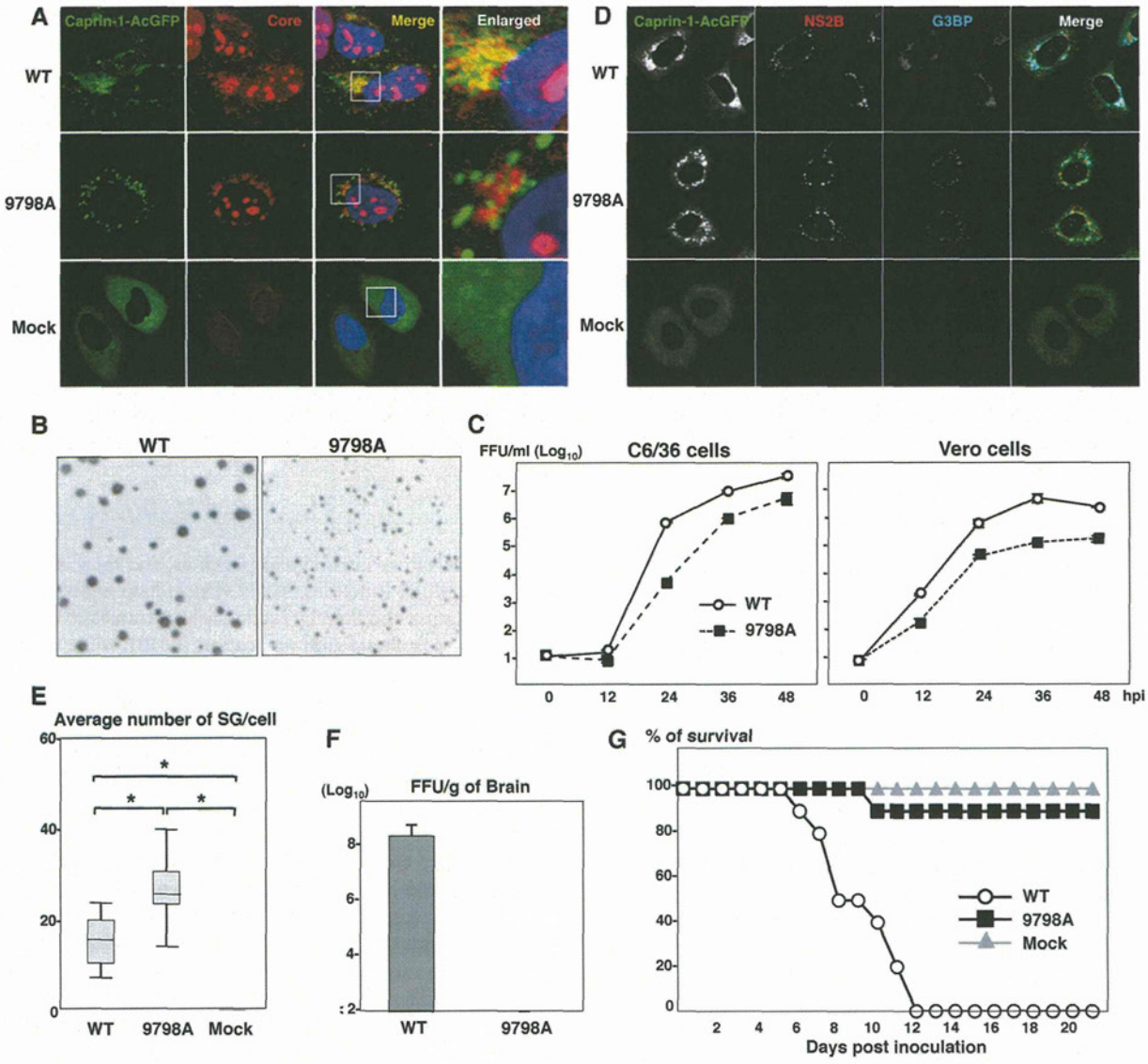

FIG 9 Interaction of JEV core protein with Caprin-1 plays crucial roles not only in viral replication *in vitro* but also in pathogenesis in mice through the suppression of SG formation. (A) Huh7/Caprin-1-AcGFP cells were infected with JEV (WT or 9798A mutant) at an MOI of 1.0, and the cellular localizations of Caprin-1-AcGFP and JEV core protein were determined at 24 h postinfection by immunofluorescence analysis with rabbit anti-core PAb and AF594-conjugated anti-rabbit IgG. Cell nuclei were stained with DAPI (blue). (B) Focus formation of JEV (WT or 9798A mutant) in Vero cells incubated in methylcellulose overlay medium at 48 h postinfection. The infectious foci were immunostained as described previously (20). (C) Growth kinetics of JEV (WT or 9798A mutant) in C6/36 and Vero cells infected at an MOI of 0.1. Infectious titers in the culture supernatants harvested at the indicated times were determined by focus-forming assays in Vero cells. Means of three experiments are indicated. (D) Huh7/Caprin-1-AcGFP cells were infected with either WT or 9798A at an MOI of 0.5, and cellular localizations of Caprin-1-AcGFP, G3BP (blue), and JEV NS2B (red) were determined at 24 h postinfection by immunofluorescence analysis with mouse anti-G3BP MAb and rabbit anti-NS2B PAb, followed by AF633-conjugated anti-mouse IgG and AF594-conjugated anti-rabbit IgG, respectively. (E) Numbers >of G3BP-positive foci in 30 cells prepared as described in panel D were counted. Lines, boxes, and error bars indicate the means, 25th to 75th percentiles, and 95th percentiles, respectively. The significance of differences between the means was determined by Student's *t* test. *, $P < 0.01$. (F) Infectious titers in the cerebrums of mice at 7 days postintraperitoneal inoculation with 5×10^4 FFU/100 μl of either WT or 9798A virus were determined in Vero cells. The means of titers in the homogenates of the cerebrums from three mice are indicated. The detection limit is 10^2 FFU/g of cerebrum. (G) Percentages of surviving mice ($n = 10$) after intraperitoneal inoculation with 5×10^4 FFU of either WT or 9798A virus. Mock, inoculation with DMEM.

Caprin-1 exhibited reduced replication *in vitro* and attenuated pathogenicity in mice.

