

# Interferon-Stimulated Genes as Influenza Virus Host Restriction Factors

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Influenza virus exploits host factors to promote each step of its lifecycle. In turn, the host deploys antiviral or restriction factors that inhibit or restrict the influenza virus lifecycle at each of those steps. Two broad categories of host restriction factors can exist in virus-infected cells: (1) encoded by the interferon-stimulated genes (ISGs) and (2) encoded by the constitutively expressed genes that are not stimulated by interferons (non-ISGs). There are hundreds of ISGs known, and many, e.g., Mx, IFITMs, and TRIMs, have been characterized to restrict influenza virus infection at different stages of its lifecycle, by (1) blocking viral entry or progeny release, (2) sequestering or degrading viral components and interfering with viral synthesis and assembly, or (3) bolstering host innate defenses.

Keywords: interferon-stimulated genes (ISGs) ; Influenza virus ; Mx ; IFITM3 ; TRIM ; Host Restriction ; Restriction Factors ; Antiviral Factors

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## 1. Introduction

A variety of host factors facilitate and restrict the influenza virus lifecycle at each stage <sup>[1]</sup>. The host factors that restrict the infection are called host restriction factors or antiviral factors and, broadly, can be of two types: (1) encoded by the interferon-stimulated genes (ISGs) and (2) encoded by the genes that are constitutively expressed or are not stimulated by interferons (non-ISGs). Many host restriction factors in both categories have been identified, some through the latest genetic techniques, such as RNA interference and CRISPR-Cas9 and characterized to restrict influenza virus infection.

## 2. Interferon-Stimulated Genes

The expression of ISGs, as the name suggests, is induced by interferons. Interferons are the first line of defense molecules produced by host cells after sensing the virus infection through pattern recognition receptors. The existence of ISGs was first detected in the later part of the 20th century <sup>[2][3]</sup>. Since then, several hundreds of ISGs have been identified <sup>[4]</sup> and characterized to inhibit the infection of many viruses <sup>[5]</sup>. Likewise, many ISGs, encoding both proteins and non-coding RNAs (ncRNAs), have been identified to express in response to the influenza virus infection and restrict its infection at different stages of the viral lifecycle.

### 2.1. Mx Proteins

The Mx (myxovirus) gene encoding an ~75 kDa protein was the first ISG to be discovered to confer resistance to influenza virus infection <sup>[6][7][8][9][10]</sup>. Except for chickens <sup>[11][12][13][14]</sup>, Mx proteins in the majority of influenza virus hosts, e.g., humans <sup>[15]</sup>, pigs <sup>[16][17]</sup>, and horses <sup>[18]</sup>, exhibit antiviral activity. Mx proteins are dynamin-like GTPases <sup>[19][20][21]</sup>, which oligomerize into ring-like structures <sup>[22][23][24][25][26]</sup> and target influenza virus vRNPs to exert their antiviral function <sup>[27][28]</sup>. Human Mx protein interacts with viral NP and PB2 to sense and sequester the incoming vRNPs in the cytoplasm and inhibit their nuclear import and subsequent viral RNA transcription and replication <sup>[18][27][28][29][30][31]</sup>. Human Mx protein is a barrier to the zoonotic transmission of avian influenza viruses and recently discovered bat influenza viruses to humans <sup>[32][33][34][35][36][37]</sup>. To escape this barrier, avian influenza viruses acquire human-adaptive mutations in their NPs or increase their RNA polymerase activity or vRNP nuclear export <sup>[33][36][37][38][39][40][41]</sup>. Some influenza viruses can also escape this barrier in humans and animals carrying naturally occurring Mx allele variants, which either lack or exhibit reduced antiviral activity <sup>[16][42][43][44][45][46]</sup>.

