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## Multi-Step Regulation of Interferon Induction by Hepatitis C Virus

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**Abstract** Acute hepatitis C virus (HCV) infection evokes several distinct innate immune responses in host, but the virus usually propagates by circumventing these responses. Although a replication intermediate double-stranded RNA is produced in infected cells, type I interferon (IFN) induction and immediate cell death are largely blocked in infected cells. In vitro studies suggested that type I and III IFNs are mainly produced in HCV-infected hepatocytes if the MAVS pathway is functional, and dysfunction of this pathway may lead to cellular permissiveness to HCV replication and production. Cellular immunity, including natural killer cell activation and antigen-specific CD8 T-cell proliferation, occurs following innate immune activation in response to HCV, but is often ineffective for eradication of HCV. Constitutive dsRNA stimulation differs in output from type I IFN therapy, which has been an authentic therapy for patients with HCV. Host innate immune responses to HCV RNA/proteins may be associated with progressive hepatic fibrosis and carcinogenesis once persistent HCV infection is established in opposition to the IFN system. Hence, innate RNA sensing exerts pivotal functions against HCV genome replication and host pathogenesis

MAVS has been identified as the adaptor for RIG-I and MDA5 by four independent groups, and then also known as IPS-1, Cardif or VISA (Kawai and Akira 2009). TICAM-1 has been identified as the adaptor for TLR3 and TLR4 by two independent groups, and thus also described as TRIF (Oshiumi et al. 2003). In accordance with the HUGO Gene Nomenclature Committee-approved nomenclature, here we refer to these adaptor molecules as MAVS and TICAM-1, respectively.

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through modulation of the IFN system. Molecules participating in the RIG-I and Toll-like receptor 3 pathways are the main targets for HCV, disabling the anti-viral functions of these IFN-inducing molecules. We discuss the mechanisms that abolish type I and type III IFN production in HCV-infected cells, which may contribute to understanding the mechanism of virus persistence and resistance to the IFN therapy.

**Keywords** Hepatitis C virus · TLR3 · TICAM-1 (TRIF) · MAVS (IPS-1, Cardif, VISA) · Interferon-inducing pathway · Double-stranded RNA

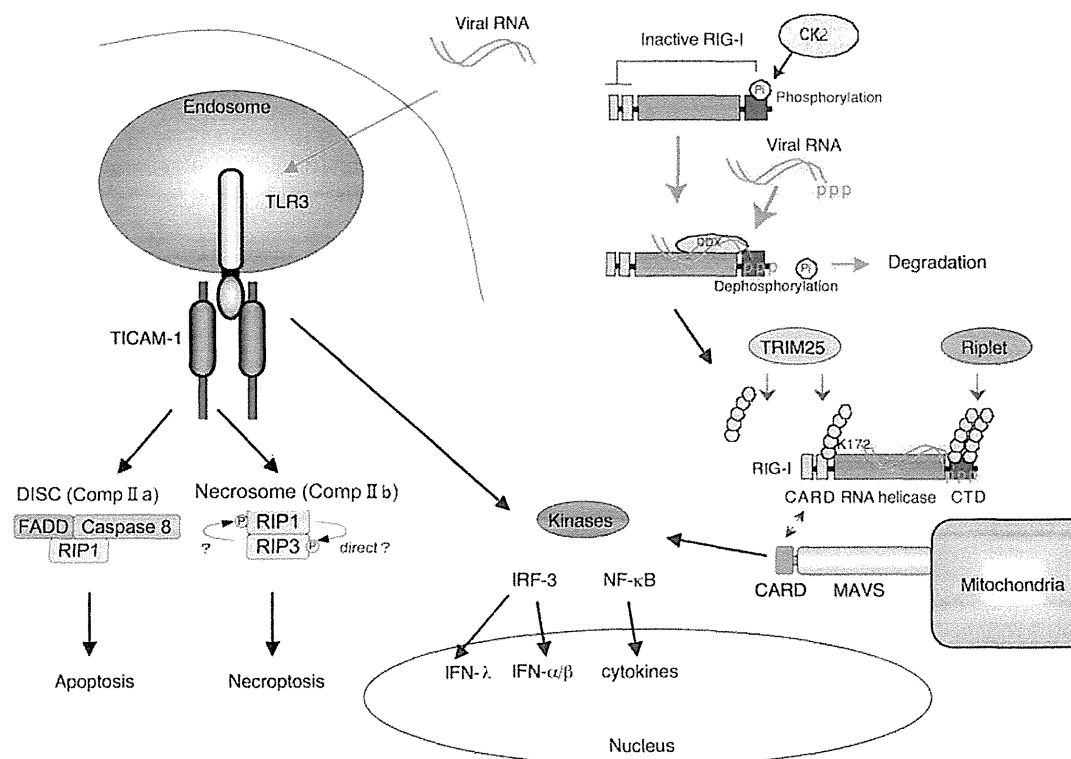
### Abbreviations

BMDC	Bone marrow-derived dendritic cells
CTL	Cytotoxic T lymphocytes
DAMP	Damage-associated molecular pattern
DC	Dendritic cell
dsRNA	Double-stranded RNA
IFN	Interferon
LD	Lipid droplet
MAM	Mitochondrial-associated endoplasmic reticulum membranes
MAVS	Mitochondrial antiviral signaling protein
Mφ	Macrophages
mRNA	Messenger RNA
NK	Natural killer
NS	Non-structural
RIG-I	Retinoic acid-inducible gene I
RIP	Receptor-interacting protein
STING	Stimulator of IFN genes
TICAM-1	Toll-IL-1-homology domain-containing adaptor molecule-1
TLR	Toll-like receptor
TNF	Tumor necrosis factor
TNFR1	TNF- $\alpha$ receptor 1

## Introduction

Hepatitis C virus (HCV) mainly infects human hepatocytes, and triggers induction of cytokines and type I (IFN- $\alpha/\beta$ ) and type III interferons (IFN- $\lambda$ ) (Fig. 1). Although cells expressing IFN receptors respond to the released IFN and amplify type I IFN production, IFN induction is not always robust in the infected cells due to the fact that HCV proteins inhibit host IFN-inducing pathways. IFN-stimulated genes (ISGs), such as IRF-7, MAP3K14, RIG-I, IRF-2, and IRF-1 are known to inhibit HCV replication (Schoggins et al. 2011). In particular, type III IFNs are more produced than IFN- $\alpha/\beta$  in HCV-infected hepatocytes via the mitochondrial antiviral signaling protein (MAVS) pathway to induce a set of ISGs (Thomas et al. 2012). Cytokines and chemokines are released from infected hepatocytes and myeloid cells in the liver. These mediators affect the formation of inflammatory environments and modify homeostasis of the host cell community, including the recruited bystander cells. Although these scenarios generally reflect the signs of patients with HCV, what

occurs following initial virus entry into host cells remains obscure at the molecular level. HCV genome RNA is internalized via fusion and a portion of 3'-polyU/UC or 5'-triphosphate-short stem RNA acts directly as a ligand for RIG-I (Saito et al. 2008). The HCV genome functions as a messenger (m)RNA for HCV polyprotein production and, at the same time, HCV genome replicates in the cytoplasm (Lindenbach et al. 2007). Double-stranded (ds)RNA accumulating in infected cells is the main pattern molecule (PAMP) and, once liberated, provokes activation of innate immunity in myeloid cells. How host cells sense HCV RNA or dsRNA during infection and replicon transfection has been investigated, and has led to an understanding of the importance of the cytoplasmic RNA recognition pathways (Fig. 1), particularly, the MAVS pathway (Cheng et al. 2006; Li et al. 2005a, b). The current concept is that MAVS signals the kinases, TANK-binding kinase 1 (TBK1) and I $\kappa$ B kinase epsilon (IKK $\epsilon$ ), to phosphorylate IFN regulatory factors (IRF)-3 and IRF-7, resulting in the induction of type I IFN (Kawai and Akira 2009). Likewise, IRF-3 and nuclear factor (NF)- $\kappa$ B appear to participate in



**Fig. 1** Cytoplasmic and endosomal sensors for virus dsRNA in HCV infection. Live signal (*right*) and cell death signal (*left*) in response to viral dsRNA are illustrated. The live signal occurs with stimulation of TLR3 or RIG-I-like receptors and essentially induces activation of NF- $\kappa$ B to support induction of pro-inflammatory cytokines and type I/type III interferons (IFNs) (*right*). This live signal may be amplified by the function of a small amount of IFN- $\beta$  that is required for the

maintenance of homeostasis of the cellular microenvironment. In contrast, death signal occurs with TLR3: caspase 8 is a key molecule for discriminating between apoptosis and necroptosis, and its functional absence sustains the RIP1/RIP3 necrosome signal leading to necroptosis (*left*). Viral dsRNA recognition by RIG-I is induced by RIG-I ubiquitination (*right*). The two modes of K63 polyubiquitination activate RIG-I

the induction of IFN- $\lambda$  (Ding et al. 2012). Because RIG-I-like receptors are IFN-inducible genes, only trace levels are found in resting cells or those in the early stage of virus entry. Thus, how RIG-I/MDA5 captures internalized or replicating virus RNA to evoke an antiviral response in such situations remains unexplained.

