PE-CD40, FITC-CD69, and allophycocyanin-CD11c Abs were from eBioscience. An ELISA kit for IFN-β was purchased from PBL Biomedical Laboratories, and ELISA kits for mouse IL-28 (IFN-λ2/3) were purchased from Abcam and eBioscience. An ELISA kit for mouse IFN-γ was purchased from eBioscience. ELISA was performed according to the manufacturer's instructions. Mouse IFN-α and IFN-λ3 (IL-28B) were purchased from Miltenyi Biotec and R&D Systems, respectively.

Cell preparation

Spleen $CD8^+$ and $CD4^+$ DCs were isolated using $CD8^+$ DC isolation kit and CD4-positive isolation kit, according to manufacturer's instruction (Miltenyi Biotec). Spleen $CD11c^+$ DCs were isolated using CD11c microbeads. To obtain splenic double-negative (DN) DCs, $CD4^+$ and $CD8^+$ cells were depleted from mouse spleen cells using CD4 and CD8 MicroBeads (Miltenyi Biotec), and then $CD11c^+$ DCs were positively selected using CD11c MicroBeads (Miltenyi Biotec). We confirmed that >90% of isolated cells were $CD4^-$, $CD8^-$, and $CD11c^+$ DCs. Splenic NK cells were isolated using mouse DX5 MicroBeads (Miltenyi Biotec). The cells were analyzed by flow cytometry on a FACSCalibur instrument (BD Biosciences), followed by data analysis using FlowJo software.

Generation of bone marrow–derived DCs and bone marrow–derived macrophages

Bone marrow cells were prepared from the femur and tibia. The cells were cultured in RPMI 1640 medium with 10% FCS, 100 μM 2-ME, and 10 ng/ml murine GM-CSF or culture supernatant of L929 expressing M-CSF. Medium was changed every 2 d. Six days after isolation, cells were collected.

Hydrodynamic injection

Total RNA from the human hepatocyte cell lines O cells and Oc cells was extracted using TRIzol reagent (Invitrogen). HCV genotype 1b 3′ UTR RNA, including the polyU/UC region, was synthesized using T7 and SP6 RNA polymerase and purified with TRIzol, as described previously (20). RNA was i.v. injected into a mouse by a hydrodynamic method using a TransIT Hydrodynamic Gene Delivery System (Takara), according to the manufacturer's instruction.

Quantitative PCR

For quantitative PCR, total RNA was extracted using TRIzol reagent (Invitrogen), after which 0.1–1 μg RNA was reverse transcribed using a high-capacity cDNA transcription kit with an RNase inhibitor kit (Applied Biosystems), according to the manufacturer's instructions. Quantitative PCR was performed using a Step One real-time PCR system (Applied Biosystems). The expression of cytokine mRNA was normalized to that of β-actin mRNA, and the fold increase was determined by dividing the expressions in each sample by that of wild type at 0 h. PCR primers for mouse IFN-λ amplified both IFN-λ2 and λ3 mRNA. The primer sequences are described in Supplemental Table 1.

Activation of NK cells in vitro

NK cells and $CD11c^+$ DCs were isolated from spleens using DX5 and CD11c MicroBeads (Miltenyi Biotec), respectively. A total of 2×10^5 NK

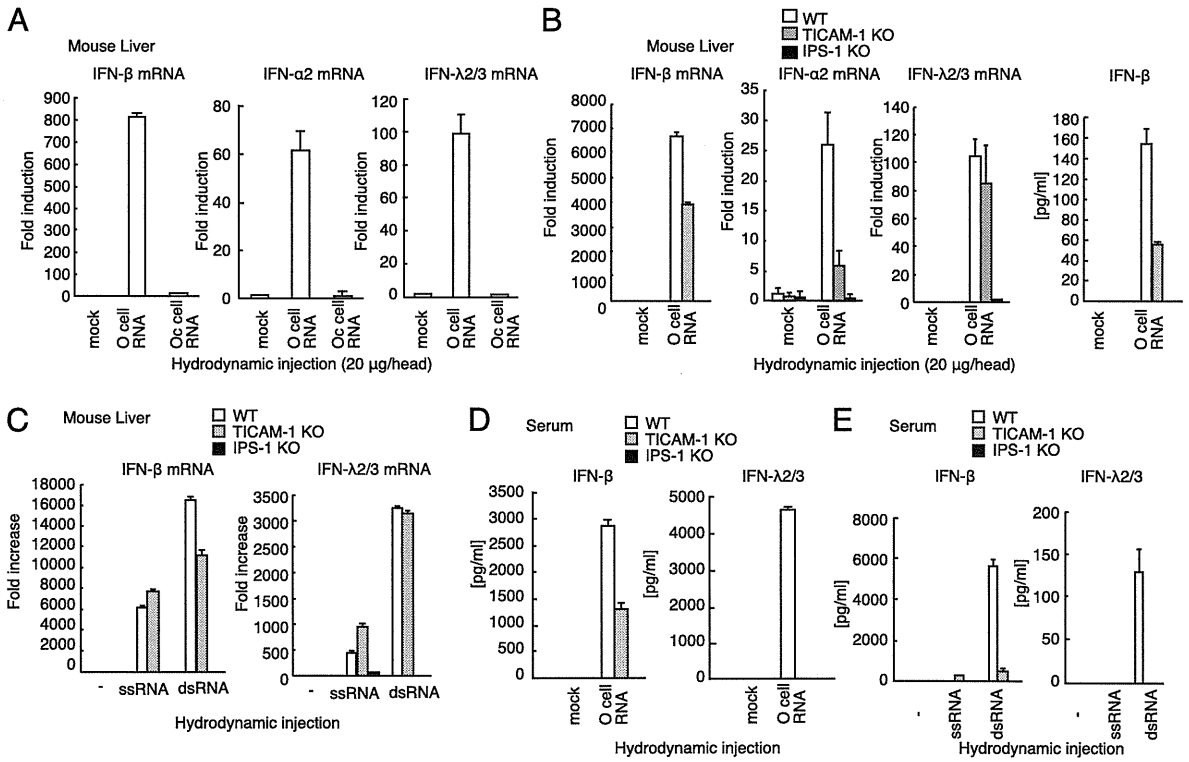


FIGURE 1. Type I and type III IFN productions in response to HCV RNA in vivo. (**A**) O cell and Oc cell RNA (20 μg) were hydrodynamically injected into wild-type mice. Six hours later, mouse livers were excised, and IFN-β, α2, and -λ2/3 mRNA levels were determined by quantitative RT-PCR. (**B**) O cell RNA (20 μg) with HCV replicons was hydrodynamically injected into wild-type, TICAM-1 KO, and IPS-1 KO mice. Six hours after injection, IFN-β, α2, and -λ2/3 mRNA levels in liver were determined by quantitative RT-PCR. IFN-β protein levels in mouse livers were determined by ELISA. (**C**) HCV ssRNA or HCV dsRNA (5 μg) was hydrodynamically injected into wild-type, TICAM-1 KO, and IPS-1 KO mice. Six hours after injection, IFN-β and -λ2/3 mRNA levels in liver were determined by quantitative RT-PCR. (**D**) O cell RNA (20 μg) with HCV replicons was hydrodynamically injected into wild-type, TICAM-1 KO, and IPS-1 KO mice. Six hours after injection, serum IFN-β and -λ2/3 concentrations were determined by ELISA. (**E**) HCV ssRNA or HCV dsRNA (5 μg) was hydrodynamically injected into wild-type, TICAM-1 KO, and IPS-1 KO mice. Six hours after injection, serum IFN-β and -λ2/3 concentrations were determined by ELISA.

Downloaded from http://www.jimmunol.org/ at National Institute of Infectious Disease on February 27, 2014

cells and 1×10^5 DCs was cocultured with IFN-λ, IFN-α, or polyI:C. After 6, 12, and 24 h, IFN-γ concentrations in the supernatants were determined by ELISA. To determine CD69 expression, $NK1.1^+$ and $CD3e^+$ cells in 24-h sample were gated.

Ag-specific T cell expansion in vivo

OVA (1 mg) and IFN-λ (0.5 μg) or 1×10^5 IU IFN-α were i.p. injected into mice on day 0, and then 0.5 μg IFN-λ or 1×10^5 IU of IFN-α was injected into mice on days 1, 2, and 4. On day 7, spleens were homogenized and stained with FITC CD8α Ab and PE-OVA tetramer for detecting OVA (SL8)-specific $CD8^+$ T cell population. For a negative control, PBS in place of IFN was injected on days 0, 1, 2, and 4. For a positive control, 100 μg polyI:C and OVA were injected into mice on day 0.

Results

TICAM-1 is essential for type III IFN production in response to polyI:C

DCs require the TLR3 adaptor TICAM-1 to produce type III IFN in response to polyI:C (15). Adding polyI:C to culture medium for mouse bone marrow–derived macrophages (BM-Mf) induced IFN-β, IFN-α2, IFN-α4, and IFN-λ2/3 mRNA expression, and TICAM-1 KO abolished IFN-λ2/3 mRNA expression (Supplemental Fig. 1A). These results suggested an essential role for TICAM-1 in type III IFN expression by BM-Mf.

Next, we examined cytokine mRNA expression in mouse tissues in response to i.p. injected polyI:C. IFN-β, IFN-α2, and IFN-α4 mRNA expression was detectable in both wild-type and TICAM-1 KO mice livers, whereas IFN-λ2/3 mRNA expression was not detected in TICAM-1 KO mouse liver (Supplemental Fig. 1B–1E). A recent study showed that TLR3 KO abolished IFN-λ serum levels in response to i.v. polyI:C injection (15). Our results and those in the previous study confirmed that TICAM-1 is essential for type III IFN expression in response to polyI:C.

IPS-1 plays a crucial role in type III IFN production in response to HCV in vivo

IPS-1 is essential for type I IFN production in response to HCV RNA and polyI:C in vivo (2, 3). We investigated whether IPS-1 could induce type III IFN production. An ectopic expression study using IPS-1 and TICAM-1 expression vectors showed that both TICAM-1 and IPS-1 activated the IFN-λ1 promoter (Supplemental Fig. 2A, 2B), which suggested that IPS-1 has the ability to induce IFN-λ1 expression. A deletion analysis showed that a 150- to 556-aa region of TICAM-1 and the transmembrane region of IPS-1 were essential for IFN-β, -λ1, and 2/3 promoter activations (Supplemental Fig. 2C, 2D).

Hydrodynamic injection is a highly efficient procedure to deliver nucleic acids to the mouse liver (21), and Gale Jr. and colleagues

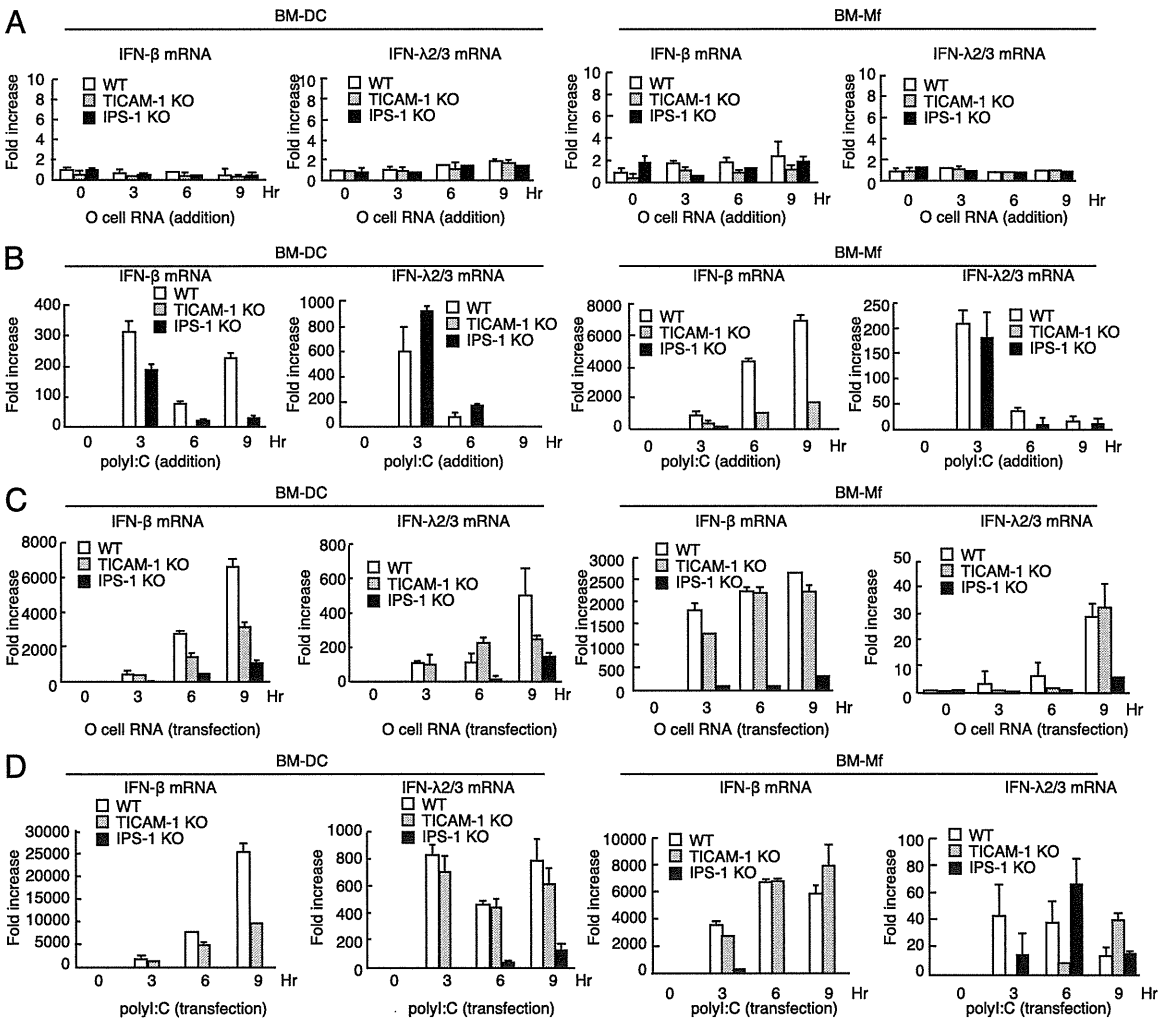


FIGURE 2. Type I and type III IFN expression in mouse DCs and Mfs in response to HCV RNA. (**A** and **B**) O cell RNA (A) or polyI:C (B) (20 μg) was added to the culture medium of BM-DCs and BM-Mfs derived from wild-type, TICAM-1 KO, and IPS-1 KO mice. IFN-β and IFN-λ2/3 mRNA levels were determined by quantitative RT-PCR at indicated hours. (**C** and **D**) O cell RNA (C) or polyI:C (D) (1 μg) was transfected into BM-DCs and BM-Mfs derived from wild-type, TICAM-1 KO, or IPS-1 KO mice. IFN-β (C) and -λ2/3 (D) mRNA levels were determined by quantitative RT-PCR.

