Production and Action of Type I Interferons in Host Defense

Paul J. Hertzog

Introduction

The interferons (IFNs) are a family of cytokines that function in the host response to environmental stress [1]. The evolution of the IFN response has adapted to perform a wide range of physiological and pathological functions. The IFNs are classified into three types distinguished by amino acid similarity; cognate receptors, through which they signal; and to a lesser extent, the production stimulus and cell. Type I IFNs are a multi-gene family composed of 13 IFN α subtypes, a single IFN β , IFN ε and IFN ω , and other species-specific members, produced by most cell types and acting via IFNAR 1 and 2 receptors [2]. Type II IFN has a single member, IFNy, produced mainly by activated NK and T cells and signaling via IFNGR1 and 2 receptors [3]. Type III or IFN λ has two members, produced by many cell types stimulated by pathogens and acting via IFNL1 and IL10R β receptors [4]. This review will focus on type I IFNs, setting the scene for their role in host defence against bacterial infections. IFNs have multiple effects on cells, which include rendering them resistant to viral infection, modulating proliferation, differentiation, survival and migration, as well as other specialized functions [5]. Thus, IFNs can regulate the development and activation of most effector cells of the innate and adaptive immune response. Type I IFNs signal via the JAK/STAT signaling pathway to regulate the expression of genes that encode the effector proteins of the response including antiviral and antibacterial effectors. Their broad effects on a range of target cells, necessitates a fine balance in the IFN response to ensure protection of the host against insult and a return to homeostasis, but avoid potential toxicity or chronic disease. Excessive IFN production contributes to acute septic shock in animal

P.J. Hertzog (🖂)

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Centre for Innate Immunity and Infectious Diseases, MIMR-PHI Institute, Monash University, Clayton, VIC, Australia e-mail: paul.hertzog@monash.edu

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models, and long-term deregulation of type I IFN signaling contributes to the pathogenesis of autoimmune diseases such as systemic lupus erythematosus. Understanding the regulation of type I IFN production and the actions of this family of proteins on cells is necessary to gain insights into their role in the pathogenesis of bacterial infections. In some cases, particularly with extracellular pathogens, IFNs are protective, whereas they increase susceptibility to intracellular pathogens.

Production of Type I IFNs

The production of type I IFNs was first described in response to viral infection and remains best characterized in response to these pathogens [6-8]. Nevertheless, it is increasingly evident that type I IFN production is activated by a wide variety of stimuli, including bacteria [9], physiological stimuli [10, 11] and cancer cells [12, 13]. The deluge in information characterizing the pattern recognition receptors (PRRs) that sense "danger" signals has provided considerable explanation of the mechanism whereby type I IFNs are produced [14-16]. Once PRRs bind ligand, they engage intracellular signaling molecules, often specific for the PRR family involved, and then activate kinases that in turn activate a restricted range of transcription factors such as NFkB and the interferon regulatory factors (IRFs) that stimulate the induction of pro-inflammatory cytokines and type I IFNs, respectively. The IRFs are a nine-member family of latent transcription factors involved in type I IFN production (IRF1, 3, 5, 7) and signaling (IRF9), among other functions [17]. As discussed in detail below, IRF3 is activated by many PRRs to induce IFNB gene expression (in conjunction with NF κ B and AP1) but not the expression of IFN α s. On the other hand, IRF7 is also activated by many PRRs, but can activate expression of IFN β and IFN α subtypes. In addition, IRF5 and IRF1 appear more restricted in their upstream activation pathways and these also activate IFN α gene expression.

TLRs 1, 2, 4, and 6 are cell surface PRRs that sense cell surface or secreted ligands, or pathogen-associated molecular patterns (PAMPs). The TLR4 signaling pathway activated by Gram negative bacterial lipopolysaccharide (LPS) in complex with MD2 and LBP is the best characterized and prototypic PRR signaling pathway. Ligand activated TLR4 engages four TIR domain-containing adaptor molecules: MyD88 and Mal, which activate the NFκB pathway, and TRAM and TRIF, which activate the IRF3 previously phosphorylated upstream by TBK and IKKε [14–16]. This pathway, in conjunction with NFκB, activates expression of IFNβ specifically, since this is the only type I IFN with neighboring IRF3 and NFκB binding elements in its promoter. *Escherichia coli* and *Salmonella* are strong activators of TLR4, whereas other bacteria such as *Helicobacter pylori* produce LPS that only weakly stimulates TLR4, which may explain their relative virulence [9].

