Chicken Interferon-Inducible Transmembrane Protein 3 Restricts Influenza Viruses and Lyssaviruses In Vitro

S. E. Smith,a M. S. Gibson,b R. S. Wash,a F. Ferrara,c E. Wright,d N. Temperton,c P. Kellama,ef M. Fifeb

Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, United Kingdom;a The Pirbright Institute, Compton Laboratory, Compton, Berkshire, United Kingdom;b Viral Pseudotype Unit, School of Pharmacy, University of Kent, Chatham Maritime, Kent, United Kingdom;c Viral Pseudotype Unit (Fitzrovia), School of Life Sciences, University of Westminster, London, United Kingdom;d MRC/UCL Centre for Medical Molecular Virology, Division of Infection and Immunity, University College London, London, United Kingdome

Interferon-inducible transmembrane protein 3 (IFITM3) is an effector protein of the innate immune system. It confers potent, cell-intrinsic resistance to infection by diverse enveloped viruses both in vitro and in vivo, including influenza viruses, West Nile virus, and dengue virus. IFITM3 prevents cytosolic entry of these viruses by blocking complete virus envelope fusion with cell endosomes membranes. Although the IFITM locus, which includes IFITM1, -2, -3, and -5, is present in mammalian species, this locus has not been unambiguously identified or functionally characterized in avian species. Here, we show that the IFITM locus exists in chickens and is syntenic with the IFITM locus in mammals. The chicken IFITM3 protein restricts cell infection by influenza A viruses and lyssaviruses to a similar level as its human orthologue. Furthermore, we show that chicken IFITM3 is functional in chicken cells and that knockdown of constitutive expression in chicken fibroblasts results in enhanced infection by influenza A virus. Chicken IFITM2 and -3 are constitutively expressed in all tissues examined, whereas IFITM1 is only expressed in the bursa of Fabricius, gastrointestinal tract, cecal tonsil, and trachea. Despite being highly divergent at the amino acid level, IFITM3 proteins of birds and mammals can restrict replication of viruses that are able to infect different host species, suggesting IFITM proteins may provide a crucial barrier for zoonotic infections.

Type I and II interferons (IFNs) are critical for the development of the cell intrinsic antiviral state and achieve this by inducing the expression of genes collectively named IFN-stimulated genes (ISGs). Expression of the interferon-inducible transmembrane (IFITM) genes (new members of the ISG family) restricts the replication of several highly pathogenic human viruses, including severe acute respiratory syndrome (SARS) coronavirus, filoviruses (Marburg virus and Ebola virus), influenza A viruses (IAVs), and flaviviruses (dengue virus) (1, 2). Although restriction of HIV-1 infection has also been reported in some studies (3, 4), others have failed to demonstrate such activity (1). IFITM proteins are small, with an average size of 130 amino acids, and share a topology (5) defined by a conserved CD225 domain (6). This domain consists of two intramembrane (IM) regions and a conserved intracellular loop (CIL).

As their names suggest, IFITM proteins are upregulated by type I and II IFNs; however, some cell and tissue types express constitutive levels of one or more of these proteins (7). In humans, IFITM1, -2, and -3 are expressed in a wide range of tissues, while IFITM5 expression is limited to osteoblasts. Mice have orthologues for IFITM1, -2, -3, and -5 and additional IFITM genes, Ifitm6 and Ifitm7 (8). Genome analysis of chickens has predicted the existence of two IFITM genes, orthologous to human IFITM10 (huIFITM10) and huIFITM5 (9). However, such in silico analysis is often confounded by inappropriate identification of pseudogenes and incorrect assignment of orthologues, due to an incomplete knowledge of IFITM gene duplication and evolutionary history of this locus during speciation. Under such circumstances, careful genome analysis of syntenic regions and functional characterization of genes are required to attempt to unambiguously define orthologous genes.