Downloaded from http://www.jimmunol.org/ at National Institute of Infectious Disease on February 27, 2014

(2) previously used a hydrodynamic assay to assess the role of RIG-I in type I IFN production in response to HCV RNA in vivo. Thus, to investigate the response to HCV RNA in vivo, we also used a hydrodynamic assay. We used RNA extracted from hepatocyte cell lines, O cells and Oc cells. O cells are derived from HuH-7 cells and contain HCV 1b full-length replicons (22). Oc cells were obtained by eliminating these replicons using IFN-α treatment (22). RNAs extracted from O cells (with HCV RNA) and Oc cells (without HCV RNA) were hydrodynamically injected into mouse livers, after which the cytokine expressions in mouse livers were determined. In wild-type mouse liver, O cell but not Oc cell RNA induced IFN-α2, β, and λ mRNA expression (Fig. 1A), which indicated that these cytokines were expressed in response to HCV RNAs within O cells that contained the HCV genome and replication intermediates in hepatocyte. Knockout of IPS-1 severely reduced IFN-β and α2 mRNA expressions in mouse liver in response to hydrodynamically injected O cell RNA (Fig. 1B). IFN-β protein level in mouse liver was also reduced by IPS-1 knockout (Fig. 1B). Although TICAM-1 was essential for IFN-λ2/3 mRNA expression in liver in response to i.p. injected polyI:C (Supplemental Fig. 1), TICAM-1 was dispensable for IFN-λ2/3 mRNA expression in response to hydrodynamically injected O cell RNA (Fig. 1B). In contrast, IPS-1 was essential for IFN-λ2/3 mRNA expression in response to hydrodynamically injected O cell RNA (Fig. 1B). A requirement for IPS-1 for IFN-λ2/3 mRNA expression in the liver was also found when in vitro synthesized HCV dsRNAs and ssRNAs were used for the hydrodynamic assay (Fig. 1C). These results suggested that IPS-1 plays a crucial role in type III IFN production in response to HCV RNA in vivo.

To corroborate the role of IPS-1 in type III IFN production, we next measured serum IFN-λ and -β levels in response to hydrodynamic injection of O cell RNA, HCV ssRNA, and HCV dsRNA. Interestingly, IPS-1 KO markedly reduced serum IFN-λ2/3 levels (Fig. 1D, 1E). Unexpectedly, TICAM-1 KO also reduced serum IFN-λ levels (Fig. 1D, 1E). Because TICAM-1 was dispensable for IFN-λ mRNA expression in the liver, it is possible that serum IFN-λ was produced from DCs in other tissues in a TICAM-1–dependent manner, as described below. Our data indicated that both TICAM-1 and IPS-1 are essential for type III IFN in response to HCV RNA in vivo. When polyI:C was hydrodynamically injected, knockout of TICAM-1 or IPS-1 moderately reduced IFN-λ2/3 levels in sera (Supplemental Fig. 3).

DCs produce type III IFN through an IPS-1–dependent pathway in response to cytoplasmic HCV RNA

HCV proteins and minus strands of its genome are detected in DCs and macrophages (Mfs) of chronically HCV-infected patients (23, 24), and recent study showed that DCs produce type I and III IFNs in response to HCV (17, 25). Thus, we assessed the role of IPS-1 in type III IFN production by DCs and Mfs in response to HCV RNA. Surprisingly, adding O cell RNA into the culture medium did not induce any IFN-β and -λ2/3 mRNA expression (Fig. 2A), whereas adding polyI:C into culture medium efficiently induced IFN-β and -λ2/3 mRNA expression (Fig. 2B), and TICAM-1 KO abolished the IFN-λ2/3 mRNA expression in bone marrow–derived DCs (BM-DCs) and BM-Mfs (Fig. 2B). It has been shown that polyI:C is preferentially internalized and activates TLR3 in human monocyte-derived DCs, whereas in vitro transcribed viral dsRNA hardly induced IFN-β production in monocyte-derived DCs (26). Thus, there is a possibility that, unlike polyI:C, TLR3 ligand in O cell RNA was not delivered to endosome where TLR3 is localized. Next, cells were stimulated with O cell RNA or polyI:C by transfection. BM-DCs and BM-Mfs expressed IFN-β and -λ2/3

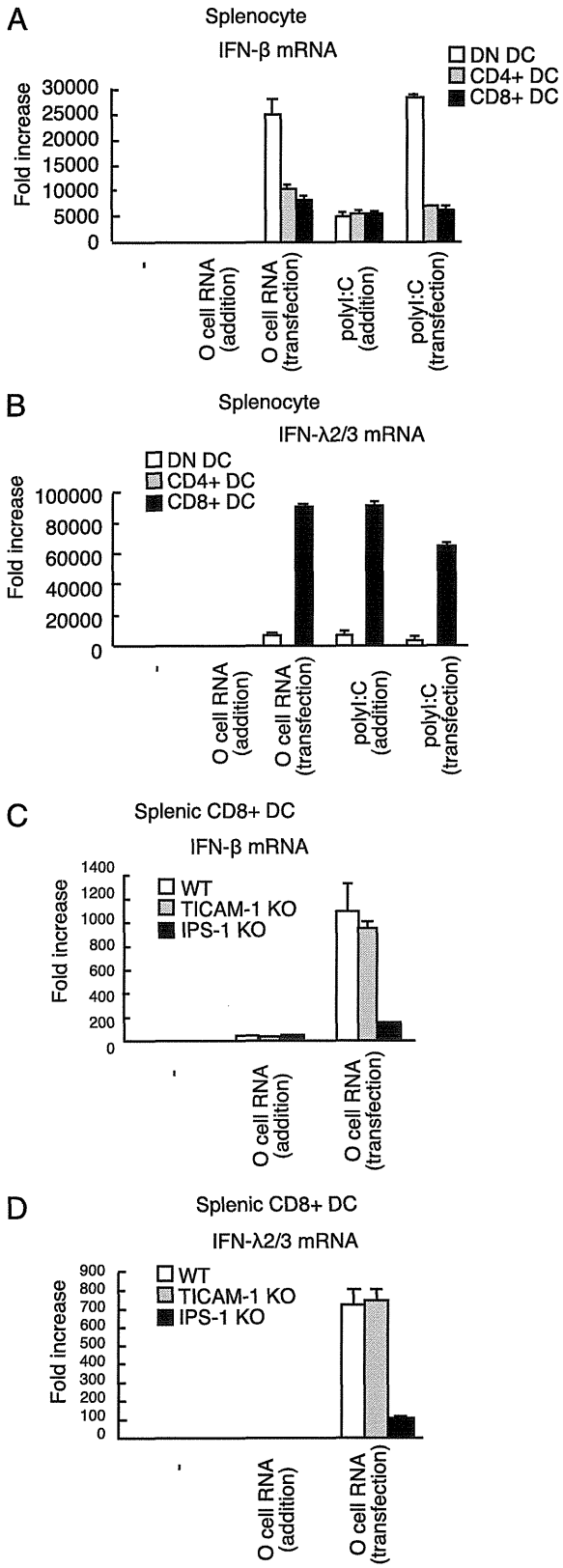


FIGURE 3. Type III IFN production by $CD8^+$ DCs. (**A** and **B**) $CD4^+$, $CD8^+$, and DN DCs were isolated from mouse spleens and stimulated with 20 μg O cell RNA without transfection or stimulated with 1 μg O cell RNA by transfection for 6 h. IFN-β (A) and -λ2/3 (B) mRNA levels were determined by quantitative RT-PCR. (**C** and **D**) $CD8^+$ DCs were isolated from wild-type, TICAM-1 KO, or IPS-1 KO mouse spleens. O cell RNA (20 μg) was added to the culture medium, or 1 μg O cell RNA was transfected into $CD8^+$ DCs. Six hours after transfection, IFN-β (C) and -λ2/3 (D) mRNA levels were determined by quantitative RT-PCR.

Downloaded from http://www.jimmunol.org/ at National Institute of Infectious Disease on February 27, 2014

mRNAs in response to O cell RNA and polyI:C (Fig. 2C, 2D). IPS-1 KO severely reduced IFN-λ2/3 mRNA expression in BM-DCs and BM-Mfs in response to O cell RNA (Fig. 2C). These results indicated that IPS-1 in BM-DCs and BM-Mfs plays a crucial role in IFN-λ2/3 mRNA expression in response to cytoplasmic HCV RNA.

Mice have $CD4^+$, $CD8^+$, and DN DCs. Thus, we next examined the IFN-β and -λ2/3 mRNA expression in these mouse DC subsets. As seen with BM-DCs, the mouse DCs expressed IFN-β and -λ2/3 mRNA in response to polyI:C but not O cell RNA in the culture medium, whereas stimulation with polyI:C or O cell RNA by transfection strongly induced their expression (Fig. 3A, 3B). Interestingly, $CD8^+$ DCs highly expressed IFN-λ2/3 mRNA in response to stimulation with polyI:C or O cell RNA by transfection compared with $CD4^+$ and DN DCs (Fig. 3A, 3B), and IPS-1 KO but not TICAM-1 KO severely reduced IFN-λ2/3 expression in $CD8^+$ DCs in response to O cell RNA transfection (Fig. 3C, 3D). This indicated that IPS-1 was essential for IFN-λ2/3 mRNA expression in $CD8^+$ DCs in response to cytoplasmic HCV RNA.

It was recently reported that exosomes mediate cell-to-cell transfer of HCV RNA from infected cells to cocultured DCs (27). We examined the production of IFN-β and -λ2/3 by $CD8^+$ DCs that were cocultured with O cells and Oc cells. Coculture with O cells but not Oc cells induced IFN-β and -λ2/3 production by $CD8^+$ DCs (Fig. 4A, 4B). Interestingly, TICAM-1 KO abolished IFN-λ2/3 mRNA expression and protein production, whereas IPS-1 KO failed to reduce IFN-λ2/3 mRNA expression and protein production in $CD8^+$ DCs (Fig. 4C, 4D). This suggested that TICAM-1 but not IPS-1 was essential for IFN-λ2/3 production by $CD8^+$ DCs when cocultured with hepatocytes with HCV replicons.

Type III IFN increases RIG-I expression in $CD8^+$ DC

The receptor for type III IFN consists of IL-10RB and IL-28Rα subunits (8). DN and $CD4^+$ DCs and NK cells did not express IL-28Rα mRNA, whereas $CD8^+$ DCs expressed both IL-10RB and IL-28Rα mRNAs (Fig. 5A). Thus, we investigated the effects of IFN-λ on DC function.

First, we examined DC cell surface markers. Unlike IFN-α, IFN-λ3 hardly increased CD40, 80, and 86 surface marker expressions on $CD8^+$ DCs (Fig. 5B). Second, we examined the effects of IFN-λ3 on cross-priming because $CD8^+$ DCs have high cross-priming capability. OVA, IFN-α, and/or IFN-λ3 were i.p. injected into mice according to the indicated schedules (Fig. 5C). Seven days after injection, OVA (SL8)-specific $CD8^+$ T cells in spleens were quantified by tetramer staining. For a positive control, OVA and polyI:C were i.p. injected into mice. The results showed that IFN-λ3 failed to increase OVA-specific $CD8^+$ T cells in the spleens and suggested that IFN-λ3 failed to promote cross-priming at least in our experimental condition (Fig. 5C).

Third, we examined NK cell activation by DCs. NK cells and DCs were isolated from mouse spleens and were cocultured for 24 h in the presence of IFN-α, λ3, or polyI:C. Although IFN-γ production was increased by IFN-α stimulation, IFN-λ3 failed to increase IFN-γ production (Fig. 5D). Next, we investigated a cell surface marker for NK cells when cocultured with DCs. The expression of CD69, a NK cell activation marker, was not increased by IFN-λ3 stimulation (Fig. 5E). These results indicated that, unlike IFN-α, IFN-λ3 failed to enhance the activation of NK cells by DCs.

Fourth, we investigated the expression of antiviral genes in $CD8^+$ DCs in response to IFN-λ3 stimulation. Interestingly, IFN-λ3 stimulation increased RIG-I and Mx1 but not TLR3 mRNA expression in $CD8^+$ DCs (Fig. 6A). In addition, pretreatment with IFN-λ3 augmented IFN-λ2/3 mRNA expression in $CD8^+$ DCs in response to HCV RNA (Fig. 6B). Taken together, type III IFN induced RIG-I and antiviral protein expression but failed to promote DC-mediated NK cell activation and cross-priming.

Hepatocytes express type III IFN receptors. Thus, we examined the effects of IFN-λ on mouse hepatocytes. As with IFN-α, IFN-λ3 stimulation induced both TLR3 and RIG-I mRNA expression in mouse hepatocyte (Fig. 6C). Antiviral nucleases, ISG20 and RNaseL, and an IFN-inducible gene, Mx1, were induced by IFN-λ3 or IFN-α treatment (Fig. 6C). Pretreating mouse hepatocytes with IFN-λ3 enhanced IFN-β and -λ2/3 mRNA expression in response to stimulation with HCV RNA by transfection (Fig. 6D). These results indicated that IFN-λ3 induced cytoplasmic antivirus protein expression in mouse hepatocytes. We confirmed that IFN-λ3 treatment significantly reduced HCV RNA levels in O cells with HCV replicons (Fig. 6E). A previous study also reported that IFN-λ inhibits HCV replication (13).

Discussion

Previous studies have established the importance of the TLR3 pathway for type III IFN production in response to polyI:C (15) or HCV (17). In this study, we established the importance of IPS-1–dependent pathway for type III IFN production in response to cytoplasmic HCV RNA in vivo and in vitro using a mouse model. These data indicated that there are at least two main pathways for type III IFN production in vivo, as follows: one is TICAM-1 dependent, and the other is IPS-1 dependent.

We revealed that IFN-λ was efficiently produced by $CD8^+$ DCs, the mouse counterpart of human $BDCA3^+$ DCs, in response to

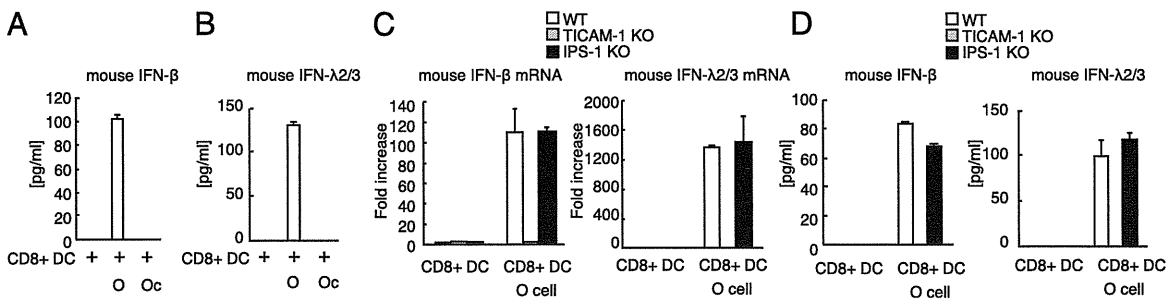


FIGURE 4. IFN-β and –λ production by $CD8^+$ DCs cocultured with hepatocytes with HCV replicons. (**A** and **B**) $CD8^+$ DCs isolated from wild-type spleens were cocultured with O cells (with HCV replicons) or Oc cells (without HCV replicons). After 24 h of coculture, IFN-β (A) and –λ2/3 (B) concentrations in culture medium were determined by ELISA. (**C**) $CD8^+$ DCs isolated from wild-type, TICAM-1 KO, or IPS-1 KO spleens were cocultured with O cells with HCV replicons for six hours, and then IFN-β and –λ2/3 mRNA expression was determined by RT-qPCR. (**D**) $CD8^+$ DCs isolated from wild-type, TICAM-1 KO, or IPS-1 KO spleens were cocultured with O cells with HCV replicons. IFN-β and –λ2/3 concentrations in culture medium were determined by ELISA.

