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The expanding regulatory network of STING-mediated signaling Guy Surpris¹ and Alexander Poltorak^{1,2,3}



The identification and characterization of DNA-sensing pathways has been a subject of intensive investigation for the last decade. This interest, in part, is supported by the fact that the main outcome of DNA-responses is production of type I interferon (IFN-I), which, if produced in excessive amounts. leads to various pathologies. STING (stimulator of interferon genes) is positioned in the center of these responses and is activated either via direct sensing of second messengers or via interaction with upstream sensors of dsDNA. STING mediates responses to pathogens as well as host-derived DNA and is, therefore, linked to various autoimmune diseases, cancer predisposition and ageing. Recent mouse models of DNA damage showed the adaptor STING to be crucial for heightened resting levels of IFN-I. In this review, we will focus on recent advances in understanding the regulation of STINGsignaling and identification of its novel components.

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STING: a central player in the immune response to cytosolic DNA

In eukaryotic cells, the DNA is packaged in the nucleus or mitochondria. During infection or in response to a variety of stress signals, DNA may be exposed within the endosomal or cytoplasmic compartment, where it is recognized by several DNA sensors that ultimately activate caspase-1 and signaling mediated by STING [1]. The name implies that the production of IFN-I as well as the subsequent activation of IFN-stimulated genes (ISGs) [2] is the main outcome of STING activation.

STING (Tmem173/MPYS/MITA) is a tetraspanning membrane-resident sensor that recognizes both bacterial and host-derived cyclic di-nucleotides (CDNs) and cytoplasmic nucleic acids, either directly or via other cytosolic DNA sensors, such as nuclear resident IF116 (interferon inducible 16) [3], a nucleotidyltransferase cGAS (cGAMP (GMP-AMP) synthase) [4], and helicase DDX41 (DExD/ H-box) [5]. The amino-terminal domain (NTD) of STING, which encompasses approximately the first 130 amino acids, contains four transmembrane domains, while the final 250 amino acids comprise a globular carboxy-terminal domain (CTD), several crystal structures of which have been reported.

The STING CTD resides in the cytosol and provides a platform that directs TBK1 (tank binding kinase) [6] to phosphorylate and activate IRF3 (interferon regulatory factor 3) [7]. The phosphorylation of IRF3 appears to be a conserved mechanism that selectively recruits IRF3 to activate IFN-I [7]. The activation of STING triggers conformational changes in its CTD, which serves as a platform for the recruitment and auto-phosphorylation of the serinethreonine kinase TBK1. This kinase, in turn, phosphorylates and activates the transcription factor IRF3. IRF3 then travels to the nucleus, where it initiates IFN-I production and directly promotes the expression of multiple ISGs, many of which are activated via the IFN-I $\alpha\beta$ receptor (IFNAR) pathway. The growing interest in STING-mediated DNA responses is based on the importance of IFN-I for the host defenses against DNA viruses, such as herpes viruses, and intracellular bacteria, such as Listeria *monocytogenes.* Another subject of interest is the regulation of IFN-I by STING; namely, tight regulation of IFN-I is essential, since excessive production of this cytokine leads to the development of autoimmunity [8,9], chronic inflammation [10^{••},11], or sepsis. Not surprisingly, STING is a critical component in tissue repair and tumorigenesis [12].

While recent studies have highlighted the functional importance of the STING CTD [13], particularly in the recruitment and activation of the serine-threonine kinase TBK1 and the transcription factor IRF3, less is known about the function of the NTD, although some NTD mutations have been described in humans; for example, a potentially nonfunctional allele, referred to as HAQ (R71H-G230A-R293Q), was found to be homo-zygous in $\sim 3\%$ of two American cohorts [14]. Additional

evidence has been reported from murine studies, where a hypomorphic allele of STING with detrimental mutations confined to the NTD is seen in wild-derived mice [15]. However, the role of the STING NTD in its interaction with recently discovered additional components and pathways requires further analysis.

Conceptual advances in the definition of the STING signaling pathway

Given a central role of STING in IFN-I production and regulation, it would not be surprising if additional ligands exist that activate STING-signaling. Some of these ligands, such as mitochondrial DNA (mtDNA), easily fit into the DNA-damage based model of STING-activation [16], which is counterbalanced by caspases [17]. Other ligands, such as those activated downstream of lipid membrane [18], have yet to be identified. Finally, the STING signaling pathway could converge at some level with other pathways, downstream of STING.