TLR2 usually acts as a heterodimer with TLR1 or TLR6 and recognizes different peptidoglycans to activate the NF κ B pathway driven pro-inflammatory cytokines via MyD88 and Mal. This signaling pathway is not usually associated with activation

of IRFs and IFN production. However, exceptions have been reported [18], including a study involving the commensal *Lactobacillus* [19], but the details of the pathways remain to be fully elucidated.

TLRs 3, 7, 8, and 9 are endosomal sensors of nucleic acids including dsRNA (TLR3), ssRNA (TLR7/8) and bacterial CpG DNA (TLR9). TLR3 is the only family member that does not utilize MyD88, but signals via TRIF. These endosomal TLRs recruit adaptors and activate TBK and/or IKK ϵ , which in turn activate IRF7 and 3 to drive the induction of IFN α s and IFN β [16]. TLR9 senses *Staphylococcus aureus* and activates IFN production via IRF1 [20]. Group A and B *streptococci* are recognized by TLR7 and activate IFNs via IRF1 [21].

The RIG I-like family of receptors (**RLRs**) including RIG-I, MDA5 and LGP2 were originally identified as cytosolic sensors of viral 5'-triphosphorylated RNA [22]. Once activated, they are recruited to mitochondria or associated membranes, bind adaptors MAVS/IPS and subsequently activate TBK/IKK ε , which phosphorylate IRFs, which themselves translocate to the nucleus and induce expression of IFN α and IFN β genes [23, 24].

STING was discovered as a molecule that mediated the induction of IFN β in response to cytosolic DNA from pathogens or necrotic cells [25]. Subsequent studies cast doubt on whether the endoplasmic reticulum-localized STING directly bound DNA (reviewed in [26]). It was found that STING was the receptor for cyclic di-nucleotides such as c-di AMP or c-di GMP which act as PAMPs, for example in macrophages infected with *Listeria monocytogenes*, after listerolysin O-mediated (LLO) their release from vacuoles, possibly via DDX41 [27–29]. Another STING activating PAMP is cGMP-AMP generated by the IFN-inducible enzyme cGAS, which is important in sensing cytosolic DNA and initiating the innate immune response to pathogens. DNA from *Chlamydia muridarum* [30], *Myocbacterium tuberculosis* [31] and *Legionella pneumophilia* [32] have also been shown to activate STING and induce IFN β expression.

Cytosolic Sensors

DAI was the first reported cytosolic sensor of DNA from viruses or bacteria, inducing IFN via TBK and IRF3 [33]. DAI senses *Streptococcus pneumoniae* [34]. Another study showed that **DNA-dependent RNA polymerase III** converts cytosolic DNA into RNAs that act as PAMPs to activate RIG-I [35]. DNA released into the cytosol during infection with *Francisella tularensis* is sensed by the **AIM2** inflammasome which in turn activates IRF3 and type I IFN production [36, 37]. *L. monocytogenes* also activates the AIM2 inflammasome [38]. **NOD 1 and 2** have been speculated to induce IFN production in response to sensing muramyl dipeptide (MDP) from organisms including *M. tuberculosis* [39–41].

