

Fig. 1. Structure of the hepatitis B virus polymerase/Reverse Transcriptase gene and amino acid substitutions associated with resistance to nucleoside analogs. a.a., amino acids

of LAM administration, in 24% after 52 weeks, and in 65% after 5 years.⁴ In Japan, in an extensive study on the clinical course of both HBeAg-positive and HBeAg-negative chronic hepatitis B patients, the rate of emergence of LAM-resistant strains was 50%, 5 years after the start of LAM administration.¹¹ Not all patients having rtM204V/I develop hepatitis. Although the incidence of amino acid mutation of polymerase is high in patients with hepatitis, no specific mutation has been observed.¹²

The case of a patient who was LAM-resistant despite the absence of mutation in the YMDD motif was reported recently. The 181st alanine (A) in the Pol domain was replaced by threonine (T) (rtA181T) in this patient. An experiment using chimeric mice bearing human hepatocytes demonstrated that this mutation causes LAM resistance.¹³

Resistance to adefovir dipivoxil

The use of adefovir dipivoxil (ADV) in combination with LAM has been approved in Japan for patients showing LAM resistance. The emergence of ADV-resistant viral strains was first studied with regard to the administration of ADV alone. ADV resistance occurs in approximately 6% of patients 3 years after the start of ADV administration.¹⁴ The replacement of the 236th asparagine (N) in the Pol domain by T (rtN236T) and that of the 181st A in the Pol domain by V (rtA181V) were observed in ADV-resistant strains.

Following the administration of ADV to patients exhibiting LAM resistance, strains with rtA181V/T or rtN236T emerged in 18% of the patients 1 year after the start of ADV administration.¹⁵ rtA181T was also observed in LAM-resistant strains in the absence of mutation in the YMDD motif. It was reported recently that

some patients exhibiting LAM resistance are non-responders to ADV from the start of ADV administration. These resistant strains had the rtI233V mutation.¹⁶

Resistance to entecavir

Administration of entecavir (ETV) for more than 52 weeks to patients with LAM-resistant chronic hepatitis B leads to the emergence of resistant viral strains in 1.4% of patients,¹⁷ although no results have been reported for long-term administration of ETV. The amino acid sequence of the RT domain in resistant viral strains was analyzed in two patients, and strains with rtM250V and rtI69T were found in one patient and strains with rtT184G and rtS202I in the other.²¹ In Japan, strains with rtS202G and rtL269I have been detected.²² It is notable that all of the patients who acquired ETV resistance were resistant to LAM. Thus, initial treatment with ETV alone may be less likely to lead to ETV-resistant viral strain emergence, but this hypothesis should be confirmed in future studies (Table 1).

HCV infection

HCV is a positive-strand RNA virus belonging to the family *Flaviviridae*. Approximately 170 million HCV carriers or patients are estimated to be persistently infected with HCV worldwide, and approximately 1.8 million in Japan. HCV is transmitted to humans by direct contact with infected or contaminated blood. The routes of infection include transfusion of contaminated or HCV-tainted blood or blood products, which have now been eliminated in Japan, sharing needles among drug abusers, acupuncture, and tattoos. Acupuncture and

Table 1. Clinical trial of entecavir for the treatment of chronic hepatitis B

No.	Authors	HBeAg	Lam resistance at baseline	ETV resistance at baseline	ETV resistance at end point (1 year)	Biochemical rebound (1 year)	Reference No.
1	Chang et al.	Positive	No		0/339	6/339 (2%)	9
2	Sherman et al.	Positive	Yes	11/186 (6%)	7/134 (5%)		17
3	Colonna et al.	Positive	No		0/354	6/354 (2%)	18
		Negative			1/325 (0.3%)	8/325 (2%)	
4	Lai et al.	Negative	No		0/211	5/211 (2%)	19
5	Chang et al.	Positive	Yes	6/181 (3%)	2/181 (1%)		20
		Negative					

HBeAg, hepatitis B e antigen; LAM, lamivudine; ETV, entecavir

depilation are invasive treatments and should be considered to involve risk for infection with HCV unless disposable medical instruments are used.²³

HCV infection develops into persistent infection at a very high rate, becoming persistent in 70%–80% of patients with acute HCV infection. Generally, patients develop acute hepatitis 2 to 3 months after their initial infection with HCV. However, many patients are unaware of the onset of hepatitis because of the mild subjective symptoms and mild jaundice, if any. Although 20%–30% of patients developing acute hepatitis recover from the disease spontaneously, acute hepatitis develops into chronic hepatitis (by definition, hepatitis persisting for more than 6 months) in the remaining 70%–80% of patients. Then, chronic hepatitis enters an inactive phase that lasts 10–15 years. Serum ALT level, which indicates the destruction of hepatocytes, is within normal limits during the inactive phase, but viral growth continues.

Chronic hepatitis enters an active phase after 10–15 years in many patients, although there are marked individual differences. Serum ALT level increases to about two to three times the normal level when chronic hepatitis enters the active phase. Once chronic hepatitis C enters the active phase, it will not improve spontaneously. If the disease is left untreated, the risk of progressing from chronic hepatitis to cirrhosis increases. Hepatitis C characteristically progresses gradually but steadily.²⁴ The risk of developing HCC is high among patients with cirrhosis. The risk of HCC development in cirrhosis patients is 5%–7%.²⁵ Patients infected with HCV should be diagnosed during the inactive phase of chronic hepatitis C and start treatment for HCV elimination (antiviral treatment) as soon as the hepatitis enters the active phase.

Treatment of HCV infection

HCV infection is treated mainly with IFN-based drugs. The treatment efficacy is evaluated 6 months after the end of IFN-based drug administration. If HCV-RNA is

not detected by the sensitive RT-PCR test, the patient is considered to show a sustained virological response (SVR), indicating that HCV has been virtually eliminated.

At present, polyethylene glycol-interferon (Peg-IFN) treatment in combination with ribavirin plays a key role in the treatment of HCV infection. Peg-IFN, an IFN molecule covalently bonded to Peg, is a sustained-release formulation. It needs to be injected only once weekly from the start of treatment, whereas conventional IFN preparations require administration three times weekly. Administration of Peg-IFN alone is more effective than that of a conventional IFN-based drug alone, but the administration of Peg-IFN in combination with ribavirin is even more effective.^{26–28} An SVR rate of approximately 50% can be expected even in cases of chronic hepatitis infected with a high viral load of HCV of genotype 1, and an SVR rate of approximately 60% can be generally expected. Peg-IFN is usually administered for 48 consecutive weeks. It is important to continue the treatment for 48 weeks, although the dose may be reduced if adverse drug reactions appear. In addition, extending the administration period to a total of 72 weeks recently proved effective in patients who became HCV-negative after 12 weeks of treatment.²⁹

There is a long history of treatment with IFN alone: treatment of non-A, non-B hepatitis with IFN alone dates back to around 1985, before the discovery of HCV. A nationwide survey conducted by the Study Group of the Ministry of Health, Labour and Welfare of Japan in 1995 showed that the SVR rate for treatment with IFN alone for 6 months (administration of 6 to 10 million units) was approximately 30% in all patients. However, in patients with the genotype 1 HCV, which is the major genotype worldwide and in about 70% of Japanese HCV patients, particularly those with high viral loads (determined as an HCV-RNA load of 100 KIU/ml or more), SVR was obtained in only about 2%–7%. The efficacy of treatment with IFN alone is thus low. Hence, Peg-IFN in combination with ribavirin

Table 2. Relationship between the ISDR and the response to interferon treatment for chronic hepatitis patients with genotype 1 hepatitis C virus infection

No.	Authors	Interferon	Ribavirin	Relationship between ISDR and viral load	Relationship between ISDR and response	Ethnicity	Ref. no.
1.	Enomoto et al.	α	No	Yes	Yes	Japanese	30
2.	Kurosaki et al.	β	No	Yes	Yes	Japanese	31
3.	Chayama et al.	α	No	ND	Yes	Japanese	32
4.	Zeuzem et al.	α	No	No	No	German	33
5.	Squadrito et al.	α	No	No	No	French	34
6.	Hofgartner et al.	α	No	ND	No	American	35
7.	Khorsi et al.	α	No	ND	No	French	36
8.	Saiz et al.	α	No	ND	Yes	Spanish	37
9.	Frangoul et al.	α	No	ND	No	French	38
10.	Odeberg et al.	α	No	ND	No	Sweden	39
11.	Chung et al.	α	No	ND	No	American	40
12.	Ibarrola et al.	α	Yes	ND	No	Spanish	41
13.	Sarrazin et al.	α	Yes	ND	Yes	German	42
14.	McKechnie et al.	α	No	ND	No	English	43
15.	Yoshioka et al.	α	No	ND	Yes	Japanese	44
16.	Stratidaki et al.	α	No	ND	No	American	45
17.	Murphy et al.	α	Yes	ND	No	American	46
18.	Cappiello et al.	PEG α	Yes	ND	No	Italian	47
19.	Aslan et al.	α	No	ND	No	Turkish	48
20.	Murayama et al.	α	Yes	ND	Yes	Japanese	49

ISDR, interferon sensitivity determining region; ND, not described; PEG, pegylated

is the first choice for patients with intractable disease, as mentioned above.

Emergence of antiviral resistance in HCV infection

In the treatment of chronic hepatitis C with IFN alone or IFN (or Peg-IFN) in combination with ribavirin, HCV-RNA does not disappear in some patients, particularly in those with genotype 1 HCV. Approximately 10% of genotype 1 HCV patients with high viral loads never become HCV-RNA-negative during the period of treatment with IFN (or Peg-IFN) in combination with ribavirin.

Not only host factors but also viral factors have been identified as causes for the nonelimination of HCV. The HCV genotype is a typical viral factor, and patients infected with genotype 1 or 4 are more resistant to treatment than those with genotype 2 or 3.

Another reported factor is the interferon sensitivity-determining region (ISDR) in NS5A, a region consisting of 40 amino acids, first reported by Enomoto et al.³⁰ ISDR is contained in the binding site of interferon α -inducible RNA-dependent protein kinase (PKR). Mutation in ISDR may cause dysfunction in the binding between the NS5A protein and PKR, leading to a decrease in viral protein translation. In Japan, a close correlation between IFN treatment efficacy and mutation in ISDR in genotype 1b HCV patients was found.^{31,32} In Europe and the United States, however, the correlation between amino acid mutation in ISDR and IFN

treatment efficacy is not clear even in patients infected with HCV genotype 1 (Table 2).

In addition, mutation of the PKR/eIF2 α phosphorylation homology domain of the E2 domain has been reported to correlate with IFN-based drug efficacy, but this needs further clarification.

Ribavirin-resistant viral strain

Ribavirin shows low anti-HCV activity in some patients even when it is administered alone, and chronic hepatitis C has been treated with ribavirin alone. The structure of a ribavirin-resistant viral strain that has emerged has been studied. Mutation of the 415th amino acid (F415Y) in the RNA-dependent RNA polymerase (RdRp) domain of NS5B was detected in strains infecting patients treated with ribavirin alone who became ribavirin-resistant.⁵⁰ This mutation was considered to be related to IFN treatment efficacy in patients with genotype 1a HCV. In a study using a replicon, mutations of the 404th and 442nd amino acids (G404S and E442G) were detected.⁵¹

Conclusions

An overview of the mechanisms underlying the emergence of drug-resistant HBV and HCV strains has been given above. The emergence of drug-resistant strains of HBV in particular has posed problems. This resistance has resulted from the development of a wide range of

drugs for HBV, ranging from nonspecific IFN-based drugs to viral protein-specific RT inhibitors. Although no serious problem has arisen to date as regards HCV, specific anti-HCV drugs such as protease inhibitors and RNA polymerase inhibitors are beginning to be developed, so the emergence of drug-resistant viral strains is expected to be a major problem. Indeed, the emergence of a strain resistant to VX950, an HCV protease inhibitor with high antiviral activity, following a short period of administration of this drug has already been reported.⁵² HBV and HCV do not seem to be very easy to eliminate.