There are many reports suggesting that Toll-like receptor 3 (TLR3) participates in the response to HCV dsRNA (Eksioglu et al. 2011; Khvalevsky et al. 2007; Li et al. 2012) (Fig. 1). Most of the relevant studies have been performed with hepatoma cell lines due to the lack of proper systems for reproducing the HCV life cycle in culture as well as the in vivo animal model to examine the HCV immune responses. Cell death accompanied with a cytopathic effect is another phenotype of infected hepatocytes (Lim et al. 2012). Hepatocyte death is characterized as apoptosis, but the possible involvement of the pathway with receptor-interacting protein (RIP) kinases in infection-induced cell death has not been strictly ruled out (Fig. 1). Necrosis-like cell death (necroptosis) might cause a source of infectious virions and lead to the pathogenesis of HCV-associated liver damage. Ligands of the death receptor family, including FasL and TRAIL, are likely to associate with hepatocyte death induced by HCV infection (Bantel and Schulze-Osthoff 2003; Saeed et al. 2011; Zhu et al. 2007); however, what triggers the induction of the effector cells is still undetermined. Apart from these cell death family proteins, it is accepted that TLR3 is an activator of the RIP1 pathway (Meylan et al. 2004), which clearly participates in macrophage necroptosis (He et al. 2011). TLR3 is up-regulated in macrophages/dendritic cells (Mf/DC) in an IFN-dependent manner (Tanabe et al. 2003) and recognizes internalized virus dsRNA in the endosome of these phagocytes (Matsumoto et al. 2011). TLR3 has been characterized as an inducer of cellular immune effectors (Matsumoto et al. 2011; Seya and Matsumoto 2009). In accordance with the current dogma, natural killer (NK)-ligand up-regulation or cross-presentation of DCs that occurs with the internalization of dead cell-derived dsRNA may bridge the missing link between HCV dsRNA and TLR3-derived DC maturation (Ebihara et al. 2008).

Dead cells are a source of damage-associated molecular pattern (DAMP) (Kono and Rock 2008). DAMP refers to an intracellular molecule with inflammation-inducing capacities when it is released out of the cell. DAMP does not belong to the cytokine family, but resembles PAMP in its functional properties toward activation of myeloid DCs and macrophages (Kono and Rock 2008). Its function may be associated with physiological responses related to HCV immune response in a broad sense, including regeneration and tumorigenesis. Recently, necrotic or necroptotic cell death has been closely connected with innate immune responses involving pattern sensing (Kono and Rock 2008; Nace et al. 2012).

**Table 1** Sensors for nucleic acid PAMPs and DAMPs

PAMP/DAMP	Receptors
Microbial nucleic acids (PAMP)	
Cytosolic long dsRNA	MDA5
Cytosolic 5'-PPP-RNA	RIG-I
Endosomal >140 bp dsRNA	TLR3
Nonmethylated CpG DNA	TLR9
Cytosolic dsDNA	DNA sensors <sup>a</sup>
Self-molecular patterns (DAMP)	
HMGB1	RAGE, TLR2/4
Uric acid	CD14, TLR2/4
HSPs	CD14, TLR2/4 <sup>b</sup>
S100 proteins	RAGE
Self-nucleic acids (DAMP)	
Self-DNA	DNA sensors <sup>a</sup>
Self-mRNA	TLR3

*HMGB1* High-mobility group box 1, *HSPs* heat shock proteins

<sup>a</sup> See Table 2

<sup>b</sup> Scavenger receptors, CD91, etc.

How HCV patterns are sensed and linked to the cellular immunity will be an intriguing issue. DAMP contains a number of cytosolic or nucleic molecules, as in Table 1, and in particular nucleic acids from infected cells. Thus, DAMP and dsRNA of viral origin are extrinsic patterns for sensors to evoke unique features of inflammation during HCV infection.

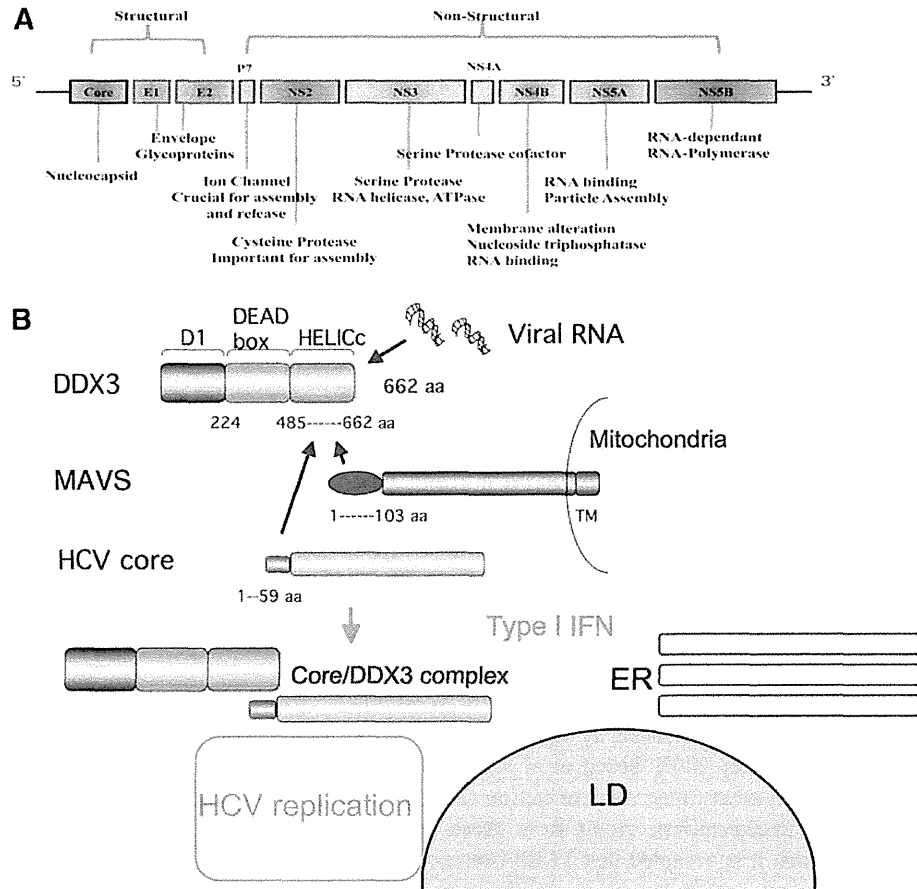
Herein, we discuss the interrelationship between these recent findings on innate immunity and HCV infection.

### Blocking IFN Induction by HCV Proteins

#### Proteolytic Control of the IFN-Inducing Pathways by NS3/4A

HCV genome RNA serves as a single mRNA that encodes ~3,000 amino acids, consisting of 10 virus proteins (Lindenbach et al. 2007). Structural proteins (core, E1, and E2) are situated at the N-terminal region of this polyprotein (Fig. 2a). The HCV polyprotein is first cleaved between 191A and 192Y by signal peptidase to separate the core protein from E1 protein and the core is retained on the endoplasmic reticulum (ER) membrane (McLauchlan et al. 2002). Then, signal peptide peptidase scissions out the core protein by cleavage at 177F and 178L from the ER membrane (Okamoto et al. 2004). E1 and E2 are also released from the remaining structural protein complex by the proteolytic function of signal peptidase (McLauchlan et al. 2002). Non-structural proteins of HCV are fragmented into functional units by NS2 and NS3/4A proteases. Hence, the release of the structural proteins precedes the mature

**Fig. 2** Two different functions of HCV core protein. HCV genome and the functions of each HCV protein. HCV core is first clipped out from the polyprotein of HCV, and later NS proteins are generated (a). HCV core protein retracts DDX3 from the MAVS–DDX3 signal complex on the mitochondria (b). DDX3 usually couples with MAVS on mitochondria and directly binds overwhelmed virus dsRNA in virus-infected cells. When the HCV core protein is produced, DDX3 binds core protein with high affinity and moves from the mitochondria to the HCV replication apparatus, where the core is recruited. The HCV replication apparatus is situated near the lipid droplet (LD) in ER. DDX3 supports HCV replication in the apparatus



processing of non-structural (NS) proteins during the HCV polyprotein processing (Lindenbach et al. 2007). Notably, two structural proteins, core and E2, exhibit regulatory functions against type I IFN induction (Florentin et al. 2012; Mulhern and Bowie 2010).

NS3/4A protease is reported to be crucial, not only for the liberation of HCV NS proteins, but also for the regulation of host anti-viral reactions by proteolytic inactivation of host cytosolic proteins, which also interfere with homeostasis of live cells. It has been reported that NS3/4A proteolytically degrades MAVS (Cheng et al. 2006; Li et al. 2005b; Loo et al. 2006). In addition, NS4B protein has been reported to target STING to repress RIG-I-mediated type I IFN induction in hepatocytes (Nitta et al. 2012). Preceding the generation of these NS proteins, HCV core (Oshiumi et al. 2010a) and E2 proteins (Florentin et al. 2012) can suppress RIG-I-mediated type I IFN production in hepatocytes and plasmacytoid DC, respectively. In particular, the generation of core protein and NS3/4A are closely associated with suppression of the HCV-mediated host IFN biological response and the promotion of HCV replication. Since core protein is produced prior to NS3/4A in HCV-infected cells, many other functions of the core are

expressed just before the proteolytic processing of HCV NS proteins within the cells.

NS3/4A cleaves MAVS (Cheng et al. 2006; Li et al. 2005b; Oshiumi et al. 2010a) and TICAM-1 (Li et al. 2005a). Hence, NS3/4A proteolytically controls at least two adaptor proteins as its substrates. In addition, Riplet is reduced in response to HCV replication (Oshiumi et al. 2010c). Whether or not Riplet is a substrate for NS3/4A is still under investigation.

