Human Cytomegalovirus IE1 Protein Disrupts Interleukin-6 Signaling by Sequestering STAT3 in the Nucleus

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ABSTRACT

In the canonical STAT3 signaling pathway, binding of agonist to receptors activates Janus kinases which phosphorylate cytoplasmic STAT3 at tyrosine 705 (Y705). Phosphorylated STAT3 dimers accumulate in the nucleus and drive the expression of genes involved in inflammation, angiogenesis, invasion and proliferation. Here we demonstrate that human cytomegalovirus (HCMV) infection rapidly promotes nuclear localization of STAT3 in the absence of robust phosphorylation at Y705. Furthermore, infection disrupts interleukin-6 (IL6)-induced phosphorylation of STAT3 and expression of a subset of IL6-induced STAT3-regulated genes including SOCS3. We show that the HCMV 72-kDa IE1 protein associates with STAT3 and is necessary to localize STAT3 to the nucleus during infection. Furthermore, expression of IE1 is sufficient to disrupt IL6-induced phosphorylation of STAT3, binding of STAT3 to the SOCS3 promoter and SOCS3 gene expression. Finally, inhibition of STAT3 nuclear localization or STAT3 expression during infection is linked to diminished HCMV genome replication. Viral gene expression is also disrupted with the greatest impact seen following viral DNA synthesis. Our study identifies IE1 as a new regulator of STAT3 intracellular localization and IL6 signaling and points at an unanticipated role of STAT3 in HCMV infection.

INTRODUCTION

Human cytomegalovirus (HCMV) is a human herpesvirus that infects the majority of the world population. Primary exposure results in a lifelong infection. HCMV is an opportunistic pathogen that causes serious disease in immunocompromised patients and is a leading cause of congenital birth defects (41, 44). The current FDA-approved antiviral compounds inhibit viral DNA replication and have significantly improved the management of HCMV-associated diseases. Although the use of antivirals usually resolves viremia, the compounds fail to remove the latent reservoirs of HCMV within the body. Moreover, their use is limited due to toxicity, poor oral bioavailability and the selection of antiviral resistant variants (5, 20, 35). Efforts are underway to identify additional antiviral compounds to increase treatment options.

The 72-kDa immediate-early 1 (IE1) protein of HCMV is a key regulatory phosphoprotein conditionally required for viral early gene expression and replication in fibroblasts (18, 19, 42). IE1 localizes to the host cell nucleus, targeting both interchromatin compartments termed nuclear domain 10 (ND10) (2, 26, 68) and chromatin (29). Our work and a consecutive study by Huh et al. has demonstrated that IE1 forms physical complexes with STAT1 and STAT2 in the nuclei of infected cells, prevents association of STAT1, STAT2, and IRF9 with promoters of type I interferon (IFN)-stimulated genes and inhibits IFN-α-induced transcription (22, 27, 46). Consequently, IE1 disrupts type I IFN-dependent STAT signaling endowing the virus with partial resistance to the antiviral effects of IFN-α and IFN-β (22, 27, 46). Notably, this activity has been subsequently shown to be conserved across IE1 homologs of the human β-herpesvirus subfamily (23). Conversely, following ectopic expression in an inducible cell model (TetR/TetR-IE1), IE1 elicited a transcriptional response dominated by the up-regulation of pro-inflammatory and immune modulatory genes normally induced by IFN-γ

(25). Although IE1-mediated gene expression proved to be independent of IFN-γ, it required the tyrosine-phosphorylated form of STAT1. Accordingly, STAT1 accumulated in the nucleus and became associated with IE1 target genes upon expression of the viral protein (25).

Another member of the STAT protein family, STAT3 is involved in regulating diverse responses. In total, four isoforms of STAT3 have been identified: full-length STAT3α and truncated STAT3β, STAT3γ, and STAT3δ (See review: 75). Although the function of the truncated isoforms is unclear, studies are beginning to suggest that they have distinct cellular activities from STAT3α (37, 72, 76). STAT3 is activated by a variety of different stimuli including interleukin-6 (IL6) and other cytokines or growth factors (1, 75). In the canonical STAT3 signaling pathway, binding of agonist to receptors activates Janus kinases (JAKs) which phosphorylate cytoplasmic STAT3 at tyrosine 705 (Y705). Phosphorylated STAT3 dimers accumulate in the nucleus and drive the expression of genes involved in inflammation, angiogenesis, invasion and proliferation (1, 75). Nuclear translocation is mediated by the importin-α and β1 heterodimer complex (9, 32). Furthermore, phosphorylation at serine 727 (S727) is necessary for maximal STAT3 transcriptional activity (66, 67). Recent studies have demonstrated that STAT3 unphosphorylated at Y705 shuttles between the cytoplasm and the nucleus and is also transcriptionally active (48, 60, 70, 71).

In this study, we have determined a mechanism used by HCMV to regulate STAT3 during infection. We demonstrate that HCMV IE1 is both necessary and sufficient to promote early nuclear localization of STAT3 which is predominately unphosphorylated at Y705. One functional consequence is the IE1-mediated disruption of STAT3-mediated IL6 signaling. In addition, inhibition of STAT3 nuclear localization was linked to reduced viral DNA replication and late gene expression.

MATERIALS AND METHODS

Biological Reagents

MRC-5 fibroblasts, ARPE-19 epithelial cells and U373 astrocytoma cells were propagated in Dulbecco's modified Eagle's medium supplemented with 7% fetal bovine serum (Life Technologies, Carlsbad, CA) and 1% penicillin/streptomycin (Life Technologies). Unless otherwise stated, cells were grown until confluent, serum starved in 0.5% fetal bovine serum for 2 days and then infected at a multiplicity ranging from 0.25 to 5 infectious units per cell (IU/cell) in DMEM supplemented with 0.5% FBS. In several experiments, cells were treated 24 h prior to infection with the indicated inhibitors: 15 µM curcumin (Sigma-Aldrich, St. Louis, MO), 30-150 µM S3i-201 (NSC 74859) (ThermoFisher Scientific, Waltham, MA), 5 µM STATTIC (Santa Cruz), 4 µM WP1066 (Santa Cruz) or DMSO (Sigma). Compounds were replaced every 24 h. As a control for pSTAT3 and STAT3-regulatable gene expression, U-373 cells were treated with 183 ng/ml of carrier free recombinant human interleukin-6 (IL6) (BioLegend, San Diego, CA) for 15 min for Western blot analysis or 45 min for gene expression studies. Studies using MRC-5 cells also included recombinant human IL6 receptor alpha (IL6Rα) (R&D Systems, Minneapolis, MN). TetR-IE1 and TetR cells have been previously described (25) and were treated with doxycycline (Dox) for 0 to 72 h at a final concentration of 1 µg/ml. Viability and total cell numbers were determined with Viacount (EMD Millipore, Billerica, MA) and Gauva EasyCyte Mini Flow Cytometer (Millipore). Control siRNAs (Cell Signaling Technology), siRNA targeting importin-β1 (Life Technologies) or siRNA targeting STAT3 (On-TARGET-SMART pool) (ThermoFisher) were transfected using Lipofectamine 2000 (Life Technologies).

BAC-derived HCMV strains AD169 (AD*wt*) (73), AD*in*27F (49) and Towne *wt* (36) were propagated in primary fibroblasts, and Towne *dl*IE1 virus (27) was propagated in TetR-IE1 cells. BAC-derived HCMV clinical virus TB40/E (54) was propagated in ARPE19 epithelial cells. Viral titers were determined by an infectious units assay (40) or standard plaque assay.

Analysis of Protein, DNA, and Gene Expression

Preparation of cell extracts, immunoprecipitation, Western blot analysis, and immunofluorescence microscopy were completed as previously described (27, 49, 59). The antibodies used are listed below. Immunofluorescence was observed using a 63× lens in a Leica DMRX inverted microscope (Leica Microsystems, Wetzlar, Germany) equipped with a Retiga-SRV digital camera and Image-Pro Plus 6.2 software (Q-Imaging, Surrey, Canada) (Figures 3, 5, and S2). Alternatively, a 60× lens in a Nikon Eclipse Ti-U inverted microscope (Nikon, Melville, NY) equipped with a CoolSNAP ES2 CCD camera (Photometrics), multifluorescent Sedat Quad ET filter set (multichroic splitter, Chroma), and NIS-Elements software (Nikon) was used for image analysis (Figures 1, 2, 6, 8, and S1). The mean fluorescent intensity of STAT3 within the nucleus and cytoplasm was obtained from an average of 20-30 cells and from at least two replicate experiments unless otherwise noted. The data is presented as nuclear to cytoplasmic ratio ± SEM. Viral DNA content and RNA expression from infected cells were determined using quantitative real-time PCR as previously described (27, 49) and primers listed below. Quantities for unknown samples were defined relative to an arbitrary standard curve consisting of 10-fold serial dilutions of one sample and completed for each primer pair. Chromatin immunoprecipitation (ChIP) coupled to qPCR was performed as described (25) using 10 μg anti-STAT3 C-20 or normal rabbit IgG and primers specific to the human SOCS3 promoter or transcribed region (see below). For flow cytometry, U373 cells were dissociated from culture plates using enzyme-free cell dissociation buffer (Millipore). Cells were resuspended in PBS with 2% BSA containing antibody-conjugate (Alexa Fluor 647) and incubated for 30 min at 4°C. Cells were washed three times using PBS with 2% BSA and then fixed with 2% paraformaldehyde. Data acquisition was performed on a BD LSR II and analyzed using FlowJo Software (Treestar, Ashland, OR).

