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STAT1-Independent Control of a Neurotropic Measles Virus Challenge in Primary Neurons and Infected Mice

Lauren A. O’Donnell,* Stephen Conway,* R. Wesley Rose, † Emmanuelle Nicolas,* Michael Slifker,* Siddharth Balachandran,* and Glenn F. Rall*

Neurons are chiefly nonrenewable; thus, cytolytic immune strategies to clear or control neurotropic viral infections could have lasting neurologic consequences. IFN-γ is a potent antiviral cytokine that is critical for noncytopathic clearance of multiple neurotropic viral infections, including measles virus (MV); however, the downstream pathways through which IFN-γ functions in neurons have not been defined. Unlike most cell types studied to date in which IFN-γ affects gene expression via rapid and robust activation of STAT1, basal STAT1 levels in primary hippocampal neurons are constitutively low, resulting in attenuated STAT1 activation and consequently slower kinetics of IFN-γ–driven STAT1-dependent gene expression. Given this altered expression and activation of STAT1 in neurons, we sought to determine whether STAT1 was required for IFN-γ–mediated protection from infection in neurons. To do so, we evaluated the consequences of MV challenge of STAT1-deficient mice and primary hippocampal neurons explanted from these mice. Surprisingly, the absence of STAT1 did not restrict the ability of IFN-γ to control viral infection either in vivo or ex vivo. Moreover, the canonical IFN-γ–triggered STAT1 gene expression profile was not induced in STAT1-deficient neurons, suggesting that IFN-γ regulates neuronal STAT1-independent pathways to control viral replication. The Journal of Immunology, 2012, 188: 1915–1923.

Central nervous system invasion is a rare, but typically severe, consequence of several human viral infections that include most herpesviruses, poliovirus, measles virus, flaviviruses (e.g., West Nile virus), and HIV (1). When CNS infections do occur, complications typically result in lasting neurologic damage and often in death, especially in the young, elderly, and immunocompromised (2). The severity of neurotropic virus pathogenicity may be due to the delicate balance that must be achieved by the antiviral immune response: effective immunity must control the infection while minimizing CTL-mediated lysis of this chiefly nonrenewable cell population. Whereas multiple animal models have demonstrated that cytokines, including IFN-γ, can limit viral spread in the brain via noncytopathic mechanisms (3–6), the downstream signaling pathways that result in clearance remain largely undefined. This becomes clinically significant in instances in which viral clearance fails, as in many cases of pediatric encephalitis including measles and St. Louis encephalitis (1, 7–10).

IFN-γ is the only type II member of the IFN family, which also consists of type I IFNs (IFN-αβ) and type III IFNs. Unlike type I IFNs, which are expressed by most cells soon postinfection, IFN-γ is chiefly produced by activated immune cells such as NK cells and T cells. IFN-γ initiates a cellular response by binding to the IFN-γ receptor complex (consisting of a heterotetramer of IFN-γR1 and R2 subunits), which triggers activation of receptor-associated JAK-1/2 and subsequent tyrosine phosphorylation of the cytoplasmic tail of the IFN-γR1 subunits. STAT1 is recruited to the phosphorylated R1 subunit, where it is phosphorylated, homodimerizes, and translocates to the nucleus. The phosphorylated STAT1 homodimer binds to γ-activated sequence elements within IFN-γ-responsive genes to initiate transcription. Over 250 genes are induced in this manner to inhibit viral spread (11). Whereas STAT1 is central to a classical IFN-γ response, a substantial number of studies has also demonstrated the presence of IFN-γ–dependent, STAT1-independent pathways (12–20).

IFN-γ is required for viral clearance of many neurotropic viral and bacterial infections (4, 6, 21–26). Of note, however, distinct immune strategies may be employed to resolve CNS infections, depending on the cell type that is infected. For example, mouse hepatitis virus can infect CNS resident astrocytes, microglia, and oligodendrocytes (27); whereas perforin is sufficient to mediate viral clearance from astrocytes and microglia, IFN-γ is sufficient for mouse hepatitis virus control in oligodendrocytes (28, 29). In addition, certain subsets of neural cells, such as neural precursors in the retina, preferentially use STAT3 instead of STAT1 in response to IFN-γ (30). Numerous studies have also shown that both STAT1-dependent and -independent pathways are likely to be important for IFN-mediated viral clearance in other regions of the body (13, 18, 19, 31, 32). For example, STAT1 plays a biphasic role in control of systemic dengue infection in mice: STAT1-dependent pathways are required for early viral control, but STAT1-independent pathways are required for later control and eventual viral clearance (13, 20, 21).