#### MAVS Inactivation by NS3/4A

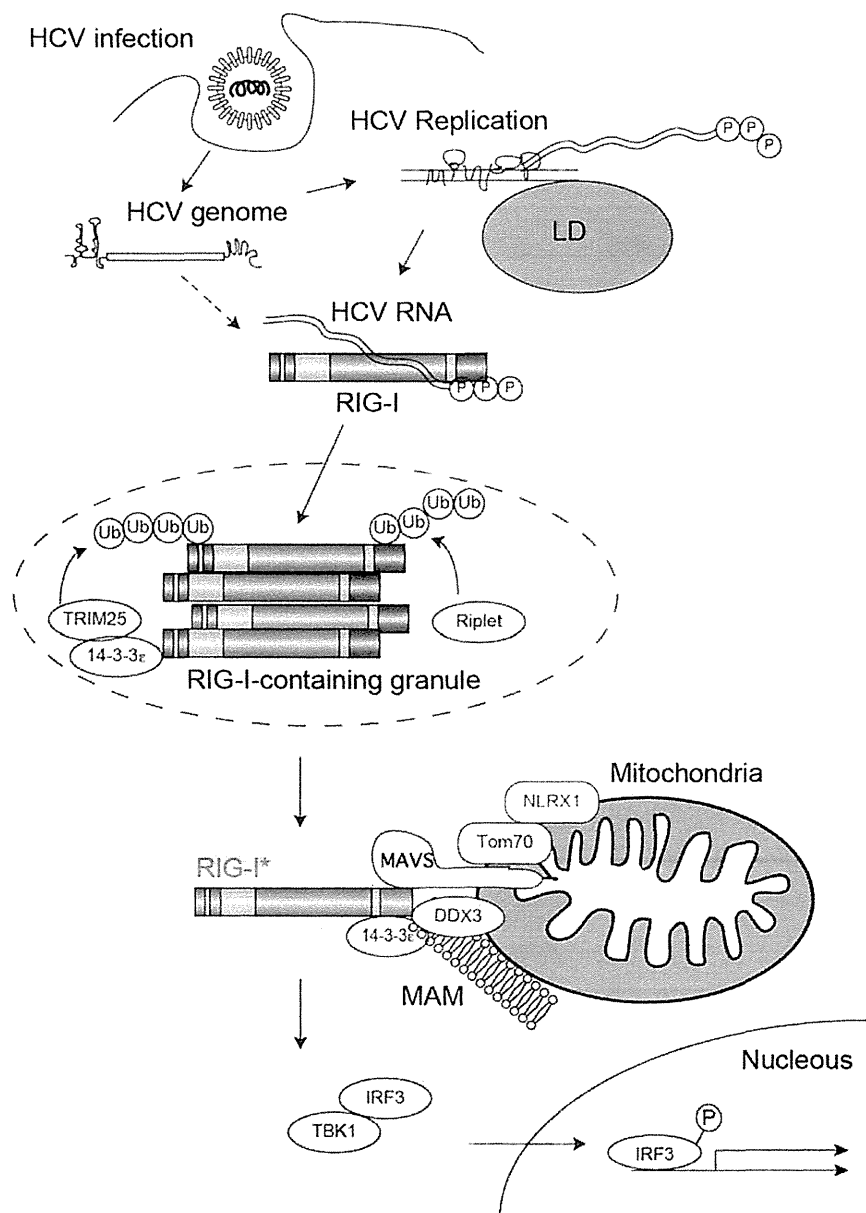
The current assumption is that the RIG-I family proteins, RIG-I and MDA5, sense viral RNA to induce type I IFN and pro-inflammatory cytokines, which in turn suppress viral infection. RIG-I and MDA5 possess the N-terminal caspase activation and recruitment domain (CARD), the central DExD/H-box helicase domain, and the C-terminal RNA-binding domain (CTD) (Fig. 1). According to crystal structure analysis, the basic region of CTD binds virus dsRNA irrespective of the presence of 5'-triphosphate (Yoneyama et al. 2004), while the CARD domain participates in interaction with the adaptor.



RIG-I recognizes HCV RNA, as well as its replication intermediate, dsRNA (Saito et al. 2008). Although MDA5 recognizes long dsRNA patterns, the role of MDA5 in HCV RNA recognition is unknown. MAVS is the key adaptor for RIG-I/MDA5-mediated IFN induction in HCV infection, although it is localized in the mitochondrial outer membrane apart from intact RIG-I molecules (Seth et al. 2005). RIG-I is not quantitatively sufficient at the protein level to capture the abundant dsRNA replicating in infected cells during the early stage; other molecules have to accept the overwhelmed dsRNA in other cytoplasmic regions (Oshiumi et al. 2010b). RIG-I is initially involved in a

molecular complex (RIG-I granule), which contains many other molecules that make up a nucleocapture complex. E3 ubiquitin ligases are involved in the RIG-I granule. Ubiquitin ligases, TRIM25 (Gack et al. 2007) and Riplet (Oshiumi et al. 2009), are also situated in the RIG-I granule together with RIG-I and confer RNA-binding capacity on RIG-I through RIG-I ubiquitination (Fig. 1). TRIM25 ubiquitinates N-terminal lysines of RIG-I (Gack et al. 2007), while Riplet ubiquitinates C-terminal lysines of RIG-I (Oshiumi et al. 2009), either or both of these molecules enable RIG-I to interact with MAVS and confer mobility on mitochondria (Fig. 3). A recent report

**Fig. 3** Translocation of RIG-I from the cytoplasm to the mitochondria. RIG-I is diffusely distributed in the cytoplasm. When minute quantities of dsRNA enter the cytoplasm (dashed line), the RIG-I granule is formed with many other molecules to sense dsRNA. Once RIG-I molecules are polyubiquitinated, they form a complex with dsRNA and becomes mobile (RIG-I\*). RIG-I\* is recruited to the mitochondria to couple with MAVS. There are many other molecules associated with mitochondrial signaling. Because DDX3 captures overwhelmed dsRNA, the RIG-I–DDX3–MAVS complex allows robust IFN production in conjunction with dsRNA/DDX3. Whether DDX3 participates in IFN- $\lambda$  induction remains undetermined



speculated that after RIG-I is up-regulated and ubiquitinated in the RIG-I granule, the 14-3-3 $\epsilon$  is coupled with newly ubiquitinated RIG-I (Liu et al. 2012). Then, RIG-I moves from the granule to the mitochondrial membrane, a distinct membrane compartment linked to the ER, which is referred to as mitochondrial-associated endoplasmic reticulum membranes (MAM) (Horner et al. 2011). MAM accumulates MAVS and may coordinate MAVS signaling of innate immunity from peroxisomes (Dixit et al. 2010) and mitochondria (Seth et al. 2005), while MAVS localized to MAM serves as a molecular platform for the IFN-inducing signal. MAVS is constitutively complexed with DDX3, which serves as an acceptor of dsRNA in resting (RIG-I-insufficient) cells (Oshiumi et al. 2010b). If this is the case, the location for RIG-I ubiquitination (i.e., RIG-I granule) may differ from the site at which RIG-I interacts with the MAVS–DDX3 complex for signaling. Validating this issue will be of great interest in understanding initial viral RNA recognition.

Our previous data suggested that three forms of MAVS are detected in HCV-replicating hepatocyte lines by imaging analysis, as follows: intact MAVS, sequestered MAVS, and proteolytically liberated MAVS (Oshiumi et al. 2010a). These forms of MAVS simultaneously exist in hepatocytes expressing the HCV replicon or those infected with HCV. The MAVS proteolytically released from mitochondria appear to have decreased ability to activate IRF-3. MAVS is also diminished in some HCV-infected cells to lose its IFN-inducing function (Oshiumi et al. 2010a), suggesting that NS3/4A is a protease that determines the inactivation state of MAVS in HCV-replicating hepatocytes. A recent report suggested that Riplet is depleted during HCV replication (Oshiumi et al. 2010c),

indicating the possibility that participation of the expressed NS3/4A protease in degrading other molecules upstream of MAVS is more important for IFN regulation than clipping out of MAVS in infected cells (Fig. 1). Similarly, other factors independent of proteolytic control may be critical for dsRNA-mediated IFN inducibility, as demonstrated by Cheng et al. (2006).

#### Blocking of the DDX3-Augmented IFN Production by Core Protein

Three reports have independently showed that DEAD/H Box 3 (DDX3, also known as DBX) acts as a positive regulator for MAVS-mediated type I IFN induction (Table 2; Fig. 2b). Elevation of MAVS pathway-mediated type I IFN production by DDX3 is modally different in these three reports (Mulhern and Bowie 2010). Like RIG-I and MDA5, DDX3 is a member of the DExD/H-box family of RNA helicases and is ubiquitously expressed in a variety of cells (Kim et al. 2001). The DExD/H motif of the members in this family of proteins is predictive of a role in RNA-binding and RNA-dependent cellular processing (Schroder 2009). Schroder et al. (2008) showed that the vaccinia virus protein K7 binds DDX3 and inhibits pattern-recognition receptors-induced IFN- $\beta$  promoter activation. They suggested that DDX3 interacts with IKK $\epsilon$  to enhance IRF-3 activation, while K7 counters DDX3 activity of MAVS-mediated IFN- $\beta$  induction. This IFN-enhancing function of DDX3 in IRF-3 activation is located at the N-terminus of DDX3, which is the same region of the protein targeted by K7 for IRF-3 inhibition. Structure analysis of K7 complexed with a peptide from the N-terminus of DDX3 (Oda et al. 2009) has confirmed this finding.

**Table 2** Nucleic acid sensors related to IFN induction in innate immunity

Pattern-recognition receptors	Adaptors	Agonists (references)	Origin
MDA5	MAVS	Cytosolic long dsRNA (Yoneyama et al. 2008)	RNA viruses
RIG-I	MAVS	Cytosolic 5'-PPP-RNA (Yoneyama et al. 2008)	RNA viruses
NOD2	MAVS	Cytosolic ssRNA (Morosky et al. 2011)	RNA viruses
TLR3	TICAM-1	Endosomal >140 bp dsRNA viruses, host (Jelinek et al. 2011)	DNA/RNA viruses
TLR7/8	MyD88	Endosomal ssRNA (Uematsu and Akira 2007)	RNA viruses, bacteria
TLR9	MyD88	Nonmethylated CpG DNA (Uematsu and Akira 2007)	RNA viruses, bacteria
DDX3	MAVS	dsRNA, ssRNA (Oshiumi et al. 2013; this review)	Viruses, host
DDX1/21, DHX36	TICAM-1	dsRNA (Rathinam and Fitzgerald 2011)	Viruses?
DDX60	MAVS	dsRNA, ssRNA, dsDNA (Oshiumi et al. 2013; this review)	Viruses, host
DHX9/DHX36 MyD88	STING	dsDNA (Rathinam and Fitzgerald 2011)	DNA viruses
DDX41	TBK1	dsDNA (Rathinam and Fitzgerald 2011)	DNA viruses
DAI (ZBP1)	STING	dsDNA (Takaoka and Taniguchi 2008)	DNA viruses
IFI16	$\beta$ -Catenin	dsDNA (Rathinam and Fitzgerald 2011)	DNA viruses
LRRFIP1		dsDNA (Rathinam and Fitzgerald 2011)	DNA viruses

ssRNA single-stranded RNA

The second study indicated that DDX3 constitutively interacts with MAVS via the C-terminal region of DDX3 (Oshiumi et al. 2010b). The binding of DDX3 to MAVS is constitutive and not through the N-terminus, in contrast to the case of the virus-dependent interaction between DDX3 and IKK $\epsilon$  (Schroder et al. 2008). RIG-I-induced IFN- $\beta$  promoter reporter gene activity is inhibited by DDX3 small interfering RNA and enhanced by overexpression of DDX3 (Oshiumi et al. 2010b). Thus, DDX3 synergistically activates the IFN- $\beta$  promoter together with MAVS. The C- and N-terminal regions of the DDX3 regulate MAVS-mediated IFN induction (Hogbom et al. 2007) (Fig. 1).