G3BP is one of the key molecules involved in the SG aggregation process and self-oligomerizes in a phosphorylation-dependent manner to sequester mRNA in SGs (4). Therefore, G3BP knocked down cells (6) and G3BP knockout mouse embryonic fibroblast cells are deficient in the SG formation. In addition, G3BP sequestration inhibits SG formation in response to arsenite treatment (32). Caprin-1, known as RNA granule protein 105 or p137 (33), also participates in SG formation through phosphorylation of eIF2α (28) and is ubiquitously expressed in the cytoplasm. Caprin-1 regulates the transport and translation of mRNAs

of proteins involved in the synaptic plasticity in neurons (34) and cellular proliferation and migration in multiple cell types (28) through an interaction with G3BP. USP10, another SG-associated molecule, also interacts with G3BP and forms the G3BP/USP10 complex (29), suggesting that several SG-associated RBPs participate in the formation of a protein-protein network. In this study, the JEV core protein was shown to directly interact with Caprin-1, to sequester several key molecule complexes involved in SG formation to the perinuclear region in cells infected with JEV, and to facilitate viral propagation through the suppression of SG formation.

Flaviviruses replicate at a relatively low rate in comparison with most of the other positive-stranded RNA viruses, and thus rapid shutdown of host cellular protein synthesis would be deleterious for the viral life cycle. In cells infected with JEV, several SG components were colocalized with the core protein in the perinuclear region, while in those infected with WNV or DENV, SG components were accumulated in a replication complex composed of viral RNA and nonstructural proteins. In addition, the phosphorylation of eIF2α induced by arsenite was completely canceled by the infection with WNV or DENV, whereas the suppression of the phosphorylation was limited in JEV infection (15). Incorporation of the nascent viral RNA into the membranous structure induced by viral nonstructural proteins prevents PKR activation and inhibits SG formation in cells infected with WNV (17). In cells infected with hepatitis C virus (HCV), which belongs to the genus *Hepacivirus* in the family *Flaviviridae*, induction of SG formation was observed in the early stage of infection, in contrast to the inhibition of the arsenite-induced SG formation in the late stage (35). Several SG components, such as G3BP1, PABP1, and ataxin-2, were colocalized with HCV core protein around lipid droplets (35), and G3BP1 was also associated with the NS5B protein and the 5′ terminus of the minus-strand viral RNA (36) to mediate efficient viral replication. Collectively, these data suggest that flaviviruses have evolved to regulate cellular processes involved in SG formation through various strategies.