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moved, the neurons were washed twice in Dulbecco’s PBS (DPBS), and the cells were placed in conditioned Neurobasal media.

For cells treated with IFN-γ, murine IFN-γ (BD Transduction Laboratories) was diluted in B27-free Neurobasal media, added to the cultures (100 U/ml final concentration), and incubated for the indicated times prior to collection.

**Immunofluorescence assay**

At the indicated time points post–IFN-γ addition, cells on coverslips were fixed in a 1:1 solution of methanol:acetone for 5 min at 20°C and rehydrated in DPBS. To prevent nonspecific Ab binding, cells were incubated in a 10% goat serum/20% FBS solution in DPBS for 1 h at room temperature (RT). A primary Ab was then added in blocking solution for 1 h at RT. Abs, sources, and concentrations used included the following: monoclonal anti–phospho-STAT1 (pY701), BD Pharmingen (1:500); rabbit polyclonal anti-MAP2, Chemicon (1:250); rabbit polyclonal anti-GFAP, Novus Biologicals (1:250); and Keller anti-MV human serum, a gift of M. Oldstone (The Scripps Research Institute) (1:1000). After three washes in DPBS, the cells were incubated in the appropriate secondary Ab in blocking solution for 1 h at RT; anti-mouse AlexaFluor-555 (1:10,000) or anti-rabbit AlexaFluor-488 (1:10,000) with Hoechst 33342 (10 μM) nuclear stain, all from Molecular Probes. After three washes in DPBS, coverslips were mounted onto glass slides using Citi-Flour AF1 (Electron Microscopy Sciences). Images were captured using an Inverted TE2000 with Nikon C1 confocal scanhead (original magnification ×40 objective) in the Fox Chase Cancer Center Confocal Facility.

**ImmunobLOTS**

Cells were treated with IFN-γ and collected at the indicated times, and immunoblots were performed, as previously described (35). Abs used included the following: anti–STAT1 (1:1000); phospho-specific STAT1 (pY701; 1:1000); Keller anti-MV (1:1000); and anti–GAPDH (1:10,000; Chemicon). All were diluted in PBS-Tween 20 (PBS-T) containing 5% milk. For quantitative analysis of immunoblots, densitometric analysis was performed using National Institutes of Health Image software (v. 1.63). When reprobing was necessary, strips were blotted in an acidic glycine/SDS solution for 2 h at RT.

**Immunohistochemical analysis of mouse tissues**

Brains from four to five mice/time point were removed, immersed in tissue-embedding compound (Fisher), snap frozen in a dry ice-isopentane bath, and stored at −70°C. Horizontal cryosections (10 μm) were air dried and stored at −70°C. Standard immunohistochemistry using diaminobenzidine precipitation (3, 41) was performed. To detect MV-infected cells, Keller anti-MV serum was used at a dilution of 1:2000, followed by a biotinylated anti-human secondary Ab (1:300; Vector). Rat anti-mouse CD4 (clone RM4-5; 1:100; BD Pharmingen) or rat anti-mouse CD8 (clone 43D8 B Abs (clones 53-6-7 and 53-5, respectively; 1:100 each; BD Pharmingen) were used to identify T lymphocyte subsets. Sections were then sequentially incubated for 1 h at RT with a biotinylated anti-rat IgG secondary Ab (1:200; Vector Laboratories), 30 min with a streptavidin-peroxidase conjugate (ABC Elite; Vector Laboratories), and, finally, the addition, cells on coverslips were rehydrated (1:250), Keller anti-MV serum was used at a dilution of 1:2000, followed by a biotinylated anti-human secondary Ab (1:300; Vector). Rat anti-mouse CD4 (clone RM4-5; 1:100; BD Pharmingen) or rat anti-mouse CD8 (clone 43D8 B Abs (clones 53-6-7 and 53-5, respectively; 1:100 each; BD Pharmingen) were used to identify T lymphocyte subsets. Sections were then sequentially incubated for 1 h at RT with a biotinylated anti-rat IgG secondary Ab (1:200; Vector Laboratories), 30 min with a streptavidin-peroxidase conjugate (ABC Elite; Vector Laboratories), and, finally, for 5–10 min with diaminobenzidine (0.7 mg/ml in 60 mM Tris) and urea-H2O2 (0.2 mg/ml), purchased as preweighed tablets (Sigma-Aldrich). All were diluted in PBS-Tween 20 (PBS-T) containing 5% milk. For quantitative analysis of immunoblots, densitometric analysis was performed using National Institutes of Health Image software (v.1.63). When reprobing was necessary, strips were blotted in an acidic glycine/SDS solution for 2 h at RT.