Thus, the various PRRs constitute a repertoire of sensors, strategically located through evolution, at different subcellular locations to ensure the detection of a pathogen component, be it outside the cell, in endosomes, free in the cytoplasm, associated with organelles or in the nucleus. The various PRR signal transduction pathways activate one of the IRFs (1, 3, 5, or 7) and occasionally NF κ B, to bind promoter elements in type I IFN genes. To complement the upstream signaling pathways, the promoters of the 13 IFN α subtypes and IFN β genes each contain a distinct number and arrangement of transcription factor binding sites to ensure that one or some of these essential cytokines are produced in response to infection with a broad range of pathogens—both viral and bacterial. This promoter diversity is also likely to be important in determining the IFN subtypes produced by different cell types. A thorough investigation of the many transcription factor binding sites in the promoters of the various type I IFN genes is yet to be performed. However, type I IFNs are not only produced by haemopoietic cells as traditionally thought (originally called "leukocyte" IFN), and recent studies have brought attention to their production by epithelial cells as well [42, 43]. Depending on the expression of signaling molecules, different cell types will differ in their pathways, the repertoire of type I IFNs and the amounts they produce. For example, plasmacytoid dendritic cells (DC) express high levels of constitutive IRF7 and therefore rapidly produce high levels of IFN α compared to other cells. Other cell types respond slower because signaling molecules like IRF7 have to be first induced by IFN.

Two decades of studies in mice deficient in Ifnar 1, through which all type I IFNs signal, have demonstrated the crucial role of this family of cytokines in sculpting the response to viral and bacterial infections [44, 45]. Consistent with this scenario, type I IFNs are never all produced, rarely singly (except IFN β discussed below) and usually in subsets: for example, some IFN α s +/– IFN β .

In addition to the mammalian cell components, properties of the pathogen also determine the nature of the type I IFN response. For viruses, whether they constitutively harbor RNA or DNA, single or double stranded, determines the cellular PRR response. Pathogens also activate different PRRs depending on their cellular niche. For bacteria, whether they are intracellular or extracellular pathogens and the nature of virulence factors (such as pore-forming toxins) that might be necessary to "release" PAMPs to the responding cellular compartment, will determine the nature of the response.

Type I IFN Signaling:Receptors

All type I IFNs characterized to date transduce signals via interaction with the receptor components, IFNAR1 and IFNAR2. IFNAR2 is the high affinity binding chain and can be differentially spliced to produce a "long" form which transduces signals (IFNAR2c); a truncated transmembrane isoform that contain little or no signaling capacity (IFNAR2b); and a soluble form (IFNAR2a). IFNAR2a and c isoforms are conserved between human and mouse, whereas IFN2b is specific to humans [46–48]. Studies in the murine model have demonstrated that *in vitro*, soluble IFNAR2a has the capacity to either block signaling or facilitate signaling via a process called trans-signaling whereby soluble receptor binds ligand and presents it

to the signaling receptor chain [49]. This process can be a major form of signaling as for IL6, but remains to be determined for the type I IFNs. is [50]. In vivo studies have recently indicated that soluble IFNAR2a does not block responses to IFN β [51]. The IFNAR 1 chain has been shown to have very low affinity for binding type I IFNs (with one exception, discussed below), but combines with IFNAR2 to generate a high affinity trimeric complex. IFNAR1 is essential for transducing signals for all type I IFNs characterized so far, as determined from numerous studies of IFNAR1 deficient mice. Both receptors appear to be expressed broadly making most cells responsive to IFN, but there have not been extensive studies on the surface expression of receptor components on individual cell types or at different stages of the host responses.

Type I IFN Signaling: Signal Transduction Pathways

Once ligand engages the receptors, the IFNAR1-associated TYK2 and the IFNAR2associated JAK1 kinases are activated and phosphorylate receptor tyrosine residues [52, 53]. These form docking sites for signal transducers and activators of transcription (STATs), which are themselves phosphorylated, dissociate from the receptors, dimerize and translocate to the nucleus via interaction with importins, and activate the transcription of IFN-regulated genes (IRGs) [54]. Studies have shown that the docking sites for STATs are in the IFNAR2 component of the receptor [52, 55, 56]. The canonical transcription factors of the type I IFN pathway is ISGF3 (composed of a STAT1:STAT2) and IRF9 (also called p48 or ISGF3 γ because it is induced by IFN γ). Nevertheless, type I IFNs also activate STAT3, and dimers of STAT3:STAT3 or STAT1:STAT3 can bind GAS sites (interferon-gamma activated sites) in IRGs (sometimes wrongly thought to be IFN γ -specific) [54]. Indeed, type I IFNs can activate all STATs (4, 5, and 6) depending on the cell type. Indeed in PBMCs, STAT5 is the main STAT activated [57, 58].