### 2.2. IFITM Proteins

The IFITM (interferon-inducible transmembrane) genes encoding 14–16 kDa proteins were identified as ISGs around the same time as the Mx gene <sup>[47][48][49][50]</sup>. However, the antiviral function of IFITM proteins 1, 2, and 3 during influenza virus

infection was discovered much later in a genomic screen [51]. IFITM proteins are broad host restriction factors of the influenza virus, as IFITMs from multiple host tissues and species (including bacteria [52]) are capable of inhibiting influenza virus infection [53][54][55][56][57][58][59][60][61][62][63][64][65][66][67]. IFITMs 1, 2, and 3 are closely related proteins and share 70–90% homology, and all three inhibit influenza virus infection by inhibiting its entry to the host cells [51]. IFITM3 is a type II transmembrane protein and localizes to the endosomes and lysosomes, where it interacts with influenza virus HA and prevents the fusion of viral envelope with the endosomal membrane by interfering with lipid homeostasis, consequently preventing vRNP release into the cytoplasm [68][69][70][71][72][73][74][75][76][77][78][79].

The antiviral activity of IFITM3 is regulated by posttranslational modifications like palmitoylation, ubiquitination, and methylation [59][80][81][82][83][84][85][86]. Specifically, the palmitoylation of IFITM3 promotes its antiviral activity by enhancing its membrane affinity and endosomal localization [59][80][81][82][87]. In contrast, the ubiquitination of IFITM3 reduces its antiviral activity by decreasing its stability and localization to the endosomes [81][85]. Also, the methylation of IFITM3 reduces its antiviral activity and influenza disease severity [83][86]. The phosphorylation of IFITM3 reduces its ubiquitination and may indirectly promote its antiviral activity [84]. These findings indicate that the influenza virus potentially employs the ubiquitin ligases, e.g., NEDD4 [85], and methyltransferases, e.g., SET7 [86], to antagonize the antiviral function of IFITM3 and escape IFITM3 restriction. Furthermore, avian influenza A virus subtypes H5N1 and H7N9 may escape IFITM3 restriction in cells with inefficient endosomal acidification [88].

Influenza virus may also escape IFITM3 restriction and cause severe disease in humans carrying single nucleotide polymorphisms (SNPs) in the IFITM3 gene [54][89][90]. The IFITM3 allele carrying SNP rs12252-C encodes an N-terminally truncated IFITM3 variant, which is incapable of localizing to the endosomes and allows the influenza virus to escape IFITM3 restriction [54][71][91][92]. Consequently, rs12252-C has been associated with severe influenza disease [54]. However, the evidence of this association has been found in studies involving the cohorts mainly from Asian ethnicity [90][93][94][95][96][97][98][99][100] and not from other ethnicities [101][102][103][104][105][106][107]. Further, the SNPs in IFITM1 are not associated with influenza disease severity [108].

## 2.3. TRIM Proteins

TRIM (tripartite motif) proteins are a large family of proteins that comprise a conserved architecture known as RBCC (a RING finger domain, one to two B-box domains, a coiled coil domain, and a variable C-terminus) [109][110]. Among TRIMs, TRIM19, also known as promyelocytic leukemia (PML) protein, was the first to be identified as an ISG [111]. Soon after, it was discovered to inhibit influenza virus infection [112]. Now, over 80 TRIMs are known [110], of which at least 27 TRIMs have been identified as ISGs [113]. In addition to TRIM19, TRIMs 14, 21, 22, 25, 35, and 56 have been shown to inhibit influenza virus infection [114][115][116][117][118][119][120][121]. TRIMs are E3 ubiquitin ligases and are part of the ubiquitin–proteasome system, which degrades proteins. Hence, most TRIMs exert their antiviral function by targeting the viral proteins for degradation. Specifically, TRIM14 [117] and TRIM22 [114] target viral NP, TRIM21 targets viral M1 [122], and TRIM35 targets viral PB2 [118] for ubiquitin ligase-dependent degradation. However, the NP of some influenza A virus H1N1 subtypes is resistant to TRIM22-mediated restriction [123]. The TRIM25 [116][120] and TRIM56 [115] interfere with viral RNA synthesis or stability though in an E3 ligase-independent manner. Also, TRIM25 has been reported to inhibit influenza virus infection by facilitating its RIG-I-mediated host sensing in a ubiquitin ligase-dependent manner [124][125][126][127]. However, influenza virus antagonizes the latter function of TRIM25 via NS1 protein, which is the main influenza virus virulence factor that antagonizes host defenses. NS1 binds TRIM25 and interferes with its ubiquitin ligase activity [124][125][126][127][128].