Antibodies

The following antibodies were used in these studies: normal rabbit immunoglobulin G (IgG) (Sigma-Aldrich), mouse anti-FLAG M2 (Sigma-Aldrich), mouse anti-GAPDH clone 0411 (Santa Cruz Biotechnology), rabbit anti-GAPDH ab9485 (Abcam), mouse anti-HA clone HA-7 (Sigma-Aldrich), rabbit anti-STAT1 E-23 (Santa Cruz Biotechnology), rabbit anti-STAT2 H-190 (Santa Cruz Biotechnology), mouse anti-STAT3 clone 124H6 (Cell Signaling Technology), rabbit anti-STAT3 C-20 (Santa Cruz Biotechnology), rabbit anti-pSTAT3 (Y705) (Cell Signaling Technology), rabbit anti-pSTAT3 (S727) (Cell Signaling Technology), rabbit anti-H2A ab15653 (Abcam), and rabbit anti-importin β1 (Cell Signaling Technology). The antibodies against HCMV proteins were mouse anti-pUL123 clone 1B12, mouse anti-pUL122 clone 3A9, mouse anti-pTRS1, mouse anti-pUL99, mouse anti-pUL37 clone 2A1D, and mouse anti-pUL38 clone 3D12 (generously provided by Dr. Tom Shenk, Princeton University) and mouse anti-pUL44 (Virusys). Secondary antibodies include goat anti-mouse HRP and donkey anti-rabbit HRP (Jackson ImmunoResearch) for Western blot analysis and anti-mouse Alexa Fluor 488, anti-mouse Alexa Fluor 568, anti-mouse Alexa Fluor 594, anti-rabbit Alexa Fluor 488 (Life Technologies), and Alexa Fluor 647 conjugated to anti-CD126 (IL-6Rα) (Biolegend, San Diego, CA) for immunofluorescence. Cellular DNA was stained with 4′,6-diamidino-2-phenylindole (DAPI) (Life Technologies).

PCR Oligonucleotides

The following oligonucleotide pairs were used in these studies: IL6 (5’-AGCCACTCACCTCTTCAGAACGAA-3’ and 5’-AGTGCCTCTTTGCTGCTTTCACAC-3’), SOCS3 (5’-ATTCGCCTTAAATGCTCCCTGTCC-3’ and 5’-TGGCCAATACTTACTGGGCTGACA-3’) and (5’-GGCCACTCTTCAGCATCTC-3’ and 5’-ATCGTACTGGTCCAGGAACTC-3’), SOCS3 promoter (5’-AGCCTTTCTCTGCTGCGAGT-3’ and 5’-CCCGATTCCTGGAACTGC-3’), TUBB (5’-TATCAGCAGTACCAGGAT GC-3’ and 5’-TGAGAAGCCTGAGGTGATG-3’), GAPDH (5’-ACCCACTCCTCCACCTTTGAC-3’ and 5’-CTGTTGCTGTAGCCAAATTCGT-3’), UL123 (5’-GCCTTCCCTAAGACCACCAAT -3’ and 5’-ATTTCTGGGCATAAGCCATAATC-3’), UL122 (5’-CCAGTATGCACCAGGTGTTAG-3’ and 5’-CTGGATGCCCTTGTTGTTC-3’), UL38 (5’-ACGGTGCTATCGTGCTGGAGTATT-3’ and 5’-AAGACCATCACCAGGTCGTCC ATA-3’), UL99 (5’-TTCACAAGGTCCACCCACC-3’ and 5’-GTGTCCCATTCCGACTCG-3’), and UL83 (5’-TGAGCATCTCAGGTAACCTGTTG-3’ and 5’-CAGCCACGGGATCGTACTG-3’).

Statistical Analysis

The data are representative of at least two independent experiments, and values are given as the mean of replicate experiments ± standard error of the mean (SEM) unless otherwise stated. For all experiments using the Student's t-test, we have determined that the variances were not different using an F-test prior to using a t-test. A significant p value ($p < 0.05$) is indicated by an asterisk in the figures.

RESULTS

HCMV infection localizes unphosphorylated STAT3 to the nucleus and disrupts IL6-induced gene expression. Limited information is available on the impact of HCMV infection on the cellular transcription factor STAT3. To determine whether HCMV influences STAT3, we evaluated subcellular localization at 2 and 24 hpi. We infected U373 astrocytoma cells using HCMV strain AD169 (AD*wt*) at a multiplicity of 5 infectious units (IU) per cell in 0.5% serum. As a control, uninfected cells were treated with or without human IL6 to stimulate phosphorylation of STAT3. Reduced serum conditions allowed for more robust IL6-stimlulated responses. Cells were fixed and stained using antibodies against STAT3 and phosphorylated STAT3 (pSTAT3) at Y705. To quantify changes in localization, we determined the ratio of mean fluorescent intensities between nuclear and cytosolic staining (N/C). We detected increased STAT3 within the nuclei of infected cells at 2 hpi (N/C=2.95±0.05) and 24 hpi (N/C=6.71±0.68) as compared to uninfected cells (N/C=1.25±0.16) (Figure 1A). As expected, we observed increased nuclear localization of STAT3 (N/C=3.42±0.35) and pSTAT3 in mock plus IL6-treated cells (Figure 1A). To our surprise, we detected little to no pSTAT3 within the nuclei of infected cells (Figure 1A). These data suggest that HCMV infection rapidly promotes nuclear localization of STAT3 in the absence of robust phosphorylation at Y705.

In general, phosphorylation of cytoplasmic STAT3 at Y705 occurs following cytokine and growth factor stimulation and results in STAT3 nuclear accumulation and DNA binding (1, 75). We next investigated whether HCMV influences STAT3 phosphorylation during both infection and cytokine stimulation. U373 cells were infected at an MOI of 5 IU/cell and cultures were treated at the indicated times post infection with or without IL6 (Figure 1B). We evaluated steady-state protein levels using Western blot analysis on whole cell lysates isolated from a population of cells. Compared to mock infection treated with IL6, HCMV infection suppressed IL6-induced phosphorylation of STAT3 at Y705 by 2 hpi and continued through 48 hpi (Figure 1B). In contrast, phosphorylation at S727 occurred regardless of infection and was independent of IL6 stimulation (Figure 1B). At a lower MOI, we observed increased STAT3 phosphorylation at Y705 by Western blot analysis which is likely occurring within uninfected cells in the population as determined by immunofluorescence analysis (Figure S1). To determine whether the response also occurs using a clinically relevant HCMV strain, we completed the experiment using the TB40/E virus (54). Similar to AD169, TB40/E infection suppressed IL6-induced phosphorylation at Y705 but not S727 (Figure 1C). These data demonstrate that HCMV infection disrupts IL6-induced phosphorylation of STAT3 at Y705.

We evaluated the impact of infection on the expression of two genes known to be regulated by STAT3, IL6 and SOCS3 (74, 75). We infected U373 cells at 1 IU/cell using AD*wt* virus with or without IL6 at the indicated times post infection and determined changes in gene expression using quantitative RT-PCR (qRT-PCR) relative to GAPDH RNA levels. Compared to mock control, infection significantly decreased gene expression of IL6 and SOCS3 following IL6 stimulation (Figure 1D). These data support the conclusion that HCMV infection disrupts expression of two IL6-induced STAT3-regulated genes. To exclude the possibility that disruption of IL6 signaling is a consequence of decreased IL6 receptor cell surface expression, we measured the impact of infection on IL6Rα. We infected U373 cells at 3 IU/cell and surface levels of IL6Rα were determined using flow cytometry. Compared to mock, we observed similar levels of IL6Rα during HCMV infection at 6 and 24 hpi (Figure 1E). These data rule out the possibility of HCMV-mediated loss of endogenous IL6Rα surface expression during the time of altered gene expression.

To test whether HCMV-mediated inhibition of IL6 signaling depends on STAT3 nuclear localization, we evaluated the effects on STAT3 phosphorylation after disruption of nuclear import. Nuclear translocation of STAT3 is mediated by the importin-α and β1 heterodimer complex (9, 32). We transfected U373 cells with either a control siRNA or an siRNA targeting importin-β1 expression and observed a reduction in importin-β1 levels (Figure 2A). Under these conditions, reduced importin-β1 resulted in increased pSTAT3 in IL6-treated HCMV-infected cells (Figure 2A). Furthermore, disrupting importin-β1 reduced IL6-induced STAT3 nuclear accumulation in both mock (N/C=1.27±0.11) and HCMV-infected cells (N/C=1.55±0.12) as compared to control siRNA mock (N/C=2.19±0.03) and infected (N/C=4.15±0.10) (Figure 2B). These data suggest that HCMV is promoting nuclear accumulation of STAT3 early during infection thereby moving STAT3 away from the cytosolic regulators.

Changes in STAT3 phosphorylation and localization are detectable as early as 2 hpi indicating a role for HCMV virions or newly expressed proteins in manipulating STAT3. To identify the source of the activity, U373 cells were infected with either untreated AD*wt* or UV-irradiated virus and evaluated by immunofluorescence microscopy. STAT3 nuclear localization occurred following infection with untreated (N/C=3.27±0.15) but not UV-irradiated virus (N/C=1.09±0.02) (Figure 2C). Under these conditions of UV treatment, we did not detect IE1 RNA expression (Figure 2D). These data demonstrate that viral gene expression is necessary for relocalization of STAT3.

HCMV IE1 promotes STAT3 nuclear accumulation and disrupts IL6-induced STAT3 phosphorylation, DNA binding and target gene expression.

HCMV immediate early protein IE1 is known to regulate both STAT1 and STAT2 (22, 25, 27, 46). To determine whether IE1 expression could influence STAT3 localization, MRC-5 fibroblasts were mock-infected or infected with either wild-type (*wt*) or an IE1-deficient virus (*dl*IE1) of the HCMV Towne strain at 3 PFU/cell. Using immunofluorescence microscopy, we observed increased staining of STAT3 within the nuclei of IE2-positive infected cells by 6 hpi using *wt* virus (N/C=1.73±0.04) but not *dl*IE1 (N/C=0.99±0.15) as compared to mock (N/C=1.09±0.13) (Figure 3A). This increase was also observed at both 24 (N/C=1.73±0.55) and 72 hpi (N/C=2.13±0.56) (Figure 3A). At these later times, we did observe a few cells in the *dl*IE1 infections that had increased nuclear STAT3 staining; however, this was not significant among the population as indicated by the N/C ratio determined from a random selection of cells (n=95). These data demonstrate that IE1 is necessary for the efficient nuclear localization of STAT3 during infection. HCMV IE1 has been previously demonstrated to localize to mitotic chromatin (27). In cells undergoing mitosis in the infected population, we observed colocalization of STAT3 with DAPI-stained chromatin (Figure 3B, left and right panel). Moreover, STAT3 and IE1 colocalized in *wt*- but not *dl*IE1-infected cells (Figure 3B, right panel). To assess a possible physical interaction between IE1 and STAT3, we isolated whole cell lysates at 24 hpi and immunoprecipitated protein complexes using an antibody against IE1. Following immunoprecipitation, we detected the slower migrating STAT3α but not the smaller STAT3 isoform by Western blot analysis from TN*wt*-infected cells (Figure 3C). We did not observe an interaction when using an antibody against IE2 or following infection by the *dl*IE1 virus (Figure 3C). IE1 was also specifically detected throughout the viral infectious cycle (6 to 72 h) in protein complexes isolated by immunoprecipitation using a STAT3-directed antibody

(Figure 3D). These data demonstrate that HCMV IE1 associates with at least one STAT3 isoform during infection.