In contrast, Soulat et al. (2008) demonstrated a positive role for DDX3 in IFN- $\beta$  promoter induction in another distinct manner. Specifically, DDX3 is shown to be a kinase substrate for TBK1 to synergistically enhance IFN- $\beta$  promoter activation by TBK1. Furthermore, they demonstrated that DDX3 is recruited to the IFN- $\beta$  promoter via its N-terminal region (Soulat et al. 2008). Together, these findings show that DDX3 is a positive regulator targeting the multiple sites of the RLR-induced IFN pathway. A role for DDX3 in cell cycle control and apoptosis has also been proposed in response to dsRNA (Schroder et al. 2008).

DDX3 facilitates viral replication in a variety of viruses, including HCV. The N-terminus of HCV core protein binds the C-terminus of DDX3 (Owsianka and Patel 1999). According to a recent finding, the HCV core protein participates in the suppression of DDX3-augmented MAVS signaling for IFN- $\beta$  induction (Fig. 2b), which may also be related to the function of DDX3 described in the second study mentioned before (Oshiumi et al. 2010b). Unlike the DEX/H-box helicases, such as RIG-I and MDA5, DDX3 is constitutively expressed and co-localized with MAVS around mitochondria (Table 2). However, HCV core protein interferes with DDX3 function to enhance MAVS signaling by coupling with DDX3 to dissociate it from MAVS in the mitochondria. In hepatocytes with the HCV replicon, DDX3/MAVS-enhanced IFN- $\beta$ -induction is largely abrogated, even when DDX3 is co-expressed. Whether DDX3 enhances IFN- $\lambda$  induction like RIG-I remain untested. DDX3 is spotted with minimal merging with MAVS in confocal analysis, and partly assembles in the HCV core protein located near the lipid droplet (LD) in replicon-positive hepatocytes, although in some cells MAVS is diminished or disseminated apart from mitochondria. Thus, HCV core retracts DDX3 from MAM, where RIG-I moves from the RIG-I granule to assemble together with MAVS (Figs. 2b, 3).

Our consensus is that the binding of HCV core protein to DDX3 and suppressing DDX3–MAVS complex formation are crucial for inhibition of the MAVS pathway. However, multiple functions of DDX3 may be reflected in other functional aspects of core protein; specifically, the DDX3–

core interaction is required for HCV replication (Ariumi et al. 2007). Although DDX3 promotes efficient HCV infection by accelerating HCV RNA replication, the processes appear independent of its interaction with the viral core protein (Angus et al. 2010). In addition, the association between DDX3 and core protein implicates DDX3 in HCV-related hepatocellular carcinoma progression (Chang et al. 2006). Based on its core protein association and MAVS-regulatory properties, DDX3 appears to be switched by the core protein from an HCV-suppressing (i.e., IFN-inducing) mode to an HCV replication-supporting mode (Fig. 2b). The results enable us to conclude that HCV infection is promoted by modulating the dual function of DDX3.

Evidence is accumulating that HCV assesses many steps in the IFN-inducing pathway throughout the early and late infection stages, and suppresses IFN production by multiple means. Disruption of MAVS function by NS3/4A and core protein may be crucial in HCV-infected Huh7.5 cells, even though the cells harbor dysfunctional RIG-I (Binder et al. 2007). Type I IFN suppresses tumor progression by causing expression of p53 and other tumor-suppressing agents (Takaoka et al. 2005). E2 and NS4B may affect tumor progression by controlling type III IFN induction. These unique features of the HCV proteins require further confirmation and should be in the focus of investigation regarding HCV persistence, chronic infection, and progression to cirrhosis and carcinoma.

#### Inactivation of the TICAM-1 Pathway by NS3/4A

TICAM-1 pathway has been associated with chemokine production, apoptosis, necroptosis, and IL-12p40 production in hepatoma cell lines expressing TLR3 (Li et al. 2012); however, such immune responses are predominantly absent in primary cultured cells. This might be explained by the TLR3 signaling that is likely to be shut off in most normal hepatocytes, but executed in hepatocytes of the infectious liver during chronic states of HCV infection or exposure to dsRNA stimulation. Despite the constitutive expression of the adaptor molecule TICAM-1 in human hepatocytes, only trace amount of TLR3 is being expressed in comparison to RIG-I that is commonly expressed. This gives us an insight of the role played by other cytoplasmic dsRNA sensors such as DDX1/DDX21/DHX36 (Table 2), in the activation of TICAM-1 pathway (Zhang et al. 2011). It remains unknown whether these cytoplasmic dsRNA sensors participate in IFN- $\lambda$  induction.

Although there are positive findings supporting the importance of TLR3 in the pathogenesis of HCV infection (Eksioglu et al. 2011; Khvalevsky et al. 2007; Li et al. 2012), the expression level of TLR3 is still a contentious issue. TLR3 protein is undetectable by immunostaining with monoclonal antibody (TLR3.7) against huTLR3 in

uninfected human hepatocytes (Nakamura et al. 2008) or Huh-7 hepatoma cells that are commonly used for propagation of HCV (Wang et al. 2009). Only a few reports have shown evidence that TLR3 protein is weakly detected in resting primary cultured hepatocytes (Wang et al. 2009). On the other hand, several reports have suggested that the TLR3 at the messenger level was observed in cultured hepatocytes and hepatoma cell lines by real-time polymerase chain reaction (Khvalevsky et al. 2007). Since TLR3 expression is partly regulated by p53, mutated p53 in Huh-7 cells as well as other hepatocellular carcinoma cell lines may attribute to the specific lacking of the TLR3 expression. In addition, Tanabe et al. (2003) demonstrated that the lack of TLR3 expression in Huh-7 cells may be due to other transcriptional regulations.

TLR3 expression appears to be up-regulated in cultured hepatocytes in response to polyI:C (Wang et al. 2009). Similarly, TLR3 is up-regulated in hepatocytes of patients with chronic HCV infection or polyI:C-injected mice (McCartney et al. 2009; Nakamura et al. 2008). These results lead to the assumption that TLR3 can be up-regulated in hepatocytes in an infectious milieu in response to the produced dsRNA or liberated type I IFN by HCV-infected hepatocytes via the RIG-I-mediated IFN-inducing pathway. A similar mechanism of secondary induction of the TLR3 expression by type I IFN may as well occur in hepatoma cells. Thus, HCV infection or malignant transformation allows hepatocytes to turn TLR3 positive, enabling the activation of the TICAM-1 pathway by external virus dsRNA. This would explain the finding that TLR3 is highly expressed in biliary epithelial cells and certain hepatoma cell lines (Harada et al. 2007; Nakamura et al. 2008). Li et al. (2012) showed that TLR3 senses HCV infection and induces ISG expression when TLR3 is over-expressed artificially in the Huh7.5 cells that are deficient in RIG-I signaling. They demonstrated that HCV replication is partially restricted when the cells are infected at a low multiplicity. However, such protective effect is dismissive when the infection is overwhelmed at high multiplicity partly due to the limitation of the TLR3.

TLR3 has a distinct feature from RIG-I as TLR3 can potentially sense viral dsRNA released into the extracellular environment by other cells. Considering the fact that NS3/4A protease that interferes with the host anti-viral reactions is only expressed within infected cells, TLR3-mediated immune responses might be triggered in the uninfected hepatocytes or other cell types. On top of that, it has been reported that TICAM-1 is also a substrate for NS3/4A protease in hepatoma cell lines (Li et al. 2005a). Ferreon et al. (2005), has confirmed this in the corollary biochemical studies. TICAM-1 and its signal pathway are intact within the cells around infected hepatocytes

(Shimoda et al. 2011). This may contribute to the IFN responses observed in some patients.

TLR3 is highly expressed in biliary epithelial cells where biliary atresia occurs in response to the interaction between TLR3-stimulated monocytes and liver NK cells (Harada et al. 2007; Shimoda et al. 2008, 2011). However, it remains intriguing whether the up-regulated TRAIL or FasL in NK cells resulted from the IFN-signaling (Estornes et al. 2012) are responsible for the induction of cell death in hepatocytes. Nevertheless, TICAM-1-mediated cell death in some HCV-infected hepatocytes is also likely to occur via autophagy or *trans*-acting of dsRNA generated by HCV replication.

### DAMP and dsRNA in HCV Pathology

Live or death signals are usually raised by viral dsRNA in virus-infected cells. Type I/type III IFNs and proinflammatory cytokines (IL-6, IL-12, TNF- $\alpha$  etc.) are liberated through IRF-3/7 and NF- $\kappa$ B activation as the output from virus-infected cells that are alive. In contrast, DAMP and cytoplasmic cytokines converted to active forms by caspase 1 eventually result from activation of inflammasome and often links to cell death events (Yeretssian 2012). TLR, Nod-like receptor and other cytosolic nucleic acid sensors are closely associated with PAMP/DAMP recognition (Table 2), therefore inflammation states are fundamentally modified by these factors (Bortolucci and Medzhitov 2010).