PKR is one of the interferon-stimulated genes and plays a crucial role in antiviral defense through phosphorylation of eIF2α, which leads to host translational shutoff (37, 38). In the early stage of flavivirus infection, both positive- and negative-stranded RNAs transcribe at low levels, while genomic RNA predominantly synthesizes in the late stage of infection (39). It was shown that activation of PKR was suppressed (40) or only induced in the late stage of WNV infection (41) and impaired by the expression of HCV NS5A (42–44). Very recently, JEV NS2A was shown to suppress PKR activation through inhibition of dimerization of PKR in the early stage but not in the late stage of infection (45). In this study, we have shown that JEV core protein interacts with Caprin-1 and inhibits SG formation downstream of the phosphorylation of eIF2α in the late stage of infection, suggesting that JEV has evolved to escape from host antiviral responses in the multiple stages of viral replication by using structural and nonstructural proteins.

The flavivirus core protein is a multifunctional protein involved in many aspects of the viral life cycle. In addition to the formation of viral nucleocapsid through the interaction with viral RNA (as a structural protein) (46), flavivirus core proteins interact with various host factors, such as B23 (47), Jab1 (48), hnRNP K (49), and hnRNP A2 (23), and regulate viral replication and/or modify the host cell environment (as a nonstructural protein). Although further investigations are needed to clarify the precise mechanisms underlying the circumvention of SG formation through the interaction of JEV core protein with Caprin-1, leading to efficient propagation *in vitro* and pathogenicity in mice, these findings could help not only to provide new insight into strategies by which viruses escape host stress responses but also to develop novel antiviral agents for flavivirus infection.

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Molecular Biology | Virology | Cell Biology

BioTechniques Rapid Dispatches

Benchmarks

Attenuated protein expression vectors for use in siRNA rescue experiments

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Transient transfection of small interfering RNA (siRNA) provides a powerful approach for studying cellular protein functions, particularly when the target protein can be re-expressed from an exogenous siRNA-resistant construct in order to rescue the knockdown phenotype, confirm siRNA target specificity, and support mutational analyses. Rescue experiments often fail, however, when siRNA-resistant constructs are expressed at suboptimal levels. Here, we describe an ensemble of mammalian protein expression vectors with CMV promoters of differing strengths. Using CHMP2A rescue of HIV-1 budding, we show that these vectors can combine high-transfection efficiencies with tunable protein expression levels to optimize the rescue of cellular phenotypes induced by siRNA transfection.

Keywords: siRNA; CMV promoter; mammalian protein expression; phenotypic rescue; HIV-1 budding; ESCRT; CHMP2

Small interfering RNAs (siRNAs) are commonly employed, both individually and on a genome-wide scale, to degrade specific mRNAs and test the cellular requirements for their encoded proteins (1–7). The basic siRNA depletion experiment can be extended further using "rescue" experiments in which the target protein is re-expressed from a transiently transfected vector that encodes an altered mRNA resistant to siRNA silencing (8–10). This experiment is useful for confirming siRNA specificity because the exogenously expressed protein should rescue the loss-of-function phenotype. The experiment also enables genetic analyses in cultured mammalian cells because the functional effects of specific mutations can be tested. Phenotypic rescue experiments can fail, however, when the rescuing protein is expressed at such a high level that it dominantly inhibits the pathway of interest. This problem can often be alleviated by reducing the quantity of transfected expression vector, but this approach fails if the overall transfection efficiency is reduced. To address this problem, we created an ensemble of seven mammalian expression vectors designed to allow more precise control of exogenous protein expression levels. These vectors have nested deletions that successively eliminate transcription factor binding sites within the human cytomegalovirus (CMV) intermediate early enhancer/promoter (summarized in Figure 1 and Supplemental Table 1, and see Supplemental Figure 1 for promoter DNA sequences and a summary of the design strategy). The deletions were made in the context of the mammalian expression vector pcDNA3.1/myc-His(-)A, that contained a custom-designed multiple cloning site (MCS) cassette. These vectors allow optimized expression of siRNA-resistant constructs, while maintaining the high transfection efficiencies necessary for potent phenotypic rescue.