Finally, we evaluated the functional impact of IE1 on STAT3 following IL6 stimulation. These studies were completed by adding both IL6 and soluble IL6 receptor alpha (IL6Rα) to the culture media, because MRC-5 cells are largely unresponsive to IL6 alone. Following the addition of exogenous IL6/IL6Rα, infection by *wt* but not *dl*IE1 virus resulted in reduced levels of Y705-phosphorylated STAT3 at 16 hpi as compared to mock (Figure 4A). Under these conditions in mock infected cells, IL6/IL6Rα triggered robust STAT3 DNA binding at the SOCS3 promoter and little binding at the SOCS3 transcribed region, as determined by chromatin immunoprecipitation (ChIP) assay (Figure 4B). During infection, IL6/IL6Rα-induced STAT3 DNA binding was substantially diminished using *wt* virus but not the *dl*IE1 virus (Figure 4B). Concordantly, SOCS3 gene induction was significantly reduced during *wt* infection (Figure 4C). Infection by the *dl*IE1 virus altered SOCS3 expression, but to a lesser degree than *wt* virus (Figure 4C). Expression of HCMV IE2 was unaltered between the different conditions of infection (Figure 4C). Our results support the conclusion that HCMV IE1 binds to STAT3α and is necessary to localize STAT3 to the nucleus at early times of infection. Furthermore, expression of IE1 disrupts IL6-induced phosphorylation of STAT3, DNA association by STAT3, and SOCS3 gene induction during infection.

To determine whether IE1 expression is sufficient to mediate these changes, we induced IE1 in the absence of infection using a tetracycline repressor-regulated expression system in human fibroblasts (TetR/TetR-IE1) (25). Following induction of IE1 expression using doxycycline, we observed strong accumulation of STAT3 within the nuclei of TetR-IE1 cells (Figure 5A). STAT3 relocalization did not occur in control TetR cells (Figure 5A). By 24 to 72 h post stimulation, greater than 90% of the IE1-positive cells contained STAT3 within the nucleus (Figure 5B), but these nuclei did not exhibit detectable pSTAT3 (Figure S3). Furthermore, STAT3 again colocalized with the viral protein and DAPI-stained mitotic chromatin upon induction of IE1 (Figure 5C). Consistent with previous studies (25), induction of IE1 expression relocalized only a fraction of STAT1 to the nucleus with delayed kinetics as compared to STAT3 (Figure S2A and C) while not apparently altering the subcellular distribution of STAT2 (Figure S2B and C). We also evaluated changes in STAT3 phosphorylation upon IE1 expression. Increased expression of IE1 correlated with decreased levels of phosphorylation at Y705, while the total levels of STAT3 remained constant (Figure 5D). Under these conditions, IE1 was sufficient to suppress the levels of SOCS3 RNA (Figure 5E). Finally, induction of IE1 suppressed exogenous IL6/IL6Rα-stimulated phosphorylation of STAT3 (Figure 5F and S3), SOCS3 promoter binding by STAT3 (Figure 5G) and SOCS3 expression (Figure 5H). These data indicate that expression of IE1 is sufficient to promote the nuclear accumulation of mostly unphosphorylated STAT3 inactive for sequence-specific DNA binding at the SOCS3 promoter and alter expression of the STAT3-regulated gene SOCS3.

Disruption of STAT3 relocalization inhibits HCMV DNA replication. The rapid accumulation of unphosphorylated STAT3 in the nucleus during infection suggests that HCMV might utilize STAT3 for viral replication. To test this hypothesis, we evaluated the impact of chemical inhibitors of STAT3 on HCMV infection. The inhibitors included S3i-201 which inhibits STAT3 dimerization and DNA binding (53), curcumin, a natural plant polyphenol which functions, in part, by inhibiting STAT3 DNA binding (3, 7, 15, 28), STATTIC which interferes with STAT3 phosphorylation and dimerization (51), and WP1066 which blocks upstream JAK2-

mediated phosphorylation (14). Initially, we tested whether the compounds would influence HCMV-mediated localization of STAT3. U373 cells were pretreated with DMSO or non-cytotoxic concentrations of each compound (Figure 6A). We infected cells at a multiplicity of 5 IU/cell and evaluated STAT3 by immunofluorescence microscopy. Compared to DMSO (N/C=5.30±0.12), both S3i-201 (N/C=1.26±0.10) and curcumin (N/C=1.13±0.40) treatments significantly reduced the accumulation of STAT3 in the nucleus of infected cells (Figure 6B). STATTIC treatment resulted in an intermediate phenotype (N/C=2.64±0.80) while inhibiting JAK-mediated phosphorylation using WP1066 failed to block the HCMV-mediated change in STAT3 localization (N/C=5.45±0.90) (Figure 6B).

Next, we quantified the impact of inhibiting STAT3 on HCMV replication. U373 cells were pretreated with DMSO or compound and infected at 0.25 IU/cell using AD*wt* virus. We quantified changes in HCMV viral DNA levels using qPCR. The addition of S3i-201 resulted in a 99.7% reduction in viral DNA levels, curcumin in a 94.0% reduction, STATTIC in an 89.5% reduction and WP1066 had no effect on DNA replication (Figure 6C). Interestingly, the percent reduction was proportional to the change in the nuclear/cytosolic ratio for STAT3 (Figure 6B). Using S3i-201, we observed the greatest decrease in DNA replication at ≥120 μM (Figure 7A). The efficacy of S3i-201 inhibition was influenced by MOI. Although still inhibiting replication, infection at 3 IU/cell resulted in approximately 71.2 % decrease in viral DNA replication (Figure 7B). We also evaluated the antiviral efficacy of S3i-201 during infection of primary human foreskin fibroblasts and retinal pigmented epithelial cells. Fibroblasts and U373 cells were infected at 0.25 IU/cell using AD*wt* virus while epithelial cells were infected using the clinical isolate TB40/E. Chemical inhibition of STAT3 significantly reduced viral DNA replication at 72 hpi in all of the cell types and viral strains (Figure 7C). Finally, we determined the impact of

STAT3 inhibition on viral titers at 96 hpi from cells treated with either DMSO or S3i-201. We observed that the addition of S3i-201 resulted in an average 2.3 log reduction in viral titers (Figure 7D). These data suggest that STAT3 nuclear localization is linked to efficient HCMV DNA replication and virus production in multiple cell types.

To provide evidence that the disruption is STAT3-dependent, we knocked-down STAT3 expression by transfecting U373 cells with an siRNA targeting STAT3 or control siRNA. We analyzed changes in STAT3 protein expression by Western blot and observed a reduction in STAT3 levels using the specific siRNA as compared to control (Figure 8A). Albeit reduced, we did observe STAT3 within the nucleus in cells transfected with the specific siRNA (Figure 8B). To evaluate the impact on HCMV viral DNA replication, siRNA-transfected U373 cells were infected a 0.25 IU/cell and we quantified changes in viral DNA levels using qPCR. Compared to control, we observed a 5-fold reduction in viral DNA replication upon reduced levels of STAT3 (Figure 8C). These data provide additional evidence that STAT3 is necessary for fully efficient viral DNA replication.

Herpesvirus gene expression is temporally regulated with kinetic classes defined as immediate early (IE), early (E), early-late (E-L) and late (L). Efficient late gene expression is dependent upon DNA replication (41). To identify the steps in replication which require STAT3, we quantified changes in viral gene expression. U373 cells were pretreated with DMSO or S3i-201 and infected using AD*wt* virus at 0.25 IU/cell. Total RNA was harvested and viral gene expression was quantified relative to GAPDH RNA. We observed similar levels of expression for the IE and E genes UL123 (IE1) and UL38, respectively, between mock and S3i-201 treatments (Figure 9A). However, beginning around 24 hpi, the addition of S3i-201 significantly decreased expression of UL122 (IE2), UL83, and UL99 (Figure 9A). We confirmed these changes using Western blot analysis of whole cell lysates from HCMV-infected U373 cells (Figure 9B). In addition to changes in the IE2-86 kDa (pUL122) protein, we observed decreased expression of the IE2-60 kDa late isoform following S3i-201 treatment (Figure 9B). Furthermore, expression levels of two viral proteins with E-L kinetics, pTRS1 and pUL44, were also inhibited (Figure 9B) beginning at 24 hpi. These data demonstrate that inhibition of STAT3 disrupts viral gene expression beginning around 24 hpi with the greatest impact seen after 48 hpi on HCMV IE2, E-L and L genes.

The accumulation of E-L and L transcripts as well as UL122 is dependent on viral DNA synthesis (12, 57, 58). Furthermore, HCMV IE2, pUL44, and pTRS1 have been demonstrated to contribute to genome replication (21, 33, 34, 36, 50, 56, 65). To test the timing of STAT3's contribution to HCMV replication, we treated U373 cells with S3i-201 at different times during infection. Cells were infected at 0.25 IU/cell using AD*wt* virus and treated with S3i-201 at 2 hpi or at 48 hpi for 24 h. We isolated DNA at 72 hpi and quantified viral genomes using qPCR. Consistent with previous data, S3i-201 treatment early during infection resulted in a significant decrease in viral DNA levels (Figure 9C). Conversely, treatment at 48 hpi resulted in no significant difference in viral DNA compared to control infection (Figure 9C). These data suggest that HCMV relocalizes STAT3 early to regulate early and late events during infection, including efficient viral DNA replication.

DISCUSSION

We have determined that HCMV infection promotes the nuclear accumulation of STAT3 that is predominantly or entirely unphosphorylated at tyrosine 705 (Y705). In the canonical pathway from uninfected cells, STAT3 is activated by a variety of different stimuli including cytokines and growth factors, resulting in phosphorylation of Y705 (pSTAT3) and accumulation in the nucleus (1, 75). Unlike HCMV, herpesviruses that infect cells of lymphoid origin including Epstein-Barr virus (EBV) (17, 64), Kaposi's sarcoma-associated herpesvirus (KSHV) (47), herpesvirus saimiri (HVS) (8), and varicella-zoster virus (VZV) (52) exploit the survival and oncogenic effects of pSTAT3. Beyond herpesviruses, several oncogenic viruses utilize pSTAT3 while other viruses employ mechanisms to inhibit STAT3 signaling (62, 63). Within our studies, we observed that disrupting the nuclear accumulation of STAT3 or STAT3 expression inhibited HCMV infection at the stage of viral DNA replication. These studies are the first example of a virus that inhibits phosphorylation of STAT3 at Y705 yet still requires its activities for viral replication.