**Quantitative RT-PCR**

Mouse brains were snap frozen in liquid nitrogen and stored at −80°C. RNA was isolated by TRIzol, according to the manufacturer’s instructions (Sigma-Aldrich). Contaminating DNA was removed from RNA preparations using DNase I treatment (Invitrogen). Purified RNA was quantified using a Nanodrop instrument. RNA was reverse transcribed using Moloney murine leukemia virus reverse transcptase (Ambion) and a mixture of anchored oligo-dT and random decanucleotides. For each sample, two reverse transcription reactions were performed with inputs of 100 and 20 ng. An aliquot of the cDNA was used for 5′-nuclease assays using TaqMan chemistry. For IFN-γ expression, Assay-on-Demand Mm00801778_m1 would include the following: anti-STAT1 (1:1000); phospho-specific STAT1 (pY701; 1:1000); Keller anti-MV (1:1000); and anti–GAPDH (1:10,000; Chemicon). All were diluted in PBS-Tween 20 (PBS-T) containing 5% milk. For quantitative analysis of immunoblots, densitometric analysis was performed using National Institutes of Health Image software (v.1.63). When reprobing was necessary, strips were blotted in an acidic glycine/SDS solution for 2 h at RT.

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Statistical analysis was applied using a paired t test. Sequences were as follows: forward, 5'-CGCACGACAGTCGAAAGTCT-3'; reverse, 5'-TTCCGA-GATTCCCTGCATG-3'; probe, 5'-6Fam-TGACGCCCCTAGTGGCTGCAA-BHQ1-3'. Assays were used in combination with Universal Master mix and run on a 7900 HT sequence detection system (Applied Biosystems). Cycling conditions were 95°C, 15 min, followed by 40 (two-step) cycles (95°C, 15 s; 60°C, 60 s). The assay for MV-N was validated with a 4-fold five-points dilution curve of cDNA. The slope was -3.54, corresponding to a PCR efficiency of 95%. For each sample, the values are averaged and SD of data are derived from two independent PCRs. Relative quantification to the control was done using the comparative cycle threshold method.

Flow cytometric analysis of brain infiltrates

On the indicated day postinfection (dpi), mice were deeply anesthetized with 400 μl 3.8% chloral hydrate in PBS, delivered i.p. Once animals were confirmed to be nonresponsive, the mice were perfused with 30 ml PBS. Following perfusion, each brain and spleen were removed and processed using a nylon mesh cell strainer in PBS. Dissected tissue was run over a 30/70% discontinuous Percoll gradient for 20 min at 4°C. Mononuclear cells were recovered from the interface, washed with PBS, treated with 0.84% ammonium chloride to remove contaminating RBCs, and washed again. Collected mononuclear cells were counted using a hemocytometer and plated into a 96-well plate for subsequent Ab staining for multicolor flow cytometry. The following Abs (eBioscience) were used: PE-Cy5-CD8α, allophycocyanin-Ax750-CD4, PE-CD3ε, FITC-CD11c, allophycocyanin-CD161ε (NK1.1), PB-CD19, PE-Cy5.5 Gr-1 (Ly-6G), PE-Cy7-CD49b (DX5), and Ax700-CD11b. Cells were allowed to incubate with Ab for 1 h at 4°C and then washed following the incubation period. Pelleted, stained cells were resuspended and read in a BD LSR II system. Percentages obtained from flow cytometry were combined to calculate total cell numbers.

Microarray

Primary hippocampal neurons were plated in poly-L-lysine–coated 6-well plates at a density of 1 × 10⁶ cells/well. RNA was purified from whole-cell lysates using the RNeasy mini kit (Qiagen), and contaminating DNA was removed using a RNase-free DNase set. A quantity amounting to 500 ng total RNA was amplified and labeled using the low RNA input linear amplification kit (Agilent). Labeled cRNA targets were hybridized onto Agilent 4X44k mouse whole genome arrays. Microarray images were processed using Agilent Feature Extraction software (version 9.5). Data were background corrected using the normexp method (PMID: 17720982) implemented in the Bioconductor package limma (42, 43), and quantile normalized. Identification of differentially expressed genes was performed with empirical Bayes moderated t tests using limma. Biological pathways and networks were examined with Ingenuity Pathway Analysis software (www.ingenuity.com). The dataset is at the Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo/), accession number GSE33057.