HIV-1 and many other enveloped viruses recruit the cellular endosomal sorting complexes required for transport (ESCRT) pathway to facilitate the final membrane fission step of virus budding (11–14). As is true for many other cellular pathways, siRNA depletion/rescue experiments have contributed to our understanding of the role of the ESCRT pathway in HIV-1 budding (9,15). We have found, however, that it is often difficult to rescue virus budding to wild type levels following siRNA depletion because many ESCRT proteins, particularly those of the ESCRT-III family, can potently inhibit HIV-1 budding when overexpressed at elevated levels (16–20). The ESCRT-III/HIV-1 system therefore represents an attractive test case for examining the utility of our family of attenuated CMV expression vectors.

HIV-1 budding from cultured 293T cells can be potently inhibited by co-depletion of both members of the human CHMP2 family of ESCRT-III proteins (denoted CHMP2A and CHMP2B) (15). Hence, vector titers were dramatically reduced 48 h after co-transfection of a proviral HIV-1 vector together with siRNAs that targeted both CHMP2 proteins (Figure 2A, 24 ± 5-fold reduction, compare lanes 1 and 2). CHMP2 depletion also blocked virus release into the culture supernatant, as measured by immunoblotting for the virion-associated structural proteins, MA and CA (Figure 2A, panel

Method summary:

We have created a family of mammalian protein expression vectors with cytomegalovirus promoters of differing strengths and shown that these vectors can combine high-transfection efficiencies with tunable protein expression levels to optimize the rescue of cellular phenotypes induced by siRNA transfection.

2, compare lanes 1 and 2). Western blots of the 293T producing cells demonstrated that both CHMP2A and CHMP2B were depleted efficiently (Figure 2A, panels 4 and 5, compare lanes 1 and 2) and that cellular levels of the structural HIV-1 Gag protein and its MA and CA cleavage products were not altered significantly by CHMP2 protein depletion (Figure 2A, panel 3, compare lanes 1 and 2).

To test for rescue of virus budding, 500 ng of each of the different siRNA-resistant pCMV-CHMP2A expression vectors were co-transfected together with the siRNA and proviral HIV-1 (Figure 2A). As expected, CHMP2A expression levels were highest for the construct that carried the wild type CMV promoter (denoted pCMV(WT)-CHMP2A) and decreased successively over two orders of magnitude as larger and larger promoter deletions were introduced (denoted pCMV(Δ1)-CHMP2A to pCMV(Δ7)-CHMP2A, (Figure 2A, panel 4, compare lanes 3–10)). In contrast, the rescue of virus budding was biphasic: virion release and infectivity were low when CHMP2A levels were highest, increased when CHMP2A was expressed at intermediate levels, and then decreased again at the lowest CHMP2A expression levels (Figure 2A, panels 1 and 2, compare lanes 3–10). Levels of virion release and infectivity generally correlated well, but maximal infectivity occurred at slightly higher CHMP2A levels, perhaps because rapid virus release kinetics contribute more to viral infectivity than to total virion release as measured in the end point release assay. The pCMV(Δ4)-CHMP2A and pCMV(Δ5)-CHMP2A constructs expressed CHMP2A at levels that most closely approximated the normal level of the endogenous protein (Figure 2A, panel 4, compare lanes 7 and 8 to lane 1). These two CHMP2A expression constructs also rescued virus release and infectivity best (Figure 2A, panels 1 and 2). Importantly, the pCMV(Δ4)-CHMP2A construct rescued viral titers very efficiently, to 102 ± 12% of untreated control levels. These data imply that: *(i)* CHMP2A alone can fully rescue HIV-1 budding, even in the absence of CHMP2B; *(ii)* CHMP2A functions best when expressed at near-native levels; and *(iii)* the attenuated pCMV(Δ4)-CHMP2A and pCMV(Δ5)-CHMP2A constructs can express near-native levels of CHMP2A under conditions where transfection efficiencies apparently remain high.