Downloaded from http://www.jimmunol.org/ at National Institute of Infectious Disease on February 27, 2014

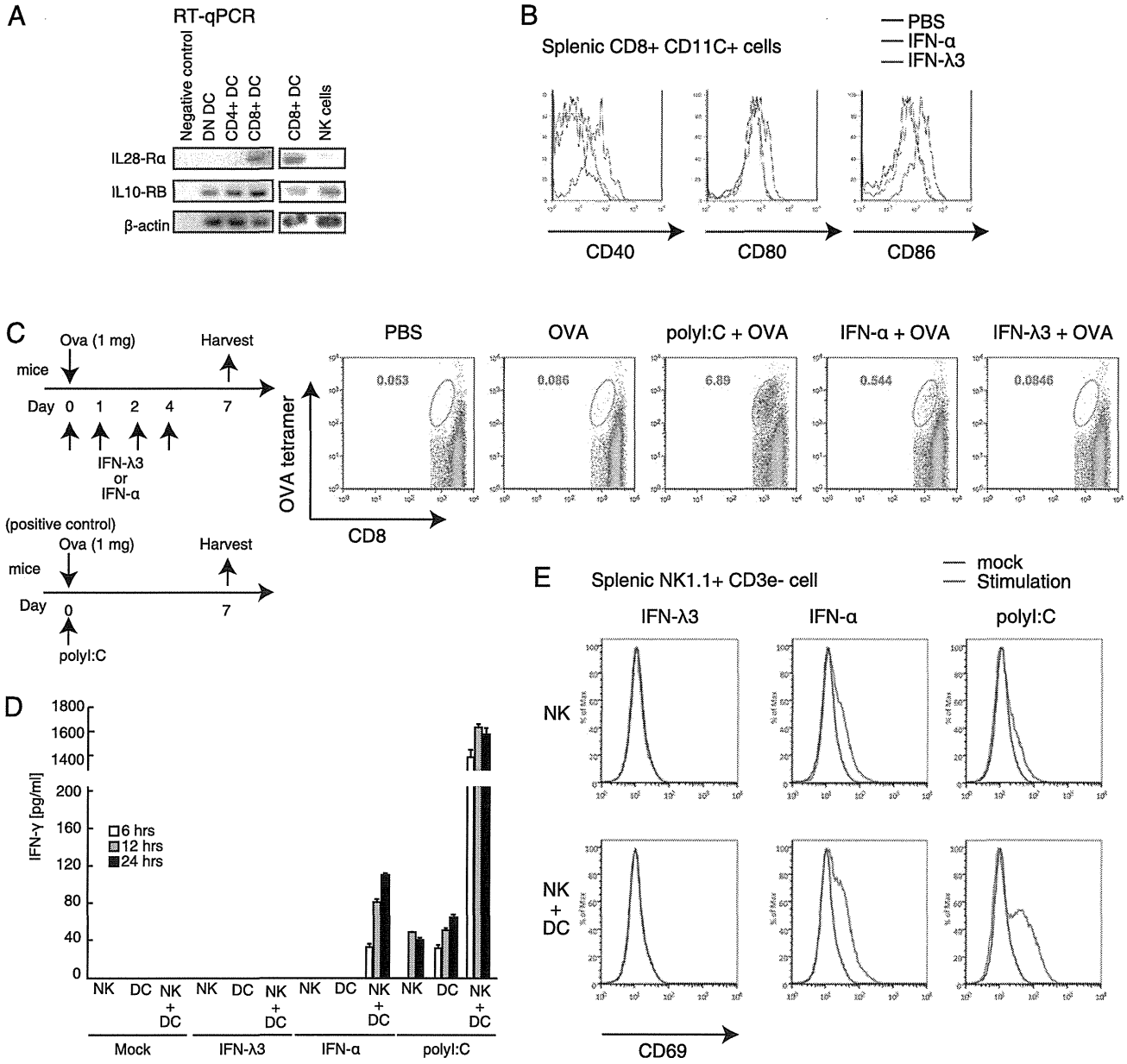


FIGURE 5. IFN-λ effects on DC functions. (**A**) DN, $CD4^+$, $CD8^+$ DCs, and NK cells were isolated from wild-type mouse spleens. IL-28Rα and IL-10RB mRNA were determined by RT-PCR. (**B**) A total of 0.5 μg IFN-λ3 or 1×10^5 IU IFN-α was i.p. injected into mice. Six hours after injection, spleen $CD8^+$ DCs were isolated, and cell surface expressions of CD40, 80, and 86 were determined by FACS analysis. (**C**) OVA and IFN-λ or IFN-α were i.p. injected into mice on day 0, and then IFN-λ or IFN-α was injected into mice on days 1, 2, and 4. Spleens were excised on day 7, and OVA (SL8)-specific $CD8^+$ T cells were determined by a tetramer assay. For a negative control, PBS in place of IFN was injected on days 0, 1, 2, and 4. For a positive control, polyI:C and OVA were injected into mice on day 0. (**D**) NK cells and $CD11c^+$ DCs were isolated from mouse spleens and then stimulated with 1000 U/ml IFN-α, 100 ng/ml IFN-λ3, or 100 μg/ml polyI:C. IFN-γ concentrations in the culture medium at the indicated times were determined by ELISA. (**E**) NK cells were isolated from mouse spleens and then cultured with or without spleen $CD11c^+$ DCs. Cells were stimulated with 1000 U/ml IFN-α, 100 ng/ml IFN-λ3, or 20 μg polyI:C. CD69 expression on NK cells was determined by FACS analysis.

cytoplasmic HCV RNA. Moreover, our data showed that IFN-λ stimulation increased the mRNA expression of RIG-I but not that of TLR3 in $CD8^+$ DCs, and $CD8^+$ DCs required IPS-1 to produce IFN-λ in response to stimulation with cytoplasmic HCV RNA. Furthermore, IFN-λ enhanced the mRNA expression of IFN-λ itself in $CD8^+$ DCs, which suggested a positive feedback loop for IFN-λ mRNA expression in $CD8^+$ DCs. IFN-λ failed to promote DC-mediated NK activation or cross-priming at least in our experimental conditions, whereas antiviral proteins, such as ISG20 and RNaseL, were efficiently induced by IFN-λ stimulation in hepatocytes and $CD8^+$ DCs. These results established a novel role of IPS-1 in innate immune response against HCV via IFN-λ production. IFN-λ pretreatment markedly increased IFN-β mRNA expression in response to HCV RNAs in mouse hepatocyte but not in $CD8^+$ DCs (Fig. 6B, 6D). Although the underlying mechanism is unclear, it is possible that there is a cell-type–specific role of IFN-λ.

It was recently reported that $BDCA3^+$ DCs require TLR3 for type III IFN production in response to cell-cultured HCV (17). They used a HCV 2a JFH1 strain that cannot infect human DCs in vitro (5). We also showed that the TLR3 adaptor TICAM-1 was essential for type III IFN production by $CD8^+$ DCs when cocultured with O cells with HCV replicons. Thus, TLR3 appears to be essential for type III IFN production by DCs that are not infected with HCV. It

Downloaded from http://www.jimmunol.org/ at National Institute of Infectious Disease on February 27, 2014

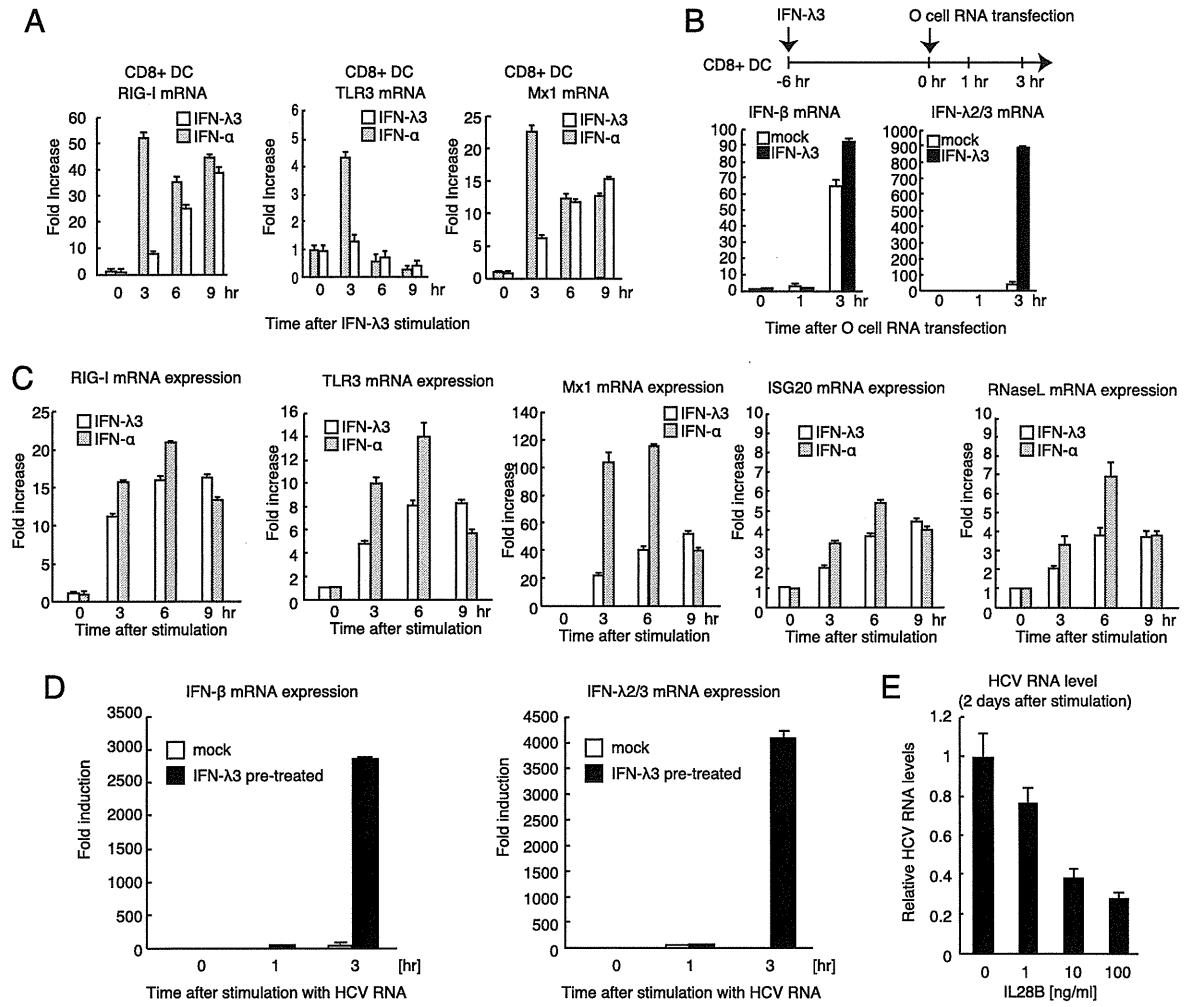


FIGURE 6. Antiviral responses induced by IFN-λ. (**A**) Mouse spleen CD8$^+$ DCs were stimulated with 100 ng/ml IFN-λ3 or 1000 IU/ml IFN-α, after which RIG-I, TLR3, and Mx1 mRNA levels were determined by quantitative RT-PCR. (**B**) Mouse spleen CD8$^+$ DCs were treated with 100 ng/ml IFN-λ3 for 6 h. O cell RNA was transfected into CD8$^+$ DCs, and IFN-β and -λ2/3 mRNA levels were determined by quantitative RT-PCR at the indicated times. (**C**) Mouse hepatocyte cell line cells were stimulated with 1000 U/ml IFN-α or 100 ng/ml IFN-λ3. RIG-I, TLR3, Mx1, ISG20, and RNaseL mRNA levels were determined by quantitative RT-PCR. (**D**) Mouse hepatocyte cell line cells were treated with 100 ng/ml IFN-λ3 for 6 h, and then O cell RNA was transfected into these cells. IFN-β and -λ2/3 mRNA levels were measured by quantitative RT-PCR at the indicated times. (**E**) O cells that contain HCV 1b full-length replicons were treated with human IL-28B at indicated concentration for 2 d. HCV RNA levels were determined by quantitative RT-PCR. HCV RNA levels were normalized to GAPDH mRNA expression.

has been shown that exosomes are internalized efficiently by DCs and sorted into early endosomes, where TLR3 is localized (28, 29). Unlike the transfected HCV RNA, exosome-enclosed HCV RNA might be efficiently sorted and released within early endosomes of CD8$^+$ DC, where TLR3 is localized, leading to TLR3-dependent IFN-λ2/3 production. Although HCV JFH1 infection particles fail to infect DCs in vitro, previous studies indicated that HCV infects DCs in chronically infected patients (23, 24, 30). In human patient DCs and hepatocytes infected with HCV, the IPS-1 pathway could play a pivotal role in type III IFN production.

Knockout of TICAM-1 failed to reduce IFN-λ2/3 mRNA expression in mouse liver after HCV RNA hydrodynamic injection, whereas knockout of TICAM-1 abolished IFN-λ2/3 levels in sera after HCV RNA hydrodynamic injection (Fig. 1B, 1D). Considering that there is a positive feedback loop for IFN-λ production, it is possible that TICAM-1 and IPS-1 pathways augment IFN-λ production each other in vivo; however, we do not exclude a possibility that TICAM-1 is involved in posttranscriptional step of IFN-λ production.

HCV NS3-4A protease cleaves IPS-1 to suppress host innate immune responses (31, 32). However, it is notable that a mutation within the *RIG-I* gene in HuH7.5 cells increases cellular permissiveness to HCV infection (33). This indicates that the RIG-I pathway is functional at least during the early phase of HCV infection before NS3-4A cleaves IPS-1. Thus, we propose that IPS-1 is important for type III IFN production during the early phase of HCV infection.

IFN-α augmented DC-mediated NK cell activation and cross-priming, whereas IFN-λ failed to augment DC-mediated NK cell activation and cross-priming in our experimental conditions. However, as seen with IFN-α, IFN-λ could induce RNaseL and ISG20 mRNA expression. These data indicated that IFN-λ induces cytoplasmic antiviral proteins to eliminate infected virus. A previous study showed that IPS-1 is required for initial antiviral response but dispensable for the protective adaptive immune response to influenza A virus (34). Thus, it is expected that IPS-1–mediated IFN-λ production would be required for initial antiviral response to HCV infection.

In summary, our results provide insights into type III IFN production mechanism in response to HCV RNA in vivo and identify IPS-1 as a molecule crucial for producing type III IFN from hepatocyte and CD8$^+$ DCs in response to cytoplasmic HCV RNA.

Downloaded from http://www.jimmunol.org/ at National Institute of Infectious Disease on February 27, 2014

Acknowledgments

IFN-λ1 and 2/3 reporter plasmids and O cells with HCV replicons were gifted from T. Imamichi (National Institutes of Health) and N. Kato (Okayama University), respectively.

Disclosures

The authors have no financial conflicts of interest.