Replication of virus RNA allows hepatocytes to induce type III IFN, IL-7 and chemokines (Apolinario et al. 2005; Zeremski et al. 2007). HCV also regulates production of chemokines (Sillanpaa et al. 2008) and type III IFNs (Thomas et al. 2012) by infected cells. Polymorphisms around the IL-28B gene have been associated with clearance of HCV in human, indicating a role for type III IFNs rather than type I in HCV infection (Thomas et al. 2012), although little is known about the function of type III IFNs in intrinsic antiviral responses. IFNs and IL-7 released from HCV-infected hepatocytes possibly act on myeloid cells and lymphocytes expressing their receptors to induce IFN- $\gamma$  (Sawa et al. 2009). Once type I/type III IFN and IFN- $\gamma$  are systemically distributed, synergistic function of these IFNs allows the systemic cells to produce ISGs including CXCL10 (IP-10) and CCL5 (RANTES) (Larrubia et al. 2008; Zeremski et al. 2007). In addition, dsRNA-induced IL-7 forms a positive amplifying loop with T-cell-derived IFN- $\gamma$  to promote macrophage recruitment and CXCR3 ligand (CXCL10) expression by these macrophages (Andersson et al. 2009). Since CXCR3 is mainly expressed on activated T and NK cells, these cytotoxic effectors gather around the inflammatory nest as well as secondary affected organs. HCV-related extrahepatic

disorders are likely to occur in conjunction with ectopic T-cell immune response (Antonelli et al. 2008, 2009). In addition, these immunological aberrances may be modulated by viral factors. In fact, in mouse models, NS5A expression impairs clearance of other viruses from the liver due to the inhibition of IFN- $\gamma$  production (Kanda et al. 2009). By any means, induction of IFN- $\gamma$  in concert with activation of cellular immunity is a major array for live signal in HCV infection.

Necrosis-like cell death occurs contrarily in a cell type-specific manner as a result of death signal. Tumor necrosis factor (TNF)- $\alpha$  and its receptor, TNFR1, are implicated in this process. The coupling of RIP1 with RIP3, termed a necrosome, is responsible for the switching of apoptosis to necroptosis (Cho et al. 2009; He et al. 2009). Caspase 8 acts as a key protease for blocking the formation of the necrosome; the RIP1/RIP3 complex can assemble only in the absence of functional caspase 8. It has been reported that virus dsRNA often induces apoptosis in infected cells, which is known as cytopathic effect (Lim et al. 2012). TICAM-1 and RIP1 may be involved in the virus-derived apoptosis. Yet, possible involvement of RIG-I/MDA5 in cell death cannot be ruled out in some cases of viral infection (Eksioglu et al. 2011). In HCV-infected hepatocytes, how the TLR3/TICAM-1 pathway is involved in necroptotic inflammation is the next issue to be elucidated with respect to HCV pathogenesis (Fig. 1). HCV dsRNA and DAMP can be liberated from infectious hepatocytes, as well as virus particles. TNF- $\alpha$  and IL-6 are the pro-inflammatory cytokines released during HCV infection. Hence, a characteristic feature of the HCV-infected hepatocytes is that DAMP is released together with viral dsRNA from necroptotic HCV-infected cells to the surrounded environment. These factors stimulate nucleic acid sensors of myeloid DC/Mf in the draining region (Table 2). We expect that necroptosis will be of enormous interest in HCV infection following smoldering inflammation. Because each virus species harbors distinct strategies for escaping the innate dsRNA-sensing system, the physiological role of TLR3-mediated necroptosis should be analyzed in a HCV-specific fashion.

### Cellular Immunity Induced by HCV-Infected Cell Debris

Once DC/Mf responds to these unusual innate stimulators, DAMP and dsRNA, cellular immunity is provoked against HCV Ag with irregular modification by these immune enhancers during HCV infection. NK cells and cytotoxic T lymphocytes (CTL) are known to be driven in myeloid DCs by stimulation with dsRNA, and in fact are the main effectors against HCV-infected hepatocytes based on several different systems (Ebihara et al. 2008; Saeed et al.

2011; Zhu et al. 2007). DCs express NK-activating ligands by recognizing dsRNA to activate NK cells (Ebihara et al. 2007), and cell damage is reported to play a role in the regulation of NK-activating ligands (Wen et al. 2008), thereby dsRNA and DAMP are involved in the elimination of HCV-infected cells. Subsequently, DCs cross-prime CD8 CTLs through incorporation of dsRNA and HCV Ag-mounted cell debris (Jin et al. 2007). FasL and TRAIL are major effectors for the ligands of death receptors. HCV-infected cells will be eliminated if the cells express high levels of MHC class I with HCV antigen.

Our laboratory has reported that a dsRNA analog (polyI:C) has strong ability to activate NK cells in vivo (Akazawa et al. 2007; Matsumoto and Seya 2008). Two main routes for NK cell activation have been reported. First, DCs secrete several cytokines, such as IL-12, IL-18, IL-15 and IFN- $\alpha/\beta$  in response to dsRNA, and these mediators act on NK cells (Lucas et al. 2007; Matsumoto et al. 2011). Second, DCs express NK-activating ligands on their cell surface and the ligands make a balance shift to activation of NK cells through cell–cell contact (Ebihara et al. 2010). In mouse studies, IL-15 and cell-surface NK-activating ligands are crucial in polyI:C-mediated NK cell activation (Ebihara et al. 2010; Lucas et al. 2007). A main NK-activating ligand induced by polyI:C is IRF-3-inducing NK-activating molecule (INAM) (Ebihara et al. 2010). In a human system with bone marrow-derived DCs (BMDC) and HCV-infected debris (a source of dsRNA), NK cells are activated by BMDC via the TLR3-TICAM-1 pathway in BMDC (Ebihara et al. 2008). Thus, INAM may be a factor that participates in HCV-derived NK activation.

However, how dsRNA and DAMP modify the maturation of DC in an infectious milieu to induce CD4 and CD8 T cells is largely unknown because the functional properties of DAMP generated in HCV-infected hepatocytes have not been well documented (Azuma et al. 2012). Once antigens are presented on MHC class II in DCs upon internalization of infectious debris, CD4 T cells (Longhi et al. 2009), including Th1, Th2, Th9, Th17, and Tregs, are driven in a sophisticated manner. In this context, DAMP and dsRNA could act as the second signal of TLRs triggering DCs to induce cross-presentation, which leads to mounting Ag on MHC class I and subsequently induce the proliferation of CD8 T cells (CTL) (Caskey et al. 2011). Furthermore, the so-called innate lymphocytes may respond to intrinsic stimuli in an Ag-independent fashion. Thus, the function of nucleic acid sensors for DAMP and dsRNA in the presentation of exogenous antigen by DCs is an issue to be tackled (Caskey et al. 2011). Cross-presentation is enhanced by molecules, such as type I IFN and CD40, and by immune cells, including CD4 T cells, NK cells, and NKT cells (Matsumoto and Seya 2008). Yet, the role of type III IFN in T-cell cross-priming and innate lymphocyte activation are

yet unknown. TLR3/TICAM-1 is a main pathway for inducing cross-presentation in response to dsRNA in DCs (Azuma et al. 2012). PolyI:C or virus dsRNA is an example of the TLR3 ligand, and their cross-presentation-inducing activity was first described by Schulz et al. (2005). The effective adjuvancy of polyI:C has been subsequently reported by Steinman group (Caskey et al. 2011; Longhi et al. 2009); however, no report has been definitively determined which DAMPs participate in cross-presentation and possess latent cross-priming (CTL-inducing) ability.

Why HCV circumvents the host immune system of both innate and acquired arms of the immune system remains an ambiguous question. Hepatocytes stand with unique properties with lipid droplet (LD) and the bile secretion system, where hepatocytes secrete bile into canaliculi, which flows into choledochus. HCV and hepatitis B virus induce smoldering inflammation, which is believed to be a nest of carcinogenesis. These viruses have no common properties in their viral-side factors, but the host factors including hepatocytes are common bases for triggering inflammation. Thus, the host factors are undoubtedly critical in inducing infection-driven inflammation and perhaps initiation of tumor progression (Seya et al. 2012). We speculate that persistent HCV infection, followed by inflammation, is caused by the immune aberration involved in HCV infections. The main factors in the innate arm of immunity are DAMP and dsRNA, each of which is reported to associate with smoldering inflammation. However, it is unknown what occurs in the liver if this combined stimulation is constitutively exerted in HCV-infected cells and myeloid cells in the liver. Examining the function of dsRNA and DAMP on chronic HCV infection with increasing studies in innate immunity, inflammation, and cell death, will help us extending our knowledge on vaccine and adjuvants against HCV infection and tumorigenesis. Further molecular analysis will provide a hint for therapeutic strategies for patients who do not respond to IFN therapy.

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# Cleaved/Associated TLR3 Represents the Primary Form of the Signaling Receptor

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TLR3 belongs to the family of intracellular TLRs that recognize nucleic acids. Endolysosomal localization and cleavage of intracellular TLRs play pivotal roles in signaling and represent fail-safe mechanisms to prevent self-nucleic acid recognition. Indeed, cleavage by cathepsins is required for native TLR3 to signal in response to dsRNA. Using novel Abs generated against TLR3, we show that the conserved loop exposed in LRR12 is the single cleavage site that lies between the two dsRNA binding sites required for TLR3 dimerization and signaling. Accordingly, we found that the cleavage does not dissociate the C- and N-terminal fragments, but it generates a very stable “cleaved/associated” TLR3 present in endolysosomes that recognizes dsRNA and signals. Moreover, comparison of wild-type, noncleavable, and C-terminal-only mutants of TLR3 demonstrates that efficient signaling requires cleavage of the LRR12 loop but not dissociation of the fragments. Thus, the proteolytic cleavage of TLR3 appears to fulfill function(s) other than separating the two fragments to generate a functional receptor. *The Journal of Immunology*, 2013, 190: 764–773.