We have demonstrated that the HCMV IE1 protein is necessary to relocalize STAT3 to the nucleus at early times during infection, and the viral protein is also sufficient to induce nuclear STAT3 accumulation. The effects of IE1 on the subcellular distribution of STAT3 seem to be independent of phosphorylation at Y705 or cytokine stimulation. IE1 (also known as IE1-72kDa or IE72) is a nuclear regulatory phosphoprotein expressed from the HCMV genome at the start of infection. IE1 has long been known to attach to human chromosomes (29), but is not considered to bind directly to DNA (43). We observed that IE1 expression promotes the association of STAT3 with mitotic chromatin yet disrupts STAT3 binding to the SOCS3 promoter. Unphosphorylated STAT3 has been demonstrated to shuttle between the nucleus and the cytosol (48, 60, 70, 71), and we speculate that STAT3 nuclear export may be prevented by interactions with IE1 at cellular chromatin and/or other nuclear compartments.

One functional consequence of IE1-mediated nuclear localization of STAT3 is the suppression of IL6-induced SOCS3 gene expression. When disrupting nuclear import, we were able to re-establish IL6-stimulated phosphorylation of STAT3 suggesting that HCMV is sequestering STAT3 away from its upstream kinases by nuclear localization. In addition, disruption of JAK signaling using the compound WP1066 failed to prevent HCMV-mediated nuclear localization or disrupt viral DNA replication. However, we cannot exclude the possibility of HCMV modulation of regulatory phosphatases. Previous studies have demonstrated that up-regulation of IL6 by HCMV pUS28 resulted in pSTAT3 at Y705 (55). Consistent with these and other studies (11, 55), we observed a transient increase in IL6 expression occurring only at 2 hpi which was not affected by S3i-201 (data not shown). Furthermore, we did detect increased pSTAT3 (Y705) by Western blot when infecting most but not all of the cells in culture. Under these conditions, phosphorylation of STAT3 occurred mostly in the uninfected cells within this population. Finally, Le et al. (30) have demonstrated that HCMV infection can disrupt IFN-γ-stimulated STAT3 phosphorylation starting at 24 hpi. Our studies indicate that nuclear STAT3 is predominantly unphosphorylated at Y705 in cells infected by either lab-adapted or clinical strains of HCMV.

Our data indicates that HCMV primarily utilizes unphosphorylated STAT3 to promote, either directly or indirectly, the initiation of HCMV DNA replication. Consistent with this idea, the addition of S3i-201 after 48 hpi had no effect on DNA replication. We have demonstrated that inhibition of STAT3 severely attenuates viral DNA replication, the expression of numerous viral genes, and consequently, the production of infectious viral progeny. At 24 hpi, we observed similar levels of expression for HCMV IE1, IE2 and pUL38 following STAT3 inhibition. However, we detected a substantial decrease in expression of the viral polymerase subunit, pUL44. The decrease in pUL44 levels may be attributed to decreased pTRS1 since pTRS1 functions in cooperation with IE1 and IE2 to stimulate UL44 expression (10, 56). After 24 hpi, the increase in IE2-86kDa, IE2-60kDa, pTRS1 and pUL99 levels failed to occur upon inhibiting STAT3. These changes have been shown to be dependent upon viral DNA replication (4, 13, 38, 45). A similar phenotype occurred upon deletion of the HCMV protein pUL21a which, along with pUL97 kinase, negatively regulates the anaphase promoting complex (12, 13, 61). Disruption of pUL21a resulted in reduced DNA replication and late expression of a subset of proteins including IE2 and pUL99 (13).

We have demonstrated that chemical antagonists of STAT3 significantly inhibit HCMV infection. Similar observations have been made using inhibitors of STAT3 and VZV infection (52). Numerous malignancies are characterized by elevated STAT3 expression and activity (24). As a result, STAT3 inhibitors are being developed and are currently entering clinical trials as anti-cancer agents (24). Several FDA-approved compounds have been shown to inhibit STAT3 activity, such as Celebrex and Sorafenib (16, 31, 69), which also inhibit HCMV replication *in vitro* (6, 39). Overall, our studies indicate that HCMV manipulates STAT3 to promote an environment that supports efficient viral DNA replication and implicate STAT3 as a possible target of anti-HCMV antiviral research.

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FIGURE LEGENDS

Figure 1. Infection increases the levels of unphosphorylated STAT3 in the nucleus and inhibits IL6-stimulated gene expression.

(A) Serum-starved U373 cells were mock-infected or infected with AD*wt* at 5 IU/cell in 0.5% serum. Samples were fixed at the indicated times, incubated with antibodies against STAT3 (green) and pSTAT3 at Y705 (red), and counterstained for DNA with DAPI (blue). Where indicated, mock samples were treated with IL6 at 183 ng/ml. The mean fluorescent intensity of STAT3 within the nucleus and cytoplasm was obtained from an average of 20-30 cells and from at least two replicate experiments. The data is presented as nuclear to cytoplasmic ratio ± SEM.

(B) Cells were infected as above and treated with IL6 or DMSO for 15 min prior to Western blot analysis using the indicated antibodies. The α- and β-STAT3 isoforms are evident upon sufficient electrophoretic separation.

(C) The above experiment was repeated using the clinical isolate TB40/E.

(D) Cells were infected at 1 IU/cell and treated with IL6 or DMSO for 45 min just prior to harvest at 24 and 48 hpi. Levels of the indicated mRNAs were quantified by qRT-PCR and presented relative to GAPDH. Data represent two biological replicate experiments and are presented as the mean ± SEM ($*p < 0.05$).

(E) Serum-starved U373 cells were infected as described in (A). Cells were fixed, stained with anti-IL6Rα antibody conjugate to Alexa-Fluor 647and analyzed using flow cytometry. As a control, cells were treated with trypsin solution for 15 min prior to antibody staining (grey) and the values represent the mean fluorescence intensity from two biological experiments.

Figure 2. Nuclear accumulation of STAT3 reduces IL6-induced phosphorylation and is dependent on viral gene expression.

(A) Serum-starved U373 cells were transfected with control siRNAs or an siRNA targeting importin-β1 24 h prior to infection. Cells were mock-infected or infected with AD*wt* virus at 5 IU/cell and treated with IL6 for 15 min prior to harvest at 24 hpi. Western blot analysis was completed using the indicated antibodies.

(B) Cells were transfected, infected, and treated with IL6 as described above. At 24 hpi, cells were processed for immunofluorescence analysis using anti-STAT3 (green) and DAPI (blue). The mean fluorescent intensity of STAT3 within the nucleus and cytoplasm was obtained from an average of 20-30 cells and from at least two replicate experiments. The data is presented as nuclear to cytoplasmic ratio ± SEM.

(C) U373 cells were mock-infected or infected at 5 IU/cell with either untreated or UV-irradiated AD*wt* virus. At 5 hpi, cells were processed for immunofluorescence analysis using anti-STAT3 (green) and DAPI (blue). The mean fluorescent intensity of STAT3 within the nucleus and cytoplasm was determined as described above.

(D) U373 cells were mock-infected or infected at 5 IU/cell with either untreated or UV-irradiated ADwt virus. At 5 hpi, cells were harvested and levels of IE1 mRNA was quantified by qRT-PCR and presented relative to GAPDH. Data represent two biological replicate experiments and are presented as the mean ± SEM.

Figure 3. HCMV IE1 interacts with STAT3 and promotes STAT3 nuclear accumulation.

(A) Growth-arrested MRC-5 cells were mock-infected or infected with *wt* or *dl*IE1 at 3 PFU/cell in 10% serum. Samples were fixed at the indicated times, incubated with antibodies against STAT3 (green) and HCMV IE2 (red), and counterstained for DNA using DAPI (blue). Scale bar, 10 μm. The mean fluorescent intensity of STAT3 within the nucleus and cytoplasm was obtained from an average of 100 cells. The data is presented as mean nuclear to cytoplasmic ratio ± standard deviation.

(B) Cells were infected with *wt* or *dl*IE1 at 3 PFU/cell. Samples were fixed at 48 hpi and stained as described in (A). STAT3 staining of IE2-positive mitotic cells (left set of panels) or STAT3 colocalization with IE1 at mitotic chromatin (right set of panels) is shown. Scale bars, 10 μm.

(C) Cells were infected as described in (B) and extracts isolated at 24 hpi. Samples were subjected to immunoprecipitation using antibodies to IE1 or IE2 and Western blot analysis was completed on lysate and IP samples using the indicated antibodies.

(D) Cells were infected as described in (B) and extracts isolated at 6 to 72 hpi. Samples were subjected to immunoprecipitation using an antibody to STAT3 or normal rabbit IgG and Western blot analysis was completed on lysates and IP samples using the indicated antibodies.

Figure 4. HCMV IE1 inhibits STAT3 phosphorylation, DNA binding and target gene expression.

(A) Serum-starved MRC-5 cells were infected with *wt* or *dl*IE1 at 3 PFU/cell and treated with IL6 and IL6Rα or solvent. Samples from 16 hpi were subjected to Western blot analysis using the indicated antibodies.

(B) Serum-starved cells were infected as described in (A) and treated with IL6 and IL6Rα or solvent for 30 min. Samples from 16 hpi were subjected to ChIP using an antibody to STAT3 or normal rabbit IgG and primers specific for sequences in the SOCS3 promoter or transcribed region. The percentage of output to input DNA was calculated and is presented as the difference between STAT3 and normal IgG ChIPs. Data represent two biological and two technical replicates, and values are given as the mean ± standard deviation.

(C) Serum-starved cells were infected and treated as described in (A). Relative SOCS3 and IE2 mRNA levels at 16 hpi were determined by qRT-PCR and presented relative to TUBB expression. Data represent three biological and two technical replicates, and values are given as the mean ± standard deviation.