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Hepatitis C Virus Nonstructural Protein 5A Modulates the Toll-Like Receptor-MyD88-Dependent Signaling Pathway in Macrophage Cell Lines[∇]

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Hepatitis C virus (HCV) infection induces a wide range of chronic liver injuries; however, the mechanism through which HCV evades the immune surveillance system remains obscure. Blood dendritic cells (DCs) play a pivotal role in the recognition of viral infection and the induction of innate and adaptive immune responses. Several reports suggest that HCV infection induces the dysfunction of DCs in patients with chronic hepatitis C. Toll-like receptor (TLR) has been shown to play various roles in many viral infections; however, the involvement of HCV proteins in the TLR signaling pathway has not yet been precisely elucidated. In this study, we established mouse macrophage cell lines stably expressing HCV proteins and determined the effect of HCV proteins on the TLR signaling pathways. Immune cells expressing NS3, NS3/4A, NS4B, or NSSA were found to inhibit the activation of the TLR2, TLR4, TLR7, and TLR9 signaling pathways. Various genotypes of NSSA bound to MyD88, a major adaptor molecule in TLR, inhibited the recruitment of interleukin-1 receptor-associated kinase 1 to MyD88, and impaired cytokine production in response to TLR ligands. Amino acid residues 240 to 280, previously identified as the interferon sensitivity-determining region (ISDR) in NSSA, interacted with the death domain of MyD88, and the expression of a mutant NSSA lacking the ISDR partially restored cytokine production. These results suggest that the expression of HCV proteins modulates the TLR signaling pathway in immune cells.

Hepatitis C virus (HCV) belongs to the family *Flaviviridae* and possesses a positive, single-stranded RNA genome that encodes a single polyprotein composed of approximately 3,000 amino acids. HCV polyprotein is processed by host and viral proteases, resulting in 10 viral proteins. Viral structural proteins, including the capsid protein and two envelope proteins, are located in the N-terminal one-third of the polyprotein, followed by nonstructural proteins. HCV infects 170 million people worldwide and frequently leads to cirrhosis and hepatocellular carcinoma (36). In over one-half of patients, acute infection evolves into a persistent carrier state, presumably due to the ability of HCV to incapacitate the activation of the host immune mechanisms. Dendritic cells (DCs) are one type of potent antigen-presenting cell in vivo and play a crucial role in the enhancement and regulation of cell-mediated immune reactions. Since DCs express various costimulatory and/or adhesion molecules, they can activate even naïve T cells in a primary response. The role of the response of HCV antigen-specific T cells in viral clearance or persistence has been in-

vestigated extensively in both humans and chimpanzees (6, 27, 48, 51). These studies suggest that acute HCV infections followed by viral clearance are associated with a high frequency of HCV-specific CD4⁺ and CD8⁺ T-cell responses that can persist (27, 51), while chronic HCV infections are characterized by weak and restricted CD4⁺ and CD8⁺ T-cell responses that are not sustained (51).

Toll-like receptors (TLRs) are membrane-bound receptors that can be activated by the binding of molecular structures conserved among families of microbes. More than 10 different TLRs have been identified to date (2). They are highly conserved among mammals and are expressed in a variety of cell types. TLR binding and stimulation by pathogen-associated molecules is followed by a cascade of intracellular events that culminate in the expression of multiple genes (2). TLR signaling is mediated primarily by the adaptor protein myeloid differentiation factor 88 (MyD88), which triggers the activation of transcription factors, such as NF- κ B, that are essential for the expression of proinflammatory cytokine genes (2). This pathway also leads to the potent production of type I interferon (IFN) through the activation of IFN regulatory factor 7 (IRF7) upon stimulation of TLR7 or TLR9 (22). In contrast, Toll/interleukin-1 (IL-1) receptor homology domain-containing adaptor-inducing IFN- β (TRIF/TICAM-1) mediates the production of type I IFNs primarily through the activation of IRF3 in response to TLR3 or TLR4 stimulation (2). Type I IFN induces the maturation of DCs by increasing both the expression of costimulatory molecules such as CD80, CD86, and CD40 and antigen presentation via major histocompatibility

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complex class I in addition to classical endogenous antigen presentation; it also facilitates the cross-presentation of viral antigens. A cumulative report has shown that DC activation via TLR signaling is a prerequisite for the subsequent induction of vigorous T-cell responses (42). Some viral proteins have been shown to inhibit the TLR-dependent signaling pathway through interactions with the downstream adaptor molecules, suggesting that the alteration of TLR-mediated signals is one of the mechanisms of virus-induced immune modulation (49). Dysfunction of DCs in patients with chronic HCV infection due to immaturation caused by the direct infection of DCs by HCV or by interactions with HCV proteins has been reported previously (4, 21). On the other hand, there have also been contrasting reports suggesting a lack of impairment of DC function in both chimpanzees and humans chronically infected with HCV (26, 32). Thus, at present, alterations in the TLR signaling pathway in the immune cells of patients with chronic hepatitis C virus infection are not well understood.

In the present study, we examined the effect of HCV proteins on TLR function in murine macrophage cell lines stably expressing HCV proteins. The expression of NS3, NS3/4A, NS4B, or NS5A was found to impair the activation of the TLR signaling pathways, and NS5A interacted with MyD88 through the IFN sensitivity-determining region (ISDR) and impaired cytokine production. To the best of our knowledge, this is the first demonstration of NS5A as an immunomodulator of TLR signaling pathways through the direct interaction with an adaptor molecule in immune cells.

MATERIALS AND METHODS

Cell culture. Human embryonic kidney 293T cells and mouse macrophage RAW264.7 cells were maintained in Dulbecco's modified Eagle's medium (Sigma, St. Louis, MO) containing 10% fetal calf serum. All cells were cultured at 37°C in a humidified atmosphere with 5% CO₂.

Plasmids and viruses. DNA fragments encoding each of the HCV structural and nonstructural proteins were generated from a full-length cDNA clone of genotype 1b strain J1 (1) by PCR using *Pfu* Turbo DNA polymerase (Stratagene, La Jolla, CA). The fragments were cloned into pCAGGs-puro/N-Flag, in which the sequence encoding a Flag tag is inserted at the 5' terminus of the cloning site of pCAGGs-puro (37). A protease-deficient NS3/4A mutant with Ser¹³⁹ replaced with Ala (S139A) was generated by the method of splicing by overlap extension and cloned into pCAGGs-puro. NS5A genes were amplified by PCR from HCV clones of strains of J1 (genotype 1b), H77c (genotype 1a, kindly provided by J. Bukh), and JFH1 (genotype 2a, kindly provided by T. Wakita) and cloned into pcDNA3.1Flag/HA (38). The NS5A deletion mutants were prepared as described previously (16). DNA fragments encoding a human MyD88, human TRIF-related adapter molecule (TRAM) were amplified by reverse transcription-PCR from total RNA of THP-1 cells and cloned into pcDNA3.1-C-Myc-His (Invitrogen, Carlsbad, CA) and pcDNA3.1Flag/HA. Murine IPS-1 (mIPS-1) was amplified from total RNA of RAW264.7 cells by reverse transcription-PCR and cloned into pcDNA3.1Flag/HA. Human MyD88 deletion mutants and a mIPS-1 mutant with Cys⁵⁰⁸ replaced by Ala (C508A) were generated by the method of splicing by overlap extension and cloned into pcDNA3.1Flag/HA. pCMVIRAK1-myc and pCMVIRAK4-myc, encoding IL-1 receptor-associated kinase 1 (IRAK-1) and IRAK-4, respectively, were prepared as described previously (53). pEFBosTICAM-1-HA was kindly provided by T. Seya (44). All PCR products were confirmed by sequencing by using an ABI PRISM 310 genetic analyzer (Applied Biosystems, Tokyo, Japan). Vesicular stomatitis virus (VSV) (Indiana strain, NCP12.1) (19) was kindly provided by M. A. Whitt.

Establishment of stable cell lines expressing HCV proteins. pCAGGs-puro/N-Flag plasmids encoding HCV proteins were transfected into RAW264.7 cells by liposome-mediated transfection using Lipofectamine 2000 (Invitrogen) and selected with 10 µg/ml of puromycin (InvivoGen, San Diego, CA). After about 2 to 3 weeks of selection, several clones were isolated, and cell lysates of each clone were immunoblotted with each of specific mouse anti-HCV antibody (1) or

anti-Flag M2 mouse monoclonal antibody (Sigma). Macrophage cell lines stably expressing HCV proteins and a control cell line obtained by transfection with an empty pCAGGs-puro vector were maintained in the presence of puromycin (10 µg/ml) throughout the experiments.

Immunoprecipitation and immunoblotting. Cells were seeded onto a six-well tissue culture plate 24 h before transfection. The plasmids were transfected by the lipofection method, and the cells were harvested at 48 h posttransfection, washed three times with 1 ml of ice-cold phosphate-buffered saline (PBS), and suspended in 0.4 ml lysis buffer containing 20 mM Tris-HCl (pH 7.4), 135 mM NaCl, 1% Triton X-100, 10% glycerol, and protease inhibitor cocktail tablets (Roche Molecular Biochemicals, Mannheim, Germany). Cell lysates were incubated for 30 min at 4°C and centrifuged at 14,000 × g for 15 min at 4°C. The supernatant was immunoprecipitated with 1 µg of mouse monoclonal anti-Flag M2, anti-hemagglutinin (HA) 16B12 (HA.11; BabCO, Richmond, CA), or anti-hexahistidine (Santa Cruz Biotechnology, Santa Cruz, CA) antibody and 10 µl of protein G-Sepharose 4B Fast Flow beads (Amersham Pharmacia Biotech, Franklin Lakes, NJ) at 4°C for 90 min. The immunocomplex was precipitated with the beads by centrifugation at 5,000 × g for 1 min and then washed five times with 0.4 ml of 20 mM Tris-HCl (pH 7.4) containing 135 mM NaCl and 0.05% Tween 20 (TBST buffer) by centrifugation. The proteins binding to the beads were boiled in 20 µl of sample buffer and then subjected to sodium dodecyl sulfate–12.5% polyacrylamide gel electrophoresis and transferred onto polyvinylidene difluoride membranes (Millipore, Tokyo, Japan). The membranes were blocked with TBST containing 5% skim milk at room temperature for 1 h; incubated with mouse monoclonal anti-Flag M2, anti-HA 16B12, or anti-hexahistidine monoclonal antibody at room temperature for 1 h; and then incubated with horseradish peroxidase-conjugated anti-mouse immunoglobulin G (IgG) antibody at room temperature for 1 h. The cell lines (2 × 10⁶ cells/well) were stimulated with various doses of lipopolysaccharide (LPS) derived from *Salmonella enterica* serovar Minnesota (Re-595) (Sigma), peptidoglycans (PGN) derived from *Staphylococcus aureus* (Sigma), R-837 (InvivoGen), or phosphorothioate-stabilized mouse CpG (mCpG) oligodeoxynucleotides (ODN1668) (TCC-ATG-ACG-TTC-CTG-ATG-CT) (Invitrogen) for the times indicated, and the phosphorylation status of extracellular signal-regulated kinase (ERK) was determined by immunoblotting using antibodies specific to ERK1/2 or phosphorylated ERK1/2 (T202/Y204) (Cell Signaling Technology, Inc., Beverly, MA). Cells (1 × 10⁶ cells/well) were treated with various doses of mouse IFN-α (PBL Biomedical Laboratories, New Brunswick, NJ) or VSV for 24 h, and the phosphorylation status of double-stranded RNA-dependent protein kinase (PKR) and signal transducer and activator of transcription 1 (STAT1) was determined by immunoblotting using antibodies specific to STAT1 (Cell Signaling), phosphorylated STAT1 (Cell Signaling), or phosphorylated PKR (BioSource International, Inc., Camarillo, CA). The immune complexes were visualized with Super Signal West Femto substrate (Pierce, Rockford, IL) and detected by using a LAS-3000 image analyzer system (Fujifilm, Tokyo, Japan).