There are other signaling pathways activated by type I IFNs. Indeed JAK kinases have other substrates [59] and also function to stabilize the IFNAR1 at the plasma membrane [60]. STAT independent signaling was reported for both type I and type II IFNs in STAT-deficient cells using transcriptional profiling [61], but the signaling pathways responsible were not pursued in those studies. Numerous "alternative" type I IFN signaling pathways have been described, including MAPK (p38 and ERK), NFkB and PI3K/AKT pathways [57, 62]. The best characterized of these is the p38 and Erk MAP kinase (MAPK) pathways, which modulate IRG mRNA translation via activation of Mnk kinases [63]. Activation of AKT/mTOR (mammalian target of rapamycin) signaling is also initiated by IFNs, impacting on translation of IRG mRNA [64, 65]. The relative contribution of these and other alternative IFN signaling pathways is likely to be cell and context dependent. For example, type I IFN signaling in T cells has been reported to utilize T cell receptor signaling molecules for antiproliferative activities [66].

Type I IFN Signaling: Interferon Regulated Genes

There have been many studies documenting the nature of IRGs individually for past decades and more recently by transcriptional profiling by microarrays. In an attempt to capture an overview of the response, we have catalogued available microarray datasets of IFN treated cells or organisms; the data is reanalyzed and annotated then placed in a searchable database called the Interferome (v 2.0 http://interferome.its. monash.edu.au) [67, 68]. This represents a tool for identifying a gene as an IRG, or more importantly, for searching a dataset for IRGs. This collection has identified more than 2,000 IRGs (more depending on the statistical cut-off applied) across species, IFNs, and tissue types. These genes encode the effector proteins that mediate the different biological activities of the IFNs. The number of genes in any given condition is usually smaller, often hundreds, and there is considerable difference between different cells or tissues. There are overlaps between type I, II, and III regulated genes and some apparently IFN type-specific genes, although comparisons are often difficult because of differences in experimental conditions [69]. Tools such as the Interferome are important in finding IRG "signatures" associated with disease that might represent modulation of a particular pathway. We have used Interferome and associated tools to identify an IFN signature activated in HIV infected dendritic cells (a gene set regulated by IRF1, despite HIV suppression of IFN production [70]) and another gene signature suppressed in breast cancer metastases (regulated by IRF7; [13]). Interestingly, an IFN signature has been characterized in latent *M. tuberculosis* infection that appears to correlate with disease pathogenesis and is consistent with studies in animal models showing a role for type I IFN signaling in susceptibility to this pathogen (reviewed in [71]).

The best characterized IRGs are those involved in protecting cells from viral infection; individual ones such as 2'-5' oligoadenylate synthetase, PKR and Mx proteins, having been well characterized for many years [72]. Recently, elegant, comprehensive screening studies of 350 IFN inducible genes have highlighted new IRGs with direct antiviral activities [72]. The studies may inform similar rationales for characterizing the effector functions (anti-bacterial, immunoregulatory) of the many other IRGs. In broad terms the broad repertoire of antiviral IRGs has the ability to restrict different stages of the viral life cycle and different types of viruses, providing broad protection against infection.

Type I Interferon Regulated Antibacterial Responses

Unlike the antiviral effects of type I IFNs, the effects of IFN on bacterial infections are relatively poorly characterized. In general, type I IFNs are protective against extracellular bacterial infections, yet exacerbate infections with intracellular bacteria. This is at least in part due to the differences in organ and cell specificity, the direct effects of IFNs, the impact on cell survival and indirect actions via regulation

of the innate and adaptive immune responses [43, 73, 74]. Examples of direct acting antibacterial IRGs include iNOS, NADPH oxidase, nox-2 [73, 75]; TRAIL [76]; and phospholipidscramblase 1 (PLSCR1) [77]; GTPases [78].