IFITM proteins are the only mediators of innate immunity known to inhibit viral infection by blocking cytoplasmic entry and replication of diverse enveloped viruses (10). IFITM-mediated viral restriction occurs at entry sites of susceptible viruses, in the late endosomal and lysosomal compartments, where the proteins are predicted to adopt an intramembrane structure. The N and C termini of the proteins are predicted to be cytoplasmic, the two intramembrane domains are buried within the cytoplasmic facing lipid bilayer, and the CD225 domain is thought to be facing the cytoplasm (11). IFITM proteins inhibit formation of a fusion pore between the virus and endosomal membranes following acidic activation of virus envelope fusion proteins. Recently, the ability of IFITM proteins to alter cellular membrane fluidity was demonstrated, leading to the arrest of fusion pore formation at the stage of hemimembrane fusion (12). Furthermore, it was recently found that IFITM3 interacts with vesicle-membrane-protein-associated protein A (VAPA) and prevents its association with oxysterol-binding protein (OSBP) (13), which disturbs intracellular cholesterol homeostasis and thus causes inhibition of viral fusion in the late endosome, by an unknown mechanism.

The high constitutive levels of IFITM proteins observed in many tissues potentially provide a first line of defense against virus infection. The induction of type I IFNs further promotes IFITM expression, increasing their protective effect on sur-
rounding uninfected cells. Depletion of Ifitm3 in mouse cells results in a loss of 40% to 70% of IFN-α’s protective effect against endosomal entering viruses (1). A similar attenuation is also observed from cells derived from IfitmDel mice, lacking Ifitm1, -2, -3, -5, and 6, suggesting IFITM3 accounts for most of the antiviral activity of this locus for the viruses investigated (14). Importantly, mice homozygous for Ifitm3 deletion suffer fulminant viral pneumonia when challenged with low-pathogenicity IAV (14, 15). Direct clinical relevance of IFITM3’s involvement in restricting human IAV infection has recently been shown in individuals hospitalized with seasonal or pandemic influenza H1N1/09 viruses (15), where a statistically significant number of hospitalized patients show overrepresentation of a minor C allele in IFITM3 (rs12252-C) that correlates with a decrease in the ability of IFITM3 to restrict influenza virus infection in vitro. Importantly, the significance of the association of the rs12252-C allele with severe influenza infection was recently replicated in a Chinese cohort of patients (16). Together, these data reveal that the action of IFITM3 profoundly alters the course of influenza virus infection in mammals and that allelic variation in IFITM3 alters host susceptibility to severe influenza virus infection. Although IFITMs have been well characterized in humans and mice, little compelling functional data exists for this ISG family in other species.

Avian IAVs represent a continuing threat to human populations both as a source for direct human infection and as a reservoir for IAV genetic variation. These reservoirs provide the conditions for the generation of reassorted IAVs with altered host ranges and pandemic potential (17). Furthermore, endemic and emerging avian viral pathogens create major challenges to the poultry industry through loss of productivity and mortality. Similarly, lyssaviruses, particularly rabies virus (RABV), pose a substantial public health threat, with half of the world’s population living in areas of endemicity (18), although reports of avian lyssavirus infections are rare. The clinical presentations of an infection are identical for all lyssavirus species; however, while current vaccines and postexposure prophylaxis provide sterilizing immunity against RABV and genetically similar species, no such protection is conferred by HA flow cytometric analysis. Transfected cells were harvested at 1 × 10⁷ cells well on coverslips in a 12-well plate 1 day prior to transfection with an IFITM-encoding plasmid (1 μg DNA with 3 μl of Fugene 6 (Promega)). Cells were fixed with 100% methanol for 10 min followed by being blocked in 1% bovine serum albumin (BSA) for 30 min. The HA epitope was targeted by an anti-NA antibody conjugated to Alexa Fluor 550 (ab17513), and endosomes were visualized by a Lamp1 antibody with human (ab25630; Abcam) or chicken (LEP100 IgG; Developmental Studies Hybridoma Bank) specificity, followed by incubation with a secondary antibody conjugated to Alexa Fluor 488 (ab96871; Abcam).