Results

IFN-γ-mediated STAT1 signaling is attenuated in CNS neurons

We previously showed that IFN-γ is required for control of MV in a transgenic mouse model (NSE-CD46⁺), in which infection is neuron restricted (3). To define the mechanism by which IFN-γ functions, we determined the efficacy of IFN-γ-mediated control of MV replication in primary neurons. Explanted CD46⁺ hippocampal neurons were treated with murine rIFN-γ (100 U/ml) or an equivalent amount of heat-inactivated IFN-γ; 18 h thereafter, the neurons were infected with MV-Ed (MOI = 1), and relative infection levels were determined by quantifying viral protein load. Note that standard plaque assays cannot be used to measure viral levels because no infectious virus is released from infected neurons (44). Neuronal lysates were harvested 48 hours postinfection (hpi) for Western blot analysis. As shown in Fig. 1A and 1B, viral protein levels were >75% reduced in the presence of IFN-γ, whereas heat-inactivated IFN-γ had no effect. These results confirm that IFN-γ limits MV replication in primary neurons.

FIGURE 1. IFN-γ treatment limits MV neuronal infection, despite low basal levels of STAT1 and delayed STAT1 phosphorylation. A, Hippocampal neurons explanted from NSE-CD46⁺ embryos were treated with IFN-γ (100 U/ml, 18 h) or heat-inactivated (ΔH) IFN-γ (100 U/ml, 18 h) and infected with MV-Ed (MOI = 1). At 48 hpi, neurons were lysed in protein solubilization buffer and subjected to Western blot for MV Ag and GAPDH as a loading control. B, Western blots from A were quantified by densitometry using ImageJ software. MV signal was normalized to GAPDH as loading control. Statistical analysis was applied using a paired t test (n = 4, **p < 0.05 versus MV infected). C and D, Hippocampal neurons and cortical astrocytes from NSE-CD46⁺ embryonic mice were treated with IFN-γ (100 U/ml) for the indicated times and collected for Western blot analysis (C) or fixed for immunofluorescence (D). For Western blots (C), whole-cell lysates were subjected to Western blot for phosphorylated STAT1 (STAT1-P; tyrosine 701), total STAT1, and GAPDH. D, Coverslips were stained with a mAb against STAT1-P (red), and a polyclonal Ab against GFAP or MAP2 as astrocyte or neuronal markers, respectively (green). All experiments were conducted in triplicate. Original magnification ×400.
Our previous work (35) suggested that the downstream signaling response of primary neurons following IFN-γ engagement was distinct from classical IFN-γ-activated STAT1-dependent signaling (11). To determine whether this altered signaling profile was true for other brain parenchymal cells, primary hippocampal neurons were compared with primary astrocytes, which are derived from the same pool of neural precursor cells (45). Both primary cultures were consistently >95% pure, as defined by MAP2 and GFAP staining, respectively (Fig. 1D). Cultures were treated with IFN-γ (100 U/ml) for the indicated times, and samples were then analyzed for both total and phosphorylated STAT1 by Western blot (Fig. 1C) and by immunofluorescence (Fig. 1D). Like MEFs (35), astrocytes expressed abundant endogenous levels of STAT1, which was rapidly phosphorylated after IFN-γ treatment (Fig. 1C, 1D, top row). In contrast, primary hippocampal neurons expressed low basal levels of STAT1, and phosphorylated STAT1 was detectable in neurons only after extended IFN-γ stimulation (24 h), coincident with an increase in available STAT1 protein (Fig. 1C). These data demonstrate that delayed STAT1 phosphorylation is not a general characteristic of resident brain parenchymal cells, but rather is unique to neurons. STAT1 is not required for MV control in primary neurons

Despite reduced expression and activation of neuronal STAT1, it was possible that these low levels were still sufficient to initiate an effective antiviral signal. Thus, to determine what role STAT1 played in IFN-γ-mediated MV clearance, CD46+/− and CD46+/−/STAT1-KO neurons were treated with IFN-γ and infected with MV, as described above; neurons were then harvested for Western blot analysis for MV Ag or fixed for immunofluorescence. Quantified results are shown in Fig. 2A, and representative images are shown in Fig. 2B. Without IFN-γ, increasing levels of MV Ag were detectable in both CD46+ and CD46+/−/STAT1-KO neurons from 24 to 72 hpi, evidenced by the increasing size of viral Ag-positive foci (Fig. 2B). In contrast, infected CD46+ and CD46+/−/STAT1-KO neurons treated with IFN-γ showed equivalently less MV Ag at each time point; there were no statistical differences between STAT1-expressing and KO neurons. These data suggest that STAT1 is not required for IFN-γ-mediated control of MV in neurons.