Cytokine production and enzyme-linked immunosorbent assay (ELISA). To evaluate cytokine production in macrophage cell lines expressing HCV proteins, cells were seeded onto 96-well plates at a concentration of 1 × 10⁵ cells/well and stimulated with various doses of LPS, PGN, R-837, or mCpG. After 24 h of incubation, culture supernatants were collected, and IL-6 production was determined by using an OptEIA mouse IL-6 set purchased from BD Pharmingen (San Diego, CA).

Real-time PCR. The cell lines (3 × 10⁶ cells/well) were stimulated with R-837, LPS, PGN, mCpG, VSV, and polyinosine-poly(C) [poly(I:C)] (InvivoGen) for the times indicated, and the expression of mRNA of cytokines, chemokines, and TLR genes was determined by real-time PCR. Total RNA was prepared from the macrophage cell lines using an RNeasy Mini kit (QIAGEN). First-strand cDNA was synthesized using a ReverTra Ace (TOYOBO, Japan) and oligo(dT)₂₀ primer. Each cDNA was estimated by Platinum SYBR Green qPCR SuperMix UDG (Invitrogen) according to the manufacturer's protocol. Fluorescent signals were analyzed by using an ABI PRISM 7000 apparatus (Applied Biosystems). Mouse *Ccl2*, *IFN-β*, *IFN-α1*, *IFN-α4*, and *IL-1-α* genes were amplified with primer pairs 5'-GCATCCACGTGTTGGCTCA-3' and 5'-CTCCAGCCTACTCATTGGGACTCA-3', 5'-ACACCAGCTGGCTTCCATC-3' and 5'-TTGGAGCTGGAGCTGCTTATAGTTG-3', 5'-AGCCTTGACACTCCTGGTACAAATG-3' and 5'-TGGGTCAGCTCACTCAGGACA-3', 5'-GCTCAAGCCATCTCTGTGCTAA-3' and 5'-CATTGAGCTGATGGAGGTC-3', and 5'-TTGGTTA AATGACCTGCAACAGGA-3' and 5'-AGGTCGGTCTCACTACCTGTGATG-3', respectively. The mouse *TLR2*, *TLR3*, *TLR4*, *TLR7*, *TLR9*, and *GAPDH* (glyceraldehyde-3-phosphate dehydrogenase) genes were amplified using primer pairs 5'-AGCTCTTTGGCTCTTCTG-3' and 5'-AGAAGTGGGGATATGC-3', 5'-AAATCCTTGGTTCGGAAGTG-3' and 5'-TCAGTTGGGCGTGTGTTCAAGAG-3', 5'-GCCTCGAATCCTGAGCAACA-3' and 5'-CTTCTGGCCGGTAAGGTCCA-3', 5'-TCTGCAGACTCTGTCCTTGA-3' and 5'-CAAGGCATGCTCCTAGGTGGTGA-3', 5'-ACCAATGGCACCTGCCTAA-3' and 5'-

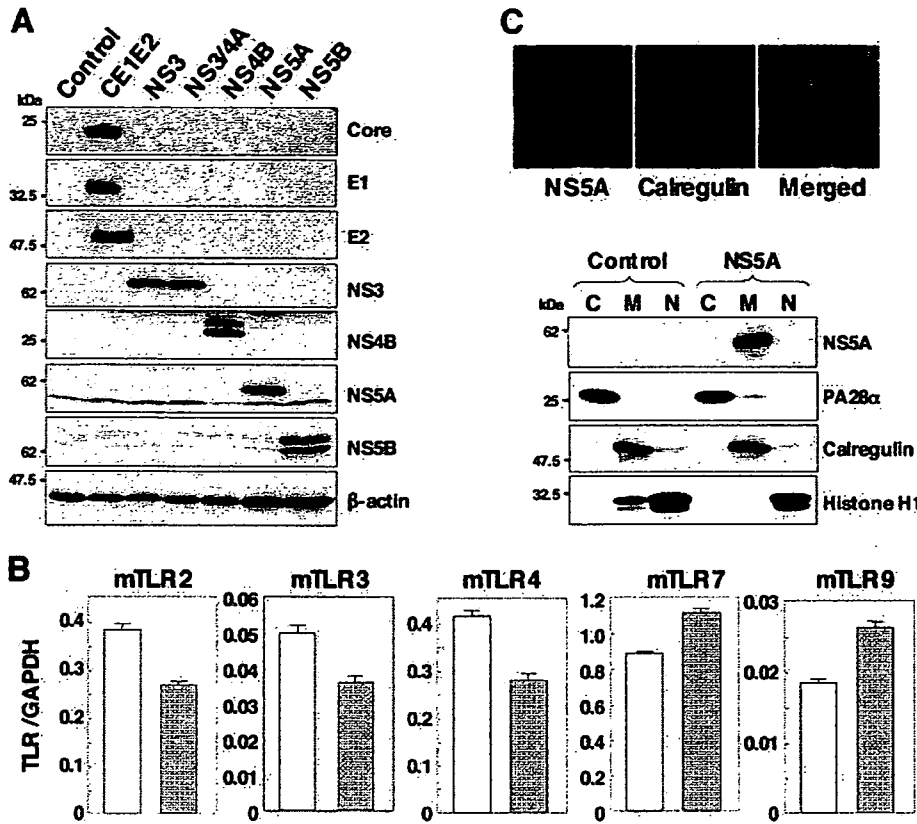


FIG. 1. Establishment of stable macrophage cell lines expressing HCV proteins. (A) Cell lysates were prepared from macrophage cell lines expressing each of the HCV proteins (4×10^6 cells) and immunoblotted with antibodies against HCV proteins or β -actin. (B) Total RNA was extracted from macrophage cell lines expressing NS5A (gray bars) or control (white bars), and the expression of mRNA of TLRs was determined by real-time PCR. (C) The subcellular localization of NS5A was examined by confocal microscopy. Cells were fixed with 4% paraformaldehyde-PBS, permeabilized with 0.5% Triton X-100, and stained with specific antibodies. Cells expressing NS5A or control cells were extracted into cytosol (C), membrane-organelle (M), and nuclear (N) fractions. Each fraction was concentrated and subjected to immunoblotting with specific antibodies. PA28 α , calregulin, and histone H1 were used as markers for cytosol, membrane-organelle, and nuclear fractions, respectively.

CGTCTTGAGAAATGTTGTGGCTGA-3', and 5'-ACCACAGTCCATGCCATC AC-3' and 5'-TCCACCACCTGTGTCIGTA-3', respectively. The expression of mRNAs of each of the chemokines, cytokines, and TLR was normalized with that of GAPDH mRNA.

Immunofluorescence microscopy and subcellular localization of HCV proteins in stable macrophage cell lines. Cells were seeded onto an eight-well chamber slide at 1.5×10^4 cells per well, washed twice with PBS, fixed with PBS containing 4% paraformaldehyde at 18 h of cultivation, and permeabilized with PBS containing 0.5% Triton X-100 at 15 min. The cells were then incubated at 4°C for 1 h with 1 μ g of mouse anti-NS5A antibody (Austral Biologicals, San Ramon, CA) or rabbit polyclonal antibody against calregulin (Santa Cruz Biotechnology) in PBS containing 10% fetal calf serum (PBSF) and then incubated at room temperature for 1 h with 0.5 μ g of Alexa Fluor 488-conjugated anti-mouse IgG (Molecular Probes) or Alexa Fluor 594-conjugated anti-rabbit IgG (Molecular Probes) after three washes with PBSF. After extensive washing with PBSF, the samples were examined with a Fluoview FV1000 laser scanning confocal microscope (Olympus, Japan). To confirm the subcellular localization of the HCV proteins in the macrophage cell lines, each stable cell line was fractionated with a Subcellular Proteome Extraction kit (Calbiochem, Darmstadt, Germany). Stepwise extraction resulted in four distinct fractions, which contained primarily cytosolic, membrane-organelle, nuclear, and cytoskeleton proteins, respectively. Each fraction was concentrated by Microcon (Millipore) and subjected to immunoblotting. PA28 α (Biomol International, Plymouth Meeting, PA), calregulin, and histone H1 (Santa Cruz Biotechnology) were used as cytoplasmic, membrane, and nuclear markers, respectively.

RESULTS

Establishment of macrophage cell lines stably expressing HCV proteins. To examine the effect of HCV proteins on the TLR function of immune cells, we established murine macrophage cell lines stably expressing HCV structural or nonstructural proteins. We selected mouse macrophage RAW264.7 cells due to their high level of expression of various TLRs (3) and their high sensitivity to stimulation with TLR ligands. Processed HCV structural and nonstructural proteins were detected in each of the cell lines by immunoblot analyses using specific monoclonal antibodies (Fig. 1A). To examine the effect of HCV proteins on TLR expression in macrophage cell lines, the mRNA of TLRs in cells expressing NS5A was determined by real-time PCR (Fig. 1B). Although slight reductions in TLR2, TLR3, and TLR4 or enhancement of TLR7 and TLR9 was observed, a substantial amount of mRNA of the examined TLRs was detected in the cell lines expressing NS5A and other HCV proteins (data not shown). To determine the subcellular localization of HCV proteins in macrophage cell lines, the expression of HCV proteins was examined by con-