Flow cytometric analysis. Transfected cells were harvested using 300 μl 0.25% trypsin-EDTA (Life Technologies), neutralized with 300 μl of cell culture medium plus 10% FBS, and pooled with the supernatant. The cells were spun at 2,000 × g for 5 min, and the pellet was resuspended in 100 μl PBS and transferred to a 96-well V-bottomed plate (Nunc). The plate was centrifuged, and the cells were fixed and permeabilized in 100 μl of Cytofix/Cytoperm buffer (Becton, Dickinson) and washed according to the manufacturer’s guidelines. The cells were resuspended with the anti-NA antibody conjugated to fluorescein isothiocyanate (FITC) (A190-108F; Cambridge Bioscience) and incubated for 1 h at 4°C, followed by two rounds of washing. IAV replication was detected by antinucleoprotein (anti-NP) antibody (ab128193; Abcam) followed by incubation with anti-mouse Alexa Fluor 650 (ab96882; Abcam). Cells were resuspended in 300 μl of PBS before analysis by flow cytometry (FACSCalibur II; Becton, Dickinson).

Infection of IFITM-expressing cell lines with pseudotyped viruses. Chicken or human IFITM-expressing A549 cell lines were seeded at 3 × 10⁵ cells/well in 96-well plates 1 day prior to infection with either green fluorescent protein (GFP)-expressing pseudotyped lyssaviruses, RABV challenge virus standard 11 (CVS-11; GenBank accession no. EU352767) and Lagos bat virus (LBV) (LBV.NIG56-RV1; GenBank accession no. HM623779), luciferase-expressing pseudotyped influenza viruses (H1A1 [GenBank accession no. AF172241], H5 [GenBank accession no. EF541394], H7 [GenBank accession no. AJ491720], and H10 [GenBank accession no. CY014671]) or amphotrophic murine leukemia virus (MLV-A). GFP expression, as a measure of lentivirus infection, was determined by fluorescence microscopy at 48 h postinfection following fixation (20 min) with 4% (vol/vol) paraformaldehyde (USB) and permeabilization (10 min) using 0.3% Triton X–PBS. Cells were washed with 100 μl of PBS-Hoechst solution (Life Technologies) (200 ng/ml), and a plate seal was adhered. The fixed cells were analyzed to determine the proportion of cells expressing GFP (Cellomics ArrayScan VTI; Thermofisher).
using the Target Activation bioapplication. Briefly, this method counts every cell on the plate by drawing a perimeter around each of the nuclei (detected by Hoechst) and calculates the percentage of these cells also expressing GFP. Luciferase activity, as a measure of lentivirus infection, was determined at 48 h postexposure using 50 μl Bright-Glo reagent (Promega). The cells were allowed to lyse for 2 min before the level of luciferase activity was measured using the FLUOstar Omega (BMG Labtech). GFP and luciferase levels are reported relative to infection of A549 cells in the absence of IFITM protein overexpression.

**siRNA knockdown studies.** DF-1 chicken cells were seeded at 5 × 10^4 cells/well in a 24-well plate and transfected with a small interfering RNA (siRNA) against chIFITM3 (GCCGAGTACCTGGAACATCCAG) or a nonspecific siRNA (UUUCCGACAGGUUGACGUGG), using Lipofectamine RNAiMAX (Life Technologies) 48 h prior to IFN stimulation. The cells were stimulated by addition of either 200 ng/ml of chicken IFN-γ (RP0115c; Kingfisher Biotech) or chicken IFN-α (PAP004; AbD Serotec) for a further 24 h or infected with IAV (A/WSN/1933 [WSN/33]) for 1 h at a multiplicity of infection (MOI) of 0.1. RNA was extracted according to the manufacturer’s instructions (RNeasy minikit; Qiagen). Reverse transcription-PCR (RT-PCR) was performed (QuantiTect Multiplex RT-PCR kit; Qiagen) using probes and primers from ABI (chicken glyceraldehyde-3-phosphate dehydrogenase [GAPDH], 4484889; and chicken IFITM3, custom assay). Influenza virus infection was measured by flow cytometric analysis (see above) using an anti-NP antibody (ab20921; Abcam) to determine cell infection.