Type I Interferon Regulated Immune Responses

There are many different IRGs, intrinsic or extrinsic to immune cells that can affect the trafficking, development, differentiation, survival, and activity of most innate and adaptive immune cells in response to infections, cancer, and inflammatory diseases (reviewed in [74, 79]). Particular cells and responses have been documented to be important in the response to bacterial infections. TNF α and IFN γ up-regulation by type I IFNs increases protection from S. pneumoniae infection [21]. Repression of type I IFN induced chemokines CXCL10 and CCL5 reduces cells neutrophil infiltration and impairs clearance of *Pseudomonas aeruginosa* from infected lungs [80, 81]. By contrast, type I IFNs suppress the production of other chemokines such as CCL2, CXCL4 and CXCL9, which recruit monocyte/macrophage and neutrophils [75] leading to exacerbation of infection by C. muridarum. Other IRGs include cytokines that activate or repress immune responses including IL10 [82], IL27, and IL17 [83] and FOXP3 which is important in Treg function [74]. Another IFN induced effect that is important in regulating responses to bacterial infection is the induction of apoptosis in infiltrating cells [84]. It is well known that IFNs can regulate the expression of different cell death pathways including bcl-2 and bcl-X [85] and caspase 11 [86] and that IFNs play a role in mediating necroptosis of Salmonella typhimurium infected macrophages [87].

Cross-Talk, Feedback, and Feed Forward

There have been numerous publications about cross-talk of type I IFNs with other systems. In general terms, many of the receptors and signaling components of other signaling systems are, in fact, IRGs and the positive or negative regulation of these factors underlie the basis of cross-talk [88]. These include other cytokines (reviewed in [5]) likely due to priming of STAT levels [89], TLRs and RLRs [5], and the inflammasome [90, 91]. Indeed, we and others have demonstrated that type I IFNs prime the basal levels of hundreds of IRGs, many of which play central roles in signaling by other systems [42, 92]. Important among these are negative regulators such as SOCS1, which are not only rapidly and strongly IFN inducible but play important roles in dampening responses to type I and type II IFNs, other cytokines and TLRs [93–95]. Indeed neonatal mice deficient in SOCS 1 die from multi-organ inflammation in the absence of SOCS1 suppression of type I [94] and type II IFN signaling [93].

Special Case Study of IFNβ

As discussed above, IFN β is different from other type I IFNs in being the only one induced by LPS, thus playing a central role in response to bacteria [92, 96]. In addition, the promoter of IFN β is unusual in having AP1 sites that can be activated by the fos/jun and MAP kinase pathway. This pathway is activated during macrophage development in response to M-CSF and in osteoclast development in response to RANK Ligand [11]. The inhibitory effect of on IFN β on the proliferation of these myeloid cells may be important in the regulation of pathogen responses. In addition to selective production of IFN β relative to other type I IFNs, it has a higher binding affinity to receptors and is more potent than the members of the IFN α family in antiproliferative assays on certain cell types. It is a singularly effective therapeutically in multiple sclerosis [97]. However, until recently, there has been no mechanistic explanation for differential activities of IFNb relative to other type I IFNs..

De Weerd et al. [97] demonstrated that IFN β but not IFN α formed a complex with IFNAR1 in the absence of IFNAR2. Crystallization of the IFN β :IFNAR1 complex showed extensive contacts of this IFN with the receptor over a much larger surface area in that crystal structure than any potential IFN α :IFNAR1 [98]. Further studies of *Ifnar2* null cells showed that while the binding of IFN β to IFNAR1 did not induce canonical STAT signaling as expected, there were signals transduced. Approximately 230 genes were induced by this novel IFN β :IFNAR1 signaling axis by an uncharacterized pathway. Induced genes included several such as TREM1, TREML4, TGM2, and CCL2, which had known roles in the response to sepsis. Using an in vivo murine model of LPS-induced septic shock, it was demonstrated that this unique IFN β :IFNAR1 signaling axis was important in mediating the previously described IFN-mediated toxicity.