Mitochondrial stress protects against viral infection

Mitochondria are known to respond to stress by DNA leakage, a process that induces innate immune responses [19]. Not surprisingly, stressed mitochondria release DNA in response to HSV-1 (herpes simplex virus) and, thus, provide protection against infection [20[•]]. Hemizygosity for *Tfam* (transcription factor a mitochondrial), which encodes an abundant mitochondrial protein responsible for nucleoid maintenance and architecture, keeps the mitochondria intact, but leads to a 50% loss of mtDNA. This results in IRF3 nuclear translocation and elevation of several IFNs and ISGs in a STING-dependent manner. IFN production is also dependent on cGAS, which is co-localized with mtDNA, suggesting that cGAS binds mtDNA.

Accordingly, *Tfam*-hemizygous MEFs (mouse embryonic fibroblasts) showed resistance to VSV (vesicular stomatitis virus) and HSV-1 infection and lower viral loads, whereas inhibition of release of mtDNA promoted viral replication. Although the authors identified the viral protein UL12.5 as responsible for mitochondrial stress induction, it seems counterintuitive that the virus activates an antiviral mechanism of defense, particularly since numerous other viral homologues of UL12.5 induce mitochondrial stress. It is possible that a synergy exists between mitochondrial stress and induction of other, independent of DNA-damage, immune responses [21], that is, a for potential engagement and cross-talk with other pathways. Altogether, this work supports the theory that mitochondria serve as important sensors of particular pathogens.

Two pathways are required for resistance to the smallpox virus infection

In support of alternative and synergistic ways of IFNproduction, He *et al.* report [22] that TLR9, MyD88, STING and IRF7 are required for resistance to mouse smallpox virus and for the production of IFN in draining lymph nodes (dLN). Either STING-deficiency or MyD88-deficiency leads to a decrease in IFN-I production and to an increase in mortality in infected mice. The authors show that inflammatory monocytes (iMos) recruited into the dLN are the main producers of IFN-I in response to infection and use STING to activate IRF7 and NF-kB for production of IFN-I. However, it remains to be determined which particular DNA sensor activates STING signaling in iMos. For example, there could be a specialized sensor that stimulates STING in an exclusive manner in these cells. It would also be interesting to see whether STING activates IRF7 directly in iMos or through TLR9-IRF7-STING interaction.

Posttranslational modifications provide additional regulation of STING signaling. For example, IFI16 is a DNA sensor that resides in the nucleus and binds to the sugarphosphate backbone of dsDNA. The details of how IFI16 moves to the cytosol of infected cells and activates STING have been clarified in a recently published report, which shows that acetylation regulates IFI16 trafficking and DNA binding [23]. A key molecular step is the acetylation of DNA-bound nuclear IFI16 via p300, which decreases DNA-IFI16 binding with the viral genome and expels IFI16 from the DNA, changes its conformation, exposes nuclear import signals, and binds STING in the cvtosol. Thus, IFI16 acetvlation defines IFI16 location and allows this sensor to switch from BRCA1-assisted [24] binding the viral DNA to interacting with STING. These findings contradict the canonical paradigm that the nucleus is 'immune privileged' with regard to sensing foreign DNA and suggest that both cytoplasmic and nuclear IFI16 participate in viral DNA surveillance.

A second STING-mediated pathway is targeted by the influenza virus

In an intriguing extension of their previous report [25], Holm et al. now describe the interference of the influenza virus with, presumably, a second pathway that is mediated by STING in a DNA-independent manner [26^{••}]; namely, they show that infection with enveloped RNA viruses leads to STING-dependent, but cGAS-independent, IFN-I production, a discovery that is surprising, since it suggests the existence of another (unknown) sensor located upstream of STING. In this study, STING co-localized with viral hemagglutinin (HA) and physically interacted with the NTD of the HA fusion protein (FP) via STING's173-163 region. The FP inhibited STING dimerization and translocation in response to the activation of cells with fusogenic liposomes [26^{••}]. The same team made another exciting discovery when they identified Arg168 of STING to be important in fusion-mediated, but not ligand-induced, IFN-I production, thus functionally separating the two pathways. It is tempting to speculate that another, novel cytosolic component, possibly related to a Ca²⁺ related membrane perturbation [27[•]], transduces the activation signal from the lipid membrane to STING. It also suggests that enveloped viruses and fusogenic liposomes both mediate STINGdependent, ligand-independent IFN-I response independently of cGAS; whether this second pathway evolved for better recognition of viruses or enveloped viruses developed additional tools for interfering with the host response remains to be further investigated.