**Plaque assays.** Material to be assayed was serially diluted in serum-free DMEM and used to infect MDCK cells in 12-well plates. After 1 h of incubation, the inoculum was removed, and the wells were overlaid with DMEM containing 0.2% BSA (Sigma-Aldrich), 1.25% Avicel (FMC Biopolymer), and 1 μg trypsin ml⁻¹ (21). After 2 days, the overlay was removed, and the wells were fixed with 4% formal saline–PBS solution for 20 min before being stained with 0.1% toluidine blue solution (Sigma-Aldrich) so that the number of PFU could be calculated.

**Expression of IFITM proteins in different chicken tissues.** Tissues were removed from 3-week-old specific pathogen-free (SPF) Rhode Island Red (RIR) chickens, specifically thymus, spleen, bursa of Fabricius, cecal tonsil, gastrointestinal tract, trachea, bone marrow, brain, muscle, heart, liver, kidney, lung, and skin. RNA was DNase treated, and reverse transcription was carried out (SuperScript III reverse transcriptase; Life Technologies). The cDNA from each tissue was amplified by PCR using the following primer sets: chIFITM1 (5'-AGGACACCACTGATCAACA TGG, R'-CTACCAAGTCTCTGGAAGATGA), chIFITM2 (5'-AGGGTGAC ATCCCGGCTCAC, R'-ACCAGGAGAACCTTCCAGG), chIFITM3 (5'-GGAGTCCACCGTTATGAC, R'-GGGGCTCCTACGTCACA), and chicken GAPDH (glyceraldehyde-3-phosphate dehydrogenase) (5'-ACTGTCAGAGGCTGAGAACGG, R'-GCTGAGGGAGCTGAGATGA).

**RESULTS**

**Identification of the chicken IFITM locus.** The chicken genome (ENSEMBL version, version 2.1) contains two putative IFITM genes on chromosome 5, the so-called IFITM5 (ENSGALG000000004239; chromosome 5:1620304 to 1621805:1) and IFITM10 (ENSGALG00000020497; chromosome 5:15244061 to 15249351:1). The putative IFITM5 gene is located next to an uncharacterized gene (ENSGALG00000006478), with which it shares 30% amino acid identity. Immediately adjacent to this are three sequence gaps whose estimated sizes are 1 kb, 1 kb, and 400 bp in the ENSEMBL chicken genome build. Importantly, the putative IFITM genes in chicken are flanked by the telomeric β-1,4-N-acetyl-galactosaminitoltransferase 4 (B4GALNT4) gene and the centromeric acetylaspartic acid transferase-like 1 (ATHL1) gene. The B4GALNT4 and ATHL1 genes flank the antiviral IFITM 1, 2, -3, and -5 gene block in mammalian genomes. Sequence similarity searches of the most recent build of the chicken genome (v4.0, NCBI) using TBLASTN analysis and the putative IFITM5 amino acid sequence, revealed several transcripts with high amino acid identity to IFITM5. Additionally, BLAST hits were also identified to putative genes LOC770612 and LOC422993, within the locus flanked by B4GALNT4 and ATHL1. Between these putative genes, two BLAST hits span the exons of genes designated chicken IFITM3-like (NCBI, LOC422993; GenBank accession no. XM_420925.4) and IFITM1-like (NCBI LOC770612; GenBank accession no. XM_001233949.3). A third BLAST hit matches an uncurated gene, “gene 376074,” which is positioned between IFITM3-like and IFITM5. Further analysis of gene 376074 showed it shared amino acid sequence identity with both IFITM3-like and IFITM1-like genes. Sequence similarity searches of the NCBI chicken expressed sequence tag (EST) database suggests gene 376074 is expressed. All of the chIFITM paralogues, like mammalian IFITMs, are comprised of two exons, and the location of the intron-exon boundary is conserved across all of the chicken IFITM genes. Therefore, the chicken genome contains an intact IFITM locus with four putative IFITM genes flanked by the genes B4GALNT4 and ATHL1 (Fig. 1A).