References

1. Lauer, G. M., and B. D. Walker. 2001. Hepatitis C virus infection. *N. Engl. J. Med.* 345: 41–52.
2. Saito, T., D. M. Owen, F. Jiang, J. Marcotrigiano, and M. Gale, Jr. 2008. Innate immunity induced by composition-dependent RIG-I recognition of hepatitis C virus RNA. *Nature* 454: 523–527.
3. Kumar, H., T. Kawai, H. Kato, S. Sato, K. Takahashi, C. Coban, M. Yamamoto, S. Uematsu, K. J. Ishii, O. Takeuchi, and S. Akira. 2006. Essential role of IPS-1 in innate immune responses against RNA viruses. *J. Exp. Med.* 203: 1795–1803.
4. Matsumoto, M., and T. Seya. 2008. TLR3: interferon induction by double-stranded RNA including poly(I:C). *Adv. Drug Deliv. Rev.* 60: 805–812.
5. Ebihara, T., M. Shingai, M. Matsumoto, T. Wakita, and T. Seya. 2008. Hepatitis C virus-infected hepatocytes extrinsically modulate dendritic cell maturation to activate T cells and natural killer cells. *Hepatology* 48: 48–58.
6. Yamamoto, M., S. Sato, H. Hemmi, K. Hoshino, T. Kaisho, H. Sanjo, O. Takeuchi, M. Sugiyama, M. Okabe, K. Takeda, and S. Akira. 2003. Role of adaptor TRIF in the MyD88-independent Toll-like receptor signaling pathway. *Science* 301: 640–643.
7. Oshiumi, H., M. Matsumoto, K. Funami, T. Akazawa, and T. Seya. 2003. TICAM-1, an adaptor molecule that participates in Toll-like receptor 3-mediated interferon-beta induction. *Nat. Immunol.* 4: 161–167.
8. Sheppard, P., W. Kindsvogel, W. Xu, K. Henderson, S. Schlutsmeyer, T. E. Whitmore, R. Kuestner, U. Garrigues, C. Birks, J. Roraback, et al. 2003. IL-28, IL-29 and their class II cytokine receptor IL-28R. *Nat. Immunol.* 4: 63–68.
9. Thomas, D. L., C. L. Thio, M. P. Martin, Y. Qi, D. Ge, C. O'Huigin, J. Kidd, K. Kidd, S. I. Khakoo, G. Alexander, et al. 2009. Genetic variation in IL28B and spontaneous clearance of hepatitis C virus. *Nature* 461: 798–801.
10. Tanaka, Y., N. Nishida, M. Sugiyama, M. Kurosaki, K. Matsuura, N. Sakamoto, M. Nakagawa, M. Korenaga, K. Hino, S. Hige, et al. 2009. Genome-wide association of IL28B with response to pegylated interferon-alpha and ribavirin therapy for chronic hepatitis C. *Nat. Genet.* 41: 1105–1109.
11. Suppiah, V., M. Moldovan, G. Ahlenstiel, T. Berg, M. Weltman, M. L. Abate, M. Bassendine, U. Spengler, G. J. Dore, E. Powell, et al. 2009. IL28B is associated with response to chronic hepatitis C interferon-alpha and ribavirin therapy. *Nat. Genet.* 41: 1100–1104.
12. Ge, D., J. Fellay, A. J. Thompson, J. S. Simon, K. V. Shianna, T. J. Urban, E. L. Heinzen, P. Qiu, A. H. Bertelsen, A. J. Muir, et al. 2009. Genetic variation in IL28B predicts hepatitis C treatment-induced viral clearance. *Nature* 461: 399–401.
13. Marcello, T., A. Grakoui, G. Barba-Spaeth, E. S. Machlin, S. V. Kotenko, M. R. MacDonald, and C. M. Rice. 2006. Interferons alpha and lambda inhibit hepatitis C virus replication with distinct signal transduction and gene regulation kinetics. *Gastroenterology* 131: 1887–1898.
14. Le Bon, A., N. Etchart, C. Rossmann, M. Ashton, S. Hou, D. Gewert, P. Borrow, and D. F. Tough. 2003. Cross-priming of CD8+ T cells stimulated by virus-induced type I interferon. *Nat. Immunol.* 4: 1009–1015.
15. Lauterbach, H., B. Bathke, S. Gilles, C. Traidl-Hoffmann, C. A. Luber, G. Fejer, M. A. Freudenberg, G. M. Davey, D. Vremec, A. Kallies, et al. 2010. Mouse CD8alpha+ DCs and human BDCA3+ DCs are major producers of IFN-lambda in response to poly IC. *J. Exp. Med.* 207: 2703–2717.
16. Schulz, O., S. S. Diebold, M. Chen, T. I. Näslund, M. A. Nolte, L. Alexopoulou, Y. T. Azuma, R. A. Flavell, P. Liljeström, and C. Reis e Sousa. 2005. Toll-like receptor 3 promotes cross-priming to virus-infected cells. *Nature* 433: 887–892.
17. Yoshio, S., T. Kanto, S. Kuroda, T. Matsubara, K. Higashitani, N. Kakita, H. Ishida, N. Hiramatsu, H. Nagano, M. Sugiyama, et al. 2013. Human blood dendritic cell antigen 3 (BDCA3)(+) dendritic cells are a potent producer of interferon-λ in response to hepatitis C virus. *Hepatology* 57: 1705–1715.
18. Oshiumi, H., M. Okamoto, K. Fujii, T. Kawanishi, M. Matsumoto, S. Koike, and T. Seya. 2011. The TLR3/TICAM-1 pathway is mandatory for innate immune responses to poliovirus infection. *J. Immunol.* 187: 5320–5327.
19. Aly, H. H., H. Oshiumi, H. Shime, M. Matsumoto, T. Wakita, K. Shimotohno, and T. Seya. 2011. Development of mouse hepatocyte lines permissive for hepatitis C virus (HCV). *PLoS One* 6: e21284.
20. Oshiumi, H., M. Ikeda, M. Matsumoto, A. Watanabe, O. Takeuchi, S. Akira, N. Kato, K. Shimotohno, and T. Seya. 2010. Hepatitis C virus core protein abrogates the DDX3 function that enhances IPS-1-mediated IFN-beta induction. *PLoS One* 5: e14258.
21. Liu, F., Y. Song, and D. Liu. 1999. Hydrodynamics-based transfection in animals by systemic administration of plasmid DNA. *Gene Ther.* 6: 1258–1266.
22. Ikeda, M., K. Abe, H. Dansako, T. Nakamura, K. Naka, and N. Kato. 2005. Efficient replication of a full-length hepatitis C virus genome, strain O, in cell culture, and development of a luciferase reporter system. *Biochem. Biophys. Res. Commun.* 329: 1350–1359.
23. Goutagny, N., A. Fatmi, V. De Ledinghen, F. Penin, P. Couzigou, G. Inchauspé, and C. Bain. 2003. Evidence of viral replication in circulating dendritic cells during hepatitis C virus infection. *J. Infect. Dis.* 187: 1951–1958.
24. Sansonno, D., A. R. Iacobelli, V. Cornacchiulo, G. Iodice, and F. Dammacco. 1996. Detection of hepatitis C virus (HCV) proteins by immunofluorescence and HCV RNA genomic sequences by non-isotopic in situ hybridization in bone marrow and peripheral blood mononuclear cells of chronically HCV-infected patients. *Clin. Exp. Immunol.* 103: 414–421.
25. Stone, A. E., S. Giugliano, G. Schnell, L. Cheng, K. F. Leahy, L. Golden-Mason, M. Gale, Jr., and H. R. Rosen. 2013. Hepatitis C virus pathogen associated molecular pattern (PAMP) triggers production of lambda-interferons by human plasmacytoid dendritic cells. *PLoS Pathog.* 9: e1003316.
26. Itoh, K., A. Watanabe, K. Funami, T. Seya, and M. Matsumoto. 2008. The clathrin-mediated endocytic pathway participates in dsRNA-induced IFN-beta production. *J. Immunol.* 181: 5522–5529.
27. Dreux, M., U. Garaigorta, B. Boyd, E. Décembre, J. Chung, C. Whitten-Bauer, S. Wieland, and F. V. Chisari. 2012. Short-range exosomal transfer of viral RNA from infected cells to plasmacytoid dendritic cells triggers innate immunity. *Cell Host Microbe* 12: 558–570.
28. Morelli, A. E., A. T. Larregina, W. J. Shufesky, M. L. Sullivan, D. B. Stolz, G. D. Papworth, A. F. Zahorchak, A. J. Logar, Z. Wang, S. C. Watkins, et al. 2004. Endocytosis, intracellular sorting, and processing of exosomes by dendritic cells. *Blood* 104: 3257–3266.
29. Matsumoto, M., K. Funami, M. Tanabe, H. Oshiumi, M. Shingai, Y. Seto, A. Yamamoto, and T. Seya. 2003. Subcellular localization of Toll-like receptor 3 in human dendritic cells. *J. Immunol.* 171: 3154–3162.
30. Pham, T. N., S. A. MacParland, P. M. Mulrooney, H. Cooksley, N. V. Naoumov, and T. I. Michalak. 2004. Hepatitis C virus persistence after spontaneous or treatment-induced resolution of hepatitis C. *J. Virol.* 78: 5867–5874.
31. Meylan, E., J. Curran, K. Hofmann, D. Moradpour, M. Binder, R. Bartenschlager, and J. Tschopp. 2005. Cardif is an adaptor protein in the RIG-I antiviral pathway and is targeted by hepatitis C virus. *Nature* 437: 1167–1172.
32. Li, X. D., L. Sun, R. B. Seth, G. Pineda, and Z. J. Chen. 2005. Hepatitis C virus protease NS3/4A cleaves mitochondrial antiviral signaling protein off the mitochondria to evade innate immunity. *Proc. Natl. Acad. Sci. USA* 102: 17717–17722.
33. Saito, T., R. Hirai, Y. M. Loo, D. Owen, C. L. Johnson, S. C. Sinha, S. Akira, T. Fujita, and M. Gale, Jr. 2007. Regulation of innate antiviral defenses through a shared repressor domain in RIG-I and LGP2. *Proc. Natl. Acad. Sci. USA* 104: 582–587.
34. Koyama, S., K. J. Ishii, H. Kumar, T. Tanimoto, C. Coban, S. Uematsu, T. Kawai, and S. Akira. 2007. Differential role of TLR- and RLR-signaling in the immune responses to influenza A virus infection and vaccination. *J. Immunol.* 179: 4711–4720.

Downloaded from http://www.jimmunol.org/ at National Institute of Infectious Disease on February 27, 2014

Journal of General Virology (2014), **95**, 60–65 DOI 10.1099/vir.0.058008-0

Short Communication

Production of single-round infectious chimeric flaviviruses with DNA-based Japanese encephalitis virus replicon

Ryosuke Suzuki,[1]† Tomohiro Ishikawa,[2]† Eiji Konishi,[3] Mami Matsuda,[1] Koichi Watashi,[1] Hideki Aizaki,[1] Tomohiko Takasaki[4] and Takaji Wakita[1]

Correspondence
Ryosuke Suzuki
ryosuke@nih.go.jp
Eiji Konishi
ekon@biken.osaka-u.ac.jp

[1]Department of Virology II, National Institute of Infectious Diseases, Toyama 1-23-1, Shinjuku-ku, Tokyo 162-8640, Japan

[2]Department of Microbiology, Dokkyo Medical University School of Medicine, 880 Kitakobayashi, Mibu-machi, Shimotsuga-gun, Tochigi, 321-0293, Japan

[3]BIKEN Endowed Department of Dengue Vaccine Development, Faculty of Tropical Medicine, Mahidol University, 420/6 Ratchawithi Road, Ratchahewi, Bangkok 10440, Thailand

[4]Department of Virology I, National Institute of Infectious Diseases, Toyama 1-23-1, Shinjuku-ku, Tokyo 162-8640, Japan

A method for rapid production of single-round infectious particles (SRIPs) of flavivirus would be useful for viral mutagenesis studies. Here, we established a DNA-based production system for SRIPs of flavivirus. We constructed a Japanese encephalitis virus (JEV) subgenomic replicon plasmid, which lacked the C-prM-E (capsid–pre-membrane–envelope) coding region, under the control of the cytomegalovirus promoter. When the JEV replicon plasmid was transiently co-transfected with a JEV C-prM-E expression plasmid into 293T cells, SRIPs were produced, indicating successful *trans*-complementation with JEV structural proteins. Equivalent production levels were observed when C and prM–E proteins were provided separately. Furthermore, dengue types 1–4, West Nile, yellow fever or tick-borne encephalitis virus prM-E proteins could be utilized for production of chimaeric flavivirus SRIPs, although the production was less efficient for dengue and yellow fever viruses. These results indicated that our plasmid-based system is suitable for investigating the life cycles of flaviviruses, diagnostic applications and development of safer vaccine candidates.

Received 1 August 2013
Accepted 3 October 2013

Japanese encephalitis virus (JEV) is the leading cause of viral encephalitis with severe mortality in eastern and south-eastern Asia, and is estimated to be responsible for 67 900 cases annually, mostly in children (Campbell *et al.*, 2011). The virus is transmitted by *Culex* mosquito vectors between pigs and/or wild birds, and humans and horses are thought to be dead-end hosts. JEV is a member of the genus *Flavivirus* within the family *Flaviviridae*, which includes dengue virus (DENV), West Nile virus (WNV), yellow fever virus (YFV) and tick-borne encephalitis virus (TBEV). JEV is an enveloped single-stranded positive-sense RNA virus with an 11 kb genome that is translated as a single large polyprotein. The polyprotein is co-translationally cleaved by host and viral proteases into three structural proteins – capsid (C), pre-membrane (prM) and envelope (E) – and seven non-structural (NS) proteins (Sumiyoshi *et al.*, 1987).

For several flaviviruses, subgenomic replicons, which lack structural protein genes but can replicate in cells, have been constructed (Khromykh & Westaway, 1997; Pang *et al.*, 2001; Shi *et al.*, 2002). In addition, the expression of viral structural proteins in cells harbouring replicon RNA has been shown to produce single-round infectious particles (SRIPs), which are infectious, but progeny viruses cannot be spread from the infected cells, as the packaged genome lacks structural protein genes (Gehrke *et al.*, 2003; Jones *et al.*, 2005; Khromykh *et al.*, 1998; Ng *et al.*, 2007; Scholle *et al.*, 2004; Yun *et al.*, 2009). Furthermore, *trans*-packaging of replicons by the prM-E proteins from heterologous flaviviruses have been reported (Ansarah-Sobrinho *et al.*, 2008; Yoshii *et al.*, 2008).

A method for rapidly producing SRIPs of flaviviruses would be useful for viral mutagenesis studies, diagnostic applications and the production of vaccines with reduced

†These authors contributed equally to this paper.

One supplementary figure is available with the online version of this paper.

058008 © 2014 SGM *Printed in Great Britain*

risk of infection. In this study, to establish a DNA-based production system for SRIPs, we constructed a JEV subgenomic replicon plasmid, which lacked the C-prM-E coding region, under the control of the cytomegalovirus (CMV) promoter. As DNA-based replicons can be transfected directly into eukaryotic cells without *in vitro* transcription, SRIPs can be rapidly produced by co-transfection with structural protein-expression plasmids.