## 2.4. OAS Proteins

OAS (2',5'-oligoadenylate synthetase) proteins 1, 2, and 3, and OAS-like (OASL) protein were among the first ISGs to be discovered [129][130]. OAS 1, 2, and 3 are activated by sensing the viral RNA and then convert the ATP to 2',5'-oligoadenylate [130], which, in turn, activates the ribonuclease (RNase) L [131]. Subsequently, RNase L restricts influenza virus infection by degrading the viral RNA [132][133][134]. However, OASL restricts influenza virus infection in an RNase L-independent manner [135]. In turn, influenza virus escapes the OAS-mediated restriction via NS1, which competes with OAS proteins for viral RNA binding [132]. Furthermore, the influenza virus may escape this restriction in humans carrying the SNP rs10774671 in OAS1 gene [136].

## 2.5. IFIT Proteins

The IFIT (interferon-induced proteins with tetratricopeptide repeats) family has four proteins, IFITs 1, 2, 3, and 5 (or ISGs 56, 54, 60, and 58, respectively), which have been characterized in humans [137]. IFIT1 is the prototypic member of the family and was the first to be identified as an ISG in the IFIT family [138][139], followed by the rest [137]. The indication of an

antiviral function of human IFITs 1, 2, and 3 during influenza virus infection was first discovered in a proteomic screen [140]. Later, it was demonstrated that human IFITs 1, 2, and 3 and avian IFIT5 exhibit antiviral properties during influenza virus infection [141][142][143][144][145]. The human and chicken IFITs exert their antiviral function by sequestering the viral RNA by binding its 5'-triphosphate group, called PPP-RNA [140][143][146], whereas the duck IFIT sequesters viral NPs [142]. However, Pinto et al. found no antiviral activity of human IFIT1 during influenza virus function [147], while Tran et al. found influenza virus rather exploiting the RNA binding property of IFIT2 to promote viral mRNA translation [148].

## 2.6. hGBP Proteins

The hGBPs (human guanylate-binding proteins), like Mx proteins, belong to GTPase family [149][150], and hGBPs -1, -2, -3, and -5 have been shown to inhibit influenza virus infection [151][152][153][154]. The hGBP-3 exerts its antiviral function by targeting viral RNA polymerase activity [151], whereas hGBP-2 and hGBP-5 target the host furin protease, which primes the HA of the highly pathogenic influenza A viruses, like H5N1 subtype, for infection [153]. Nevertheless, influenza virus NS1 antagonizes the hGBP-1 by inhibiting its GTPase activity [154].

## 2.7. Tetherin

Tetherin, also known as BST-2/CD317/HN1.24, is a GPI-anchored transmembrane protein [155] and restricts virus infection by tethering the viral progeny to the cell surface. The antiviral role of tetherin during influenza virus infection is inconclusive and has been controversial. However, tetherin expression is induced in influenza virus-infected cells in an interferon-dependent manner [156]. Human tetherin was observed to effectively tether the budding influenza virus-like particles to the plasma membrane [157][158][159][160]; however, the same was not observed with live influenza virus particles [156][157][161] or tetherin from other host species [162][163]. In other studies, tetherin was observed to inhibit the influenza virus release [159][160][164][165], but this restriction was either viral NA-dependent [159][165] or countered by viral M2 protein, which facilitated the downregulation of tetherin on the cell surface [160].

## 2.8. ISG15

ISG15 gene [166] encodes a 15-kDa protein [167], which inhibits the influenza virus infection [168] by targeting critical viral [169][170] and host [171] proteins. ISG15 is a ubiquitin-like protein [167] and is conjugated to target proteins by sequential action of several conjugation enzymes, some of which are also ISGs [172][173][174][175][176][177]. This process is also called 'ISGylation'. ISG15 ISGylates influenza virus NS1 protein and cripples its ability to perform various antagonistic functions [169][170]. Further, the ISGylation of host protein Tsg101 inhibits the trafficking of viral HA to the plasma membrane, the site of influenza virus assembly [171].