We next tested whether HIV-1 budding could be rescued to comparable levels simply by varying the quantity of pCMV(WT)-CHMP2A used in the transfection reaction. 3-fold dilutions over a range of 500–0.69 ng of pCMV(WT)-CHMP2A were tested for rescue of HIV-1 budding from cells that lacked endogenous CHMP2 proteins. CHMP2A expression levels correlated well with the quantity of pCMV(WT)-CHMP2A vector used (Figure 2B, panel 4, lanes 3–9), and CHMP2A levels most closely approximated normal endogenous protein levels when 56 and 19 ng of pCMV(WT)-CHMP2A were used (compare lane 1 to lanes 6 and 7). Rescue of HIV-1 budding again followed a biphasic curve, with optimal rescue observed when CHMP2A was expressed at intermediate levels (170–19 ng pCMV(WT)-CHMP2A, lanes 5–7). In this case, however, HIV-1 titers never exceeded 26% of control levels, even when the bulk levels of exogenous CHMP2A approximated endogenous control levels (Figure 2B, panel 1, compare lane 1 to lanes 6 and 7). In a parallel control experiment, HIV-1 release was again rescued to nearly wild type levels upon co-transfection of 500 ng of the pCMV(Δ4)-CHMP2A construct (lane 10). We therefore conclude that although optimizing pCMV(WT)-CHMP2A vector levels improved HIV-1 budding, overall rescue levels were never as high as could be achieved with the attenuated pCMV(Δ4)-CHMP2 expression construct.

We hypothesized that the pCMV(Δ4)-CHMP2A and pCMV(Δ5)-CHMP2A vectors worked well in the rescue experiment because they could be used at concentrations that coupled high transfection efficiencies with restricted protein expression. To test this idea, we created pCMV(WT)-YFP, pCMV(Δ4)-YFP and pCMV(Δ5)-YFP expression vectors and used YFP fluorescence as a measure of protein expression in 293T cells. This approach allowed us to use flow cytometry to quantify transfection efficiencies and relative protein expression levels at the single-cell level. Titrations were again performed to determine the quantity of pCMV(WT)-YFP required to express YFP at levels comparable to those produced by transfections with 500 ng of pCMV(Δ4)-YFP or pCMV(Δ5)-YFP. This was achieved with 19 ng of pCMV(WT)-YFP, in reasonable agreement with the analogous CHMP2A titration experiments (Figure 3A, compare total mean fluorescence levels for 500 ng of pCMV(Δ4)-YFP or pCMV(Δ5)-YFP DNA with 19 ng of pCMV(WT)-YFP). As shown in Figure 3B, overall transfection efficiencies under these three conditions were: 94 ± 1% for 500 ng of pCMV(Δ4)-YFP, 90 ± 2% for 500 ng of pCMV(Δ5)-YFP DNA and 36 ± 8% for 19 ng pCMV(WT)-YFP (compare lanes 2, 3 and 5). Thus, overall transfection efficiencies dropped off significantly when the quantity of vector was reduced from 500 to 19 ng. We also quantified the mean fluorescence intensity (MFI) in the subsets of cells that were actually transfected in each reaction (i.e., now excluding cells in which YFP expression was undetectable). As shown in Figure 3C, transfected cells in the 19 ng pCMV(WT)-YFP reaction had a MFI of