IFN-γ could abate MV growth either by directly eliminating MV from infected neurons, by limiting trans-synaptic spread (44), or by some combination of the two. To assess this, receptor-expressing CD46+ neurons were infected with MV, and treated with IFN-γ either 24 h before, 24 h after, or coincident with MV infection. IFN-γ-mediated control was most effective when neurons were pretreated with IFN-γ (Fig. 2C, compare lanes 2 and 1); the antiviral effect was negligible when IFN-γ was added post-infection (compare lanes 4 and 1). Moreover, in the presence of IFN-γ, MV Ag-positive neurons were typically found as single immunopositive cells, in contrast to abundant multineuronal networks in the absence of IFN-γ (Fig. 2B, quantified in Fig. 2D), suggesting that IFN-γ may play a role in blocking viral spread rather than directly resolving the infection.

**FIGURE 2.** Primary neurons use STAT1-independent pathways during IFN-γ-mediated viral control. A, NSE-CD46+ and NSE-CD46+/−/STAT1-KO hippocampal neurons were treated with IFN-γ (100 U/ml) and infected with MV (MOI = 1) for 24 or 48 h. Whole-cell lysates were harvested, subjected to Western blot analysis, and quantified on ImageJ software, with MV signal normalized to GAPDH. The average MV signal is plotted with MV infection at 24 h set to 100%, and error bars represent SEM (n = 3). B, Immunofluorescence analysis of MV Ag in CD46+ and CD46+/−/STAT1-KO neurons. Neurons were treated as in A and stained for MV Ag (red), MAP2 (green), and Hoescht (blue). Original magnification ×400. C, Primary CD46+ neurons were treated with IFN-γ either 24 h before infection (lane 2), coincident with infection (lane 3), or 24 h postinfection (lane 4). Lysates were collected from infected (and corresponding uninfected) neurons, and blots probed for MV Ag and GAPDH, as described. D, CD46+ neurons were either treated with IFN-γ (100 U/ml) or left untreated and, 24 h later, infected with MV. At 48 hpi, coverslips were collected and immunostained for MV Ags, and nuclei within immunopositive clusters were counted. Clusters were “binned” into groups of 1–3, 4–6, 7–10, or >10 (n = 3). SDs are shown from three such experiments.
STAT1-deficient mice survive viral infection in CNS neurons

To determine what role STAT1 plays in the resolution of a neuronal viral infection in vivo, we infected NSE-CD46+ transgenic mice that had been backcrossed to selective immune KO mice. NSE-CD46+ mice lacking T and B cells (NSE-CD46+/RAG2-KO), IFN-γ (NSE-CD46+/IFN-γ-KO), or STAT1 (NSE-CD46+/STAT1-KO) were infected IC with MV and monitored daily for signs of illness (Table I) and mortality (Fig. 3). Consistent with our published results (3), immunocompetent NSE-CD46+ mice remained disease free, and all survived, whereas >95% of NSE-CD46+/RAG-2 KO mice and ~50% of NSE-CD46+/IFN-γ KO mice died of unrestricted MV infection between 7 and 17 dpi, during the period of maximal T cell presence within the brain parenchyma (dotted horizontal line, Fig. 3) (34). Of note, surviving NSE-CD46+/IFN-γ-KO mice showed lasting signs of neurologic damage, including ataxia, piloerection, and hunched posture (Table I). Unexpectedly, NSE-CD46+/STAT1-KO mice segregated into two groups following MV infection. Consistently, a small proportion (~25%; 9 of 35 mice in the experiment shown) died between 4 and 6 dpi, earlier than any other KO mouse tested in this model system, and prior to the entry of CD4+ and CD8+ T cells into the CNS (34). This early death was accompanied by grade 5 “popcorn” seizures [based on a modified Racine scale (46)] and temporary paralysis, followed by death within 24 h. Importantly, however, the majority of NSE-CD46+/STAT1-KO mice survived this initial 6-d period, and showed no signs of neurologic damage at any time point thereafter (Table I). Pairwise analysis contingent on survival to 8 dpi indicated no statistically significant difference between NSE-CD46+ mice and NSE-CD46+/STAT1 KO mice, although survival differences did reach significance (p < 0.05) for the other genotypes tested. Based on these observations, we conclude that STAT1 plays a biphasic role during MV infection, and that STAT1 is dispensable for MV clearance from neurons during the adaptive immune phase.