In order to generate a subgenomic replicon from the JEV Nakayama strain (McAda *et al.*, 1987), viral RNA was extracted from infected Vero cells, reverse transcribed into cDNA and amplified in individual dsDNA fragments containing T7 RNA polymerase promoter and hepatitis delta virus ribozyme (HDV-RZ) as shown in Fig. 1(a). For deletion of the C-prM-E region, a synthetic antisense oligonucleotide was used to add a *Bsp*TI site at codons 17–18 of the C-coding region following the cyclization sequence, and a sense oligonucleotide was designed that added the *Bsp*TI site before the C-terminal transmembrane domain, which consists of 30 aa of the E protein coding sequence, in order to permit ligation of C to NS1. The five individual fragments required to produce a replicon-length cDNA were readily assembled into the low-copy-number plasmid pACYC177, designated pJEVrep#97. Replication of *in vitro*-transcribed RNAs derived from the plasmid was confirmed in RNA-transfected cells (data not shown). Next, to construct a DNA-based replicon plasmid, the T7 RNA polymerase promoter was replaced with the CMV promoter, and the simian virus 40 polyadenylation signal was inserted downstream of the HDV-RZ; the resulting plasmid was designated pCMV-JErep (Fig. 1a). pCMV-JErep-fs, which contains a frameshift mutation through a 4 nt insertion upstream of the GDD motif of RNA-dependent RNA polymerase in NS5, was also constructed as a negative control with no replication activity. To characterize the replication activity of the plasmid-derived replicon, 293T cells were transfected with plasmids as described previously (Suzuki *et al.*, 2013). Indirect immunofluorescence with an anti-dsRNA antibody showed positive staining in the cytoplasm of cells transfected with pCMV-JErep plasmid or infected with JEV Nakayama strain, whereas no signal was detected in the cells transfected with pCMV-JErep-fs, indicating the ability of viral RNAs transcribed intracellularly from the plasmid pCMV-JErep to replicate in cells (Fig. 1b). It should be noted that NS1 protein was detected in the cytoplasm of cells transfected with both pCMV-JErep and pCMV-JErep-fs.

We also constructed expression plasmids for JEV C-E, mature C consisting of 105 aa, and prM-E, which we designated pCAG-JECE, pCAG-JEC and pCAG-JEprME, respectively (Fig. 2a). To reduce sequence homology and intergenomic recombination potential with the truncated C and E genes in the subgenomic replicon, 21 nt mutations were incorporated into the 5′ region of the C gene and 3′ region of the E gene. These changes also include two nucleotides in the conserved 5′ cyclization sequence (CS) (Hahn *et al.*, 1987; Khromykh *et al.*, 2001), producing a sequence that was non-complementary to the 3′ CS of the replicon genome, thereby preventing replication of a recombinant genome. To produce SRIPs of JEV, 293T cells were transfected with a mixture of two (pCMV-JErep and pCAG-JECE) or three (pCMV-JErep, pCAG-JEC and pCAG-JEprME) plasmids. The infectivity of SRIPs was determined by inoculating the culture supernatant of transfected cells into Vero cells, followed by immunostaining with anti-NS1 antibody. 293T cells produced a titre of 6.9×10^5 IU ml^{-1} (Fig. 2b) or 7.9×10^5 IU ml^{-1} (Fig. 2c) 3 days after transfection with two or three plasmids, respectively. In contrast, no infectious particles were detected in the supernatant when one of the two or three plasmids was omitted or the replicon containing a frameshift mutation was introduced. The production levels of SRIPs from cells transfected with two or three plasmids were similar, as shown in Fig. 2(d).

In order to confirm that the SRIPs have only single-round infectivity potential, Vero cells were inoculated with medium harvested from 293T cells transfected with replicon and structural protein plasmids, and were examined for antigen-positive cells. SRIPs were demonstrated to be infectious in the first round (Fig. 3a). However, no antigen-positive cells were observed in a second round, in which the supernatants of the cells infected with SRIPs were transferred to naive Vero cells (Fig. 3a). As a control, supernatant from JEV-infected cells produced antigen-positive cells in second-round infection.

We then evaluated whether the SRIPs could be used in neutralization tests instead of infectious live virus by using anti-JEV sera raised in rabbits as a representative antibody. Serial fourfold dilutions of serum were mixed with aliquots of SRIPs or virus of equivalent infectivity. The virus–antibody mixture was incubated for 1 h at room temperature, followed by titration for infectivity on Vero cell monolayers in a 96-well plate. The neutralizing activity of each antibody dilution was expressed as a percentage of the infectivity obtained with the control, which was tested in the absence of any serum. Infection with SRIPs and JEV Nakayama strain were similarly neutralized by anti-JEV antibody in a dose-dependent manner, although normal serum did not affect infection with SRIPs and JEV (Fig. 3b).

Next, to examine whether SRIPs derived from other flaviviruses could be generated using our plasmid-based method, we used prM-E expression plasmids for the following viruses: DENV1, Mochizuki strain; DENV2, New Guinea C strain; DENV3, H87 strain; DENV4, H241 strain (Konishi *et al.*, 2006); WNV, NY99-6922 strain (Ishikawa *et al.*, 2007); YFV, 17D strain; and TBEV, Oshima 5-10 strain (Yoshii *et al.*, 2003). Detection of each E protein in cells transfected with prM-E expression plasmids by immunofluorescence revealed indistinguishable efficiency of transfection as shown in Fig. S1 (available in JGV Online). Efficient production of chimaeric flavivirus SRIPs by co-transfection with JEV C and JEV replicons was achieved for

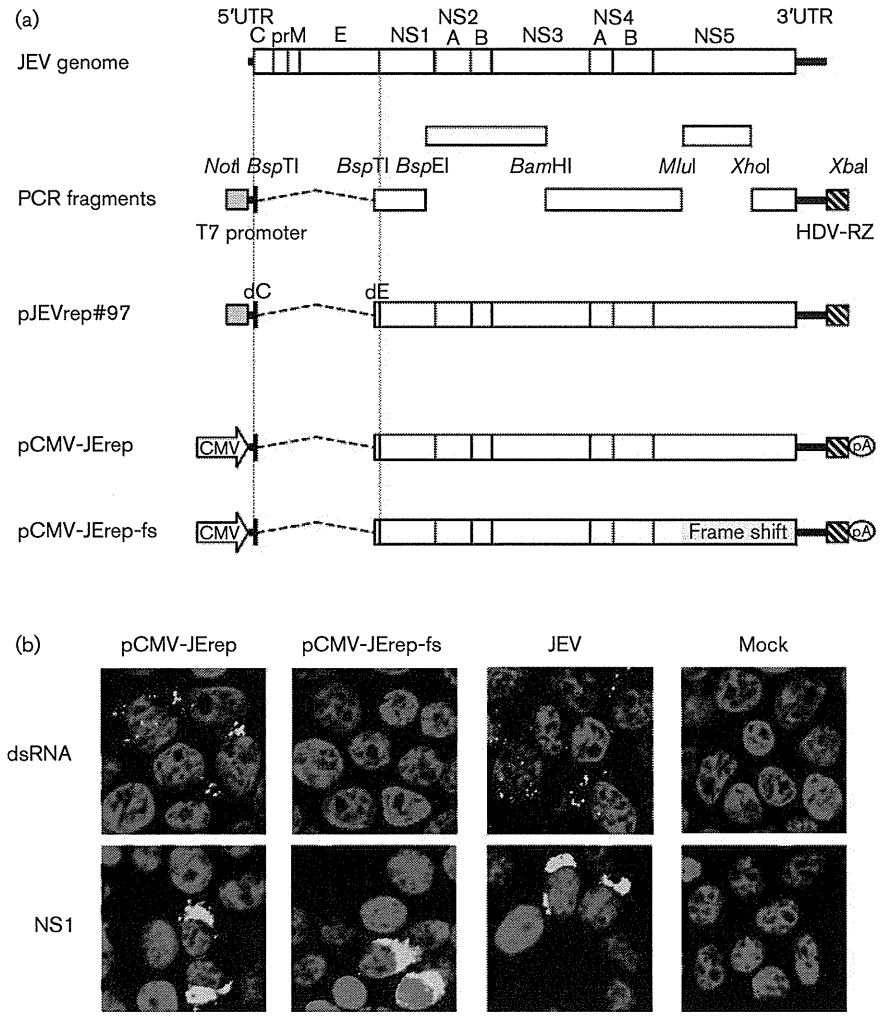


Fig. 1. (a) Schematic representation of the position of the JEV genome showing restriction enzymes sites (*Not*I, *Bsp*TI, *Bsp*EI, *Bam*HI, *Mlu*I, *Xho*I and *Xba*I), fragments used to assemble for replicon construction, position of the T7 promoter, CMV promoter (CMV), HDV-RZ and polyadenylation signal (pA). (b) 293T cells were transfected with the indicated plasmids or were infected or mock-infected with JEV. Two days post-transfection or post-infection, cells were fixed and permeabilized as described previously (Suzuki *et al.*, 2013). Samples were then incubated with anti-dsRNA antibody (J2; English & Scientific Consulting) or anti-NS1 antibody (2D5; Konishi *et al.*, 2004). Green signals were obtained with Alexa-Fluor-488-labelled goat anti-mouse IgG secondary antibody (Invitrogen). Cell nuclei were counterstained with DAPI.

WNV and TBEV, although production of SRIPs was less efficient for DENV1-4 and YFV (Fig. 3c).

It is curious that TBEV prM-E protein can be utilized efficiently for assembly of SRIPs in combination with the JEV C protein and replicon RNA producing equivalent titres to JEV and WNV, as TBEV is a tick-borne virus and is classified as a distinct serogroup from JEV. In contrast, production of DENV- and YFV-SRIPs was less efficient. The low infectious titre of SRIPs containing at least dengue prM-E may be explained by the low specific infectivity of particles encapsidated in DENV envelope protein (van der Schaar *et al.*, 2007; Winkelmann *et al.*, 2011), although we were unable to exclude the possibility that the viral assembly and/or secretion with dengue prM-E is not efficient (Chang *et al.*, 2003; Hsieh *et al.*, 2008). Adaptive mutations in structural and NS proteins could possibly enhance the production of infectious particles by improving the specific infectivity of the resulting particles (Winkelmann *et al.*, 2011). In addition, it has been reported that a chimaeric WNV genome with DENV2 prM-E genes but lacking the C gene replicates much better in DENV2-C-expressing cells than in WNV-C-expressing cells (Suzuki *et al.*, 2009), thus suggesting that the combination of homologous C protein and prM-E proteins improves the production of viral particles. Therefore, it is possible to obtain a better yield of dengue SRIPs by using DENV C protein instead of JEV C protein. Such DENV-SRIPs can be useful for studying infection-enhancing and neutralizing antibody activities.

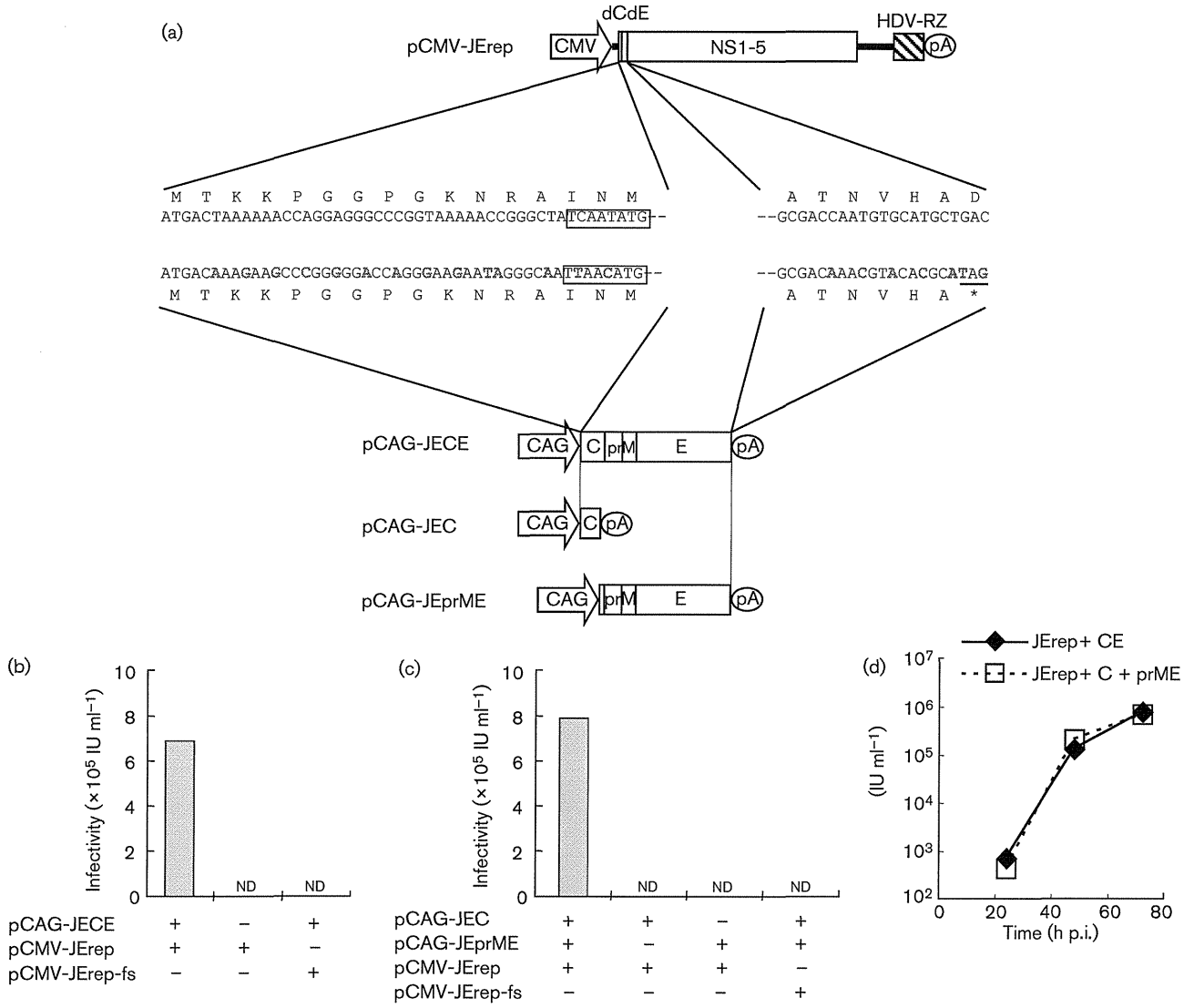


Fig. 2. Schematic representation of JEV replicon and structural protein-expression plasmids. (a) Top: JEV subgenomic replicon with deletion of structural proteins. This replicon contains a partial C and E gene. Bottom: JEV structural protein-expression plasmids showing the region of overlap with JEV replicon. Boxes indicate the 8 nt in the 5′ CS that are 100 % conserved among all mosquito-borne flaviviruses. The JEV C-E, C and prM-E coding sequences harbour silent mutations designed to prevent homologous recombinations that included two changes to the CS sequence, which must be 100 % complementary to the 3′ CS of JEV in order to permit genome replication. The termination codon is underlined. Nucleotide substitutions are shown in red. (b, c) Titres of JEV-SRIPs produced by transfection of 293T cells with replicon plasmid and structural protein-expression plasmids. Dilutions of supernatant collected at 3 days post-transfection were used to inoculate monolayers of Vero cells. Cells were fixed at 2 days post-infection and stained with anti-NS1 antibody. Stained cells were then counted to determine the titres (IU ml^{-1}) produced by transfections. ND, Not detected. (d) Time course of JEV SRIP production from transfected cells. At each time point, medium was removed and frozen for subsequent titration and fresh medium was added. JEV SRIP titres were determined by assaying infectivity in Vero cells.