**Annotation of the chicken IFITM genes.** Using genome synteny, we ascribe chIFITM5 as orthologous to mammalian IFITM5, gene 376074 as orthologous to IFITM2, LOC422993 (IFITM3-like) as orthologous to IFITM1, and LOC770612 (IFITM1-like) as orthologous to IFITM3. Multiple amino acid sequence alignments between the three predicted antiviral chIFITM genes and direct orthologues in primate species suggest this assignment is plausible. A number of conserved IFITM family motifs are present in some of the chicken sequences (Fig. 1B), and although the chicken sequences differ significantly from the human and chimpanzee orthologues, many amino acids in the CIL domain are conserved. Multiple sequence alignments also reveal important amino acids in the chicken IFITMs that help to categorize each sequence as either IFITM1 or IFITM2/3. Tyr20 is conserved in all primate IFITM2 or -3 sequences and is also present in chicken “IFITM1-like” (NCBI) but none of the other IFITM1 orthologues. This, as well as the longer N terminus, further supports our assessment of this gene as an IFITM2 or -3 gene, and by synteny, the gene is IFITM3. The alignment also reveals that other functionally significant amino acids are conserved in some of the chicken IFITM sequences, including the two cysteines (Cys75 and -76) in IM1 so that the number of PFU could be calculated.

**Subcellular localization of IFITM proteins.** Human IFITM1, -2, and -3 localize distinctly in the cell, with IFITM1 being predominantly cell surface expressed and IFITM2 and -3 being predominantly intracellular, localizing with endosomes (Fig. 2D and E). The cellular localization of IFITM proteins can further delineate their orthologous relationships. We therefore synthesized codon-optimized, C-terminal HA-tagged chIFITM1, -2, and -3 transiently transfected chicken DF-1 fibroblasts, comparing their cellular localization to the orthologous human IFITM (hu-IFITM) proteins expressed in human A549 cells. Confocal microscopy using an anti-HA antibody and an anti-LAMP1 antibody showed chIFITM1 was diffusely expressed throughout the cyto-
plasm, and chIFITM2 was present in the cytoplasm and the cell membrane, whereas chIFITM3 localized perinuclearly (Fig. 2A to C), consistent with huIFITM3. chIFITM3 therefore shares synteny, amino acid similarity, and subcellular localization with huIFITM3. In the case of the other two chIFITMs, their localization is less clearly paired with the human IFITMs; thus, our nomenclature is founded on the gene order.

**Chicken IFITM proteins restrict diverse virus infection.** We investigated if, despite considerable amino acid sequence divergence, chicken IFITMs could function as restriction factors. By expressing chIFITM3 at different levels in the cell, we show that there is a strong expression-level-dependent correlation between the level of chIFITM3 expression and the percentage of cells infected by a lentivirus vector pseudotyped with the lyssavirus envelope of LBV (Fig. 3). We then compared the level of antiviral restriction of chicken IFITM2 and -3 to that of their orthologous human proteins in A549 cells. Overexpression of chIFITM3 resulted in 79.4% and 85% reductions in infection of A549s to lentivirus vectors pseudotyped with the lyssaviruses envelopes RABV and LBV, similar to the level of restriction by huIFITM3 to the same viruses (Fig. 4A), even though chickens are rarely infected by lyssaviruses (23). chIFITM2 also restricts lyssavirus LBV and RABV infection to a similar level as chIFITM3. A similar pattern of restriction is seen for lentiviruses pseudotyped with IAV H1, H5, H7, and H10 (Fig. 4B). huIFITM3 restricts viral infection of all influenza virus hemagglutinins, reducing infection by greater than 90%, and chIFITM3 restricts H1 and H10 pseudotypes as effectively, but restricts H5 and H7 less well. chIFITM2 and huIFITM2 restrict more moderately, as shown by others. Consistent with previous studies on huIFITM3 protein (1, 2), chIFITM3 failed to restrict MLV-A (Fig. 4D). Overall, although chIFITM3 and huIFITM3 only share 42% amino acid identity, the level of viral restriction of chIFITM3 is similar to that in huIFITM3. Data are not shown for chIFITM1, as a stably expressing cell line could not be made; this lack of stability at high expression levels is supported by Hach et al. (24), who show that overexpression of unpalmitoylated murine IFITM1 is difficult to achieve.