T cell infiltration into the CNS and control and clearance of MV in neurons are STAT1 independent

Studies using STAT1 KO mice have implicated a role for STAT1 in the CNS of IFN-γ-treated neurons, with and without STAT1. Microarrays were performed on both primary MEFs and primary NSE-CD46+ and NSE-CD46+/STAT1 KO neurons following IFN-γ exposure for 0, 3, 6, or 24 h. Three individual cultures were analyzed for each time point. Heat maps, reflective of expression levels, are shown in Fig. 6. Yellow represents the baseline for each gene in numbers of infiltrating cells within the CNS, confirming IFN-γ as a chemoattractant (Fig. 4A, right panel). However, no differences in either profile (Fig. 4A, right panel) or localization (Fig. 4B) of intraparenchymal T cells were observed between MV-permissive wild-type and STAT1 KO mice.

To compare relative levels of IFN-γ, we quantified IFN-γ RNA in brain tissue at the peak of T cell infiltration (11 dpi) by quantitative RT-PCR (Fig. 5A) and compared MV RNA levels in the CNS at various dpi (Fig. 5B). As expected, NSE-CD46+/IFN-γ–KO mice did not produce IFN-γ (data not shown), and were unable to clear MV RNA to levels seen in NSE-CD46+ or NSE-CD46+/STAT1-KO mice (Fig. 5B). Brains of NSE-CD46+/STAT1-KO mice expressed significantly higher levels of IFN-γ RNA at 11 dpi than NSE-CD46+ mice, which correlated with the decrease in MV RNA seen in nonseizing NSE-CD46+/STAT1-KO brains between 4 and 11 dpi (Fig. 5B). Importantly, NSE-CD46+ mice had consistently low levels of MV RNA, indicating that STAT1 most likely plays a pivotal role in the type I IFN innate response at early times postinfection. Note also that, although ~20% of NSE-CD46+/STAT1-KO mice develop lethal seizures at 4 dpi, there was no statistical difference in viral load between seizing and healthy mice. Together, these data indicate that the adaptive immune response of NSE-CD46+/STAT1-KO mice is comparable to that made by wild-type mice, leading to viral resolution in the absence of the canonical STAT1-mediated pathway.

Canonical IFN-γ-dependent genes are not expressed in STAT1-KO neurons

Finally, to address the possibility that IFN-γ resulted in the expression of a classic profile of genes via an alternative (non-STAT1–mediated) pathway, we used a microarray strategy to identify the top 50 genes that were activated by IFN-γ and NSE-CD46+ mice lacking T and B cells (NSE-CD46+/RAG2-KO), IFN-γ (NSE-CD46+/IFN-γ-KO), or STAT1 (NSE-CD46+/STAT1-KO) were infected IC with MV and monitored daily for signs of illness (Table I) and mortality (Fig. 3). Consistent with our published

Table I. Measles virus-induced CNS disease in mice of various immunodeficient backgrounds

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Week 1</th>
<th>Week 2</th>
<th>Week 3</th>
<th>Week 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>NSE-CD46+</td>
<td>0 (100)</td>
<td>0 (100)</td>
<td>0 (100)</td>
<td>0 (100)</td>
</tr>
<tr>
<td>NSE-CD46+/RAG-2 KO</td>
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<td>2.8 (30)</td>
<td>2.3 (20)</td>
<td>2.5 (10)</td>
</tr>
<tr>
<td>NSE-CD46+/IFN-γ KO</td>
<td>0 (100)</td>
<td>1.9 (60)</td>
<td>1.8 (60)</td>
<td>1.3 (50)</td>
</tr>
<tr>
<td>NSE-CD46+/STAT1 KO</td>
<td>1.2 (70)</td>
<td>1.0 (70)</td>
<td>0.5 (70)</td>
<td>0 (70)</td>
</tr>
</tbody>
</table>

Mice were subjectively assessed for signs of morbidity every other day postinfection. Average scores (0–3) of surviving mice for a 4-wk observation interval are shown (n = 10 for each genotype), as follows: 0 = healthy; 1 = ruffled fur/piloerection, ataxic; 2 = ruffled fur/piloerection, ataxic, plus seizures; 3 = moribund.