The plasmid-based production system offers an advantage for vaccine production in terms of stability and safety, as this method is able to reduce the chance of mutations in the structural protein region, as well as the risk of infection when compared with live virus production. In addition, our replicon plasmids have the potential for application to DNA-based vaccines, as described previously (Cao *et al.*, 2011; Chang *et al.*, 2008; Huang *et al.*, 2012).

In conclusion, we established a DNA-based production system for SRIPs of flaviviruses. This system has potential value as a basic research and diagnostic tool, and could be used to enhance the safety of neutralization assay, as well as vaccine production.

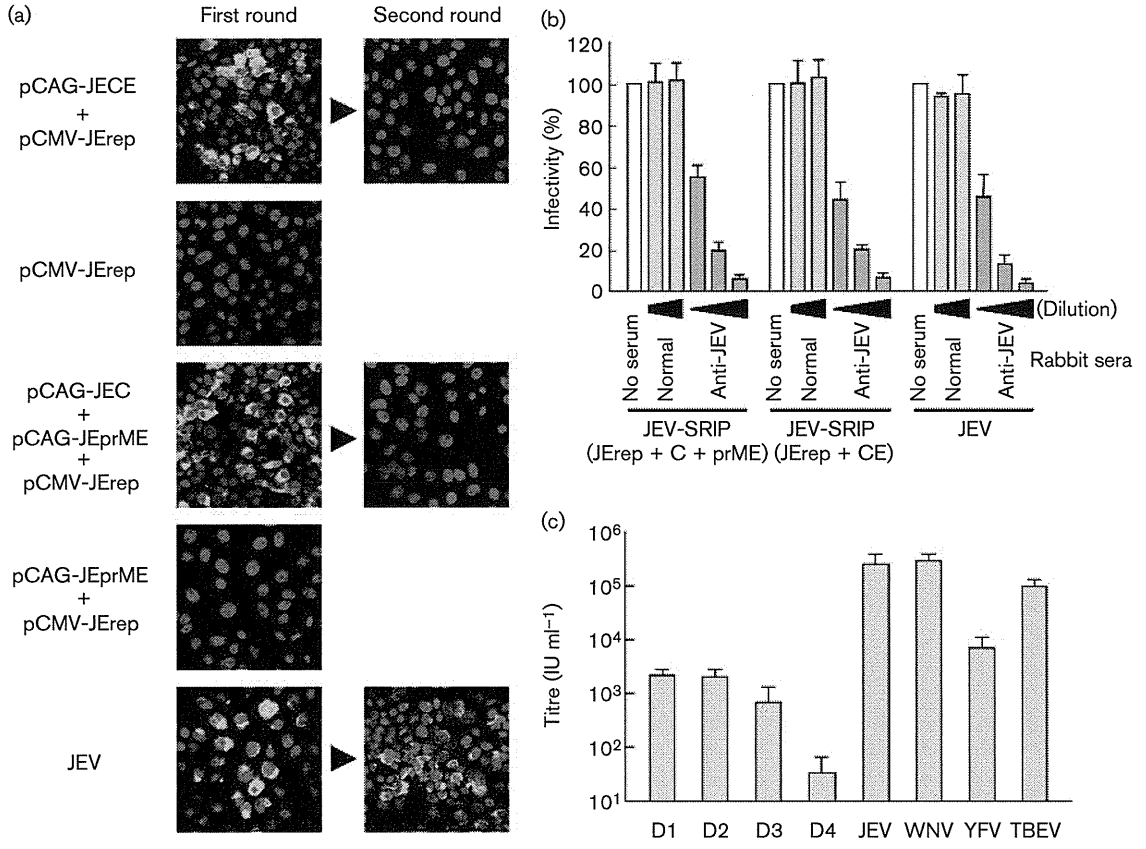


Fig. 3. Vero cells were inoculated with supernatant of 293T cells transfected with the indicated plasmids or infected with JEV. Two days post-inoculation, culture supernatants were collected, and cells were fixed and stained with NS1 antibodies (first round). Naive Vero cells were reinfected with culture supernatants from the first round. Two days post-inoculation, cells were fixed and stained with NS1 antibodies (second round). Cell nuclei were counterstained with DAPI. (b) JEV SRIP inoculum was incubated with serially diluted (1 : 2000, 1 : 8000 and 1 : 32 000) rabbit normal serum or anti-JEV serum for 1 h at room temperature, followed by inoculation onto Vero cells. Cells were immunostained with anti-NS1 antibody at 2 days post-infection, and antigen-positive cells were counted and used to calculate a titre based on f.f.u. ml^{-1} for spreading infections or IU ml^{-1} for non-spreading infections. Data for each condition are means of values obtained from three independent experiments with error bars showing SD. The value for controls without serum (no serum) was set at 100 %. (c) Infectious titres of flavivirus SRIPs, including dengue types 1–4 (D1–4), produced by transfection of 293T cells with pCMV-JErep, pCAG-JEC and flavivirus prM-E expression plasmids. Dilution of supernatant collected at 3 days post-transfection was used to inoculate monolayers of Vero cells. Cells were fixed at 2 days post-infection and stained with anti-JEV NS1 antibody, and stained cells were counted in order to determine titres.

Acknowledgements

The BIKEN Endowed Department of Dengue Vaccine Development, Faculty of Tropical Medicine, Mahidol University, Thailand, was endowed by the Research Foundation for Microbial Diseases of Osaka University, Osaka, Japan, to the Research Institute for Microbial Diseases, Osaka University, Osaka, Japan. We are grateful to K. Yoshii for providing the TBE structural protein-expression plasmid. We would also like to thank P. W. Mason, T. Kobayashi and T. Kato for their helpful discussions, as well as M. Sasaki and M. Yahata for technical assistance. This work was supported by Grants-in-Aid from the Ministry of Health, Labour and Welfare of Japan (H23-shinkou-ippan-010, H23-seisakutansaku-ippan-002). The authors declare no conflicts of interest.

References

Ansarah-Sobrinho, C., Nelson, S., Jost, C. A., Whitehead, S. S. & Pierson, T. C. (2008). Temperature-dependent production of pseudoinfectious dengue reporter virus particles by complementation. *Virology* **381**, 67–74.

Campbell, G. L., Hills, S. L., Fischer, M., Jacobson, J. A., Hoke, C. H., Hombach, J. M., Marfin, A. A., Solomon, T., Tsai, T. F. & other authors (2011). Estimated global incidence of Japanese encephalitis: a systematic review. *Bull World Health Organ* **89**, 766–774, 774A–774E.

Cao, F., Li, X. F., Yu, X. D., Deng, Y. Q., Jiang, T., Zhu, Q. Y., Qin, E. D. & Qin, C. F. (2011). A DNA-based West Nile virus replicon elicits humoral and cellular immune responses in mice. *J Virol Methods* **178**, 87–93.

Chang, G. J., Hunt, A. R., Holmes, D. A., Springfield, T., Chiueh, T. S., Roehrig, J. T. & Gubler, D. J. (2003). Enhancing biosynthesis and secretion of premembrane and envelope proteins by the chimeric plasmid of dengue virus type 2 and Japanese encephalitis virus. *Virology* **306**, 170–180.

Chang, D. C., Liu, W. J., Anraku, I., Clark, D. C., Pollitt, C. C., Suhrbier, A., Hall, R. A. & Khromykh, A. A. (2008). Single-round infectious particles enhance immunogenicity of a DNA vaccine against West Nile virus. *Nat Biotechnol* **26**, 571–577.

Gehrke, R., Ecker, M., Aberle, S. W., Allison, S. L., Heinz, F. X. & Mandl, C. W. (2003). Incorporation of tick-borne encephalitis virus replicons into virus-like particles by a packaging cell line. *J Virol* **77**, 8924–8933.

Hahn, C. S., Hahn, Y. S., Rice, C. M., Lee, E., Dalgarno, L., Strauss, E. G. & Strauss, J. H. (1987). Conserved elements in the 3′ untranslated region of flavivirus RNAs and potential cyclization sequences. *J Mol Biol* **198**, 33–41.

Hsieh, S. C., Liu, I. J., King, C. C., Chang, G. J. & Wang, W. K. (2008). A strong endoplasmic reticulum retention signal in the stem-anchor region of envelope glycoprotein of dengue virus type 2 affects the production of virus-like particles. *Virology* **374**, 338–350.

Huang, Y., Liu, S., Yang, P., Wang, C., Du, Y., Yu, W. & Sun, Z. (2012). Replicon-based Japanese encephalitis virus vaccines elicit immune response in mice. *J Virol Methods* **179**, 217–225.

Ishikawa, T., Takasaki, T., Kurane, I., Nukuzuma, S., Kondo, T. & Konishi, E. (2007). Co-immunization with West Nile DNA and inactivated vaccines provides synergistic increases in their immunogenicities in mice. *Microbes Infect* **9**, 1089–1095.

Jones, C. T., Patkar, C. G. & Kuhn, R. J. (2005). Construction and applications of yellow fever virus replicons. *Virology* **331**, 247–259.

Khromykh, A. A. & Westaway, E. G. (1997). Subgenomic replicons of the flavivirus Kunjin: construction and applications. *J Virol* **71**, 1497–1505.

Khromykh, A. A., Varnavski, A. N. & Westaway, E. G. (1998). Encapsidation of the flavivirus kunjin replicon RNA by using a complementation system providing Kunjin virus structural proteins in trans. *J Virol* **72**, 5967–5977.

Khromykh, A. A., Meka, H., Guyatt, K. J. & Westaway, E. G. (2001). Essential role of cyclization sequences in flavivirus RNA replication. *J Virol* **75**, 6719–6728.

Konishi, E., Shoda, M., Ajiro, N. & Kondo, T. (2004). Development and evaluation of an enzyme-linked immunosorbent assay for quantifying antibodies to Japanese encephalitis virus nonstructural 1 protein to detect subclinical infections in vaccinated horses. *J Clin Microbiol* **42**, 5087–5093.

Konishi, E., Kosugi, S. & Imoto, J. (2006). Dengue tetravalent DNA vaccine inducing neutralizing antibody and anamnestic responses to four serotypes in mice. *Vaccine* **24**, 2200–2207.

McAda, P. C., Mason, P. W., Schmaljohn, C. S., Dalrymple, J. M., Mason, T. L. & Fournier, M. J. (1987). Partial nucleotide sequence of the Japanese encephalitis virus genome. *Virology* **158**, 348–360.

Ng, C. Y., Gu, F., Phong, W. Y., Chen, Y. L., Lim, S. P., Davidson, A. & Vasudevan, S. G. (2007). Construction and characterization of a stable subgenomic dengue virus type 2 replicon system for antiviral compound and siRNA testing. *Antiviral Res* **76**, 222–231.

Pang, X., Zhang, M. & Dayton, A. I. (2001). Development of Dengue virus type 2 replicons capable of prolonged expression in host cells. *BMC Microbiol* **1**, 18.

Scholle, F., Girard, Y. A., Zhao, Q., Higgs, S. & Mason, P. W. (2004). *trans*-Packaged West Nile virus-like particles: infectious properties in vitro and in infected mosquito vectors. *J Virol* **78**, 11605–11614.

Shi, P. Y., Tilgner, M. & Lo, M. K. (2002). Construction and characterization of subgenomic replicons of New York strain of West Nile virus. *Virology* **296**, 219–233.

Sumiyoshi, H., Mori, C., Fuke, I., Morita, K., Kuhara, S., Kondou, J., Kikuchi, Y., Nagamatu, H. & Igarashi, A. (1987). Complete nucleotide sequence of the Japanese encephalitis virus genome RNA. *Virology* **161**, 497–510.

Suzuki, R., Winkelmann, E. R. & Mason, P. W. (2009). Construction and characterization of a single-cycle chimeric flavivirus vaccine candidate that protects mice against lethal challenge with dengue virus type 2. *J Virol* **83**, 1870–1880.

Suzuki, R., Matsuda, M., Watashi, K., Aizaki, H., Matsuura, Y., Wakita, T. & Suzuki, T. (2013). Signal peptidase complex subunit 1 participates in the assembly of hepatitis C virus through an interaction with E2 and NS2. *PLoS Pathog* **9**, e1003589.

van der Schaar, H. M., Rust, M. J., Waarts, B. L., van der Ende-Metselaar, H., Kuhn, R. J., Wilschut, J., Zhuang, X. & Smit, J. M. (2007). Characterization of the early events in dengue virus cell entry by biochemical assays and single-virus tracking. *J Virol* **81**, 12019–12028.

Winkelmann, E. R., Widman, D. G., Suzuki, R. & Mason, P. W. (2011). Analyses of mutations selected by passaging a chimeric flavivirus identify mutations that alter infectivity and reveal an interaction between the structural proteins and the nonstructural glycoprotein NS1. *Virology* **421**, 96–104.

Yoshii, K., Hayasaka, D., Goto, A., Obara, M., Araki, K., Yoshimatsu, K., Arikawa, J., Ivanov, L., Mizutani, T. & other authors (2003). Enzyme-linked immunosorbent assay using recombinant antigens expressed in mammalian cells for serodiagnosis of tick-borne encephalitis. *J Virol Methods* **108**, 171–179.

Yoshii, K., Goto, A., Kawakami, K., Kariwa, H. & Takashima, I. (2008). Construction and application of chimeric virus-like particles of tick-borne encephalitis virus and mosquito-borne Japanese encephalitis virus. *J Gen Virol* **89**, 200–211.

Yun, S. I., Song, B. H., Koo, Y., Jeon, I., Byun, S. J., Park, J. H., Joo, Y. S., Kim, S. Y. & Lee, Y. M. (2009). Japanese encephalitis virus-based replicon RNAs/particles as an expression system for HIV-1 $Pr55^{Gag}$ that is capable of producing virus-like particles. *Virus Res* **144**, 298–305.

BJ Disease

Biochem. J. (2014) **458**, 195–201 (Printed in Great Britain) doi:10.1042/BJ20131492

View this PDF in Utopia Documents for more interactive functionality
Download FREE software now

REVIEW ARTICLE

Beyond dsRNA: Toll-like receptor 3 signalling in RNA-induced immune responses

Megumi TATEMATSU*, Tsukasa SEYA* and Misako MATSUMOTO*[1]

*Department of Microbiology and Immunology, Hokkaido University Graduate School of Medicine, Kita 15, Nishi 7, Kita-ku, Sapporo 060-8638, Japan

The innate immune system recognizes pathogen- and damage-associated molecular patterns using pattern-recognition receptors that activate a wide range of signalling cascades to maintain host homoeostasis against infection and inflammation. Endosomal TLR3 (Toll-like receptor 3), a type I transmembrane protein, senses RNAs derived from cells with viral infection or sterile tissue damage, leading to the induction of type I interferon and cytokine production, as well as dendritic cell maturation. It has been accepted that TLR3 recognizes perfect dsRNA, but little has been addressed experimentally with regard to the structural features of virus- or host-derived RNAs that activate TLR3. Recently, a TLR3 agonist was identified, which was a virus-derived 'structured' RNA with incomplete stem structures. Both dsRNA and structured RNA are similarly internalized through clathrin- and raftlin-dependent endocytosis and delivered to endosomal TLR3. The dsRNA uptake machinery, in addition to TLR3, is critical for extracellular viral RNA-induced immune responses. A wide spectrum of TLR3 ligand structures beyond dsRNA and their delivery systems provide new insights into the physiological role of TLR3 in virus- or host-derived RNA-induced immune responses. In the present paper, we focus on the system for extracellular recognition of RNA and its delivery to TLR3.