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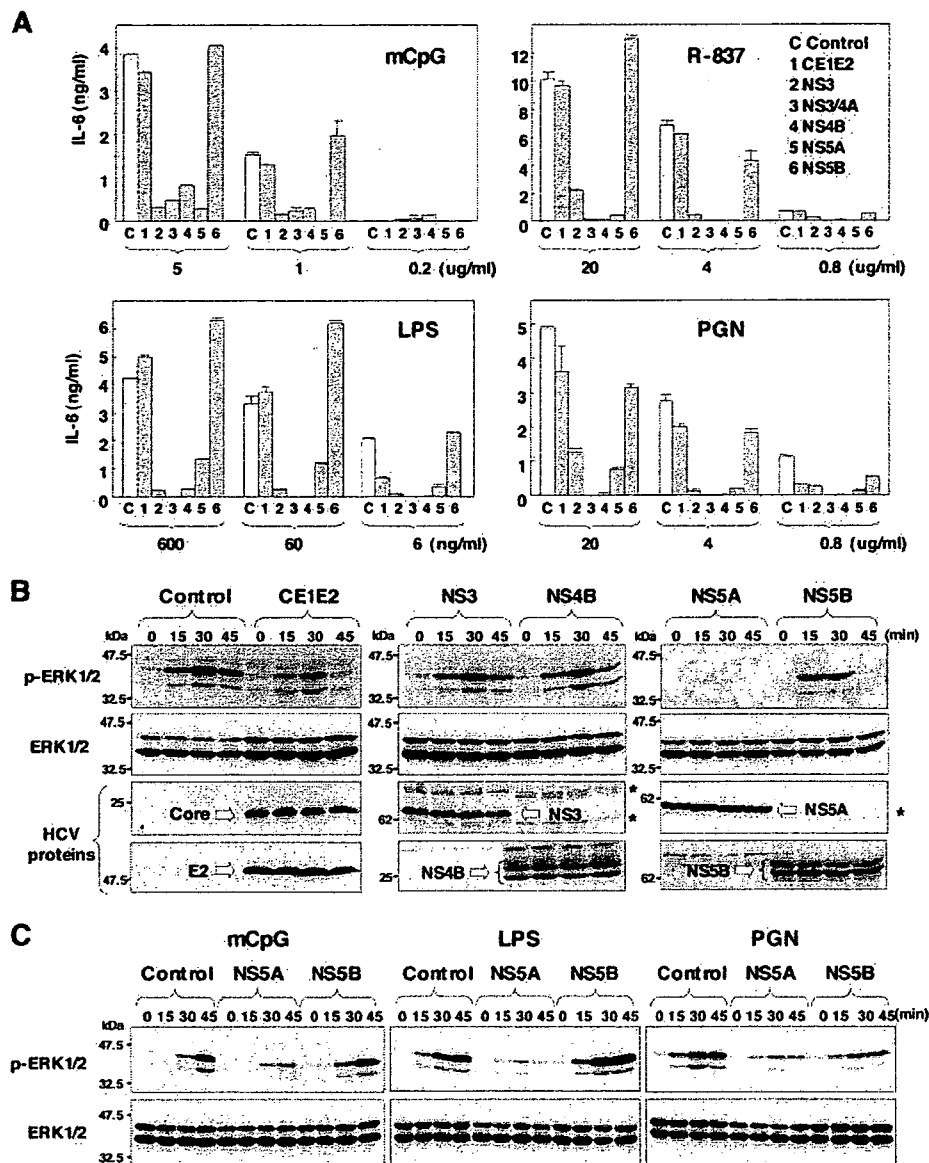


FIG. 2. Expression of HCV nonstructural proteins modulates IL-6 production and MAPK cascades through the TLR-dependent signaling pathway in macrophage cell lines. (A) Cells were seeded onto 96-well plates (1×10^5 cells/well) and stimulated with the indicated amounts of mCpG, R-837, LPS, or PGN. After 24 h of stimulation, IL-6 production in the culture supernatants was determined by sandwich ELISA. Data are shown as means \pm standard deviations (SD). (B) Cells (2×10^6 cells/well) were stimulated with $10 \mu\text{g/ml}$ of R-837 for the times indicated, and ERK1/2 phosphorylation was determined by immunoblotting with antibodies to ERK and phosphorylated ERK (p-ERK). Asterisks indicate nonspecific bands. (C) Cells (2×10^6 cells/well) were stimulated with $10 \mu\text{g/ml}$ of mCpG, 25 ng/ml of LPS, or $10 \mu\text{g/ml}$ of PGN for the times indicated, and ERK1/2 phosphorylation was determined by immunoblotting.

focal microscopy and cell fractionation (Fig. 1C). HCV NS5A was colocalized with the endoplasmic reticulum marker calregulin in the macrophage cell line as reported previously for human hepatoma cell lines (47). Other HCV proteins exhibited similar localization with NS5A (data not shown). To further confirm the subcellular localization of NS5A proteins, cytoplasmic, membrane-organelle, and nuclear fractions of the cell line expressing NS5A were analyzed by Western blotting. NS5A was detected mainly in the membrane-organelle fraction.

Expression of HCV NS3, NS3/4A, NS4B, or NS5A modulates the TLR-dependent signaling pathway in macrophage cell lines. In order to determine the effect of the expression of HCV proteins on the TLR signaling pathway in macrophage cell lines, we examined the ability of HCV proteins to inhibit NF- κ B activation via stimulation with various TLR ligands. The macrophage cell lines were stimulated with the TLR ligands, and the production of the proinflammatory cytokine IL-6 in the culture supernatants was determined by ELISA (Fig. 2A). The expression of HCV structural proteins or NS5B

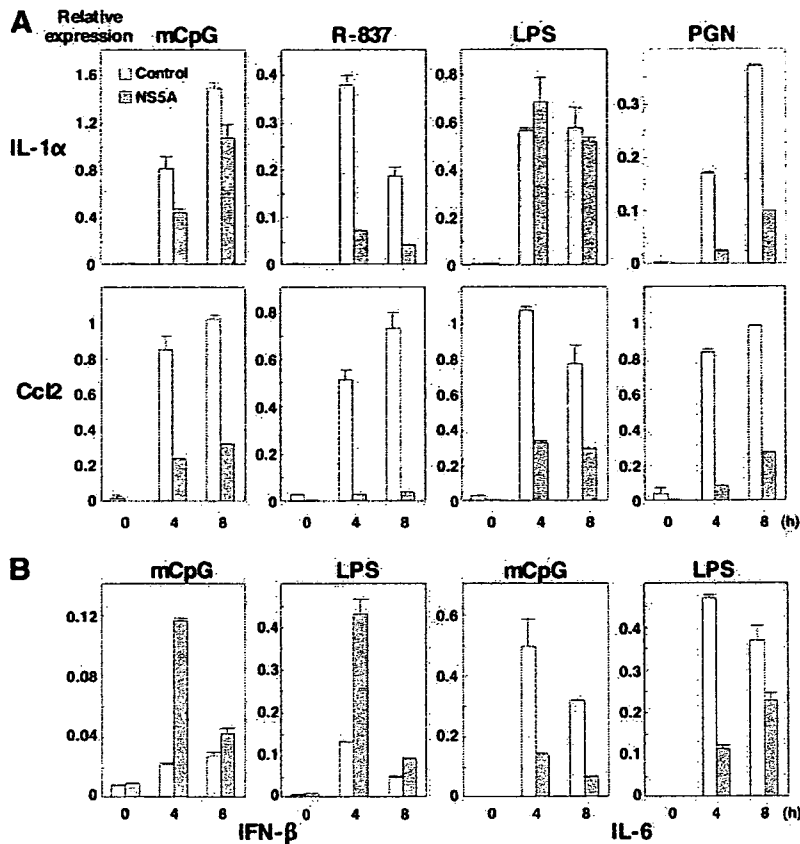


FIG. 3. Effect of NS5A expression on the production of cytokines and chemokines in response to TLR ligands in macrophage cell lines. Cells (3×10^6 cells/well) were stimulated with 10 μ g/ml of mCpG, 10 μ g/ml of R-837, 25 ng/ml of LPS, and 10 μ g/ml of PGN for the times indicated. Total RNA was extracted from macrophage cell lines expressing NS5A (gray bars) or control (white bars), and the expression of mRNA of IL-1 α and Ccl2 (A) and IFN- β and IL-6 (B) was determined by real-time PCR.

had no effect on IL-6 production after stimulation with mCpG, R-837, LPS, or PGN, which are ligands for TLR9, TLR7, TLR4, and TLR2, respectively. On the other hand, the expression of NS3, NS3/4A, NS4B, or NS5A inhibited the production of IL-6 induced by treatment with the ligands. These results indicate that the expression of NS3, NS3/4A, NS4B, and NS5A inhibits the production of IL-6 through the TLR-dependent signaling pathway in macrophage cell lines.

In addition to proinflammatory cytokine production via NF- κ B activation, stimulation of TLR also activates mitogen-activated protein kinases (MAPKs). We then examined the activation of ERK, a MAPK signaling pathway, in response to the TLR ligands in the macrophage cells expressing HCV proteins (Fig. 2B). Although the expression of the HCV structural proteins NS3, NS4B, and NS5B did not alter the phosphorylation status of ERK1/2 in response to stimulation with the TLR7 ligand R-837, the expression of NS5A exhibited a clear inhibition of the phosphorylation of ERK1/2. To further examine the effect of NS5A expression on the MAPK cascade in response to the TLR ligands, the cells were treated with mCpG, LPS, and PGN. NS5A expression was found to inhibit the phosphorylation of ERK1/2 in response to stimulation with the ligands for TLR9, TLR4, and TLR2 (Fig. 2C). In contrast, the phosphorylation of c-Jun NH₂-terminal kinase in

response to stimulation with R-837 was less impaired in the macrophage cell line expressing NS5A (data not shown). These results indicate that the expression of NS3, NS3/4A, NS4B, or NS5A inhibits the production of proinflammatory cytokines and that the expression of NS5A alone induces the inhibition of the MAPK cascade in response to stimulation by various TLR ligands in macrophage cells.

To further examine the effect of NS5A expression on the production of the other proinflammatory cytokines and chemokines in response to TLR ligands, the expression of mRNA of IL-1 α and Ccl2 in cells expressing NS5A after stimulation with TLR ligands was determined by real-time PCR (Fig. 3A). Expression of IL-1 α and Ccl2 was reduced in cells expressing NS5A by stimulation with mCpG, R-837, LPS, or PGN except for the IL-1 α expression by treatment with LPS, probably due to the TRIF-dependent activation of NF- κ B. To further confirm the specific inhibition of the MyD88-dependent signaling pathway by NS5A, we examined the effects of NS5A expression in macrophage cells on the MyD88-independent/TRIF-dependent production of IFN- β (Fig. 3B). Although the expression of IL-6 mRNA in cells expressing NS5A was impaired after stimulation with mCpG or LPS, the expression of IFN- β was enhanced. These results suggest that the expression of NS5A specifically inhibits the MyD88-dependent signaling pathway.

TLR-dependent and -independent immune activation of macrophage cells expressing NS3/4A or NS5A protein by RNA virus and dsRNA. TLR3 has been shown to sensitize cells in response to double-stranded RNA (dsRNA) generated by viral infection and a synthetic dsRNA analog, poly(I:C), through an adaptor molecule, TRIF/TICAM-1, but not MyD88. Furthermore, RIG-I and MDA5 have been identified as being cytoplasmic dsRNA detectors responding to poly(I:C) and viral RNAs (57, 58), sensitizing cells through an adaptor molecule, IPS-1/MAVS/VISA/CARDIF, in a TLR-independent manner (24, 35, 46, 55). Recently, HCV NS3/4A protease was shown not only to cleave HCV nonstructural proteins but also to inhibit viral RNA- and dsRNA-induced IFN production through the cleavage of the adaptor molecules TRIF (28) and IPS-1 (29, 30, 33, 35). Moreover, it has been shown that NS3/4A protease inhibits dsRNA-induced immune activation in a protease-dependent manner in human hepatoma cell lines (11).