**T**oll-like receptors belong to a family of pattern recognition receptors that sense the presence of pathogens and trigger a protective innate immune response (1). These germline-encoded type I integral membrane glycoproteins bind their ligands through their extracellular domain (ECD), which is composed of 19–25 leucine-rich repeats (LRRs) (2). In contrast with other members of the family that primarily recognize molecular patterns specific for nonself invaders, TLR3, TLR7, and TLR9 recognize nucleic acids originating from microbes, as well as from the host. Several fail-safe

mechanisms prevent self-polynucleotide recognition and subsequent autoimmune disorders (3). Ligands must be recognized by cell surface receptor(s) (4) that mediate their internalization before encountering the corresponding TLR exclusively in the acidic endolysosomal compartment from which signal transduction can be initiated (5). Delivery of intracellular TLRs to the endocytic compartments is also tightly regulated by the chaperone Unc93b1 (6, 7). Finally, processing by pH-dependent lysosomal proteases is an additional checkpoint for controlling TLR9 activation (8–10).

Although several studies on intracellular TLRs have been based on TLR9 trafficking and processing, less is known about TLR3. TLR3 appears to be dedicated to the recognition of dsRNA (11), and it plays a central role in the defense against HSV-1 infection in the CNS in humans (12–15). Although endogenous mRNA can activate TLR3 in vitro (16), its involvement in the autoimmune response has not been demonstrated. It was shown that TLR3 dimerization is needed for dsRNA binding and signaling (17). Moreover, analysis of the crystal structure (18, 19) and mutagenesis (18, 20, 21) of TLR3 ECD revealed that dsRNA binding requires interaction of the negatively charged ribose backbone of dsRNA with residues of TLR3 dimers located in LRR1 and LRR3, as well as with a second region formed by LRR19–LRR21 that becomes positively charged in the mildly acidified endolysosomal compartment. Therefore, the requirement for cleavage of the ECD for TLR3 signaling (9, 10, 22) raises an intriguing issue with regard to how endogenous TLR3 is processed and which forms of the receptor recognize dsRNA. In this study, we generated and used novel mAbs directed against TLR3 ECD and mutant forms of TLR3 to demonstrate that cleavage of the LRR12 loop, but not separation of the two fragments, is required for signaling.

## Materials and Methods

### Cell culture and reagents

HEK293 and HEK293-TLR3-hemagglutinin (HA) cells (InvivoGen) were grown in DMEM medium (Invitrogen) supplemented with 10% FBS and penicillin/streptomycin. Human bronchial epithelial cell line BEAS-2B (Sigma) was cultured in LHC-9 medium (Invitrogen) in bovine collagen

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The online version of this article contains supplemental material.

Abbreviations used in this article: DC, dendritic cell; ECD, extracellular domain; EEA, early endosome Ag; EndoH, endoglycosidase H; ER, endoplasmic reticulum; FL, full length; HA, hemagglutinin; HMW, high molecular weight; LMW, low molecular weight; LRR, leucine-rich repeat; mDC, monocyte-derived dendritic cell; NSCLC, non-small cell lung cancer; PNGase, peptide:N-glycosidase F; Poly(A:U), polyadenylic-polyuridylic acid; Poly(I:C), polyinosinic-polycytidylic acid; siRNA, small interfering RNA; WT, wild-type.

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type I (Invitrogen) and fibronectin (Sigma)-coated dishes. CD14<sup>+</sup> monocytes were purified from peripheral blood of healthy donors: PBMCs were isolated from human peripheral blood by standard density-gradient centrifugation on Pancoll (PAN Biotech) and then mononuclear cells were separated from PBLs on a 50% Percoll solution (GE Healthcare). Monocytes were enriched by one step of adherence and differentiated in immature dendritic cells (DCs) in complete RPMI 1640 medium supplemented with 200 ng/ml human GM-CSF (kind gift of Schering-Plough) and 50 ng/ml human rIL-4 (R&D Systems) for 6 d. NCI-H292 and NCI-H1703 non-small cell lung cancer (NSCLC) cell lines (American Type Culture Collection) were grown in RPMI 1640 medium (Invitrogen) supplemented with 10% FBS (Sigma), HEPES, NaPy, 100 U/ml penicillin/streptomycin, and 2 mM glutamine. THP1 and U937 cell lines were grown in RPMI 1640 medium (Invitrogen) supplemented with 10% FBS and 100 U/ml penicillin/streptomycin. IFN- $\alpha$  was from Schering-Plough. Z-FA-fmk, chloroquine, tunicamycin, and cycloheximide were from Sigma. Polyinosinic-polycytidylic acid [Poly(I:C)]-high molecular weight (HMW) and Poly(I:C)-low molecular weight (LMW) were purchased from InvivoGen. polyadenylic-polyuridylic acid [Poly(A:U)] was from Innate Pharma. Mouse monoclonal IgG1 anti-actin Ab was from MP Biomedicals. Anti-mouse TLR3 Ab T3.7C3 was a gift from Nadège Goutagny (Centre de Recherche sur le Cancer de Lyon, Lyon, France). HRP-conjugated donkey anti-mouse secondary Ab was from Jackson ImmunoResearch.

### TLR3.2 and TLR3.3 Ab preparation and purification

BALB/C mice were immunized with recombinant human TLR3 ECD (R&D Systems) by three i.p. injections of the immunogen in the presence of Freund's adjuvant and a final i.v. boost, 3 d before spleen isolation. Splenic cells were fused with the SP20 myeloma cell line in the presence of polyethylene glycol. Hybridoma supernatants were screened by immunofluorescent staining of pUNO-hTLR3-HA and pUNO-hTLR3-V5 transiently transfected 293T cells with Exgen 500 (Euromedex) and fixed with acetone. Only clones recognizing both transfected cells were selected.

### Western blotting

Cells were lysed in cold lysis buffer (20 mM Tris-HCl [pH 7.4], 150 mM NaCl, 0.2% Nonidet P-40, supplemented with 1 mM orthovanadate, 10 mM NaF, and a protease inhibitor mixture; Sigma) for 25 min on ice. Cell lysates were cleared by centrifugation (13,000  $\times$  g for 10 min at 4°C), and protein concentration was determined using the Bradford assay (Bio-Rad). Protein lysates were denatured or not in Laemmli buffer containing 1% SDS and 5 mM DTT and heated to 95°C for 5 min. For peptide-N-glycosidase F (PNGase)/endoglycosidase H (EndoH) digestions, lysates were treated as recommended by the manufacturer (New England BioLabs). Proteins were resolved on SDS-polyacrylamide gels and transferred onto polyvinylidene difluoride membranes by electroblooming, and nonspecific binding sites were blocked using TBS containing 0.1% Tween-20 and 5% (w/v) dry milk. After incubation with the appropriate secondary Abs conjugated to HRP, blots were revealed using ECL (GE Healthcare) or SuperSignal (Thermo Scientific) reagents. For reimmunoprecipitation experiments, anti-TLR3 or anti-HA immunoprecipitates were eluted with preheated lysis buffer containing 1% SDS and 5 mM DTT; 20% of each sample was resolved by SDS-PAGE, and the remaining 80% was diluted 10-fold in lysis buffer and then reimmunoprecipitated with TLR3.2 or anti-HA Ab, resolved by SDS-PAGE, and analyzed with either TLR3.2 or TLR3.3 Ab.

### Immunofluorescence

Cells were washed with PBS, fixed with 4% formaldehyde for 10 min at room temperature, and washed three times with PBS. Cells were then blocked using Image-iT FX signal enhancer (Life Technologies) for 30 min at room temperature and washed once with PBS. Thereafter, each washing step was done using TBS. Cells were incubated for 1 h at room temperature with TLR3.1, anti-HA, anti-calreticulin, early endosome Ag (EEA)1, or Lamp1 (Abcam) primary Abs. After washing three times, cells were incubated for 30 min at room temperature with secondary Abs (goat anti-mouse-Alexa Fluor 488 and goat anti-rabbit-Alexa Fluor 555 or Alexa Fluor 633; Life Technologies). Cells were washed again 3 min each. Cover slips were air-dried and then mounted using ProLong Gold antifade reagent with DAPI (Life Technologies). Images were acquired using a confocal microscope (Zeiss Axiovert 100 M LSM510) with a 1.4 NA Plan-Apochromat 63 $\times$  oil-immersion lens. Image noise was reduced using a Despeckle Fiji filter.

### Cytokines measurement

The supernatant from NCI-H292 and NCI-H1703 cells, cultured or not with 100  $\mu$ g/ml Poly(I:C) for 24 h, was assayed for IL-6, IP-10, and RANTES

using a MILLIPLEX MAP kit (Millipore) on a Luminex Bio-Plex 200 System Analyzer (Bio-Rad). The supernatant from monocyte-derived DCs (mDCs), cultured or not with 100  $\mu$ g/ml Poly(I:C) for 24 h, was assayed for IL-6, IP-10, TNF- $\alpha$ , and IFN- $\lambda$  using a Quantikine ELISA test (R&D Systems), as described by the manufacturer.

### DNA cloning

Preparation of the LRR1-11 and 13-21 deletion mutants was described previously (23). For the TLR3-Ins12-HA mutant, mutagenesis was performed using the QuikChange XL Site-Directed Mutagenesis Kit (Stratagene) and primer pairs containing deletion of 24 nucleotides: 5'-CTGAATTTGAAACGGTCTTTTACTCTCCCAAGATTGATGATTTTCT-3' (forward) and 5'-AGAAAAATCATCAATCTGGGGAGAGTAAAAGACCGTTTCAAAATTCAG-3' (reverse). Ten nanograms of plasmid DNA and 125 ng of primers were used, according to the manufacturer's instructions. Two colonies from each library were sequenced.

For the TLR3-Cter<sub>356</sub>-HA mutant, LRR deletion mutants of TLR3 (A<sub>22</sub>-K<sub>356</sub>) were generated by PCR with Phusion (Finnzyme), using the appropriate primers: 5'-TGTTTGGAGCACACATGGAAG-3' (forward) and 5'-GGTGGAGGATGCACACAGCATCCCA-3' (reverse). PCR was performed with the following cycling conditions: 10 s at 98°C, 2 min at 72°C for 25 cycles. The PCR product was treated with DpnI to digest the template DNA, phosphorylated with T4 PNK (New England BioLabs), and ligated using a DNA Ligation kit (New England BioLabs). Deletion constructs were sequenced. TLR3-Cter<sub>346</sub> was provided by P. Bénaroch (Curie Institute, Paris, France).