Key words: dendritic cell, dsRNA, endocytosis, innate immunity, structured RNA, Toll-like receptor (TLR), type I interferon, uptake receptor, viral infection.

INTRODUCTION

The immune system has developed a strategy for maintaining host homoeostasis through its interaction with environmental microbes. An array of PRRs (pattern-recognition receptors) in the innate immune system recognizes PAMPs (pathogen-associated molecular patterns) and induces anti-microbial immune responses [1]. Endosomal TLRs (Toll-like receptors) 3, 7, 8 and 9 serve as sensors of exogenous nucleic acids, whereas cytoplasmic RLRs (RIG-I-like receptors), AIM2-like receptors and DDX family members recognize intracellular viral nucleic acids [2,3]. The compartmentalization of PRRs is important for sensing both extra- and intra-cellular PAMPs and transmitting signals via distinct adaptor molecules.

Among the nucleic acid-sensing TLRs, TLR3 that recognizes dsRNA has a unique expression profile and subcellular localization [4,5]. It is expressed in immune cells, including myeloid DCs (dendritic cells) and macrophages, and in non-immune cells such as fibroblasts, epithelial cells and neurons [5–7]. TLR3 localizes to the early endosome in myeloid DCs [8], whereas macrophages, fibroblasts and some epithelial cell lines express TLR3 both on the cell surface and in the early endosome [5,9]. Although TLR3s on the cell surface participate in dsRNA recognition [5], TLR3-mediated signalling is initiated from endosomal compartments in either cell type [8].

In the case of TLR3, virus-derived dsRNA and poly(I:C) (polyriboinosinic:polyribocytidylic acid), a synthetic dsRNA, were first identified as TLR3 ligands [4,5]. dsRNA exists as a viral genome or is generated in the cytosol during replication of positive-strand RNA viruses and DNA viruses [10]. Thus TLR3 appears to sense extracellular viral dsRNA released from infected cells and activates antiviral immunity [11]. Indeed, TLR3 mediates a protective response against positive-strand RNA virus infection, including PV (poliovirus), coxsackievirus group B serotype 3 and encephalomyocarditis virus, and DNA virus infection such as herpes simplex virus 1 and murine cytomegalovirus (Table 1) [12–19]. On the other hand, detrimental effects of TLR3 in host immunity to some RNA and DNA viruses also have been demonstrated [20–23]. Notably, TLR3-mediated signalling exacerbates negative-strand RNA virus infection, in which dsRNA is barely detectable [22,23]. In addition, RNA released from damaged cells or mRNA is also recognized by TLR3 [24,25]. However, little is known about which RNA molecules or structures activate TLR3 during infection or inflammation. We identified recently a structural unit that can activate TLR3; surprisingly, this 'structured' RNA recognized by TLR3 contains an incomplete stem with bulge and internal loops, but sufficiently induces type I IFNs (interferons) and pro-inflammatory cytokines in both human and mouse cells [26]. Hence the spectrum of TLR3 ligand structures appeared to be beyond the canonical dsRNA. The results offer new insights into the physiological role of TLR3 in virus- or host-derived RNA-induced immune responses. In the present review, we focus on exRNA (extracellular RNA) recognition and signalling by TLR3.

Abbreviations: AP-1, activator protein-1; CTL, cytotoxic T-cell; DC, dendritic cell; ECD, ectodomain; exRNA, extracellular RNA; HEK, human embryonic kidney; IFN, interferon; IL, interleukin; iPSC, induced pluripotent stem cell; IRF-3, IFN regulatory factor-3; LRR, leucine-rich repeat; LRR-CT, LRR C-terminal; LRR-NT, LRR N-terminal; MDA5, melanoma differentiation-associated gene 5; NF-κB, nuclear factor κB; NK, natural killer; ODN, oligodeoxynucleotide; PAMP, pathogen-associated molecular pattern; poly(I:C), polyriboinosinic:polyribocytidylic acid; PRR, pattern-recognition receptor; PV, poliovirus; RIG-I, retinoic acid inducible gene-I; RLR, retinoic acid inducible gene-I-like receptor; TICAM-1, Toll–IL-1 receptor domain-containing adaptor molecule-1; TIR, Toll–IL-1 receptor; TLR, Toll-like receptor.

[1] To whom correspondence should be addressed (email matumoto@pop.med.hokudai.ac.jp).

© The Authors Journal compilation © 2014 Biochemical Society

www.biochemj.org Biochemical Journal

Table 1 Role of TLR3 in viral infections

Viral genome	Protection	Deterioration
(+) ssRNA	Poliovirus [12,13], coxsackievirus group B serotype 3 [14] and encephalomyocarditis virus [15]	West Nile virus [20]
dsRNA	Rotavirus [16]	
dsDNA	Herpes simplex virus 1 [17,18] and murine cytomegalovirus [19]	Vaccinia virus [21]
(−) ssRNA		Influenza A virus [22] and phlebovirus [23]

Table 2 Representative TLR3 ligands identified by *in vivo* or *in vitro* experiments using reporter assay and TLR3-deficient mouse DC/macrophage stimulation

Ab, antibody; PBMC, peripheral blood mononuclear cell.

RNA ligands for TLR3	Details	*In vitro* assay	Reference(s)
Exogenous RNA			
Viral dsRNA	Reovirus genome dsRNA	Mouse DC	[4]
Viral mRNA	*In vitro* transcribed HIV gag mRNA	HEK-293/TLR3	[24]
Viral structured RNA	*In vitro* transcribed PV RNA	Mouse DC and HEK-293/TLR3	[26]
Bacterial RNA	*Escherichia coli* total RNA	HEK-293/TLR3	[73]
	dsRNA of lactic acid bacteria	Mouse DC	[74]
Endogenous RNA			
RNA from necrotic cells	RNA from necrotic neutrophils	Macrophage	[25]
	UVB-irradiated U1 RNA (small nuclear RNA)	Human PBMC	[42]
Synthetic dsRNA	Poly(I:C)	HEK-293/TLR3 and Ab inhibition	[5]
	Poly(I:C_{12}U)	Mouse DC	[75]
In vitro transcribed dsRNA	Measles virus cDNA	HEK-293/TLR3	[31]
	pFastBac-CPrME plasmid	Mouse DC and HEK-293/TLR3	[37,41]

RECOGNITION OF dsRNA BY TLR3

TLR3 recognizes viral or *in vitro* transcribed dsRNA in a sequence-independent manner and mediates downstream signalling via TICAM-1 (TIR domain-containing adaptor molecule-1; also known as TRIF) [27,28]. 5′-Triphosphorylation of dsRNA is dispensable for TLR3 recognition, differing from the dsRNA recognition mode of RIG-I (retinoic acid inducible gene-I) [29,30]. Furthermore, 2′-hydroxy groups are essential for TLR3 activation by poly(I:C), because 2′-O-methyl or 2′-fluoro modification of cytidylic acid abolishes the TLR3 activating ability of the I/C duplex [31].

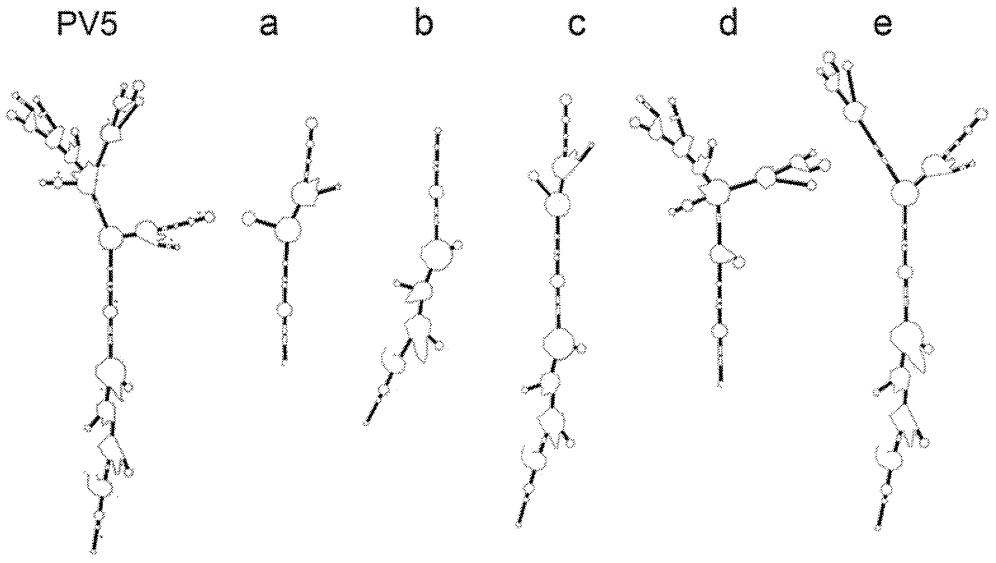
TLR3 consists of an ECD (ectodomain) containing 23 LRRs (leucine-rich repeats) and the LRR-NT (LRR N-terminal) and LRR-CT (LRR C-terminal) regions, the transmembrane domain, the cytoplasmic linker region and the TIR (Toll–IL-1 receptor) domain [32]. Crystallized human TLR3 ECD is a horseshoe-shaped solenoid assembled from 23 LRRs, of which one face is largely masked by carbohydrate, whereas the other is unglycosylated [33,34]. The N-terminal histidine residues (His^{39} in LRR-NT, His^{60} in LRR1 and His^{108} in LRR3) and the C-terminal His^{539} and Asn^{541} in LRR20 of TLR3 ECD are indispensable for dsRNA binding [33–36]. The histidine residues are protonated at endosomal pH (~pH 6.0), generating an ionic attraction with the negatively charged phosphate backbone of dsRNA. Leonard et al. [37] showed that the TLR3 ECD binds as a dimer to a 40–50 bp length of dsRNA and that multiple TLR3 ECD dimers bind to long dsRNA strands. Binding affinities increase with both buffer acidity and dsRNA length. Structural analysis of the mouse TLR3 ECD–46-bp dsRNA complex revealed that dsRNA interacts with both an N- and a C-terminal-binding site on the glycan-free surface of each TLR3 ECD, which are on opposite sides of the dsRNA [38]. The ribose-phosphate backbone is the major determinant of binding, accounting for sequence-independent dsRNA binding to TLR3. In addition, the two LRR-CT regions come together, which is essential for stable receptor–ligand complex formation and facilitates the dimerization of the cytoplasmic TIR domain [39]. Indeed, a TLR3 mutant lacking LRR21 is constitutively active, probably because of ligand-independent dimer formation due to the altered configuration of the C-terminal TLR3 ECD structure [40].

Although a biochemical study showed that a dsRNA of 40–50 bp in length forms a stable complex with dimeric TLR3 ECD under acidic conditions (pH 5.5) [36], a dsRNA of >90 bp in length is required for TLR3-mediated cytokine production and DC maturation when added to mouse DCs [41]. Given that a dsRNA of >90 bp in length is required for stable complex formation with TLR3 at the pH within the early endosome (~pH 6.0–6.5), and that TLR3 localizes to the early endosome, TLR3 oligomerization in the early endosome is essential for downstream signalling.

RECOGNITION OF VIRUS- OR HOST-DERIVED RNA BY TLR3

Several reports suggest that TLR3 recognizes RNA molecules other than dsRNA (Table 2). In negative-sense RNA virus infections, such as influenza A virus and phlebovirus, which generate little dsRNA as intermediate replication products, TLR3-mediated inflammatory cytokine and chemokine production affects virus-induced pathology and host survival [22,23]. In addition, Karikó et al. [24] reported that *in vitro* transcribed HIV gag mRNA complexed with lipofectin activates TLR3. Cavassani et al. [25] also demonstrated that mouse macrophages responded to RNA from sterile necrotic neutrophils in a TLR3-dependent manner. However, which RNA molecules or structures of the virus- or host-derived RNAs activate TLR3 is unknown. A recent study showed that RNA from UVB-irradiated keratinocytes induces cytokine production in normal

© The Authors Journal compilation © 2014 Biochemical Society



	PV5	a	b	c	d	e
length (nt)	630	191	250	367	380	469
stability: FBS- free medium	+	-	+	+	+	+
stability: FBS-containing medium	+	-	+	+	-	+
IFN-β promoter activity in HEK293 cells (FBS-free medium)	+	-	-	+	-	+
IFN-β production in mouse splenic DC (FBS-free medium)	++	-	+	++	+	++

Figure 1 RNA structures recognized by TLR3

PV5 and its derivatives (RNA a–e) were transcribed *in vitro* using PV cDNA as a template. Upper panel, secondary structure of PV5 and its derivatives (RNA a–e) predicted by the Mfold software. Thick lines indicate dsRNA regions (1–11 bp). RNAs were incubated in FBS-free or -containing medium at 37 °C for 30 min. The degradability of RNAs was assessed by electrophoresis on agarose gel. The TLR3-activating ability of RNAs was assessed by IFN-β promoter reporter assay with HEK-293 cells transiently expressing human TLR3 and IFN-β production from splenic DCs isolated from wild-type and TLR3-deficient mice in FBS-free medium [26]. All RNAs failed to induce IFN-β production in splenic DCs isolated from TLR3-deficient mice. IFN-β production in mouse splenic DCs. +, <150 pg/ml; + +, >150 pg/ml.

human epidermal keratinocytes via TLR3 [42]. UVB-damaged small nuclear RNAs, including U1 RNA (165 nt in length) were the determinants of TLR3 activation, but the precise mechanism underlying how UVB-damaged U1 RNA activates TLR3 is unknown.