Specifically, this study shows molecular mechanisms whereby IFN β can transduce specific signals with pathophysiological importance. In general terms it opens the door for discovering previously elusive selective actions of other type I IFNs by differential interaction with IFNAR1 and IFNAR2. Similarly, cells may regulate the response to type I IFNs by differential regulation of the cell surface expression of IFNAR1 and IFNAR2.

Special Case Study of IFNe

Recently, the function of a specialized type I IFN was reported. IFNe was characterized as a type I IFN based on sequence homology, the location of the gene in the type I IFN gene locus on human chromosome 9p (and syntenic murine chromosome 16) and its signaling through IFNAR1 and IFNAR2 [42, 99]. Recombinant IFNe protein induced "classical" IRGs like other type I IFNs and this signaling was abrogated in cells from *Ifnar1* or *Ifnar2* deficient mice [42]. However, the expression patterns and regulation of this gene showed unique features. Unlike other type I IFNs, it was

not pathogen inducible and was constitutively expressed. This constitutive expression was most notable in the female reproductive tract (FRT). Also unlike other type I IFNs, its expression was regulated by hormones: stimulated by estrogen and repressed by progesterone. Accordingly, its expression fluctuated during the female cycle, was dramatically reduced at the time of embryo implantation in the mouse, and was reduced to virtually undetectable in post-menopausal women, when estrogen levels decline. The in vivo functional importance of IFNE was determined in IFNE-deficient mice. These mice were more susceptible to viral infection with HSV and bacterial infection with C. muridarum. The constitutive production of IFNe in the epithelial cells of the endometrium maintained the basal expression of many IRGs including those involved in pathogen defense (Mx, ISG 15, IRGM1) and PRR sensing and primary signaling (IRF7). This priming of the innate immune response by constitutive IFNe ensures protection of the FRT mucosa from early stages of viral and bacterial infection. Furthermore, the absence of IFNE also restricted bacterial clearance, consistent with the continued production of this protective cytokine before and throughout the course of infection since this pathogen did not modulate IFNe expression in vivo. The levels of NK cells, which have been shown to aid clearance of pathogen, correlated with the levels of IFNE: administration of recombinant mu IFNE to IFNE-null mice restored the depleted levels of NK cells and decreased the number of bacteria recovered 3 days post infection. Interestingly, IFN ε is the only type I IFN that protects the FRT from *Chlamydia* infection. Ifnar1 deficient mice show less severe disease; indicating the exacerbation of disease by production of (presumably conventional, α/β) type I IFNs; shown by adoptive transfer experiments to be acting on CD8 T cells driving disease pathogenesis [75]. This is similar to infections with other intracellular bacteria such as L. monocytogenes, F. tularensis, M. tuberculosis, in which disease pathology is exacerbated by type I IFNs (refer above).

Thus, the actions of IFN ε in protecting the FRT highlight several general principles that might be applicable to IFN anti-pathogen strategies in general: (1) it is a direct example of how regulating expression in a particular way can achieve specific and functional protection; (2) it shows a specific adaptation of the innate immune response to suit organ-specific requirements of host defense; and (3) it shows how compartmentalization of an IFN response can achieve opposite outcomes—epithelial production of IFN ε is protective, whereas mucosal production of conventional IFNs exacerbates disease through their action on immune cells.

Concluding Remarks

The type I IFNs have pleiotropic effects on host defense due to their ability to regulate the parenchymal cells under attack by infectious agents or the innate and adaptive immune cells that traffic to and from the site of infection. While we have made considerable advances in understanding mechanisms of signal transduction via the IFNARs, JAK/STAT and other signal transduction pathways, we are only just beginning to understand the cell context and temporal specificities of type I IFN signaling and responses. This is manifest in the different transcription profiles identified in different cell types responding to IFNs, which represents only a part of the available repertoire of IRGs that encode the effector molecules. Understanding and harnessing the specificity of the response will make inroads into understanding and dealing with the current and emerging threats posed by bacteria and other pathogens.

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