## 2.9. PKR

PKR (protein kinase R) is a dsRNA-activated serine/threonine protein kinase and phosphorylates the eukaryotic translation initiation factor 2 (eIF-2 $\alpha$ ); this leads to the inhibition of the initiation of global protein synthesis [178]. This leads to the inhibition of viral protein synthesis too, and consequently, the influenza virus infection [179][180]. Influenza virus counteracts this restriction through NS1, which binds to dsRNA and blocks PKR activation [180][181][182]. Influenza virus NP also can block PKR activation by activating the cellular PKR inhibitor, P58 [183].

## 2.10. Other Proteins

CEACAM1 (carcinoembryonic antigen-related cell adhesion molecule 1) expression was first shown to be induced by interferon-gamma [184]. CEACAM1 inhibits influenza virus infection by suppressing the mTOR (mammalian target of rapamycin) activity, consequently inhibiting the global protein synthesis in infected cells [185].

IFI16 (interferon  $\gamma$ -inducible 16) is a ~80-kDa nucleic acid-binding protein [186][187]. IFI16 is a PYHIN (pyrin and hematopoietic interferon-inducible nuclear (HIN) domain) family protein and was initially identified as an intracellular DNA sensor [188]. Recently, IFI16 has been discovered to inhibit influenza virus infection by sensing the viral RNA and promoting the RIG-I-mediated innate antiviral response [189][190].

ISG20 (interferon-stimulated gene 20), as the name suggests, is a 20-kDa protein with 3' to 5' exonuclease activity that is specific for single-stranded RNA [191][192]. ISG20 inhibits influenza virus infection by interfering with viral RNA transcription and replication [193][194].

MOV10 (Moloney leukemia virus 10) is a member of the RNA helicase superfamily [195], and its expression can be stimulated by interferons [5]. MOV10 inhibits influenza virus infection by binding to NP and sequestering the incoming

vRNPs in the cytoplasm, consequently inhibiting their nuclear import <sup>[196][197][198]</sup>. However, the antiviral function of MOV10 is independent of its RNA helicase activity <sup>[197][198]</sup>.

MUC1 (mucin 1) is a member of mucins, a family of highly glycosylated proteins that are expressed on the surface of respiratory epithelial cells, which are the target of influenza virus infection. MUC1 potentially acts as a receptor decoy and inhibits influenza virus infection by binding to virus particles and blocking their attachment to target cells <sup>[199][200][201]</sup>.

NCOA7 (nuclear receptor coactivator 7) expression is induced by the interferon-beta <sup>[202]</sup>. NCOA7 inhibits influenza virus infection by inhibiting the fusion of viral envelope with the endosomal membrane during entry <sup>[203]</sup>.

The p21 is a cyclin-dependent kinase inhibitor and inhibits influenza virus infection by interfering with viral RNA polymerase activity <sup>[204]</sup>.

Serpin 1 or plasminogen activator inhibitor 1 (PAI-1) inhibits influenza virus infection by neutralizing host proteases, like trypsin, and preventing the cleavage of HA, which is required for influenza virus entry <sup>[205]</sup>. However, influenza virus may escape this restriction in humans carrying the naturally occurring SNP rs6092 in serpin 1 gene <sup>[205]</sup>.

SERTAD3 (SERTA domain containing 3), also called RBT1 (replication protein A binding transactivator 1), is one of the SERTA family transcription factors, and its expression is induced by the interferons <sup>[206]</sup>. SERTAD3 inhibits influenza virus infection by disrupting the formation of viral RNA polymerase complex <sup>[206]</sup>.

SLFN11 and SLFN14 are Schlafen family proteins and possess an RNA helicase domain <sup>[207]</sup>. SLFN11 and SLFN14 expression is induced by the interferons, and both inhibit influenza virus infection by contributing to host innate defenses <sup>[208][209]</sup>.

SPOCK2 (SPARC/osteonectin CWCV and Kazal-like domains 2) or testican 2 is a secreted proteoglycan, and it inhibits influenza virus infection by blocking the attachment of virus particles to cell surface <sup>[210]</sup>.