**FIGURE 3.** STAT1 is not required for T cell-mediated resolution of a neuron-restricted MV infection. Kaplan–Meier survival plot of MV-challenged NSE-CD46+ mice on various KO backgrounds. NSE-CD46+, NSE-CD46+/STAT1-KO, NSE-CD46+/IFN-γ–KO, and NSE-CD46+/RAG2-KO mice were infected, as described in Materials and Methods. Results from three separate experiments were pooled (n = 10–35 mice/condition). Mice were monitored daily for signs of morbidity and were euthanized when signs of illness were apparent. The dotted horizontal line indicates the peak of T cell entry into the CNS parenchyma of NSE-CD46+ mice. Pairwise analysis, contingent on survival to 8 dpi, was performed between infected NSE-CD46+ mice and the other three genotypes. NSE-CD46+ versus NSE-CD46+/STAT1 KO: not significant, NSE-CD46+ versus NSE-CD46+/IFN-γ KO: p < 0.05, NSE-CD46+ versus NSE-CD46+/RAG KO: p < 0.05.
each cell type; progression to red indicates induction of gene expression. The top 50 IFN-γ-activated genes in MEFs are shown in the first three columns; as expected, the majority of these genes achieved maximal levels by 3 h posttreatment. Primary STAT1+ neurons induced a similar profile of genes, although some genes were not induced at all, and most others showed delayed induction kinetics, consistent with the delayed activation of STAT1 in neurons. Importantly, despite the capacity to control MV as effectively as STAT1+ neurons, STAT1 KO neurons did not induce the majority of canonical IFN-γ-driven genes. Thus, it is likely that alternative genes are induced in STAT1 KO neurons that mediate viral control. A complete list of genes that were induced or suppressed in neurons following IFN-γ exposure, independent of STAT1 expression, is provided in Supplemental Figs. 1 and 2.

Discussion

In this manuscript, we make three key observations, as follows: 1) distinct from other parenchymal CNS cell types, the IFN-γ–triggered, STAT1-dependent signaling profile in neurons is delayed and restricted; 2) STAT1 is not required for IFN-γ-mediated control of MV either in primary neurons or in a permissive mouse model; and 3) alternative signaling pathways are most likely operative in STAT1-deficient neurons (and perhaps also in STAT1-positive neurons) to result in viral control.

A number of points warrant further discussion. First, these data add to a growing literature that shows that the cellular response to extracellular cytokines is not monolithic (15, 30, 35, 50–52). Whereas signaling pathways and the genes they regulate are generally maintained across distinct cell populations, subtle differences in expression levels can exert major changes in the antiviral response. Specifically, the delayed and muted neuronal response to IFN-γ, in contrast to the rapid and robust signal seen in MEFs (35) and astrocytes (Fig. 1C), has a marked impact on the kinetics and magnitude of IFN-γ-responsive genes expressed in neurons. Relevant to published studies, these primary neurons are ∼95% pure cultures, and, in this report, we assessed pSTAT1 levels within 3–24 h post–IFN-γ treatment; whereas untreated neurons do have detectable levels of unphosphorylated STAT1, and eventually respond to IFN-γ [as shown in other studies (53–55)], the signature of the early neuronal response is appreciably different from that observed in control cells. Of note as well, whereas these data specifically compare primary hippocampal neurons with primary astrocytes, differences may also be present in neuronal subpopulations as well. The primary neurons used in these experiments are mainly derived from the embryonic hippocampus, although dissection of this substructure from day E15 to 16 embryos can be imprecise, and most likely includes some cortical tissue. Moreover, both glutamatergic and GABAergic neurons are present in the hippocampus at this stage of development (36); thus, these cultures are most likely comprised of different neuronal subtypes. This may be relevant to the STAT1 activation profile seen in neurons since at 24 h posttreatment, about one-half of the neurons have a detectable pSTAT1 signal, whereas the remainder appears nonresponsive (Fig. 1D, lower right panel). Efforts are underway to determine whether there is a correlation between neuronal subtype in the CNS and IFN-γ responsiveness.