### RNA interference

Synthetic TRIF (L-012833-00-0005) and control nonsilencing (D-001810-03-20) small interfering RNAs (siRNAs) were from Dharmacon. TLR3 Stealth RNAi siRNA (TLR3HSS110816) was from Invitrogen. siRNAs mix was prepared in Opti-MEM medium (Invitrogen), and cells in suspension were transfected using HiPerFect reagent (QIAGEN), as described by the manufacturer. The final siRNA concentrations were 25 nM. Transfected cells were seeded in 6-well plates or 96-well white plates (Greiner) and incubated for 24 h. Medium was replaced with fresh complete medium, and cells were incubated for 48 h before Poly(I:C) treatment.

### Generation of ISRE- and NF- $\kappa$ B-luciferase reporter cell lines

HEK293, NCI-H292, and NCI-H1703 cells were transduced with luciferase ISRE- or NF- $\kappa$ B-reporter lentiviruses (SABiosciences), according to the manufacturer's recommendations, and transduced cells were selected with puromycin.

### Reporter luciferase assays

Cells were seeded in white 96-well plates (10,000 cells/well); 24 h later they were treated with 10  $\mu$ g/ml poly(I:C) in 50  $\mu$ l medium for 4 or 6 h, depending on the cell line. Then, 50  $\mu$ l Steady-Glo reactive (Promega) was added to each well before reading luminescence with a Tecan Infinite 200 microplate reader using i-control software (Tecan).

### Transient expression in HEK293 cells

Cells were seeded in 100-mm dishes to reach ~70% confluence on the day of transfection. Cells were transfected with pUNO, TLR3-wild-type (WT)-HA, TLR3-Ins12-HA, TLR3-Cter<sub>356</sub>-HA, or TLR3-Cter<sub>346</sub>-HA by incubating 8  $\mu$ l Lipofectamine 2000 (Invitrogen) with 8  $\mu$ g plasmid in 6 ml Opti-MEM medium for 5 h; subsequently, Opti-MEM was replaced by fresh medium. Twenty-four hours after transfection, cells were trypsinized and seeded in 96-well white plates and 6-well plates and incubated for 24 h.

### Stable transfections

P2.1 cells were transfected with pUNO-hTLR3 vectors, which contain WT TLR3 cDNA, TLR3-Ins12 mutant, or TLR3-Cter<sub>356</sub> mutant cDNA, or with an empty mock vector, in the presence of Lipofectamine Reagent (Invitrogen) and PLUS Reagent (Invitrogen), as described by the manufacturer. Stable transfectants were selected with medium containing blasticidin (5  $\mu$ g/ml; Invitrogen). The presence of TLR3 was confirmed by Western blotting.

### Determination of mRNA levels by RT-quantitative PCR

Total RNA was extracted from P2.1 cells. RNA was reverse-transcribed using Oligo-deoxy-thymidine. To determine mRNA levels for IL-29, quantitative PCR was performed with Assays-on-Demand probe/primer combinations and 2 $\times$  universal reaction mixture in an ABI Prism 7700 Sequence Detection System (all from Applied Biosystems). The  $\beta$ -glucuronidase (GUS) gene was used for normalization. Results are expressed according to the  $\Delta$ Ct method, as described by the manufacturer.

### Coimmunoprecipitation

Cells were cultured in 150-mm dishes, collected, washed in PBS, and lysed in 750  $\mu$ l cold lysis buffer (20 mM Tris-HCl [pH 7.4], 150 mM NaCl, 0.2% Nonidet P-40, supplemented with 1 mM orthovanadate, 10 mM NaF, and a protease inhibitor mixture; Sigma) for 25 min on ice. Cell lysates were cleared by centrifugation ( $13,000 \times g$  for 10 min at 4°C). Lysates were precleared with 50  $\mu$ l Sepharose-6B (Sigma) for 1 h at 4°C and then immunoprecipitated overnight at 4°C with 5  $\mu$ g mouse anti-TLR3.2, anti-TLR3.3, or control IgG1 Ab (R&D Systems) and the following day in the presence of 20  $\mu$ l protein G-Sepharose for 3 h at 4°C. Beads were recovered by centrifugation, and immunoprecipitates were washed extensively with lysis buffer and eluted with Laemmli buffer containing 1% SDS and 5 mM DTT and heated to 95°C for 10 min.

### TLR3 ECD modeling

The MacPyMOL software (DeLano Scientific) was used to generate the 3D representation of the TLR3 structure shown on Figs. 1C and 5A (PDB:1ZIW).

### Statistical analysis

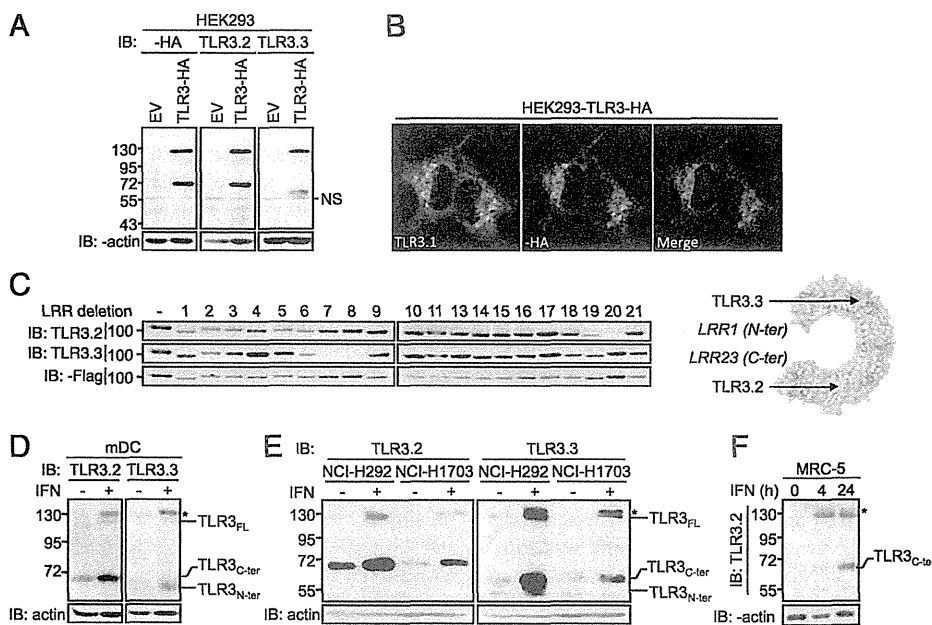
Statistical significance was determined using the Student *t* test.

## Results

### Profiling endogenous TLR3 expression

To analyze the biology of endogenous TLR3, we generated three new mAbs (designated as TLR3.1, TLR3.2, and TLR3.3) raised against the ECD of the receptor. First, the Abs were validated using HEK293 cells stably expressing TLR3 tagged with a C-terminal HA epitope (HEK293-TLR3-HA). In this model, Western blots probed with anti-HA, TLR3.2, and TLR3.3 Abs revealed an ~130 kDa band corresponding to the expected molecular mass of highly glycosylated TLR3 (Fig. 1A) (24). The stronger signal observed with TLR3.2 suggested that this Ab has a higher affinity for TLR3 than does TLR3.3. In addition, anti-HA and TLR3.2 Abs stained

a second band at ~72 kDa similar to the C-terminal fragment of TLR3 observed after cleavage by cathepsin. In addition, TLR3.3 Ab detected a third band (Fig. 1A) not recognized by anti-HA mAb and with a size ~60 kDa that could represent the N-terminal fragment of cleaved TLR3. TLR3.1 Ab did not detect TLR3 by Western blot, but it showed the same staining by immunofluorescence as observed with anti-HA Ab (Fig. 1B, Supplemental Fig. 1A). To unequivocally identify the different bands revealed by TLR3.2 and TLR3.3 Abs on Western blot, we mapped the recognized epitopes using 20 single LRR-deleted forms of the ECD of TLR3 (LRR1–11 and LRR13–21) (23). Fig. 1C establishes that TLR3.2 Ab recognizes an epitope present in LRR20, whereas TLR3.3 binds to an epitope formed by residues present in LRR7 and LRR8. We next verified whether similar expression profiles could be observed in human cells of different origins and wondered how treatment with IFN- $\alpha$ , which is known to upregulate the expression of TLR3 (25), would modify this pattern. We determined TLR3 expression by immunoblot of lysates from mDCs (Fig. 1D), from human monocytic cell lines U937 and THP1 (Supplemental Fig. 1B, 1C), and from human bronchial epithelial cells transformed by SV40-T Ag (BEAS-2B; Supplemental Fig. 1D) or derived from NSCLC (NCI-H292 and NCI-H1703; Fig. 1E). The three forms of TLR3 (130, 72, and 60 kDa) were present in every lysate with the exception of THP1, which did not appear to express TLR3 (Supplemental Fig. 1B) or respond to Poly(I:C) (Supplemental Fig. 1E). Resting MRC-5 cells were also devoid of TLR3, but kinetic analysis showed that IFN- $\alpha$  treatment led first to the detection of the high molecular mass bands (~130 and ~135 kDa) of TLR3, followed by an increase in the intensity of the lower ~72-kDa molecular mass band detected by TLR3.2 mAb (Fig. 1F), suggesting that the former might