Figure 5. IE1 is sufficient to alter STAT3 localization and to inhibit STAT3 phosphorylation, DNA binding and target gene expression.

(A) TetR-IE1 and TetR cells were treated with doxycycline (Dox) for 0 to 72 h and 72 h, respectively. Samples were fixed, incubated with antibodies against IE1 (green) and STAT3 (red), and counterstained for DNA using DAPI (blue). Scale bar, 10 µm.

(B) The percentage of positive cell nuclei was determined from 100 randomly selected cells per sample (IE1 −, no IE1 staining above background; IE1 +, weak, mostly punctate IE1 staining; IE1 ++, strong, diffuse IE1 staining; STAT3 −, STAT3 staining mostly cytoplasmic; STAT3 +, STAT3 staining cytoplasmic and nuclear; STAT3 ++, STAT3 staining mostly nuclear).

(C) TetR-IE1 and TetR cells were treated with Dox. Samples were fixed at 48 hpi and stained as described in (A). Representative mitotic cells are shown. Scale bar, 10 µm.

(D) TetR-IE1 cells were treated with Dox for 0 to 72 h and Western blot analysis was completed using the indicated antibodies.

(E) TetR-IE1 and TetR cells were treated with Dox for 0 to 72 h. Relative SOCS3 mRNA levels were determined by qRT-PCR and presented relative to TUBB expression and TetR at time 0 h. Data represent two biological and two technical replicates, and values are given as the mean ± standard deviation.

(F) TetR-IE1 and TetR cells were treated with Dox for 72 h and with IL6 and IL6Rα or solvent. Western blot analysis was completed using the indicated antibodies.

(G) TetR-IE1 and TetR cells were treated with Dox for 72 h and with IL6 and IL6Rα or solvent for 30 min. Samples were subjected to ChIP using an antibody to STAT3 or normal rabbit IgG and primers specific for sequences in the SOCS3 promoter or transcribed region. The percentage of output to input DNA was calculated and is presented as the difference between STAT3 and normal IgG ChIPs. Data represent two biological and two technical replicates, and values are given as the mean ± standard deviation. *, below detection limit.

(H) TetR and TetR-IE1 cells were treated with Dox for 72 h and with IL6 and IL6Rα or solvent. Relative SOCS3 mRNA levels were determined by qRT-PCR and presented relative to TUBB expression and TetR. Data represent three biological and two technical replicates, and values are given as the mean ± standard deviation.

Figure 6. Chemical disruption of STAT3 inhibits HCMV replication.

(A) U373 cells were treated with increasing concentrations of S3i-201, curcumin, STATTIC, or WP1066. At 72 h, cell viability was quantified. The data represent two biological replicate experiments and are presented as the mean ± SEM.

(B) Cells were pretreated with DMSO, S3i-201, curcumin, STATTIC, or WP1066. After 24 h, cells were infected at 5 IU/cell using AD*wt* and processed for immunofluorescence analysis using an antibody to STAT3 (green) and the DNA stain DAPI (blue). The mean fluorescent intensity of STAT3 within the nucleus and cytoplasm was obtained from an average of 20-30 cells and from at least two biological replicate experiments. The data is presented as nuclear to cytoplasmic ratio ± SEM.

(C) Cells were pretreated with drug as described above. After 24 h, cells were infected at 0.25 IU/cell using AD*wt*. Viral genomes were quantified at 72 hpi by qPCR and normalized to cellular DNA. Data represent two biological replicates and values are given as the mean ± SEM (∗$p < 0.05$).

Figure 7. S3i-201 inhibits HCMV replication in multiple different cell types.

(A) Cells were pretreated with increasing concentrations of S3i-201. After 24 h, cells were infected at 0.25 IU/cell using AD*wt*. Viral genomes were quantified at 72 hpi by qPCR and normalized to cellular DNA. Data represent two biological replicates and values are given as the mean ± SEM (∗$p < 0.05$).

(B) U373 cells were pretreated with 125 μM of S3i-201. After 24 h, cells were infected at 3 IU/cell using AD*wt*. Viral genomes were quantified as described above. Data represent two biological replicates, and values are given as the mean ± SEM (∗$p < 0.05$).

(C) Different cell types were pretreated with 125 μM of S3i-201. U373 and HFF cells were infected at 0.25 IU/cell using AD*wt* while ARPE19 cells were infected at 0.25 IU/cell using TB40/E. Viral genomes were quantified as above. Data represent two biological replicates, and values are given as the mean ± SEM (∗$p < 0.05$).

(D) U373 cells were pretreated with drug as described above. At 24 h, cells were infected at 0.25 IU/cell using AD*wt*. Viral titers were determined from culture supernatants obtained at 96 hpi. Data represent two biological replicates, and values are given as the mean ± SEM (∗$p < 0.05$).

Figure 8. siRNA targeting STAT3 attenuates viral DNA replication.

(A) Serum-starved U373 cells were transfected with control siRNA or siRNA targeting STAT3. After 24 h, Western blot analysis was completed using the indicated antibodies.

(B) Cells were transfected as described above. After 24 h, cells were processed for immunofluorescence analysis using anti-STAT3 (green) and DAPI (blue). The mean fluorescent intensity of STAT3 within the nucleus and cytoplasm was obtained from an average of 20-30 cells and from at least two replicate experiments. The data is presented as nuclear to cytoplasmic ratio ± SEM.

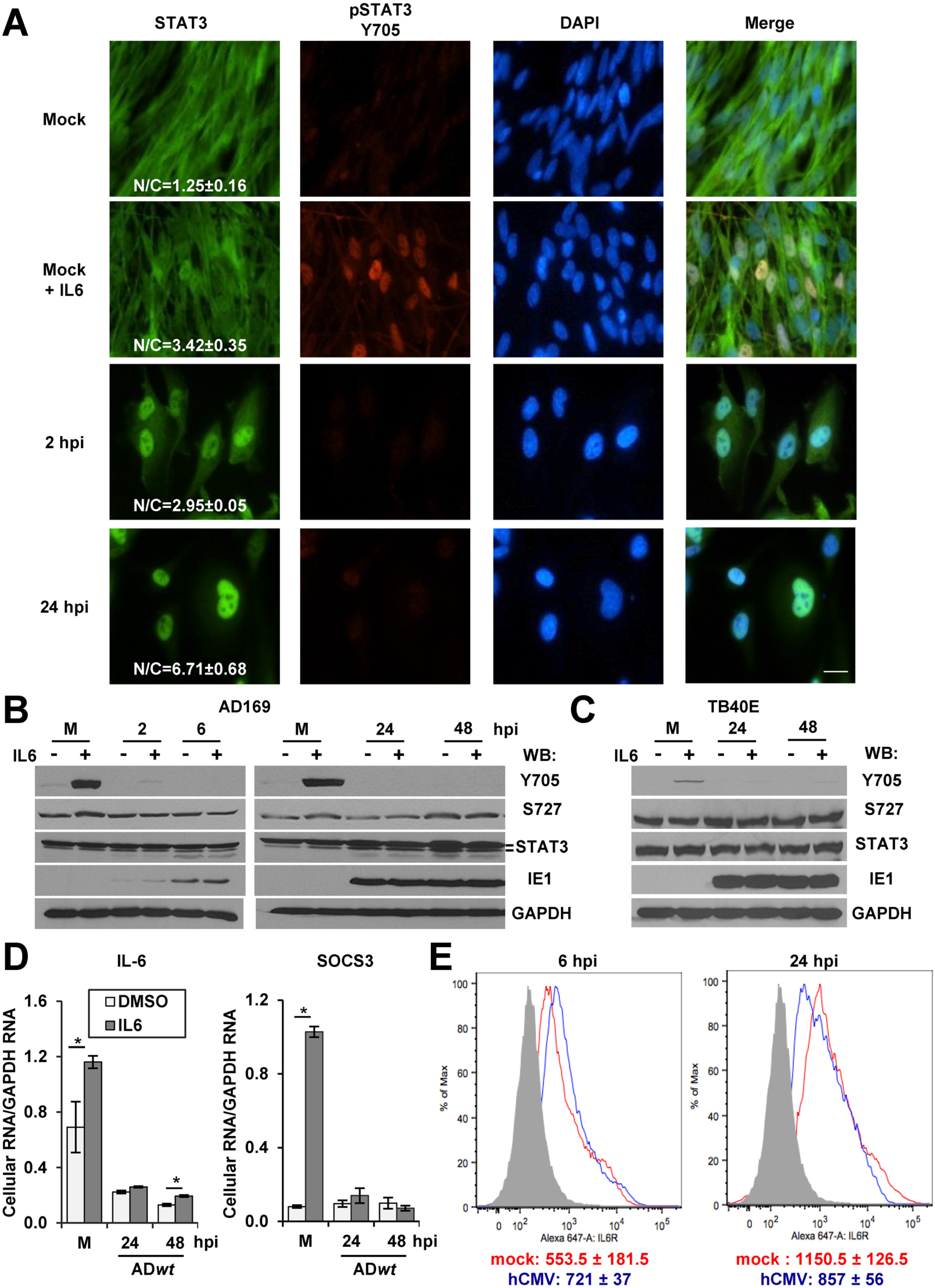
(C) Cells were transfected as described above. After 24 hr, cells were infected with AD*wt* virus at 0.25 IU/cell. Viral genomes were quantified at 72 hpi by qPCR and normalized to cellular DNA. Data represent two biological replicates and values are given as the mean ± SEM ($*p < 0.05$).