Novel mechanistic insights in the regulation of the STING-pathway

Several activation steps in STING-signaling have recently been identified, such as the interaction of STING with TRAF2 (TNF receptor associated factor 2) and the ubiquitin ligase TRAF3, as well as phosphorylation on several residues, including Ser358 [28]. Ubiquitination by TRIM56 (tripartite motif) and TRIM32 plays an important role in regulating expression of STING [29]. In addition to recruitment of TBK1 and IRF3, the STING-CTD also recruits STAT6 [30]. Tight regulation of IFN-production is achieved via inhibitory steps such as AKT-mediated inhibition of cGAS [31] or via TRM30amediated degradation of STING [32].

BTK1 phosphorylates DDX41 for activation of STING

The DNA-sensor DDX41 was known to activate the STING signaling pathway, but the specific mechanism of this activation was poorly understood. Now, Lee et al. report the importance of the BTK1 kinase in this activation [33]. BTK1-deficient cells lack phosphorylation of IRF3 and TBK1 and exhibit low levels of IFN-I. According to their model, the DEAD-box domain of DDX41 binds BTK's kinase domain, whereas the SH3/SH2 domain of BTK1 binds the transmembrane domain of STING. BTK1-mediated phosphorylation of DDX41 at Tyr414 increases the affinity of DDX41 towards dsDNA and STING and stabilizes DDX41-STING interactions, thus inducing oligomerization of STING and ultimate activation of TBK1/IRF3 and production of IFN-I. The proposed model suggests that TBK1 functions as an adaptor as well as a kinase. Although a second tyrosine at 364 is critical for the activation of STING, it is not phosphorylated by BTK1, thus leaving its role in STING activation for further investigations.

PPM1A (protein phosphatase Mg²⁺/Mn²⁺ dependent 1A) is a negative regulator of STING-activation

The phosphatase PPM1A directly interacts with STING and removes the phosphate groups from both STING and TBK1 [34], thereby acting as a negative regulator of STING signaling. This interaction prevents further oligomerization of STING and IFN β production in response to HSV-1. Using exogenously expressed proteins, the authors show that TBK1-mediated phosphorylation of STING at Ser358 is a prerequisite for STING polymerization and efficient phosphorylation of IRF3 byTBK1.

The ER (endoplasmic reticulum) adaptor SCAP (SREBP cleavage activating protein) recruits IRF3 to STING

The mechanism of IRF3 recruitment to STING was poorly understood, but Hansen et al. now provide mechanistic insight into this process [26^{••}]. Specifically, they show that silencing of SCAP, but not TBK1, abolishes IRF3 recruitment to STING and IFNB production, but does not abolish STING translocation, thus providing evidence, for the first time, that IRF3 activation and STING translocation are mechanistically separated. The N-terminal (8-pass) transmembrane of SCAP interacts with the transmembrane of STING (1-175), and the C-terminus of SCAP binds IRF3 in an activation dependent mode. SCAP-deficient mice are more sensitive to HSV-1 infection than WT mice. A major question remains as to what initiates the association of SCAP and STING at the ER upon stimulation. It is also still a mystery what regulates the STING/SCAP exit from the ER.

Diversity of DNA-sensors that confer responses to Listeria

In many instances, DNA-sensors cooperate to activate STING signaling [28]. An example of such diverse DNAresponses is recognition of Listeria [35,36]. Although the role of cGAS in mediating responses to Listeria in mice is well established, the nature of the DNA-sensor of Listeria in human cells was unclear, since human cells are neither dependent on cGAS, nor on a pump that transports CDNs into the host cytoplasm. Now Hansen *et al.* show [37] that cGAS, STING, and IFI16, but not DDX41, are important for sensing the bacterial DNA, and that it is DNA, rather than Listeria CDNs, that activates the STING-pathway in human myeloid cells. One likely explanation is that human STING is 500 times less responsive to bacterialderived CDNs with 3'5' linkage than 2'3'cGAMP. In addition, humans may have evolved to process DNA better. These data suggest a role for IFI16 in the amplification of cGAS-dependent DNA-driven responses.