**Ablation of IFITM expression in chicken DF-1 cells increases infection.** We assessed the constitutive level of expression of chIFITM3 in DF-1 cells, by quantitative RT-PCR with primers for chIFITM3. DF-1 cells abundantly express chIFITM3. DF-1 cells abundantly express chIFITM3. DF-1 cells abundantly express chIFITM3 (threshold cycles [Cₜ] of 20 for IFITM3 and 22 for GAPDH). Despite being IFN inducible, addition of IFN-γ resulted in only a moderate induction, whereas addition of IFN-α caused a 2.67-log₂ (6.4-fold) increase in chIFITM3 expression (Fig. 5A). We assessed our ability to knock down chIFITM3 expression in DF-1 cells using an siRNA
designed to the chIFITM3 transcript. Treatment with this siRNA on unstimulated DF-1 cells resulted in a 1.23-log₂ (2.4-fold) reduction in the transcript level, with no change in chIFITM3 transcript abundance with a nonspecific siRNA. Knockdown of endogenous chIFITM3 resulted in a greater than 2-fold increase in infection of DF-1 cells by replication-competent influenza A virus (A/WSN/1933) (Fig. 5B), assayed by flow cytometric analysis of NP expression. Furthermore, overexpression of chIFITM3 in DF-1 cells reduced viral replication by an average of 55% (Fig. 5D), and plaque assays show that the viral load was reduced from $1.3 \times 10^6$ PFU ml$^{-1}$ to $3.1 \times 10^5$ PFU ml$^{-1}$ after chIFITM3 overexpression (Fig. 5E). Together, these results show chIFITM3 is able to restrict IAV entry into DF-1 cells.

**Differential expression of chIFITMs in chicken tissues.** We assessed the tissue-specific gene expression pattern in chickens using a panel of RNA extracted from tissues from 3-week-old
Rhode Island Red (RIR) chickens focusing on thymus, spleen, bursa of Fabricius, cecal tonsil, trachea, gastrointestinal tract, bone marrow, brain, muscle, heart, liver, kidney, lung, and skin. Using primers specific to chIFITM1, -2, or -3 (Fig. 6), expression of chIFITM2 and -3 was detected in all tissues, although with lower levels of expression in the muscle and brain and higher levels in the cecal tonsils (Fig. 6). In contrast, expression of chIFITM1 was more restricted and confined to the bursa of Fabricius, the gastrointestinal tract, and the cecal tonsil.

**DISCUSSION**

To date, the antiviral activities of the IFITM2 and IFITM3 proteins have only been demonstrated in mammals, with a single report characterizing the function of chicken IFITM1 and IFITM5 (2). Computational analysis of vertebrate genomes suggests the IFITM gene family is present throughout vertebrates. However, this analysis and any phylogenetic reconstruction of gene history are complicated by the paralogous nature of the IFITM gene family, the presence of copy number variations, and the presence of numerous processed pseudogenes (6). Indeed, the identification of avian IFITMs as part of the dispanin protein family failed to identify chicken IFITMs in the antiviral IFITM1- to -3 subfamily defined as DSP2a to -c (25). Similarly, a more thorough analysis of vertebrate IFITMs, while identifying distantly related IFITMs in reptiles and birds, focused on eutherian clade 1 sequences for a detailed phylogenetic analysis (9). Hickford et al. (26) have undertaken a comprehensive analysis of IFITM genes across a broad range of chordates. The authors have shown that all of the species analyzed, including “lower” vertebrates, such as lampreys, possess at least one IFITM-like gene. Phylogenetic analysis of all of the IFITM paralogues they identified revealed that IFITM5 emerged in bony fish, while IFITM10 appears restricted to tetrapods. Here we have resolved the entire antiviral IFITM locus on chromosome 5 of the chicken genome, expanding the number of IFITM genes to 4 in this locus, and confirmed that the locus is flanked by the genes ATHL1 and B4GALNT4 (9). Crucially, we have shown that antiviral activity is conserved in chicken IFITMs. The low-level sequence identity and orientation change of chIFITM2 and chIFITM1 make the phylogenetic assignment of orthology problematic. Our revised nomenclature of the chicken IFITM locus is based on the syntenic gene order, as previously discussed, and functional data where possible. However, given chIFITM2 is localized to the plasma membrane, and the lack of an N-terminal extension (characteristic of huIFITM2/3), it is possible that it is analogous to huIFITM1. It is likely that similar extensive genetic and functional analyses will be essential to characterize the IFITM loci in other vertebrate species and define unambiguously IFITM1, -2, and -3 orthologues.