To determine whether murine TRIF (mTRIF) is cleaved by HCV NS3/4A protease, C-terminally His-tagged mTRIF was coexpressed with N-terminally Flag-tagged NS3, NS3/4A, or NS3/4A(S139A) in 293T cells. Immunoblot analyses revealed that mTRIF was not processed by HCV NS3/4A protease, probably due to differences in the amino acid sequences at the cleavage site in mTRIF (Fig. 4A). Amino acid sequences at the cleavage site of human TRIF are Cys³⁷² and Ser³⁷³, and those at the cleavage sites of mTRIF are Pro³⁷² and Ala³⁷³ (Fig. 4B). These results suggest that HCV NS3/4A protease could not inhibit immune activation through the TLR3-mTRIF-dependent signaling pathway in murine cells. We next determined the processing of IPS-1 by HCV NS3/4A protease. N-terminally Flag-tagged mIPS-1 or its C508A mutant, with Cys⁵⁰⁸ replaced with Ala to prevent cleavage by HCV NS3/4A protease, was coexpressed with N-terminally Flag-tagged NS3, NS3/4A, or NS3/4A(S139A) in 293T cells. Immunoblot analyses revealed that wild-type mIPS-1 was cleaved in cells coexpressing the active NS3/4A protease but not in those with NS3 (Fig. 4C). mIPS-1 processing was reduced in cells coexpressing NS3/4A(S139A) as well as in those coexpressing mIPS-1(C508A) and NS3/4A (Fig. 4C). Furthermore, we were able to detect cleavage of endogenous mIPS-1 in macrophage cell lines expressing NS3/4A but not in those expressing NS3 or NS3/4A(S139A) (Fig. 4D), indicating that mIPS-1 in murine macrophage cell lines is cleaved by HCV NS3/4A protease, as reported previously for a human hepatoma cell line.

We then examined the effect of expression of NS3/4A and NS5A on TLR-dependent and -independent immune activation induced by dsRNA. VSV and poly(I:C) were inoculated into macrophage cell lines, and the expression of mRNA of IFN- β and IL-1 α was determined by real-time PCR (Fig. 4E). The macrophage cell lines expressing NS3/4A exhibited inhibition of IL-1 α and IFN- β expression upon infection with VSV but not in response to poly(I:C), whereas no inhibition was observed in those expressing NS5A. These results suggest that the invasion of VSV and poly(I:C) is preferentially recognized in RAW cell lines by RIG-I-IPS-1- and TLR3-TRIF-dependent signaling pathways, respectively. Inhibition of IL-1 α and IFN- β expression upon infection with VSV but not in response to poly(I:C) is probably due to the selective cleavage of IPS-1 but not TRIF by NS3/4A protease in the macrophage cell lines.

In contrast, the expression of NS5A has no effect on both TLR3-TRIF and RIG-I-IPS-1-dependent signaling pathways in macrophage cells.

Although MyD88/IRF7-dependent production of IFN- α upon activation was reported in plasmacytoid DCs (pDCs) (17, 23), it is unclear whether murine macrophage cells are capable of producing IFN- α in a TLR/MyD88/IRF7-dependent manner. To examine the effect of NS5A expression on IFN- α production, the expression of IFN- α 1 and IFN- α 4 in the macrophage cell line upon infection with VSV was determined (Fig. 4E, bottom). In contrast to the effect on IFN- β production, the expression of NS5A in the macrophage cells reduced the production of IFN- α 1 and IFN- α 4 upon infection with VSV, although the inhibitory effect was weaker than that of NS3/4A. These results suggest that RAW264.7 cells are capable of producing IFN- α in a TLR/MyD88/IRF7-dependent manner upon infection with VSV as reported for pDCs, and the expression of NS5A partially counteracts this signaling pathway. However, the production of type I IFNs by the treatment with ligands for TLR7 (R-837) and TLR9 (mouse CpG) was weaker than that induced by infection with VSV in macrophage cells (data not shown). Further study is needed to clarify the precise mechanisms of the inhibition of TLR/MyD88/IRF7-dependent IFN- α production by the expression of HCV NS5A in human immune cells.

NS5A interacts with MyD88 in mammalian cells. The inhibition of the production of proinflammatory cytokines and chemokines and the MAPK cascade by NS5A expression in response to stimulation by various TLR ligands without participation of TRIF- and IPS-1-dependent signaling pathways suggests that NS5A specifically inhibits the TLR-MyD88-dependent signaling pathway in macrophage cell lines. MyD88 is a critical component of the signaling pathway and leads to the production of proinflammatory cytokines, chemokines, and MAPKs. To determine the effect of the expression of HCV proteins on the TLR signaling pathway in macrophage cell lines, the interaction of the HCV proteins with the adaptor molecules in the signaling pathway of the TLR family was examined by immunoprecipitation analysis. His-tagged MyD88 was coexpressed with Flag-tagged HCV proteins in 293T cells and immunoprecipitated with the indicated antibodies. As shown in Fig. 5A and B, MyD88 was coimmunoprecipitated with NS5A but not with structural and other nonstructural proteins in 293T cells.

To further confirm the specificity of the interaction of NS5A with MyD88, NS5A was coexpressed with other adaptor molecules in the TLR signaling pathway, TRAM, TIRAP, or TRIF, in 293T cells (Fig. 5C). NS5A interacted with MyD88 but not other adaptor molecules, suggesting that NS5A may inhibit the production of proinflammatory cytokines and chemokines and the phosphorylation of MAPKs through the counteraction of the MyD88-dependent TLR signaling pathway.

NS5A interacts with the death domain of MyD88 through the ISDR and inhibits recruitment of IRAK to MyD88. To determine the region of NS5A responsible for the interaction with MyD88, a series of deletion mutants of N-terminal Flag-tagged NS5A was constructed, and its interaction with His-tagged MyD88 was examined (Fig. 6A). The NS5A mutant covering amino acids 1 to 280 but not that covering amino

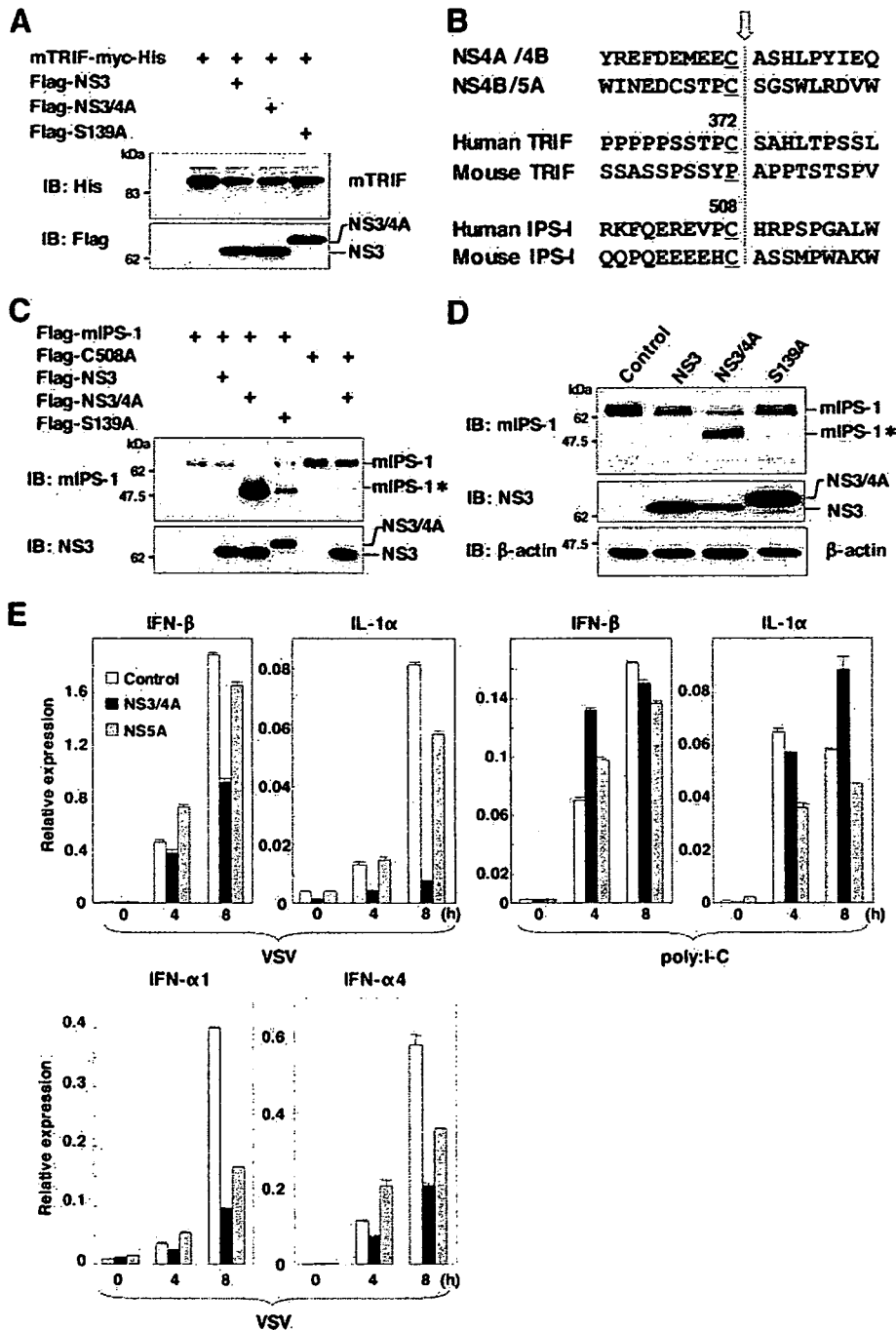


FIG. 4. TLR-dependent and -independent immune activation of macrophage cells expressing the NS3/4A or NS5A protein by RNA virus and dsRNA. (A) Myc-His-mTRIF was coexpressed with Flag-NS3, -NS3/4A, or -NS3/4A(S139A) in 293T cells and immunoblotted (IB) with antibodies against His and Flag. (B) Alignment of the flanking sequence of NS3 protease cleavage sites of NS4A/4B, NS4B/5A, TRIF, and IPS-1 of human and murine origins. The cleavage site is indicated by an arrow. (C) Flag-mIPS-1 and a mutant with Cys⁵⁰⁸ replaced with Ala (C508A) were coexpressed with Flag-NS3, -NS3/4A, or -NS3/4A(S139A) in 293T cells and immunoblotted with antibodies against mIPS-1 and NS3. (D) Processing of endogenous mIPS-1. Cell lysates of the macrophage cell lines expressing NS3, NS3/4A, and NS3/4A(S139A) were immunoblotted with antibodies against mIPS-1, NS3, and β -actin. The cleavage product of mIPS-1 is indicated as mIPS-1*. (E) Cells (3×10^6 cells/well) were stimulated with 2×10^5 PFU/ml of VSV or 50 μ g/ml of poly(I:C) for the times indicated. Total RNA was extracted from the macrophage cell lines expressing NS3/4A (black bars), NS5A (gray bars), or control (white bars), and the expression of mRNA of IFN- β , IL-1 α , IFN- α 1, and IFN- α 4 was determined by real-time PCR.