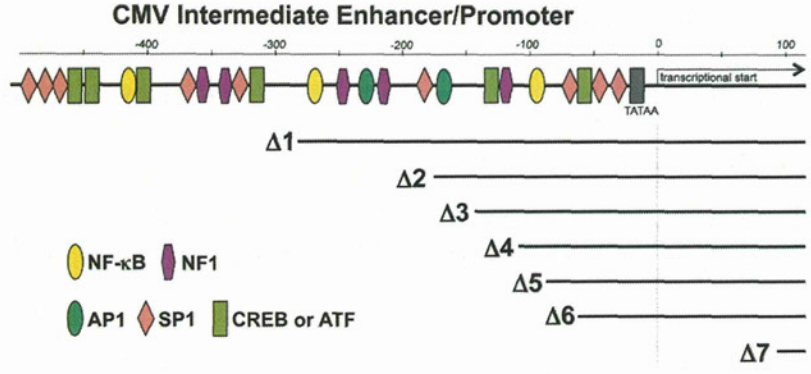

Figure 1. Human cytomegalovirus major immediate early enhancer/promoter constructs used for attenuated gene expression. The human CMV promoter structure is shown above, with the transcription start site at the +1 position and (putative) upstream binding sites for different transcription factors. Promoter deletion positions are shown below. Transcription factor binding elements were identified using the TESS analysis tool (22), with a consensus sequence cutoff of >12.0. Similar but slightly different variants of this binding site map were also generated by the program TFSEARCH (23) and have been published (24). Promoter deletions were introduced by cloning PCR fragments (*MluI*-*XbaI* sites) with the designated deletions into a pcDNA 3.1/myc-His(-)A expression vector (Life Technologies) that carried a custom multicloning site between the *XbaI* and *AflII* sites. Deletion design and DNA sequences are provided in Supplementary Figure 1, and construct numbers are provided in Supplementary Table 1.