A second issue is the apparent dispensability of STAT1 in IFN-γ–mediated viral control. In both infected mice and infected primary neurons, IFN-γ plays a central role in protection; its absence from mice results in death of ∼50% of MV-challenged animals, and permanent neurologic impairment in the survivors. Similarly, addition of murine rIFN-γ to infected neurons restricts viral load, and may afford a survival advantage to these vulnerable cells. Given the crucial role of IFN-γ in survival from MV CNS disease, we were therefore surprised that, during the period of adaptive immune cell presence in the brain of infected mice (7–17 dpi), STAT1 played no role in mouse survival. This was in contrast to an extensive body of evidence that supports a central and pivotal role for STAT1 in protection from viral infection.
role for STAT1 in mouse survival following infection by many viruses. In these papers, STAT1 KO mice demonstrated greater viremia and mortality from both peripheral viral challenges (15, 55, 56) as well as from CNS infections (55), leading to the conclusion that STAT1 was a key feature of protection against multiple infections. Yet, evidence for STAT1-independent antiviral pathways also exists for other viral infections (15, 18, 19), suggesting that particular viruses or target tissues may not be as reliant on STAT1-dependent pathways for viral clearance. The difference between our results and those that underscore the importance of STAT1 in CNS infections may be because the only cell type infected in NSE-CD46+ mice is CNS neurons, which may allow neuronal STAT1-independent pathways to be effective against this limited viral tropism.

Whereas STAT1 is not required during the 7- to 17-dpi window when T cells are abundant in the CNS, there is a small, but reproducible effect of STAT1 deficiency at early stages postinfection (3–6 dpi), resulting in death of 20–30% of infected mice. We presume that this implies participation of STAT1 in the type I IFN response (mediated by IFNs α and β), in which, along with STAT-2 and IFN regulatory factor-9, it is part of the IFN-stimulated gene factor 3 complex that binds to IFN-stimulated gene promoter elements. Whereas this hypothesis awaits confirmation, one issue that this model does not address is that neurons, in vivo, may encounter IFNs sequentially; that is, it is likely that cellular exposure to type I IFNs precedes IFN-γ exposure. As such, when a neuron encounters IFN-γ, it may already have made a transcriptional response to type I IFN. Thus, an ultimate appreciation of the role of IFNs and their subsequent signaling pathways in antiviral immunity will most likely require an integrated evaluation of the neuronal response to serial IFN encounters.

FIGURE 5. STAT1 is necessary for early MV control, but is not required for MV clearance from CNS neurons. A, Brains were removed at 11 dpi from NSE-CD46+ and NSE-CD46+/STAT1-KO mice and assessed by quantitative RT-PCR for levels of IFN-γ message (n = 8). B, MV RNA in the brains of MV-infected mice. Animals were infected IC with MV (2 × 10^4 PFU), and brains were harvested at 4, 11, and 40 dpi. RNA was extracted and subjected to quantitative RT-PCR for MV-N (n = 6–10 mice per time point). Statistical analysis was applied via unpaired t test (*p < 0.04 versus NSE-CD46+ mice on the same dpi; **p < 0.003 versus NSE-CD46+ mice on the same dpi).

FIGURE 6. Microarray expression profiles following IFN-γ stimulation. MEFs and primary NSE-CD46+ and NSE-CD46+/STAT1 KO neurons were incubated for the indicated times with IFN-γ, followed by RNA purification. RNA was then subjected to microarray, as described in Materials and Methods, and analyzed by Ingenuity software. In this heat map, yellow represents basal expression, and shades from yellow to red indicate increasing expression levels (log2 scale).
Finally, the uncoupling of STAT1 dependence from IFN-γ dependence makes it likely that a different constellation of genes is induced in neurons that influence viral control. As shown in Fig. 6, the standard IFN-γ profile is not induced in STAT1 KO neurons, and thus our current efforts are aimed at identifying what role IFN-γ-inducible, STAT1-independent genes may play in viral control.

From these data, we propose a signaling factor density model, as follows: in MEFS and astrocytes, the abundant cytoplasmic levels of STAT1 facilitate rapid and complete occupation of binding sites on the intracellular domain of the IFN-γ receptors, triggering a primarily STAT1-driven response. In contrast, neurons with lower constitutive expression of STAT1 may allow for other signal transduction factors to bind and eventually trigger transcription of a distinct subset of genes, creating a unique neuronal response profile. Indeed, the relevance of these alternative signaling pathways is supported by the impairment-free survival of STAT1 KO mice, implying that the canonical STAT1 signaling pathway plays a modest, perhaps negligible, role in viral control in neurons.

As the field of cell-specific cytokine responses progresses, one can envision that the use of cytokines as antivirals will need to be readdressed in the context of the disease or pathogen that is targeted and the cell populations affected.

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Disclosures

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References