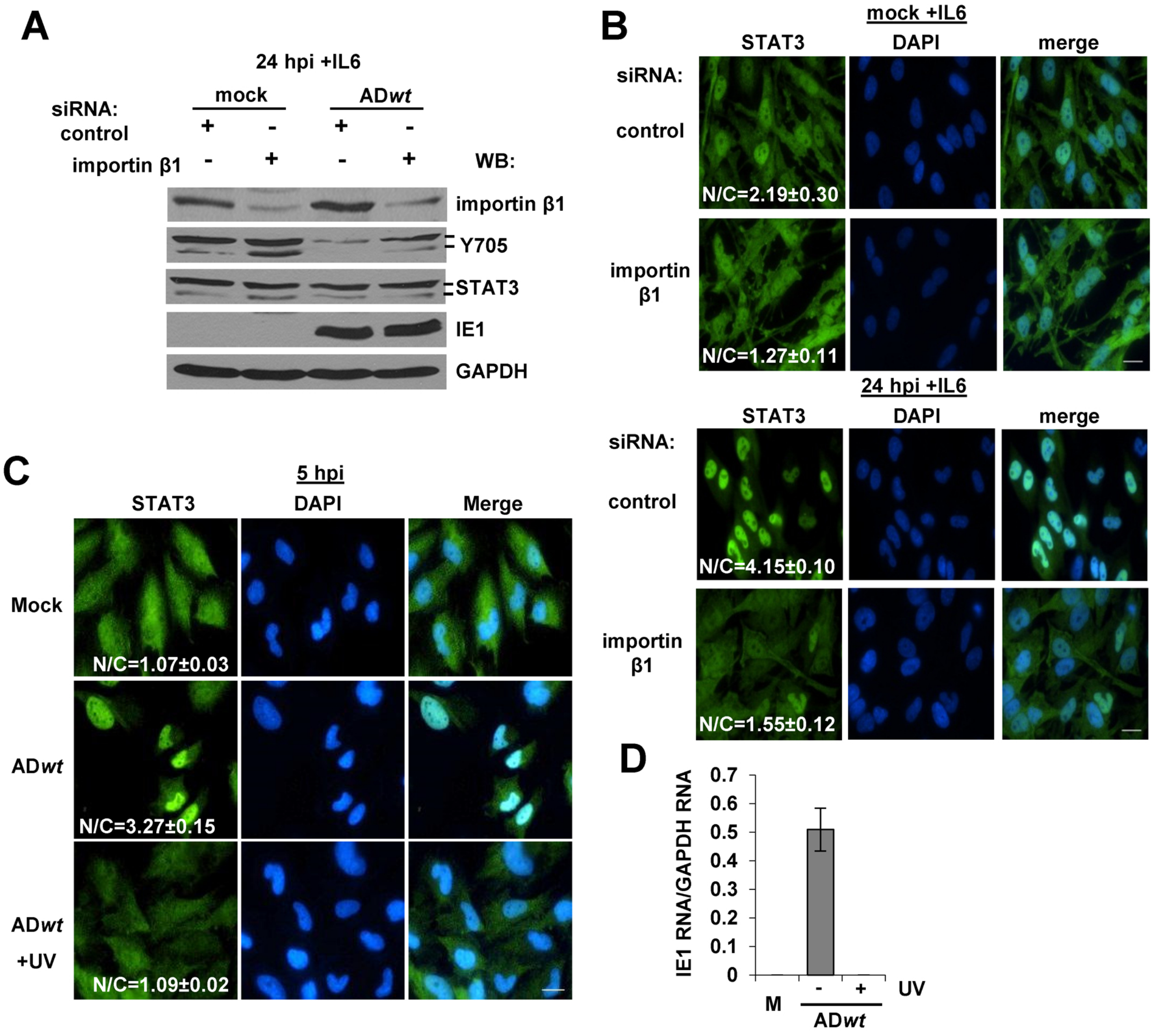
Figure 9 STAT3 is necessary for efficient HCMV gene expression and genome replication.

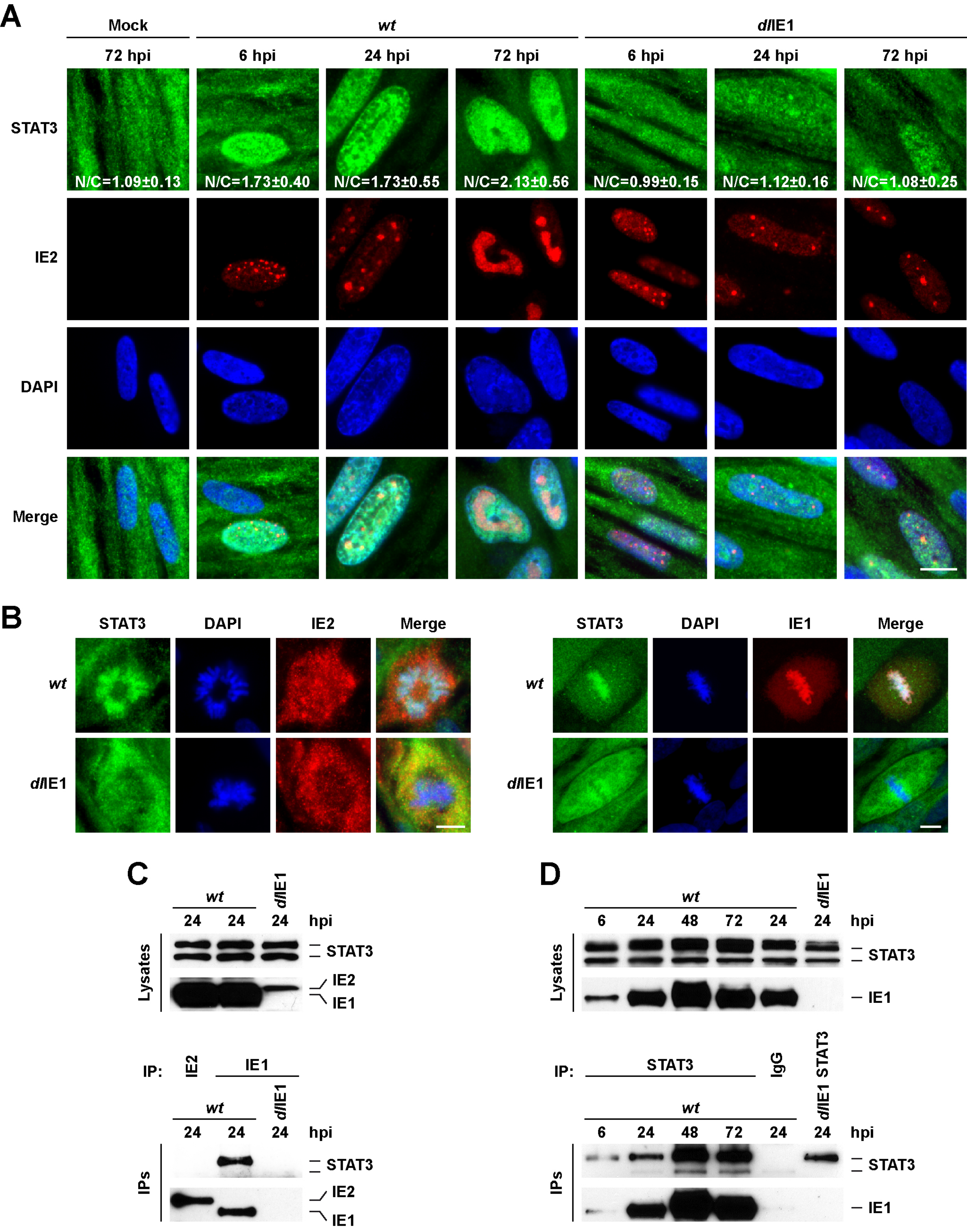
(A) U373 cells were pretreated with DMSO or 125 μM of S3i-201. After 24 h, cells were infected at 0.25 IU/cell using AD*wt*. Levels of the indicated RNAs were quantified by qRT-PCR and presented relative to GAPDH. Data represent two biological replicate experiments, and values are given as the mean ± SEM ($*p < 0.05$).

(B) U373 cells were pretreated with drug as described above, and after 24 h cells were infected for 2 to 72 h with AD*wt* at 0.25 IU/cell. Western blot analysis was completed using the indicated antibodies.

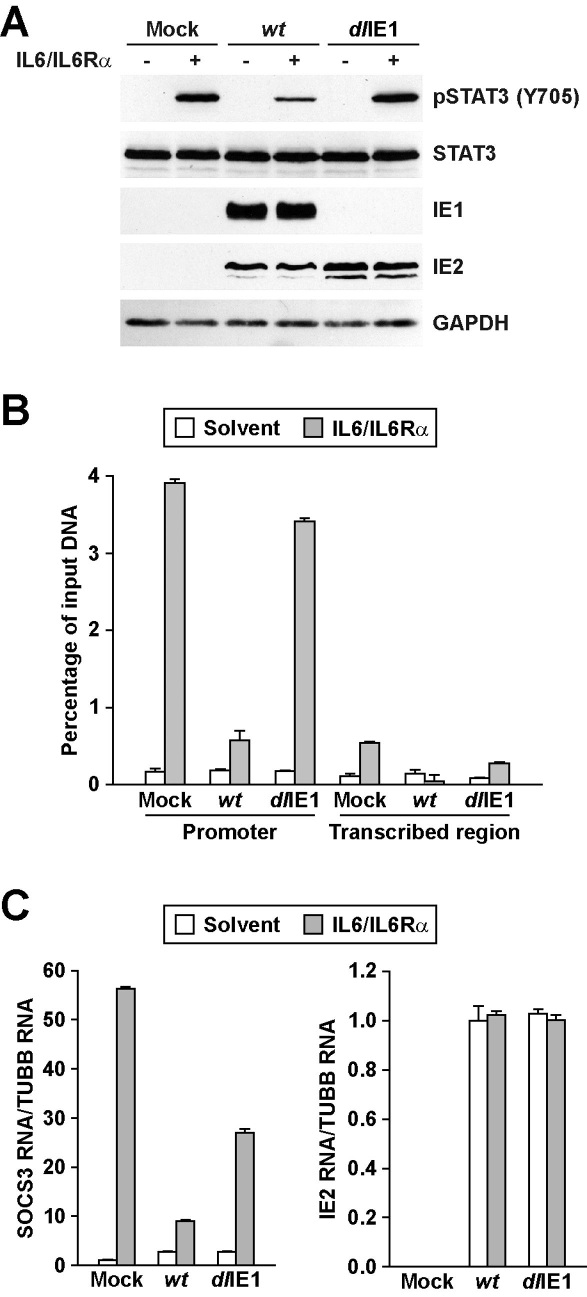
(C) U373 cells were infected at 0.25 IU/cell using AD*wt*. Cells were then treated for 24 h with 125 μM of S3I-201 at either 2 hpi or 48 hpi. After 72 hpi, viral genomes were quantified by qPCR and normalized to cellular DNA. Data represent two biological replicates, and values are given as the mean ± SEM (*p < 0.05).