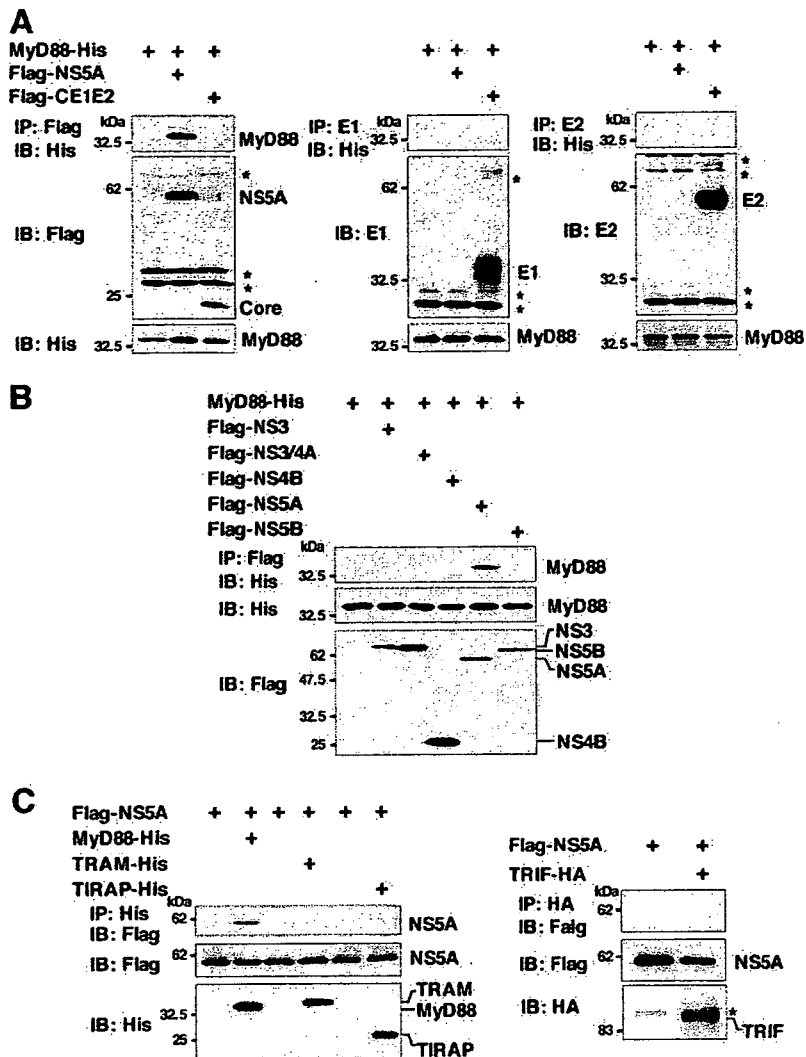


FIG. 5. NS5A interacts with MyD88. MyD88-His was coexpressed with Flag-core/E1/E2 or -NS5A (A) or Flag-NS3, -NS3/4A, -NS4B, -NS5A, or -NS5B (B) in 293T cells; immunoprecipitated (IP) with anti-Flag, E1, or E2 antibody; and immunoblotted (IB) with anti-His antibody. (C) Flag-NS5A was coexpressed with MyD88-His, TRAM-His, TIRAP-His, or TRIF-HA in 293T cells and immunoprecipitated with anti-His or -HA antibody. The immunoprecipitates were immunoblotted with anti-Flag antibody. Asterisks indicate nonspecific bands.

acids 1 to 200 exhibited binding to MyD88, suggesting that amino acid residues 200 to 280 of NS5A are required for the interaction with MyD88. Further mutational analyses of NS5A revealed that amino acid residues 240 to 280, which overlap the ISDR (amino acid residues 237 to 276), which was previously suggested to be involved in IFN resistance (10, 41), are required for the interaction with MyD88 (Fig. 6A). To determine the region of MyD88 responsible for the interaction with NS5A, His-tagged MyD88 mutants were coexpressed with Flag-tagged NS5A in 293T cells and immunoprecipitated with anti-His antibody. A MyD88 deletion mutant lacking amino acids 1 to 50, but not one lacking amino acids 1 to 80, and a mutant possessing amino acids 1 to 70 exhibited binding to NS5A, suggesting that amino acid residues 50 to 70 in the death domain of MyD88 are required for the interaction with NS5A (Fig. 6B).

MyD88 associates with TLRs and acts as an adapter that recruits IRAK, which is known as a key regulator for TLR7- and TLR9-mediated IFN- α production in pDCs (53). To determine the role of NS5A binding to MyD88 in the TLR-MyD88-dependent signaling pathway, we examined the association of IRAK with MyD88 in the presence of NS5A. Flag-tagged MyD88 was coexpressed with Myc-tagged IRAK-1 or IRAK-4 and immunoprecipitated with anti-Myc antibody (Fig. 6C, left). IRAK-1, but not IRAK-4, was coimmunoprecipitated with MyD88. Although NS5A did not bind to IRAK-1, it was not possible to assess the interaction of NS5A with IRAK-4 due to the degradation of NS5A in cells coexpressing IRAK-4 for unknown reasons (Fig. 6C, middle). To examine the interplay between IRAK-1 and MyD88 in the presence of NS5A, Flag-tagged MyD88 and Myc-tagged IRAK-1 were coexpressed with Flag-tagged NS5A in 293T cells. The interaction

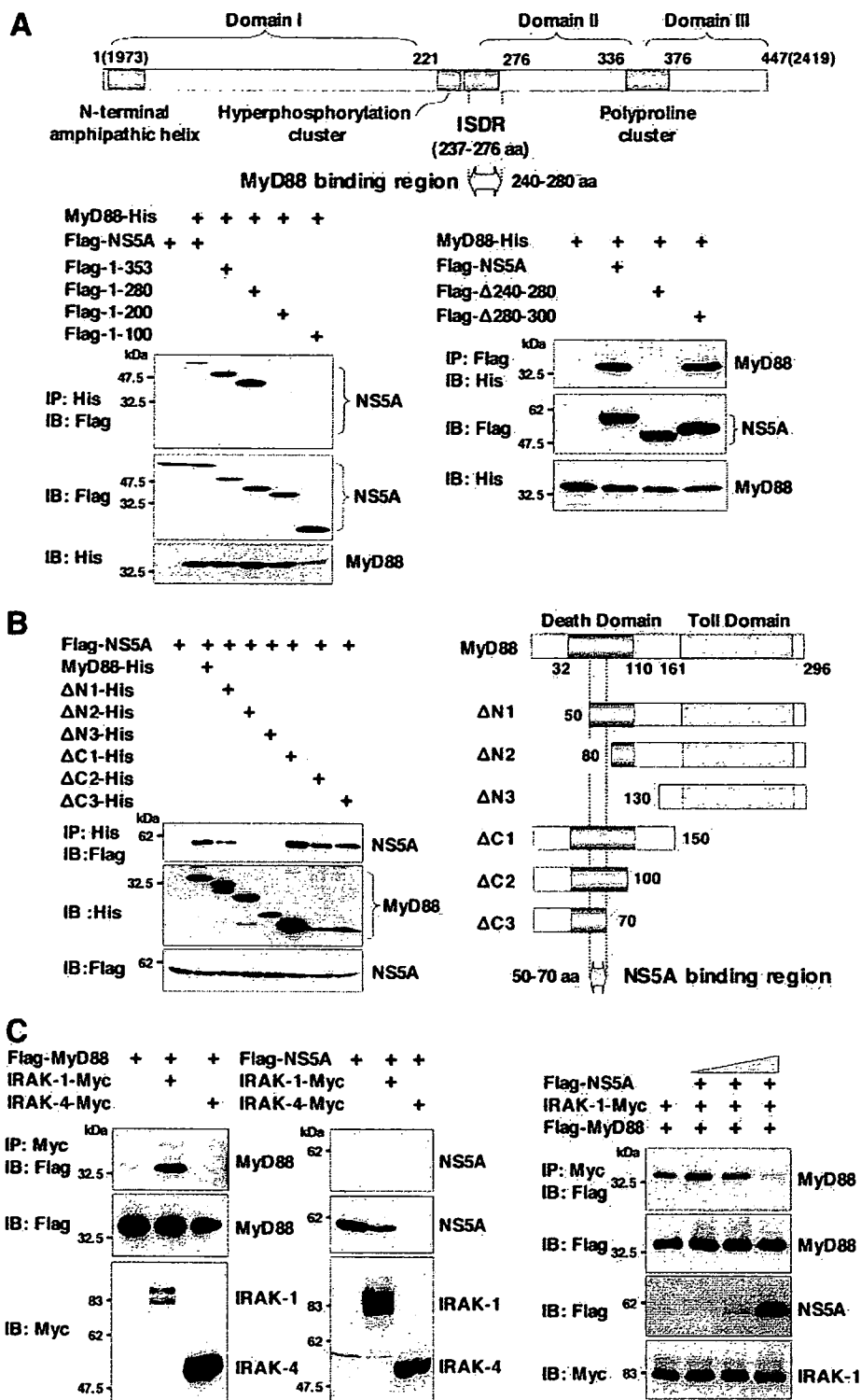


FIG. 6. NS5A interacts with the death domain of MyD88 through the ISDR and inhibits recruitment of IRAK to MyD88. (A) The structure of NS5A and the MyD88 binding region are indicated at the top. MyD88-His was coexpressed with C-terminal deletion mutants of Flag-NSSA in 293T cells, immunoprecipitated (IP) with anti-His antibody, and immunoblotted (IB) with anti-Flag antibody (left). MyD88-His was coexpressed with Flag-NSSA deletion mutants ($\Delta 240-280$ or $\Delta 280-300$) in 293T cells, immunoprecipitated with anti-Flag antibody, and then immunoblotted with anti-His antibody (right). (B) Flag-NSSA was coexpressed with N-terminal or C-terminal deletion mutants of MyD88-His ($\Delta N1$, $\Delta N2$, $\Delta N3$, $\Delta C1$, $\Delta C2$, or $\Delta C3$) in 293T cells, immunoprecipitated with anti-His antibody, and immunoblotted with anti-Flag antibody. The structures of MyD88 and the deletion mutants and the NS5A binding region are indicated on the left. (C) Flag-MyD88 (left) or Flag-NSSA (middle) was coexpressed with IRAK-1-Myc or IRAK-4-Myc in 293T cells, immunoprecipitated with anti-Myc antibody, and immunoblotted with anti-Flag antibody. Flag-MyD88 and IRAK-1-Myc were coexpressed with Flag-NSSA in 293T cells, immunoprecipitated with anti-Myc antibody, and immunoblotted with anti-Flag antibody. The effect of the increase in Flag-NSSA expression on the interaction of MyD88 with IRAK-1 was examined by transfection with 0.1, 0.5, or 2 μ g of Flag-NSSA expression plasmid (right).