NLRX1 sequesters STING to negatively regulate the interferon response

Several nod-like receptors (NLRs) have been characterized as negative regulators of the IFN-I in response to DNA [38]. Guo *et al.* now describe a mechanism by which NLRX1 blocks IFN-I responses and promotes early HIV infection [39]. NLRX1 facilitates its effect via binding the C-terminus of STING, which disrupts the STING-TBK1 interaction. The fact that NLRX1 resides in the mitochondria, whereas STING is located in the ER, challenges these findings. Furthermore, previously observed interactions between mitochondrial and ER proteins do not provide the reason for interaction between mitochondrial and ER proteins. One possibility might be that STING-signaling is specifically prohibited in MAMs (mitochondria associated membrane) and gets disrupted once STING accidently translocates to the mitochondria. Thus, the described negative regulation of STING by NLRX1 could be restricted to certain cellular compartments.

TRIM9s promotes the IFN-I response by recruiting GSK3 β to TBK1

A short isoform of TRIM9, TRIM9s, was identified as a novel positive regulator of IFN-I signaling downstream of MAVS and STING signaling [40]. Knockdown of TRIM9s resulted in higher cellular viral loads of RNA and DNA viruses. It was shown that TRIM9s binds directly to GSK3 β and TBK1 and facilitates the interaction between GSK3 β and TBK1. Binding of TRIM9s to TBK1 enhances IRF3 activation after viral infection. Finally, the authors determined that TRIM9s has E3 ligase activity and is able to auto-ubiquitinate itself in order to recruit TBK1 and GSK3 β . The negative effect of TRIM9s on IL6 and TNF-activation is likely to be linked to GSK3 β and could be confirmed by analysis of IL-10 production, which is promoted by GSK3 β .

Figure 1 summarizes some of the STING-regulatory pathways that were discussed here. The effects of these pathways are confined to phosphorylation and de-phosphorylation, or direct interactions that antagonize STING-signaling or synergize with it. The specific timing and intracellular location of these interactions is not always known but, as in case with NLRX1, spatial requirement might define specificity of the effects.

Viral interference with STING signaling

Having apparently arisen as a sensor of self-DNA and stress-signals [41[•]], the STING-pathway has evolved to counteract viral infections. It is, therefore, not surprising that viruses have developed various mechanisms to neutralize STING signaling [42,43]. In this section, we will discuss some of the recent advances in the characterization of viral strategies to hijack the STING-pathway.

HBV (hepatitis B virus) polymerase disrupts K63-linked ubiguitination of STING

To clarify the effect of HBV on the innate immune response, Liu *et al.* infected primary human hepatocytes with virus from HBV-positive sera to observe downregulation of STING-specific IFN-I production [44]. They report that viral polymerase (Pol) inhibits STING-mediated IRF3 activation and IFN-I production. They also mapped the inhibitory effect of Pol to its RT and RNAseH domains. Pol seems to physically interact with STING and does not affect expression, but rather ubiquitination, of STING via its RT domain.

KSHV (Kaposi Sarcoma Herpes Virus) targets cGAS

In the first description of viral strategy targeting cGAS, Wu et al. characterize ORF52 of Kaposi Sarcoma Herpes Virus (KSHV) as an inhibitor of cGAS. When overexpressed, ORF52 inhibited cGAS and IRF3 dimerization [45]. Because the inhibitory effect of ORF52 was attenuated by increased amounts of the DNA, this suggested that ORF52 competes with cGAS for DNA. ORF52 inhibited STING-mediated responses, but not AIM2mediated responses. The inhibitory effect was specific for DNA, but not RNA-viruses, which altogether supported direct interaction between ORF52 and cGAS. Indeed, the authors mapped the region of ORF52 responsible for binding cGAS. Ability of ORF52 to bind both DNA and cGAS provides high specificity of the inhibitory effect. The rationale behind the strategy used by herpes viruses is that DNA accounts for 10-20% of their mass, thus making it necessary for the virus to develop a mechanism that prevents recognition of DNA. This is particularly true for KSHV, which goes through lytic cycles that release viral DNA into the cytosol. Interestingly, ORF52-deficient virus showed little difference in elicited IFN-response compared with the wild type strain, suggesting redundancy in the inhibitory effects of KSHV ORFs on IFN-I production.