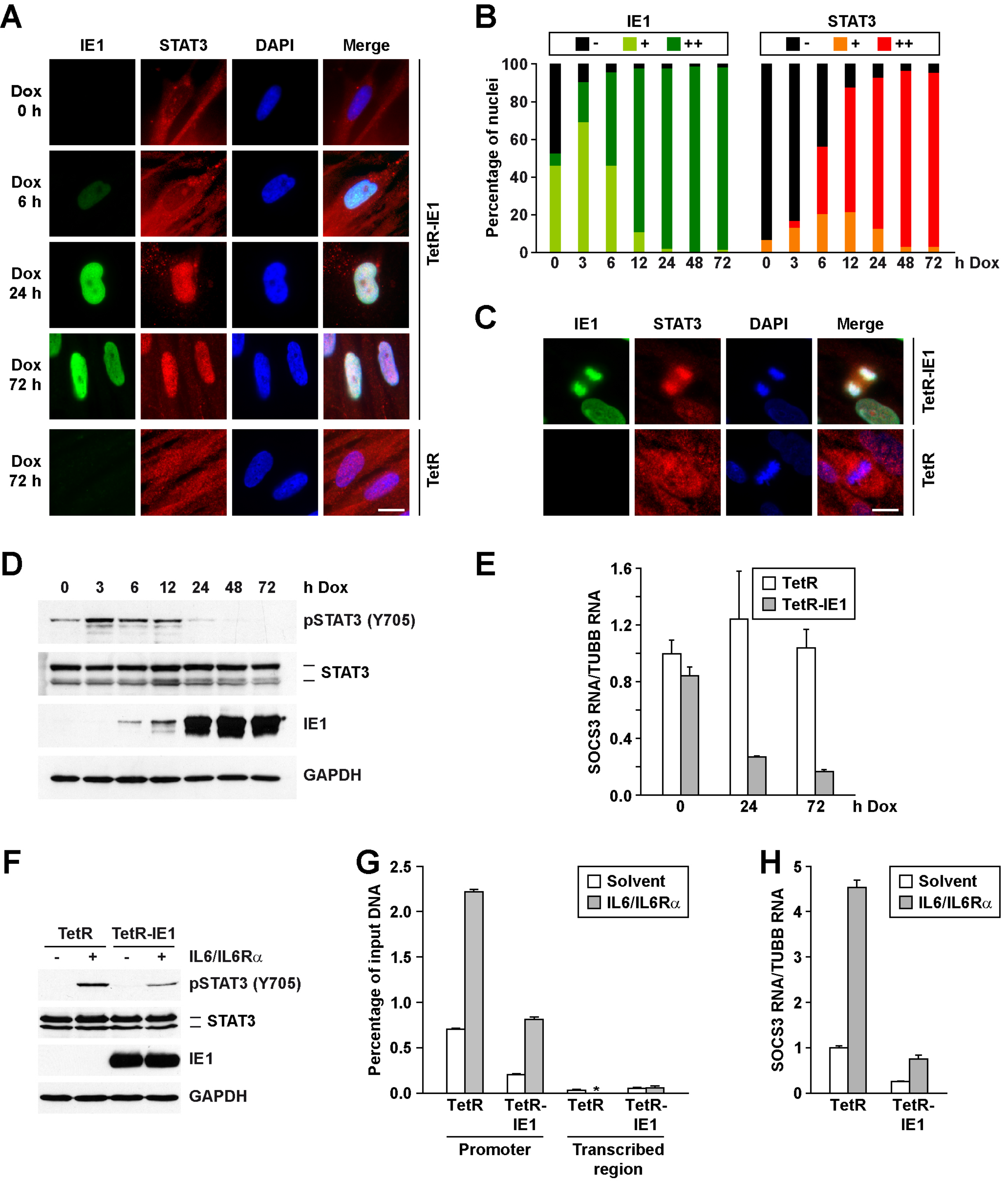

A
STAT3
pSTAT3 Y705
DAPI
Merge
Mock
Mock + IL6
2 hpi
24 hpi
N/C=1.25±0.16
N/C=3.42±0.35
N/C=2.95±0.05
N/C=6.71±0.68
B
AD169
M 2 6 M 24 48 hpi
IL6 - + - + - + - + - + - +
WB:
Y705
S727
=STAT3
IE1
GAPDH
C
TB40E
M 24 48
IL6 - + - + - +
WB:
Y705
S727
STAT3
IE1
GAPDH
D
IL-6
SOCS3
DMSO
IL6
Cellular RNA/GAPDH RNA
M 24 48 hpi
ADwt
E
6 hpi
24 hpi
% of Max
Alexa 647-A: IL6R
mock: 553.5 ± 181.5
hCMV: 721 ± 37
mock : 1150.5 ± 126.5
hCMV: 857 ± 56

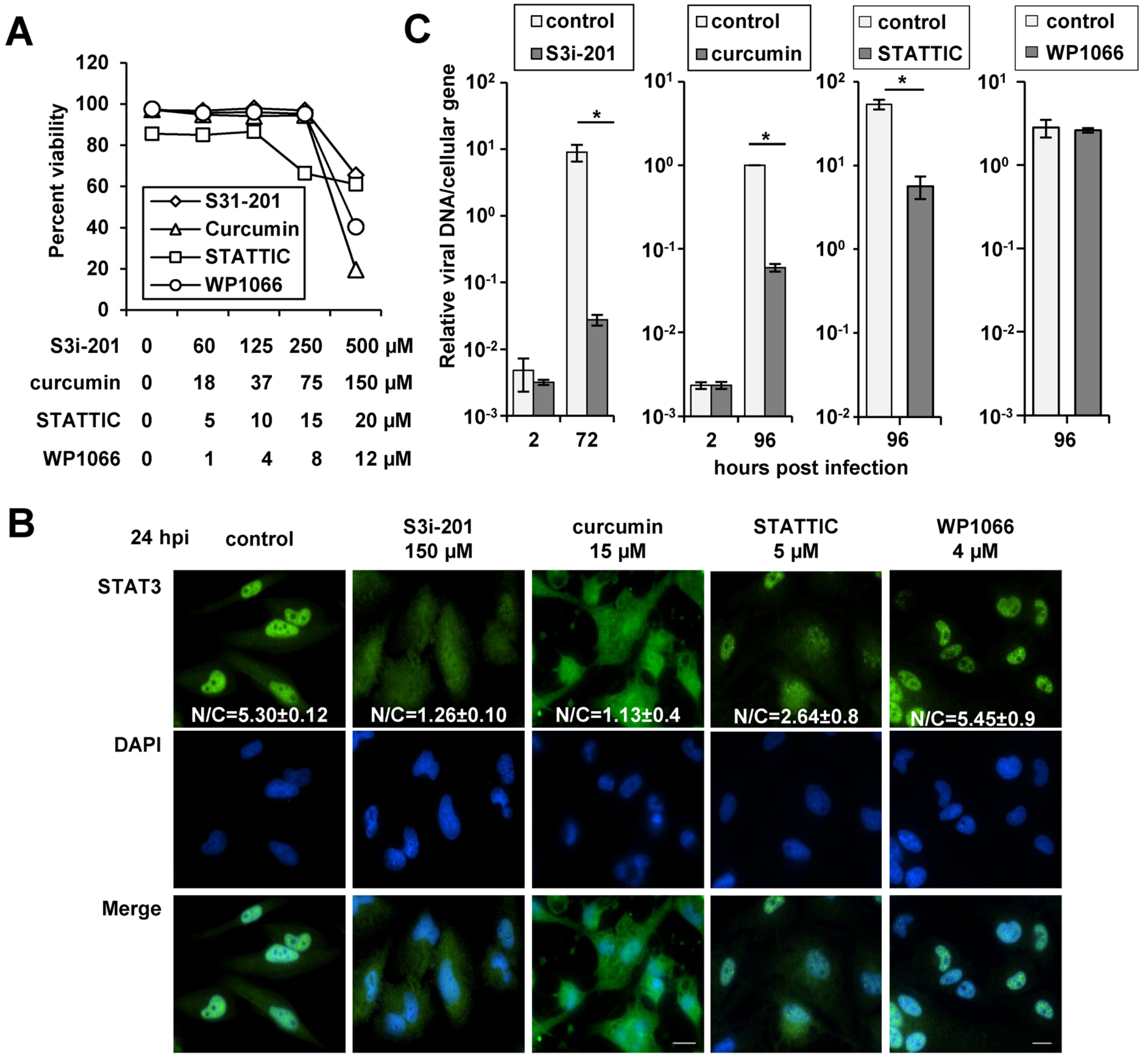

A
24 hpi +IL6
mock
ADwt
siRNA:
control
importin β1
WB:
importin β1
Y705
STAT3
IE1
GAPDH
B
mock +IL6
STAT3
DAPI
merge
siRNA:
control
N/C=2.19±0.30
importin β1
N/C=1.27±0.11
24 hpi +IL6
STAT3
DAPI
merge
siRNA:
control
N/C=4.15±0.10
importin β1
N/C=1.55±0.12
C
5 hpi
STAT3
DAPI
Merge
Mock
N/C=1.07±0.03
ADwt
N/C=3.27±0.15
ADwt +UV
N/C=1.09±0.02
D
IE1 RNA/GAPDH RNA
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
M
-
+
UV
ADwt