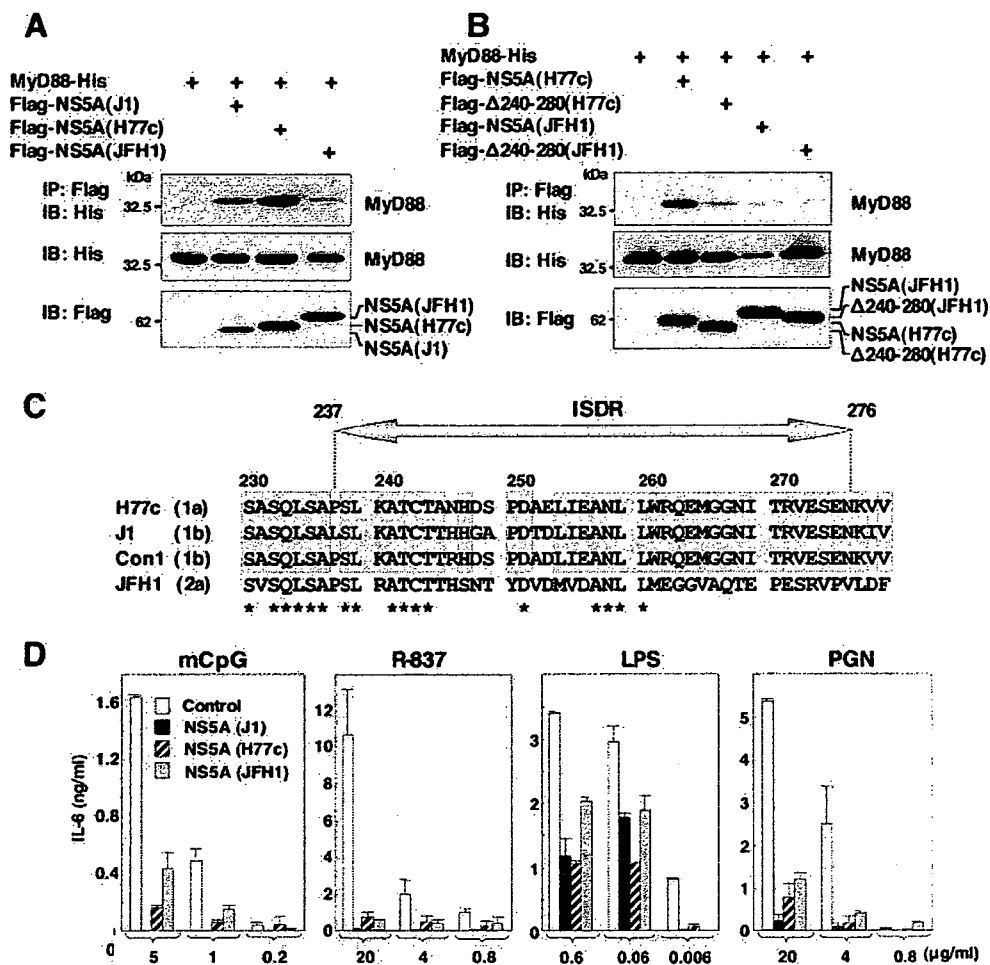


FIG. 7. NS5A of other genotypes also interacts with MyD88 and inhibits the TLR signaling pathway. (A) Flag-NS5As of other genotypes were coexpressed with MyD88-His in 293T cells, immunoprecipitated (IP) with anti-Flag antibody, and immunoblotted (IB) with anti-His antibody. (B) The wild type or a deletion mutant lacking amino acids 240 to 280 of Flag-NS5A of genotype 1a or 2a was coexpressed with MyD88-His in 293T cells, immunoprecipitated with anti-Flag antibody, and immunoblotted with anti-His antibody. (C) Amino acid sequences of ISDR and its adjacent region of strains H77c (genotype 1a), J1 (genotype 1b), Con1 (genotype 1b), and JFH1 (genotype 2a). The conserved amino acids among genotypes 1a and 1b are indicated by boxes. Conserved amino acids among all strains are indicated by asterisks. (D) Macrophage cell lines expressing NS5A of genotypes 1a (H77c), 1b (J1), and 2a (JFH1) were established. Cells were stimulated with the indicated amounts of mCpG, R-837, LPS, or PGN, and the production of IL-6 in the culture supernatants was determined by ELISA 24 h after stimulation. Data are shown as the means \pm SD.

of IRAK-1 and MyD88 decreased in accord with the increasing NS5A expression complex (Fig. 6C, right), suggesting that the expression of NS5A may interfere with the TLR-MyD88-dependent signaling pathway through the inhibition of the recruitment of IRAK-1 to MyD88.

NS5A of other genotypes also interacts with MyD88 and inhibits the TLR signaling pathway. To determine the interaction of MyD88 with NS5A of other genotypes, Flag-tagged NS5A of genotype 1a (H77c) or 2a (JFH1) was coexpressed with His-tagged MyD88 in 293T cells. MyD88 was coprecipitated with the NS5As of genotypes 1a and 2a, although it should be noted that the interaction between the MyD88 and NS5A of genotype 2a was weaker than that of the other genotypes (Fig. 7A). To determine the region of the NS5As of genotype 1a or 2a responsible for the interaction with MyD88, N-terminal Flag-tagged NS5As of genotype 1a or 2a deletion

mutants lacking amino acids 240 to 280 (Δ 240-280) were constructed, and their interaction with MyD88 was examined. Mutational analyses revealed that amino acid residues 240 to 280 of the NS5As of genotypes 1a and 2a were also required for the interaction with MyD88 (Fig. 7B). Amino acid alignment of the ISDRs of genotypes 1a, 1b, and 2a revealed that the region of genotype 2a was less conserved than those of the other genotypes (Fig. 7C).

To determine the effect of NS5A expression of other genotypes on the TLR signaling pathway, we established macrophage cell lines expressing NS5A of each genotype. NS5A expression for all genotypes was found to inhibit IL-6 production after stimulation with mCpG, R-837, LPS, or PGN (Fig. 7D). Although the association of NS5A of genotype 2a to MyD88 was weaker than that of other genotypes, the expression of genotype 2a NS5A in macrophage cells exhibited com-

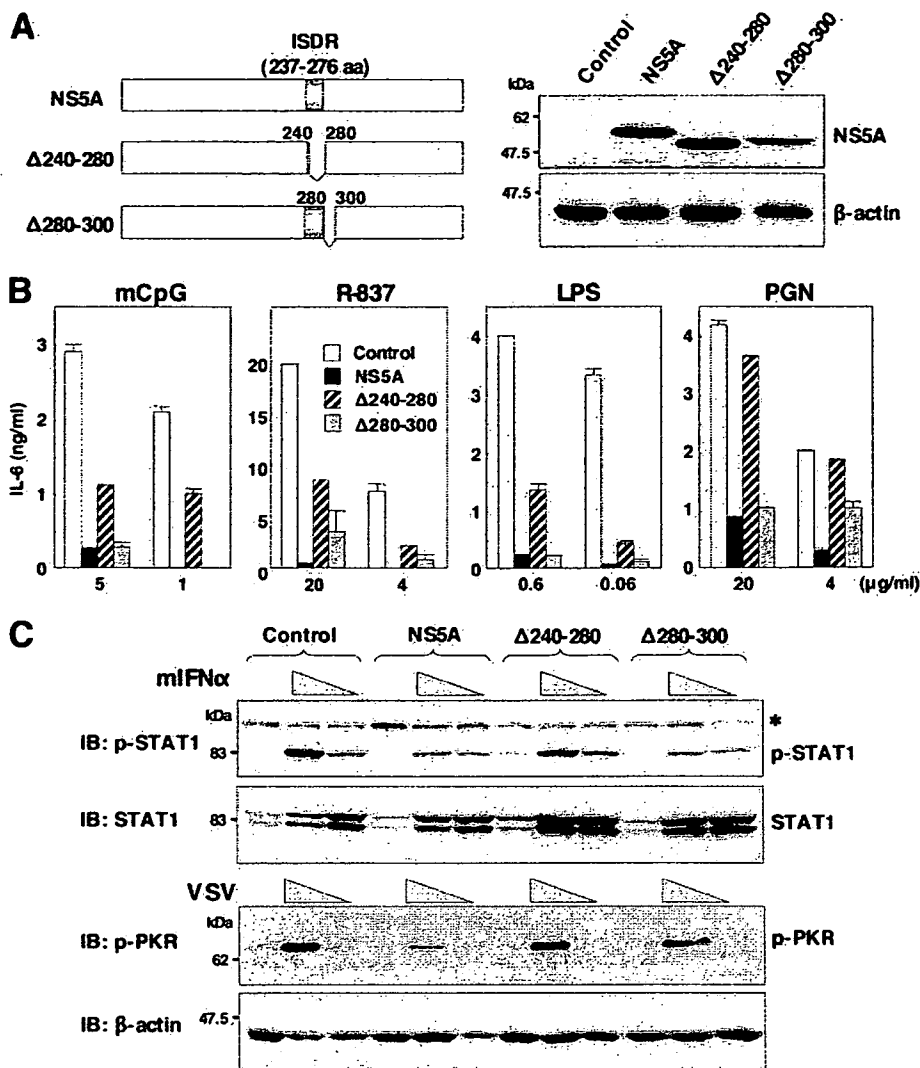


FIG. 8. ISDR in NS5A participates in the inhibition of the MyD88-dependent signaling pathway. (A) Structures of NS5A mutants lacking amino acid residues 240 to 280, in which the ISDR/MyD88-interacting region is located (Δ 240–280), and lacking amino acid residues 280 to 300 (Δ 280–300) (left). Immunoblot analyses of cells expressing wild-type or mutant NS5A (right) are shown. (B) Cells expressing wild-type or mutant NS5A were stimulated with the indicated amounts of mCpG, R-837, LPS, or PGN, and the production of IL-6 in the culture supernatants was determined by ELISA 24 h after stimulation. Data are shown as the means \pm SD. (C) Phosphorylation of STAT1 or PKR in response to treatment with murine IFN- α or infection with VSV. The cell lines were stimulated with two doses of murine IFN- α (2×10^3 and 2×10^2 units/ml) or VSV (2×10^7 and 2×10^6 PFU/ml). After 24 h of stimulation, cell extracts were immunoblotted (IB) with specific antibodies. Phosphorylated STAT1 and PKR and the total amounts of STAT1 and β -actin were determined. The asterisk indicates nonspecific bands.

parable inhibition of IL-6 production in response to stimulation by various TLR ligands with those of genotypes 1b and 1a. These results suggest that NS5As of genotypes 1a, 1b, and 2a interact with MyD88 and inhibit the TLR signaling pathway in macrophage cell lines.

ISDR participates in the inhibition of the MyD88-dependent signaling pathway by NS5A. To further confirm the inhibitory effect of NS5A on the TLR signaling pathway, we established macrophage cell lines stably expressing an NS5A mutant lacking the ISDR/MyD88 binding region (Δ 240–280) or lacking a region dispensable for the interaction with MyD88 (Δ 280–300) (Fig. 8A). The inhibitory effect of TLR signaling in response to

stimulation with mCpG, R-837, LPS, or PGN by NS5A was partially restored in the cell line expressing the NS5A lacking the ISDR (Δ 240–280), and comparable inhibition was observed in the cell line expressing the NS5A deletion mutant retaining the ISDR (Δ 280–300) (Fig. 8B). These results suggest that the interaction of NS5A with MyD88 through the ISDR is responsible for the disruption of the TLR-MyD88-dependent signaling pathway due to the expression of NS5A in macrophage cells. Partial recovery of the TLR signaling pathway by the expression of the NS5A mutant lacking the ISDR suggests the involvement of other inhibitory mechanisms by NS5A.

Previous reports suggested that the ISDR of NS5A participates in conferring IFN sensitivity (10) and in an interaction with PKR (13). To determine the effect of the interaction of MyD88 with NS5A through the ISDR on the IFN signaling pathway, we examined the phosphorylation of STAT1 and PKR in response to treatment with murine IFN- α and infection with VSV. The expression of wild-type NS5A and the Δ 280–300 mutant but not the Δ 240–280 mutant reduced the phosphorylation of STAT1 in response to IFN- α treatment (Fig. 8C, top), suggesting that the ISDR/MyD88 binding region in NS5A is involved in the IFN signaling pathway. Although cells expressing wild-type NS5A reduced PKR phosphorylation, those expressing mutant NS5A (Δ 240–280 or Δ 280–300) did not inhibit PKR phosphorylation upon infection with VSV (Fig. 8C, bottom), which is consistent with the previous observation that the 66 ISDR-inclusive amino acid residues (amino acids 237 to 302) are required for interactions with PKR (13). These results suggest that the expression of HCV NS5A in macrophage cells counteracts the IFN signaling pathway through the repression of STAT1 and PKR due to the interaction with ISDR and its adjacent region.