Figure 1



Recently described regulatory components of STING-mediated activation of type I IFN.

Pink – SCAP-mediated recruitment of IRF3 to STING; blue – TRIM9s-facilitated interaction of TBK1 with GSK3β; green – inhibitory effect of PPM1A on phosphorylation of TBK1 and STING; gray – BTK1-induced activation of DDX41 and its recruitment to STING; brown – inhibitory effect of NLRX1 on interaction between TBK1 and STING

Virus	Viral protein	Pathway inhibited	Ref.
KSHV	vIRF1	Blocks STING interaction with TBK1	[46]
Adenovirus	E1a	Blocks unknown NTD STING mediated signal	[48]
HSV1	VP24	Interacts with IRF3 and blocks phosphorylation of IRF3 by TBK1	[49]
IAV	HA2 fusion peptide	Inhibits STING dimerization in response to membrane fusion	[26**]
HTLV-1	Tax	Inhibits TBK1 phosphorylation of IRF3 by interactions with TBK1	[50]
HCV	NS4B	Inhibits STING accumulation by direct interaction with STING	[47]
KSHV	ORF52	Blocks cGAS binding of DNA	[45]
HBV	Pol	Blocks K63 ubiquitination of STING by binding STING	[44]
Coronavirus	PLP2-TM	Induces STING-Beclin1 interactions to degrade STING	[51]
SARS	PLpro-TM	Inhibits TRAF3/TBK1/STING interactions	[52]

Table 1

KSHV protein disrupts TBK1-STING interaction

In support of the 'redundancy model' Ma *et al.* [46] searched for the KSHV ORFs responsible for the inhibitory effect and identified vIRF1 as the most efficient among the tested ORFs in disrupting the TBK1-STING interaction and attenuation of IFN-production. Concordantly, depletion of vIRF1 elevated IFN-production in response to KSHV and prevented efficient viral replication. During their lifelong persistence in the host, which includes cycles of latency and lytic activation, the herpes viruses can release their DNA into the cytoplasm or in the nucleus, or induce mitochondrial stress. Thus, KSHV viruses developed various strategies to block multiple nodes in the DNA-sensing pathway.

HCV (hepatitis C virus) protein targets STING for degradation

A similar disruption of the STING-mediated pathway has been recently reported for the proteins of HCV [47], which is, similar to Influenza virus, a ssRNA virus. Using two different viral replicons, Yi *et al.* identified a transmembrane domain in NS4B that inhibited responses to cGAMP. Concordantly, activation with cGAMP inhibited replication of the HCV-cassette at the mRNA and protein level in a STING-specific manner. At the mechanistic level, NS4B induced degradation of STING, which is termed 'downregulation of STING accumulation'. Why would an RNA virus develop a strategy of interfering with STING? It is possible that STING degradation is an underlying mechanism that explains earlier reports of NS4B disrupting interaction of STING with TBK1 and MAVS.

HSV-1 serine protease VP24 inhibits DNA-response by blocking IRF3 activation

The VP24 protein is a serine protease of HSV-1 that is necessary for capsid formation of the virus. In this paper VP24 was found to dampen the interferon response to DNA by blocking the interaction between TBK1 and IRF3 and subsequent inhibition of IRF3 activation [47]. The authors show a lack of IRF3 dimerization, during HSV-1 infection that increased after the knockdown of VP24. A summary of the discussed above viral strategies of interfering with the STING-mediates signaling is provided in Table 1. Interestingly, viruses use direct physical interaction with the components of the STING-pathway rather than enzymatic modification. Another apparent conclusion from these data is that viral strategies cover all of the main components of STING-signaling thus suggesting that there are probably some unknown interferences with some (yet) unknown components. Therefore it seems promising to study the viral strategies of interfering with the host immune response.

In conclusion, STING is positioned as the main regulator of responses to host and pathogen-derived DNA. In addition, experimental data implicate STING in the regulation of DNA-responses in homeostasis (basal interferon), as well as in autoimmune models.

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