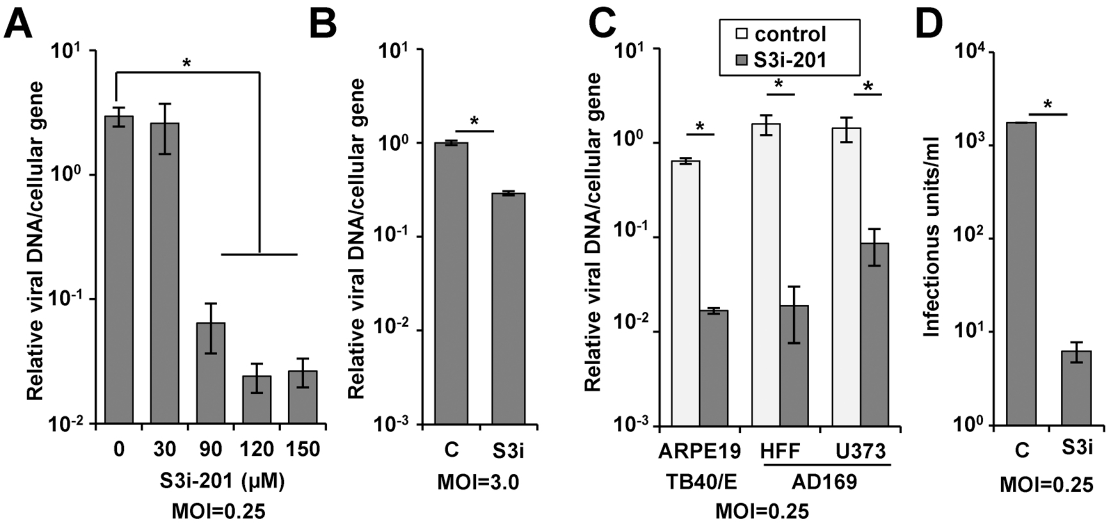


A
Mock
wt
dlIE1
72 hpi
6 hpi
24 hpi
72 hpi
6 hpi
24 hpi
72 hpi
STAT3
IE2
DAPI
Merge
N/C=1.09±0.13
N/C=1.73±0.40
N/C=1.73±0.55
N/C=2.13±0.56
N/C=0.99±0.15
N/C=1.12±0.16
N/C=1.08±0.25
B
STAT3
DAPI
IE2
Merge
wt
dlIE1
STAT3
DAPI
IE1
Merge
wt
dlIE1
C
wt
dlIE1
24
24
24
hpi
Lysates
STAT3
IE2
IE1
IP:
IE2
IE1
wt
dlIE1
24
24
24
hpi
IPs
STAT3
IE2
IE1
D
wt
dlIE1
6
24
48
72
24
24
hpi
Lysates
STAT3
IE1
IP:
STAT3
IgG
dlIE1 STAT3
wt
6
24
48
72
24
24
hpi
IPs
STAT3
IE1

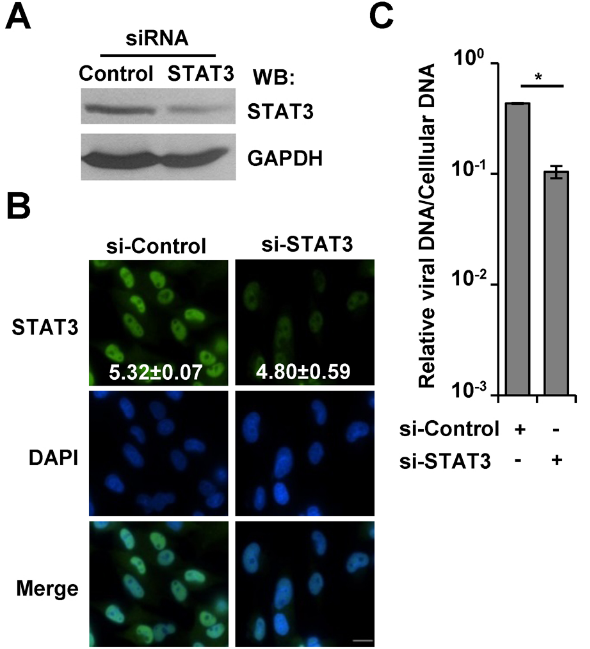

A
Mock
wt
dlIE1
IL6/IL6Rα
-
+
pSTAT3 (Y705)
STAT3
IE1
IE2
GAPDH
B
Solvent
IL6/IL6Rα
Percentage of input DNA
0
1
2
3
4
Mock
wt
dlIE1
Promoter
Transcribed region
C
SOCS3 RNA/TUBB RNA
0
10
20
30
40
50
60
IE2 RNA/TUBB RNA
0.0
0.2
0.4
0.6
0.8
1.0
1.2

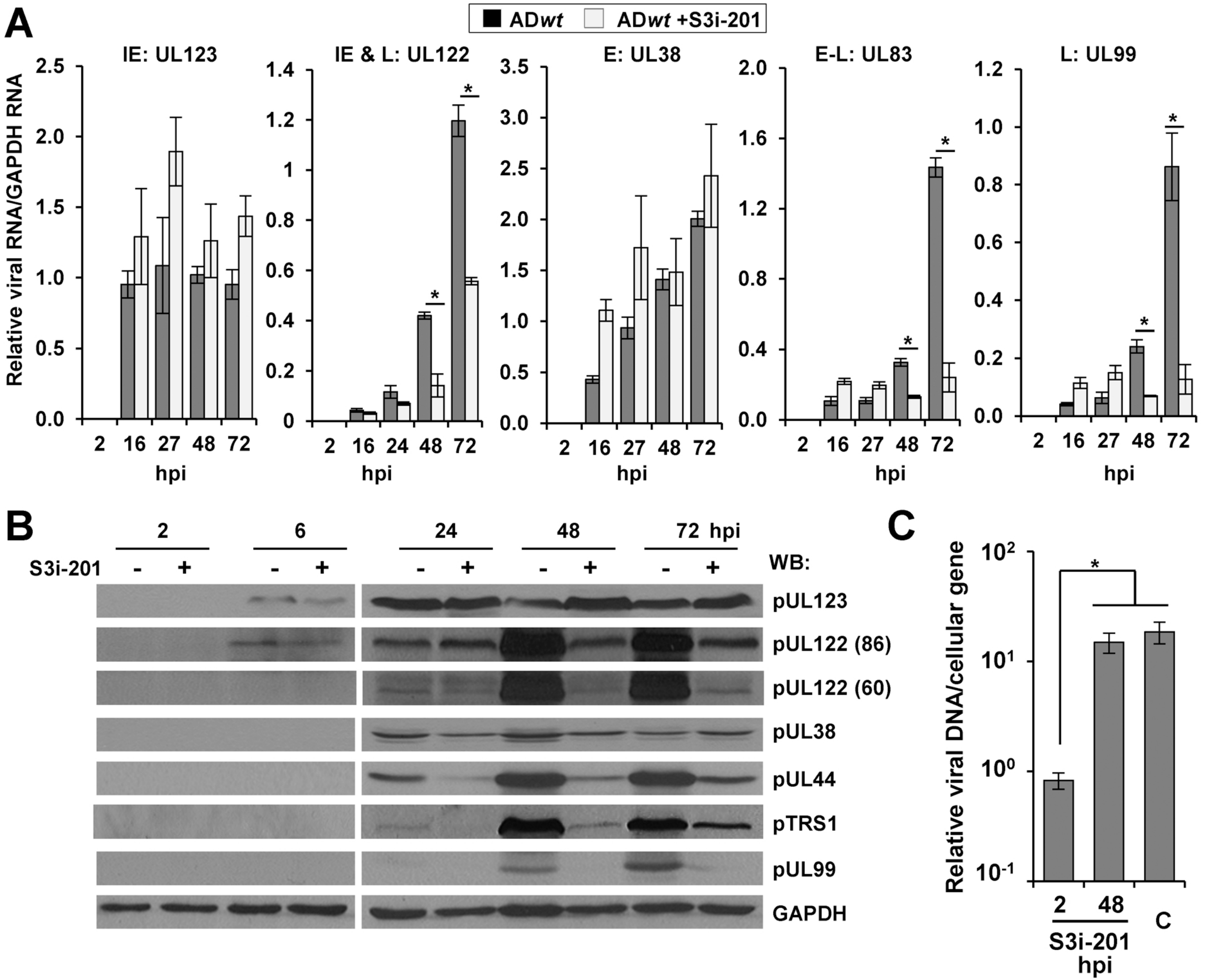

A
IE1
STAT3
DAPI
Merge
Dox 0 h
Dox 6 h
Dox 24 h
Dox 72 h
Dox 72 h
TetR-IE1
TetR
B
IE1
- + ++
STAT3
- + ++
Percentage of nuclei
100
80
60
40
20
0
0 3 6 12 24 48 72
0 3 6 12 24 48 72
h Dox
C
IE1
STAT3
DAPI
Merge
TetR-IE1
TetR
D
0 3 6 12 24 48 72 h Dox
pSTAT3 (Y705)
STAT3
IE1
GAPDH
E
SOCS3 RNA/TUBB RNA
1.6
1.2
0.8
0.4
0.0
TetR
TetR-IE1
0 24 72 h Dox
F
TetR
TetR-IE1
- + - + IL6/IL6Rα
pSTAT3 (Y705)
STAT3
IE1
GAPDH
G
Percentage of input DNA
2.5
2.0
1.5
1.0
0.5
0.0
Solvent
IL6/IL6Rα
TetR
TetR-IE1
TetR
*
TetR-IE1
Promoter
Transcribed region
H
SOCS3 RNA/TUBB RNA
5
4
3
2
1
0
Solvent
IL6/IL6Rα
TetR
TetR-IE1


A
Percent viability
120
100
80
60
40
20
0
S31-201
Curcumin
STATTIC
WP1066
S3i-201 0 60 125 250 500 μM
curcumin 0 18 37 75 150 μM
STATTIC 0 5 10 15 20 μM
WP1066 0 1 4 8 12 μM
C
control
S3i-201
curcumin
STATTIC
WP1066
Relative viral DNA/cellular gene
*
2 72
2 96
96
96
hours post infection
B
24 hpi
control
S3i-201 150 μM
curcumin 15 μM
STATTIC 5 μM
WP1066 4 μM
STAT3
DAPI
Merge
N/C=5.30±0.12
N/C=1.26±0.10
N/C=1.13±0.4
N/C=2.64±0.8
N/C=5.45±0.9



A
B
C
D
control
S3i-201
Relative viral DNA/cellular gene
Infectionus units/ml
10^1
10^0
10^-1
10^-2
10^-3
10^4
10^3
10^2
*
0
30
90
120
150
S3i-201 (μM)
MOI=0.25
C
S3i
MOI=3.0
ARPE19
HFF
U373
TB40/E
AD169
MOI=0.25
C
S3i
MOI=0.25


A
siRNA
Control
STAT3
WB:
STAT3
GAPDH
B
si-Control
si-STAT3
STAT3
5.32±0.07
4.80±0.59
DAPI
Merge
C
Relative viral DNA/Cellular DNA
10^0
10^-1
10^-2
10^-3
*
si-Control + -
si-STAT3 - +


A
ADwt
ADwt +S3i-201
IE: UL123
IE & L: UL122
E: UL38
E-L: UL83
L: UL99
Relative viral RNA/GAPDH RNA
hpi
B
2
6
24
48
72 hpi
S3i-201
WB:
pUL123
pUL122 (86)
pUL122 (60)
pUL38
pUL44
pTRS1
pUL99
GAPDH
C
Relative viral DNA/cellular gene
S3i-201
hpi
C