DISCUSSION

The majority of HCV-infected individuals become chronic carriers; however, the mechanism of progression to chronicity remains unclear. Among HCV proteins, NS3 has been shown to be immunodominant, and T cells that are reactive to NS3 have been suggested to play a crucial role in viral clearance, while HCV core protein is immunosuppressive (8). Treatment of immature DCs with core or NS3 protein inhibited DC differentiation, and DCs transduced to express core or E1 protein exhibited poor allogeneic T-cell responses (43). The immunosuppressive potential of HCV proteins has been implicated as a mechanism of the functional subversion of T cells, natural killer (NK) cells, and DCs. The association of HCV core protein with the globular domain of the C1q receptor on T cells down-regulates T-cell proliferation and IL-2 production (25). Additionally, the HCV E2 protein displays a high affinity for the tetraspanin cell surface molecule human CD81, which is one of the candidates for an HCV entry receptor (40), and E2 cross-linking with cell surface human CD81 impairs the activation of NK cells (7, 52).

In the present study, we established macrophage cell lines stably expressing HCV proteins and examined the effects of viral proteins on TLR function. The expression of the NS5A protein specifically inhibits TLR-MyD88-induced signaling by associating with the death domain of MyD88 through the ISDR spanning amino acid residues 240 to 280 in macrophage cells. HCV NS5A is a phosphoprotein that appears to possess multiple and diverse functions in viral replication, IFN resistance, and pathogenesis (34). Mutation in the ISDR has been suggested to correlate with the responsiveness of patients chronically infected with HCV genotype 1b to IFN treatment (10). Furthermore, NS5A has been shown to rescue virus replication in IFN-treated cell cultures (41) and to inhibit the antiviral activity of IFN by binding to PKR through the ISDR and its adjacent region (amino acids 237 to 302) (13, 14). However, controversial observations that the ISDR sequence variation does not account for differences in IFN sensitivity in

patients (9) and also in an HCV subgenomic RNA replicon system (15) have been made. Moreover, the expression of NS5A or the entire HCV polyprotein has been reported to counteract the antiviral effect of IFN in a PKR- and ISDR-independent manner (12). Therefore, the possibility remains that a molecule other than PKR may be involved in the NS5A-mediated inhibition of IFN (50). Restoration of the phosphorylation of STAT1 in cells expressing a deletion mutant lacking ISDR in response to IFN- α and that of PKR phosphorylation upon infection with VSV in cells expressing NS5A mutants lacking amino acid residues 240 to 280 (ISDR) or 280 to 300 may support the hypothesis that the ISDR and the adjacent region are involved in IFN sensitivity. Thus, the ISDR may participate not only in conferring IFN resistance but also in disrupting TLR-MyD88 signaling pathways in macrophage cells.

Several viral proteins have been shown to counteract TLRs and their downstream signaling cascade. The vaccinia virus A46R protein contains a Toll/IL-1 receptor domain that interacts with multiple Toll/IL-1 receptor-containing adaptor molecules, thereby inhibiting the activation of NF- κ B and IRF3 (49). Measles virus and respiratory syncytial virus have been shown to inhibit the TLR7- and TLR9-dependent IFN-inducing pathways stimulated by R848 and CpG oligodeoxynucleotides in primary human pDCs (45). HCV NS3/4A has been shown to influence the functions of adaptor molecules mediating TLR-dependent and -independent signaling pathways, resulting in an impairment of the induction of IFN- β as well as the subsequent IFN-inducible genes (11). Recently, RIG-I and MDA5 have been identified as being cytoplasmic dsRNA detectors responding to viral RNAs and poly(I:C) in a TLR-independent manner and recruit IPS-1 as an adaptor molecule for signal transduction (24). The uncapped 5'-triphosphate RNA generated by viral polymerases was shown to be selectively recognized by RIG-I (18, 39). In this study, we could demonstrate that the invasion of VSV and poly(I:C) into RAW cell lines is preferentially recognized by RIG-I-IPS-1- and TLR3-TRIF-dependent signaling pathways, respectively, and that the expression of HCV NS3/4A protease selectively inhibits cytokine production upon infection with VSV through the cleavage of IPS-1. Therefore, it is feasible that the expression of NS5A and NS3/4A proteins in macrophage cells may disrupt TLR-dependent and -independent signaling pathways, respectively. However, the mechanism for the inhibition of the TLR signaling pathway in the macrophage cells by the expression of NS3 or NS4B remains unclear.

Although there have been reports suggesting a lack of DC dysfunction in both chimpanzees and humans chronically infected with HCV (26, 32), direct infection of DCs with HCV may be a plausible mechanism for the dysfunction of DCs in patients with chronic HCV infection (4, 21). Indeed, the HCV genome has been detected in DCs by PCR (4), and HCV was detected in a monocyte/macrophage subpopulation of peripheral blood mononuclear cells from patients with chronic HCV infection (5). Further experiments are needed to exclude the possibility of contamination of viral RNA in blood samples. Pseudotype VSV-bearing chimeric HCV E1 and E2 proteins have been shown to infect immature myeloid DCs isolated from healthy donors through interactions with lectins in a Ca-independent manner (20). Recently, the *in vitro* replication

of the HCV JFH1 clone of genotype 2a isolated from an HCV-infected patient who developed fulminant hepatitis was reported (31, 54, 59). However, *in vitro* replication was limited in the combination of HCV clones derived from strain JFH1 and certain human hepatoma cell lines, and a robust cell culture of genotypes 1a and 1b, the most prevalent viruses in the world and resistant to IFN therapy, has not yet been successful except for a cell culture system for strain H77-S (genotype 1a) in which infectivity was significantly lower than that of the JFH1 clone (56). The establishment of a robust and reliable *in vitro* replication system for various HCV isolates is essential to determine the role of HCV infection in the modulation of TLR function in immunocompetent cells.

In conclusion, we have shown that the expression of the HCV nonstructural protein NS3, NS3/4A, NS4B, or NS5A impairs the activation of TLR signaling pathways in immunocompetent cells. Furthermore, the NS5A protein was shown to inhibit the TLR-MyD88 signaling pathway by a direct interaction with the death domain of MyD88 through the ISDR. These findings suggest new aspects of virus-cell interactions that may be explored to develop a greater understanding of the mechanisms of escape of HCV from the host immune surveillance system and the establishment of persistent infection. However, it remains to be proven whether the results obtained using murine macrophage cell lines are applicable to immunocompetent cells in patients with HCV infection.

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Processing of Capsid Protein by Cathepsin L Plays a Crucial Role in Replication of Japanese Encephalitis Virus in Neural and Macrophage Cells[∇]

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The flavivirus capsid protein not only is a component of nucleocapsids but also plays a role in viral replication. In this study, we found a small capsid protein in cells infected with Japanese encephalitis virus (JEV) but not in the viral particles. The small capsid protein was shown to be generated by processing with host cysteine protease cathepsin L. An *in vitro* cleavage assay revealed that cathepsin L cleaves the capsid protein between amino acid residues Lys¹⁸ and Arg¹⁹, which are well conserved among the mosquito-borne flaviviruses. A mutant JEV resistant to the cleavage of the capsid protein by cathepsin L was generated from an infectious cDNA clone of JEV by introducing a substitution in the cleavage site. The mutant JEV exhibited growth kinetics similar to those of the wild-type JEV in monkey (Vero), mosquito (C6/36), and porcine (PK15) cell lines, whereas replication of the mutant JEV in mouse macrophage (RAW264.7) and neuroblastoma (N18) cells was impaired. Furthermore, the neurovirulence and neuroinvasiveness of the mutant JEV to mice were lower than those of the wild-type JEV. These results suggest that the processing of the JEV capsid protein by cathepsin L plays a crucial role in the replication of JEV in neural and macrophage cells, which leads to the pathogenesis of JEV infection.

The genus *Flavivirus* within the family *Flaviviridae* comprises over 70 viruses, many of which are predominantly arthropod-borne viruses, such as Japanese encephalitis virus (JEV), West Nile virus (WNV), Murray Valley encephalitis virus (MVE), dengue virus (DEN), yellow fever virus (YFV), and tick-borne encephalitis virus (TBEV). They frequently cause significant morbidity and mortality in mammals and birds (5). JEV is distributed in the south and southeast regions of Asia and is kept in a zoonotic transmission cycle between pigs or birds and mosquitoes (5, 42, 45). JEV spreads to dead-end hosts, including humans, through the bite of JEV-infected mosquitoes and causes infection of the central nervous system with a high mortality rate (5, 45). JEV has a single-stranded positive-strand RNA genome of approximately 11 kb, which is capped at the 5' end but lacks a 3' polyadenine tail (24). The ability of the flaviviral genomic RNA to cyclize is crucial for viral replication (1, 14). Among mosquito-borne flaviviruses, two complementary cyclization sequences, mapped in the capsid protein-coding region and 3' untranslated region (UTR), mediated the cyclization by RNA-RNA base pairing, together with a second pair of complementary sequences, named 5' and 3' upstream AUG regions (1, 10, 14, 19, 25). The genomic RNA includes a single large open reading frame, and a polyprotein translated at the endoplasmic reticulum (ER) membrane is cleaved co- and posttranslationally by host and

viral proteases to yield three structural proteins, the capsid, precursor membrane (prM), and envelope (E) proteins, and at least seven nonstructural proteins, NS1, NS2A, NS2B, NS3, NS4A, NS4B, and NS5 (24).

Although the capsid protein has very little amino acid homology among flaviviruses—for example, the homologies of the capsid protein of JEV to those of WNV, DEN type 2 (DEN2), and TBEV were only 67%, 33%, and 25%, respectively—the structural properties, such as the hydrophobicity profile, abundance of basic amino acid residues, and secondary and tertiary structures, are well conserved (11, 18, 27). The flavivirus capsid protein commonly contains two hydrophobic sequences in the center and the carboxyl terminus. The latter serves as a signal sequence of prM. The signal/anchor sequence is cleaved off by the viral protease NS2B/3, and this cleavage is required for the subsequent liberation of the amino terminus of prM by the host signal peptidase (26, 43, 49). The mature capsid protein may be associated with the ER membrane through the central hydrophobic region (23, 29). Because the capsid protein has RNA-binding ability via the basic amino acid clusters at its amino and carboxyl termini, it is believed to bind to the genomic RNA to form a nucleocapsid (20). Unlike other envelope viruses, the nucleocapsid structures are rarely found in cells infected with flaviviruses (48), although the nucleocapsid of TBEV can assemble *in vitro* (21). Therefore, viral assembly is thought to be a coordinated process between the membrane-associated capsid protein and two envelope glycoproteins, prM and E, in the ER membrane.

In conflict with their roles as structural proteins, the capsid proteins of some flaviviruses are localized not only in the cytoplasm but also in the nuclei of the infected cells (4, 28, 32, 44, 46–48). We previously reported that the JEV capsid protein

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