The point of our recent study was that TLR3 recognizes incomplete stem structures formed in viral ssRNA and induces innate immune signalling [26]. Analyses with *in vitro* transcribed PV-derived ssRNAs and dsRNAs revealed that some PV ssRNAs activate TLR3 extracellularly, but do not activate RLRs, in human and mouse cells. Stability and length of RNA are crucial factors for TLR3 activation in that case. Functional PV RNA, 630 nt in length (PV5), bound to TLR3 ECD with high affinity, and both the N- and C-terminal dsRNA-binding sites of TLR3 ECD are required for PV5-induced IFN-β promoter activation in HEK (human embryonic kidney)-293 cells that transiently express human TLR3 (Figure 1). Furthermore, PV5 was internalized into cells via clathrin- and raftlin-mediated endocytosis and co-localized with endosomal TLR3, as observed previously with poly(I:C) uptake [43,44]. The secondary structure of PV5 predicted by Mfold software showed that PV5 possess double-strand regions (<11 bp in length) arranged in tandem, which are segmented with bulge or internal loops (Figure 1). The TLR3-activating ability of PV5 was abolished with RNaseIII treatment, indicating that the RNA duplex in PV5 is required for both the stability and functionality for the TLR3 activation. Analyses of PV5-derived RNAs partly having PV5 secondary structure (RNAs a–e in Figure 1) showed that longer stem structure with bulge and internal loops typically shown in RNA model c is the core RNA structure required for TLR3 activation in PV5 (Figure 1). Considering that dsRNA forms an A-type nucleotide duplex with 11 bp per turn [45], and that seven contiguous base pairs are needed for rapid duplex formation of DNA and RNA [46], incomplete stem structures containing contiguous base pairs may be required for stability that facilitates TLR3 binding. A fascinating model has been proposed for TLR3 dimer formation, in which shorter RNA duplexes (21–30 bp) can form less stable complexes with two TLR3 molecules [36]. Thus appropriate length or topology of multiple incomplete stems is required for TLR3 oligomerization, leading to the production of type I IFNs and pro-inflammatory

© The Authors Journal compilation © 2014 Biochemical Society

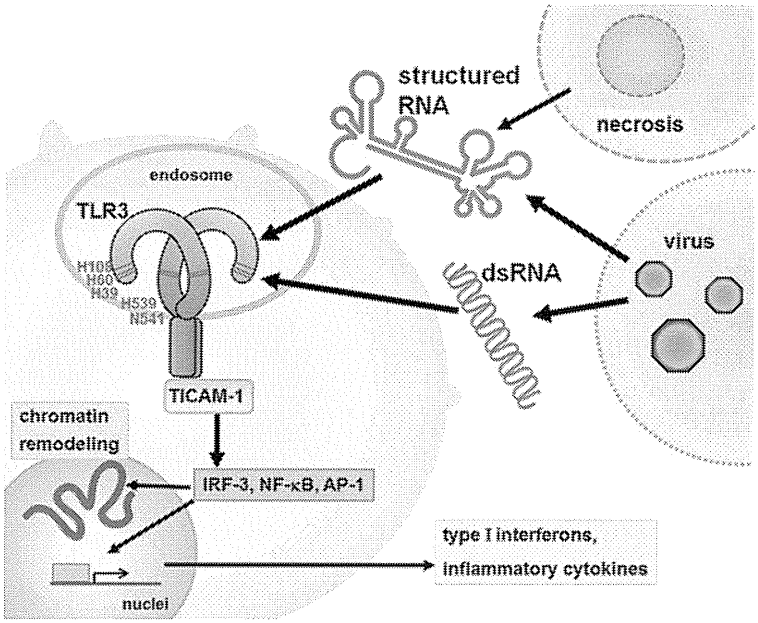


Figure 2 Model for dsRNA/structured RNA-induced TLR3-mediated immunity

Upon viral infection and sterile inflammation, virus- and host-derived RNAs are released from necrotic cells. In local environments, extracellular viral dsRNAs and virus/host-derived structured RNAs are rapidly taken up into cells via clathrin/raftlin-dependent endocytosis and delivered to endosomal TLR3. Once TLR3 is oligomerized by dsRNA/structured RNA, it recruits the adaptor protein TICAM-1 that activates the transcription factors, IRF-3, NF-κB and AP-1, leading to the production of type I IFNs and proinflammatory cytokines. The TLR3–TICAM-1 signal also induces chromatin modification in fibroblasts. In myeloid DCs, TLR3 activation triggers DC maturation capable of activating NK cells and CTLs. The key residues of TLR3, the N-terminal His^{39} in LRR-NT, His^{60} in LRR1, His^{108} in LRR3 and the C-terminal His^{539} and Asn^{541} in LRR20, which are involved in RNA binding are shown.

cytokines. RNA tertiary structure is also important for both the stability and activity of PV RNA.

Notably, mouse splenic DCs responded to shorter RNAs with mismatched duplexes that failed to activate human TLR3 expressed in epithelial cells, suggesting cell type- or species-specific RNA recognition by TLR3 (Figure 1). The precise mechanisms underlying this are currently unknown, but the high density of TLR3 expression and the potent phagocytic activity of mouse splenic DCs are advantageous for RNA-induced oligomerization of TLR3 and effective RNA uptake. In a study by Ewald et al. [47], mouse TLR3 was reported to undergo cathepsin-mediated proteolytic processing in the macrophage cell line RAW in a manner similar to that of mouse TLR9. Subsequent studies also demonstrated that human TLR3 ECD is cleaved at the loop exposed in LRR12 by cathepsins in a cell-type dependent manner [48,49], and the N- and C-terminal halves of human TLR3 remain associated after cleavage [49]. Requirement of proteolytic cleavage in TLR3 signalling appears to depend on cell type [49,50]. Potentially shorter structured RNAs may be recognized by protease-processed TLR3 in mouse DCs. Further studies are required to clarify the cell type- or species-dependent RNA recognition by TLR3.

UPTAKE OF exRNA

The ability of exRNAs to induce cellular responses primarily depends on the stability of these RNAs in the extracellular milieu and whether they are taken up into cells. dsRNA is resistant to degradation compared with ssRNA and, thus, viral dsRNA released from infected cells can be a potent activator of neighbouring virus-uninfected cells, leading to the induction of anti-viral states. Poly(I:C) is the most common dsRNA in both *in vitro* and *in vivo* studies to induce cellular responses, including type I IFN production and NK (natural killer) cell activation. Poly(I:C) is internalized into cells through clathrin-mediated endocytosis and delivered to endosomal TLR3 and to cytoplasmic MDA5 (melanoma differentiation-associated gene 5) [51]. Watanabe et al. [44] demonstrated that the cytoplasmic lipid raft protein raftlin is essential for poly(I:C) cellular uptake in human myeloid DCs and epithelial cells. In raftlin knockdown cells, surface-bound poly(I:C) neither enters the cells nor activates TLR3 and MDA5, indicating that cellular uptake is a pre-requisite for dsRNA-induced cellular responses. Upon poly(I:C) stimulation, raftlin translocates from the cytoplasm to the cell surface, where it associates with the clathrin–AP-2 (clathrin-associated adaptor protein-2) complex and induces cargo delivery. Interestingly, structured PV RNA is also internalized into cells via raftlin-mediated endocytosis and is delivered to endosomal TLR3 [26]. B- and C-type ODNs (oligodeoxynucleotides) that share the uptake receptor with poly(I:C) in humans inhibit cellular uptake of PV RNA [26,43,44,52]. Hence extracellular dsRNA/structured RNA and ODNs are recognized by a common uptake receptor and their internalization is regulated by raftlin. Mouse DCs express raftlin-2 in addition to raftlin, and raftlin knockdown does not affect poly(I:C) cellular uptake, suggesting that raftlin-2 functionally compensates for raftlin [44].

The uptake receptors for poly(I:C) have been identified by several groups. Lee et al. [53] reported that CD14 enhances poly(I:C)-induced TLR3 activation by mediating poly(I:C) uptake in mouse macrophages. Furthermore, the scavenger receptor class-A was identified as a cell surface receptor for dsRNA in human bronchial epithelial cells and mouse cells [54,55]. However, knockout of these molecules does not result in complete abrogation of poly(I:C)-induced TLR3 activation, indicating the presence of another uptake receptor. Indeed, human myeloid DCs do not express CD14 on the cell surface and an inhibitor for the scavenger receptor does not affect poly(I:C) uptake in human

© The Authors Journal compilation © 2014 Biochemical Society

myeloid DCs and epithelial cells [44]. Additionally, DEC-205 was identified as a receptor for ODNs in mouse DCs [56], but this is not the case of human DCs (M. Tatematsu and M. Matsumoto, unpublished work). Hence there must be several uptake receptors that participate in the cell entry of RNAs/DNAs in a cell type- and/or species-specific manner.

exRNA-INDUCED TLR3–TICAM-1 SIGNALLING

Following TLR3 oligomerization, TICAM-1 is recruited to the TLR3–TIR domain that activates the transcription factors, IRF-3 (IRN regulatory factor-3), NF-κB (nuclear factor κB) and AP-1, leading to the production of IFN-β and proinflammatory cytokines, as well as DC maturation [57] (Figure 2). exRNA-induced TLR3–TICAM-1-mediated signalling is classified into two categories; one that induces innate responses and the other that induces adaptive immune responses. The fibroblasts and epithelial cells that express TLR3, but not TLR7, -8 and -9, produce IFN-β and proinflammatory cytokines in response to viral dsRNA and structured RNA, which induce anti-viral states by inducing IFN-stimulated genes [26]. Host RNAs released from damaged cells could be taken up through raftlin-mediated endocytosis and activate TLR3, if they form functional structures as observed in PV RNA. Bernard et al. [42] showed that small nuclear RNAs derived from UV-damaged cells induced inflammation through activation of TLR3, but how these RNAs are delivered to endosomes and interact with TLR3 remains unknown.

Another important TLR3 signal is the induction of adaptive immune responses in myeloid DCs. TLR3 is highly expressed in the professional antigen-presenting DCs, including mouse CD8α^+ DCs and human BDCA3$^+$ DCs [58,59]. Myeloid DCs mature as a result of TLR3 activation through the expression of co-stimulatory molecules, NK-activating molecules including INAM (IRF-3-dependent NK-activating molecule) [60], and unidentified molecules involved in cross-presentation pathways, leading to the activation of NK cells and CTLs (cytotoxic T-cells) [61]. The TICAM-1–TBK1–IRF3 axis downstream of TLR3 is critical for gene induction involved in mouse DC-mediated NK/CTL activation [62,63]. In addition, mouse DCs produce the Th1-type cytokines, IFN-β and IL-12 (interleukin-12), via the TLR3–TICAM-1 pathway. This facilitates NK/CTL induction. Mouse DCs efficiently phagocytose the cell debris of virus-infected cells and mature through virus RNA-induced TLR3 activation [64].

The most intriguing finding is a link between TLR3 signals and epigenetic modifications [65]. Knockdown of TLR3 or TICAM-1 blocks the induction of human iPSCs (induced pluripotent stem cells) by retroviral reprogramming in human fibroblasts [65]. Poly(I:C)-induced TLR3 activation accelerates the development of iPSCs induced by the non-viral methods in fibroblasts. TLR3 activation leads to chromatin modification in fibroblasts by promoting genome-wide epigenetic alterations. These findings enable us to offer a new concept that RNA is an extracellular mediator that accounts for a broad range of TLR3–TICAM-1-mediated gene expression compared with other RNA-sensing receptors.

CONCLUSIONS

In plants, insects and nematodes, dsRNA-induced Dicer-mediated RNA interference is a powerful strategy for protection against viral infection [66–68]. Extracellular dsRNA is taken up into cells and systematically induces gene silencing [69,70]. In *Caenorhabditis elegans*, the membrane proteins SID-1 and SID-2 act as transporters of extracellular dsRNA, whose ability is dependent on the length of the dsRNA [71,72]. On the other hand, vertebrates have developed a wide range of anti-viral strategies, including an array of PRRs in the innate immune system, the IFN/cytokine system and the adaptive immune system. Extracellular dsRNAs are delivered to endosomal TLR3 that induce innate and adaptive anti-viral immunity. Additionally, structured RNAs with incomplete stem structures are recognized by both the dsRNA uptake receptor and TLR3, which may participate in the virus- or host-derived RNA-induced immune responses during infections or inflammation. The identification of the uptake receptor for dsRNAs and structured RNAs in human cells and also isolation of endogenous or exogenous TLR3-activating RNA molecules are important for improving our understanding of TLR3-mediated immunity.

ACKNOWLEDGEMENTS

We thank Dr Fumiko Nishikawa and our laboratory members for their valuable discussions.

FUNDING

This work was supported, in part, by Grants-in-Aid from the Ministry of Education, Science, and Culture, the Ministry of Health, Labor and Welfare of Japan, and by the Akiyama Life Science Foundation.

REFERENCES

1 Janeway, Jr, C. A. and Medzhitov, R. (2002) Innate immune recognition. Annu. Rev. Immunol. **20**, 197–216
2 Akira, S., Uematsu, S. and Takeuchi, O. (2006) Pathogen recognition and innate immunity. Cell **124**, 783–801
3 Gurtler, C. and Bowie, A. G. (2013) Innate immune detection of microbial nucleic acids. Trends Microbiol. **21**, 413–420
4 Alexopoulou, L., Holt, A. C., Medzhitov, R. and Flavell, R. A. (2001) Recognition of double stranded RNA and activation of NF-κB by Toll-like receptor 3. Nature **413**, 732–738
5 Matsumoto, M., Kikkawa, S., Kohase, M., Miyake, K. and Seya, T. (2002) Establishment of monoclonal antibody against human Toll-like receptor 3 that blocks double-stranded RNA-mediated signaling. Biochem. Biophys. Res. Commun. **293**, 1364–1369
6 Muzio, M., Bosisio, D., Polentarutti, N., D'amico, G., Stoppacciaro, A., Mancinelli, R., van't Veer, C., Penton-Rol, G., Ruco, L. P., Allavena, P. and Mantovani, A. (2000) Differential expression and regulation of Toll-like receptors (TLR) in human leukocytes: selective expression of TLR3 in dendritic cells. J. Immunol. **64**, 5998–6004
7 Cario, E. and Podolsky, D. K. (2000) Differential alteration in intestinal epithelial cell expression of toll-like receptor 3 (TLR3) and TLR4 in inflammatory bowel disease. Infect. Immun. **68**, 7010–7017
8 Matsumoto, M., Funami, K., Tanabe, M., Oshiumi, H., Shingai, M., Seto, Y., Yamamoto, A. and Seya, T. (2003) Subcellular localization of Toll-like receptor 3 in human dendritic cells. J. Immunol. **171**, 3154–3162
9 Funami, K., Matsumoto, M., Oshiumi, H., Akazawa, T., Yamamoto, A. and Seya, T. (2004) The cytoplasmic 'linker region' in Toll-like receptor 3 controls receptor localization and signaling. Int. Immunol. **16**, 1143–1154
10 Weber, F., Wagner, V., Rasmussen, S. B., Hartmann, R. and Paludan, S. R. (2006) Double-stranded RNA is produced by positive-stranded RNA viruses and DNA viruses but not in detectable amounts by negative-stranded RNA viruses. J. Virol. **80**, 5059–5064
11 Matsumoto, M., Oshiumi, H. and Seya, T. (2011) Antiviral responses induced by the TLR3 pathway. Rev. Med. Virol. **21**, 67–77
12 Oshiumi, H., Okamoto, M., Fujii, K., Kawanishi, T., Matsumoto, M., Koike, S. and Seya, T. (2011) The TLR3-TICAM-1 pathway is mandatory for innate immune responses to poliovirus infection. J. Immunol. **187**, 5320–5327
13 Abe, Y., Fujii, K., Nagata, N., Takeuchi, O., Akira, S., Oshiumi, H., Matsumoto, M., Seya, T. and Koike, S. (2012) The Toll-like receptor 3-mediayed antiviral response is important for protection against poliovirus infection in poliovirus receptor transgenic mice. J. Virol. **86**, 185–194
14 Negishi, H., Osawa, T., Ogami, K., Ouyang, X., Sakaguchi, S., Koshiba, R., Yanai, H., Seko, Y., Shitara, H., Bishop, K. et al. (2008) A critical link between Toll-like receptor 3 and type II interferon signaling pathways in antiviral innate immunity. Proc. Natl. Acad. Sci. U.S.A. **105**, 20446–20451

© The Authors Journal compilation © 2014 Biochemical Society