Using the chIFITM3 amino acid sequence, we also searched the duck genome (v1.0) and identified a scaffold (2943) containing two duck IFITM (duIFITM) orthologues. Sequence identity and conserved synteny with the chIFITM locus indicate they are IFITM5 and IFITM1. The two IFITM flanking genes, B4GALNT4 and ATHL1, are also located on the scaffold in conserved positions. Although annotated gene structures are absent in the browser, IFITM cDNAs in other avian species align with the regions adjacent to both ends of the IFITM1 structure. This suggests the duck retains four IFITM genes at a conserved locus. We would
expect the positions of duIFITM2 and duIFITM3 to be conserved with their orthologues in the chicken and other species. Following infection with two H5N1 strains of avian influenza virus (A/duck/Hubei/49/05 and A/goose/Hubei/65/05), levels of expression of duck IFITM3, -5, and -10 (measured by RNAseq) were increased to various degrees, reflecting a response befitting their expected function (27).

Control of animal pathogens, especially those with zoonotic potential, is a key component of ensuring human health and food security. RABV is responsible for approximately 70,000 human deaths each year (28), while other lyssaviruses have only been conclusively shown to cause a handful of fatalities (29), although this could be due to poor surveillance. Our results are the first to show diverse members of this genus of virus are sensitive to the inhibitory action of human IFITM proteins. Furthermore, although most warm-blooded animals are susceptible to RABV, domestic birds are rarely infected by lyssaviruses (23). Despite this, chIFITM2 and -3 were able to significantly reduce cell lyssavirus infection. Avian IAV infections, however, pose significant threats to human health, to the international poultry industry, and to small-scale poultry farmers (30). Our identification and functional characterization of the avian IFITM locus, together with knowledge that this gene family exists with copy number and allelic variants in other species (9, 15, 16), should provide a focus for identifying IFITM variants with enhanced antiviral activity for use in farm animal breeding strategies to improve animal infectious disease resistance. Specifically, we hypothesize that certain wild or outbred chicken IFITM allelic variants will confer enhanced levels of protection to pathogenic avian viruses that enter through acidic endosomes and that breeding for enhanced activity in IFITM variants will improve disease resistance in chickens. Similarly, should chicken IFITM proteins restrict IAV infection in chick embryos, the ablation of IFITM protein expression could improve vaccine production and boost yield.
We have shown that chIFITM proteins expressed in A549 cells are capable of restricting diverse viruses that enter cells through the acidic endosome pathway. Furthermore, we show that DF-1 chicken cells constitutively express chIFITM3, and this is able to restrict influenza virus infection in vitro. Despite sharing less than 50% amino acid identity, both chIFITM3 and huIFITM3 effectively restrict the entry of all lyssavirus and IAV envelope pseudotypes tested. Nevertheless, certain key amino acids in the N terminus, IM1, and CIL domain are conserved in chicken and human IFITM3, suggesting functional importance.

This work describes our elucidation of the IFITM locus in the chicken genome and provides the first functional characterization of chIFITM2 and chIFITM3. Despite this, many key questions remain; it is unclear how genes such as IFITM3 in humans and chickens, separated by 310 million years of evolution (31) and sharing less than 50% amino acid identity, maintain a conserved cellular location and a strong antiviral activity against a diverse range of viruses. It is of equal importance to determine, given the level of antiviral activity and the proposed indirect mechanism of IFITM protein restriction (12, 13), how viruses overcome the restriction either within or between species. Investigation of appropriately defined IFITM loci from different host species where cross-species transfer of virus in-
Infection occurs may help explain barriers and vulnerabilities to infection by diverse viruses.

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