RABGAP1L (RAB GTPase-activating protein 1-like) or TBC1D18 (Tre2/Bub2/Cdc16 (TBC)-domain-containing 18) protein restricts influenza virus infection by disrupting the endosome function hence virus entry <sup>[211]</sup>.

Viperin (virus inhibitory protein, endoplasmic reticulum-associated, interferon-inducible) protein <sup>[212]</sup>, also called RSAD2, inhibits influenza virus infection by disrupting the lipid rafts on the plasma membrane and inhibiting viral progeny release <sup>[213][214]</sup>.

ZAP (zinc finger antiviral) or ZC3HAV1 (Zinc finger CCCH-type antiviral 1) protein exists in two forms, short (ZAPS) and long (ZAPL), and both forms exhibit anti-influenza virus properties <sup>[215][216][217]</sup>. The ZAPS exerts its antiviral function by promoting the degradation of viral mRNA but is antagonized by NS1, which competes with ZAPS for viral mRNA binding <sup>[216]</sup>. Whereas ZAPL promotes the degradation of viral PA and PB2 and is antagonized by viral PB1, which binds ZAPL and displaces PA and PB2 <sup>[215]</sup>.

## 2.11. ncRNAs

Much of the human genome is transcribed into non-coding RNAs (ncRNAs), which do not translate into a protein. Based on their length, these ncRNAs are called microRNAs or miRNAs (~22 nucleotides), small-interfering RNAs or siRNAs (21–25 nucleotides), piwi-related RNAs or piRNAs (24–33 nucleotides), vault RNAs or vtRNAs (80–150 nucleotides), or long non-coding RNAs or lncRNAs (>200 nucleotides). Further, some lncRNAs exist as covalently-closed circular RNAs or circRNAs. Many ncRNAs are upregulated in response to the influenza virus infection and inhibit infection by targeting the viral proteins and critical host proteins <sup>[218]</sup>.

The lncRNAs are the prominent form of ncRNAs that have been identified to be upregulated in response to the influenza virus infection or interferon treatment <sup>[219][220][221][222][223][224][225][226]</sup>. Those lncRNAs inhibit influenza virus infection primarily by strengthening the antiviral state in infected cells through various mechanisms, e.g., stabilization of RIG-I–TRIM25 complex for host sensing of influenza virus <sup>[220]</sup>, epigenetic modifications of regulatory regions of innate response genes <sup>[223][225]</sup>, and manipulation of regulators (including miRNAs) of interferon signaling <sup>[219][221][224][226]</sup>.

Also, circRNAs, circVAMP3, and AIVRs are upregulated in response to influenza virus infection and restrict the infection by different mechanisms <sup>[227][228]</sup>. The circVAMP3 acts as a decoy to viral NP and NS1 and interferes with their function <sup>[228]</sup>, while the AIVR sequesters a microRNA, which degrades an enhancer of the interferon production <sup>[227]</sup>.

In addition, the miRNAs, miR-101, miR-485, ssc-miR-221-3p, and ssc-miR-222, have been identified to be upregulated in response to influenza virus infection and inhibit infection by distinct mechanisms <sup>[229][230][231]</sup>. The miR-101, like ISG CEACAM1 <sup>[185]</sup>, inhibits influenza virus infection by targeting the mTOR pathway <sup>[230]</sup>, whereas miR-485 targets host RIG-I and viral PB1 and reduces their mRNA levels <sup>[229]</sup>. Further, swine ssc-miR-221-3p and ssc-miR-222 may restrict the interspecies transmission of avian influenza viruses to pigs by targeting their viral RNA <sup>[231]</sup>.

### 3. Summary

A plethora of ISGs has been identified that restrict the influenza virus infection by inhibiting viral attachment, entry, synthesis, assembly and release, and strengthening the host innate antiviral response. However, influenza virus seems to have the upper hand and effectively antagonizes the restriction imposed by ISGs. Furthermore, the genetic diversity of some ISGs (IFITM3, Mx, OAS-1, Serpin-1) in various hosts and human populations also helps influenza virus to escape host restriction. Nevertheless, an exhaustive list of influenza virus host restriction factors and their restriction mechanisms is yet to be compiled.

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