**FIGURE 1.** Profiling endogenous TLR3 expression. **(A)** Immunoblot analysis of HEK293 cells stably expressing an empty vector (EV) or TLR3-HA; lysates were analyzed with monoclonal anti-HA, TLR3.2, TLR3.3, and anti-actin Abs. **(B)** Immunofluorescence of HEK293 cells stably expressing TLR3-HA; cells were stained with anti-HA or TLR3.1 Abs, followed by DAPI nuclear staining (blue). Original magnification  $\times 63$ . **(C)** *Left panel*, Epitope mapping of TLR3.2 and TLR3.3 Abs on HEK293 cells stably transfected with TLR3-HA WT (–) or TLR3-HA mutants carrying LRR deletions (1–11 and 13–21, as indicated). Lysates were analyzed with monoclonal TLR3.2, TLR3.3, and anti-Flag Abs, as indicated. *Right panel*, Schematic representation of epitopes recognized by TLR3.2 and TLR3.3 Abs on TLR3 ECD. **(D)** Immunoblot analysis of mDCs treated (+) or not (–) for 18 h with IFN- $\alpha$  (1000 IU/ml); lysates were analyzed with TLR3.2, TLR3.3, and anti-actin Abs. **(E)** Immunoblot analysis of NCI-H292 and NCI-H1703 cells treated (+) or not (–) for 18 h with IFN- $\alpha$  (1000 IU/ml); lysates were analyzed with TLR3.2, TLR3.3, and anti-actin Abs. **(F)** Immunoblot analysis of MRC-5 cells treated (+) or not (–) for the indicated times with IFN- $\alpha$  (1000 IU/ml); lysates were analyzed with TLR3.2 and anti-actin Abs. Values in (A) and (C)–(F) represent molecular mass (kDa). All data are representative of at least three independent experiments. NS, Nonspecific band.

represent the precursors of the latter. In other cell lines, the absolute and relative intensities of the three bands varied depending on the origin of the cells, the Ab used, and the treatment with IFN- $\alpha$ . However, under basal conditions, all cells primarily expressed the 72 and 60 kDa TLR3 forms. Treatment with IFN- $\alpha$  increased the intensity of the three bands and allowed the detection of a higher molecular mass form  $\sim$ 135 kDa in mDCs and in the four cell lines analyzed (asterisk in Fig. 1D–F and Supplemental Fig. 1D). In conclusion, our data suggest that human TLR3 is spontaneously cleaved into a C-terminal fragment  $\sim$ 72 kDa recognized by TLR3.2 and a C-terminal fragment  $\sim$ 60 kDa recognized by TLR3.3, and the relative abundance of cleaved versus uncleaved TLR3 appears to vary with the cell under consideration.

#### *TLR3 ECD cleavage by cathepsins generates two remarkably stable fragments*

To further explore the processing of endogenous TLR3 and its functional consequences, we selected the NCI-H292 and NCI-H1703 NSCLC cell lines, which triggered an innate immune response when stimulated with Poly(I:C), as indicated by cytokine secretion (Supplemental Fig. 2A) and by activation of ISRE-dependent luciferase reporter genes (Supplemental Fig. 2B). We ascertained that this response was mediated exclusively by TLR3 by showing its strict dependence on TRIF, the only known adaptor for TLR3 (Supplemental Fig. 2B). We started analyzing the effects of the cathepsin inhibitor Z-FA-fmk on the expression of the different forms of TLR3. Following Z-FA-fmk treatment, the 130 kDa band became more intense with time, whereas the 72 and 60 kDa bands gradually disappeared in both NCI-H292 and NCI-H1703 cells (Fig. 2A, Supplemental Fig. 2C, respectively), as well as in HEK293-TLR3-HA cells (Fig. 2B). These results confirm that cathepsins are necessary for TLR3 cleavage in epithelial cells (22). In NCI-H292 cells, the accumulation of full-length TLR3 was observed as early as 120 min after the addition of Z-FA-fmk (Fig. 2C), whereas in the three cell lines both C-terminal (TLR3<sub>C-ter</sub>) and N-terminal (TLR3<sub>N-ter</sub>) TLR3 fragments disappeared with an apparent  $t_{1/2} > 24$  h (Fig. 2A, 2B, Supplemental Fig. 2C). Of note, Z-FA-fmk induces a shift of TLR3 full-length (TLR3<sub>FL</sub>) from 130 kDa to 135 kDa (TLR3<sub>FL+</sub>) in both NSCLC cell lines, which is more visible after prolonged gel migration (Fig. 2D). This TLR3<sub>FL+</sub> could represent the fully glycosylated form of TLR3 leaving the post-Golgi cisternae and not cleaved yet. Published data with regard to the effects of cathepsin inhibitors on TLR3 signaling seem contradictory (8, 9). In this study, we observed that ISRE- and NF- $\kappa$ B-dependent responses to Poly(I:C) were not modified after prolonged treatment with Z-FA-fmk in NCI-H292 cells (Supplemental Fig. 2D), whereas they were significantly, but not completely, suppressed in NCI-H1703 cells (Supplemental Fig. 2E). However, considering the much higher level of TLR3 expression in resting NCI-H292 cells than in NCI-H1703 cells (Fig. 1E), the amounts of TLR3<sub>C-ter</sub> detected in NCI-H292 cells after 72 h of treatment with Z-FA-fmk was still comparable to the basal level in NCI-H1703 cells. Therefore, these results suggest that cleaved TLR3 is important for signaling, although uncleaved TLR3 might still transduce some signal. Importantly, Z-FA-fmk treatment blocked TLR3 cleavage and Poly(I:C)-induced cytokine secretion in mDCs (Fig. 2E, 2F) and TR3 signaling in macrophages U937 cells (Fig. 2G, Supplemental Fig. 2F), whereas the response to TNF- $\alpha$  was unaffected. Like with Z-FA-fmk treatment, exposure to the lysosomotropic weak base chloroquine, which prevents cathepsin activity, led to the accumulation of TLR3<sub>FL+</sub> within 3 h and to the reciprocal disappearance of the two TLR3 fragments in NCI-H292 (Fig. 2H) and NCI-H1703 (Supplemental Fig. 2G) cells after 48 h. The same results

were obtained with the specific inhibitor of vacuolar H<sup>+</sup> ATPase Bafilomycin (data not shown). Furthermore, short-term blockade of de novo protein synthesis with cycloheximide confirmed the relative high stability of endogenous TLR3<sub>C-ter</sub> (apparent  $t_{1/2} > 24$  h) (Fig. 2I, 2J) compared with TLR3<sub>FL</sub> (apparent  $t_{1/2} < 4$  h). Despite a weaker signal, a half-life similar to TLR3<sub>C-ter</sub> was estimated for TLR3<sub>N-ter</sub> (Fig. 2H, Supplemental Fig. 2G). Altogether, our data indicate that, in resting cells, TLR3 is actively transcribed and rapidly cleaved by cathepsins upon its transfer in endolysosomes into two highly stable proteolytic fragments, in agreement with a very recent report (26).

#### *TLR3 transits steadily through the Golgi before being cleaved in the endolysosomal compartments*

Although TLR3, like other intracellular TLRs, depends on the chaperone protein Unc93b1 for proper trafficking, it is unclear whether its transfer to the endolysosomes occurs constitutively or in response to its ligand. Using TLR3.1 Ab, we observed by immunofluorescence microscopy that TLR3 colocalizes extensively with Lamp1 (a lysosome marker) but not with EEA1 (an early endosome marker) (Fig. 3A, Supplemental Fig. 3) in resting epithelial cells and that the level of colocalization remained unchanged after stimulation with dsRNA (Supplemental Fig. 3). We next addressed the trafficking of TLR3 by analyzing the N-glycosylation status of the protein, which represents  $\sim$ 35% of its total mass (24). After treatments of cell lysates with PNGase, which removes all N-glycans, TLR3<sub>FL</sub> and TLR3<sub>FL+</sub> shifted from 130 and 135 kDa, respectively, to 95 kDa (Fig. 3B, 3C), corresponding to the expected molecular mass of nonglycosylated neosynthesized TLR3<sub>FL</sub> (904 aa). The TLR3<sub>C-ter</sub> band shifted from 72 to 50 kDa, indicating that both cleaved and noncleaved TLR3 are glycosylated. Treatment with EndoH, an endoglycosidase that cleaves N-glycans before their further modification in the Golgi apparatus, indicates that noncleaved TLR3<sub>FL</sub> is EndoH sensitive, whereas TLR3<sub>FL+</sub> and TLR3<sub>C-ter</sub> are partially EndoH resistant. This was similar to the presence of hybrid glycans on TLR9 even after trafficking through the Golgi (27). Cell treatment with tunicamycin, a de novo N-glycosylation inhibitor, caused the rapid fading of TLR3<sub>FL</sub> (apparent  $t_{1/2} < 8$  h) and the appearance of a band at  $\sim$ 95 kDa representing neosynthesized nonglycosylated full-length TLR3 (Fig. 3D, 3E). Altogether, our data indicate that TLR3<sub>FL</sub> corresponds to the small amounts of TLR3 present in the endoplasmic reticulum (ER), which is steadily translocated to the Golgi in resting cells, converted into fully glycosylated TLR3<sub>FL+</sub>, and exported to the endosomes/lysosomes, where it is rapidly cleaved.

#### *The endolysosomal pool of cleaved TLR3 is sufficient for signaling*

To determine which forms of endogenous TLR3 are functional, we started using specific siRNA and took advantage of the prolonged stability of cleaved fragments versus TLR3<sub>FL</sub>. We observed that 24 and 48 h after transfection, TLR3<sub>FL</sub> had completely disappeared, whereas the two cleavage fragments were still abundant (Fig. 4A, Supplemental Fig. 4A). Under these conditions, the Poly(I:C)-induced ISRE-dependent response was not reduced (Fig. 4B), suggesting that the uncleaved TLR3<sub>FL</sub> does not contribute significantly to downstream signaling, probably because of its weak expression compared with the cleaved fragments from the beginning of the experiment. Indeed, ISRE activation faded away gradually with time as the presence of cleaved TLR3 decreased (Fig. 4A, 4B). Similar results were obtained with a NF- $\kappa$ B-dependent reporter gene (Supplemental Fig. 4B). These data show that cleaved TLR3 can signal in the absence of uncleaved TLR3<sub>FL</sub> and may even represent the predominant signaling form of the receptor.