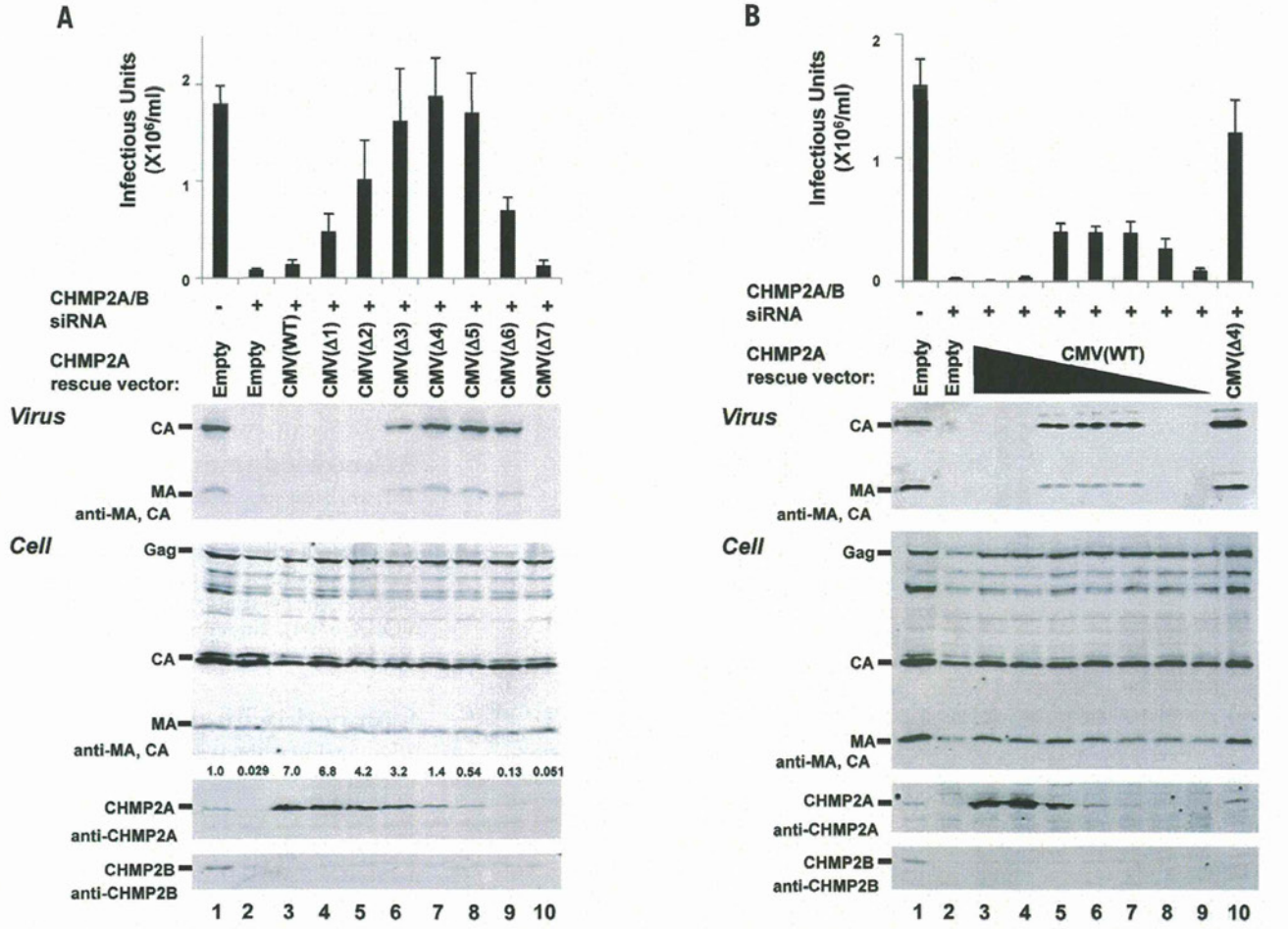

Figure 2. Rescue of HIV-1 budding from 293T cells that lack endogenous CHMP2 proteins by expression of human CHMP2A from attenuated CMV expression vectors. (A) Differential rescue of HIV-1 budding by CHMP2A proteins expressed from the ensemble of different pCMV-CHMP2A expression vectors. HIV-1 vector infectivity titers (top panel) and Western blots showing protein levels in culture supernatants (panel 2) or 293T cells (Cell, panels 3–5) co-transfected with a proviral HIV-1 vector (500 ng of pCMV-dR8.2, 500 ng pLox-GFP, 250 ng pMD-G)(25) (all lanes), either 20 nM control siRNA duplex (CGUACGCGGAAUACUUCGAtt, where "tt" represents two overhanging deoxyribothymidines, lanes 1) or 10 nM each of siRNA duplexes against CHMP2A and CHMP2B (AGGCAGAGAUCAUGGAUAUtt and GGAACAGAAUCGAGAGUUAtt, lanes 2–10)(15), and 500 ng of either an empty vector control (lane 2) or the designated pCMV-CHMP2A vector expressing an siRNA-resistant CHMP2A construct (lanes 3–10). Integrated CHMP2A band intensities, normalized to the endogenous CHMP2A level, are provided over each lane in panel 4. 293T cells (2×10^5 cells/well, 6-well plates, 2 mL volume) were seeded at t = 0, transfected with siRNA (20 nM final total concentration, 7.5 µl Lipofectamine RNAiMAX; Life Technologies, Carlsbad, CA, USA) at t = 24h, and co-transfected with siRNA, the designated pCMV-CHMP2A vector (500 ng), and the HIV-1 vector (20 nM final total siRNA concentration, 500 ng pCMV-dR8.2, 500 ng pLox-GFP, 250 ng pMD-G, 10 µl Lipofectamine 2000; Life Technologies) at t = 48h. The following silent mutations were introduced into the CHMP2A cDNA coding sequence to make the CHMP2A mRNA siRNA resistant: AGGCAGAGATCATGGATAT to AaGCtGAaATtATGGATAT (nucleotides 395–413). Cells and supernatant were collected and analyzed at t = 96h. Released virions were pelleted through a 20% sucrose cushion at 15,000× *g* and viral Gag-derived proteins were detected by Western blotting using our rabbit anti-HIV-1 CA (UT415, 1:2000) and MA (UT556, 1:1000) antisera. Cells were lysed with buffer (50 mM Tris-HCl pH 7.4, 150 mM NaCl, 1% Triton-X100, and PMSF) for Western blotting of intracellular proteins. Anti-CHMP2A and CHMP2B were detected with UT589 (our antibody) and Ab33174 (Abcam, Cambridge, MA, USA) as described (26). Secondary antibodies were anti-mouse IgG or anti-rabbit IgG polyclonal conjugated to IRdye700 or IRdye800 (1:10000, Rockland Immunochemicals Inc., Gilbertsville, PA, USA). Western blots were visualized using an Odyssey scanner (Li-Cor Biosciences, Lincoln, NB, USA). For titer measurements, 293T cells were infected with viral supernatants and GFP-positive cells were quantified by flow cytometry (FL1 channel, FACScan, BD Biosciences, San Jose, CA, USA). Values show the average of three independent repetitions with standard errors. (B) Rescue of HIV-1 budding by CHMP2A proteins expressed from different quantities of the wild type CMV expression vector, pCMV(WT)-CHMP2A. The figure and experiments are equivalent to panel (A), except that the following quantities of the siRNA-resistant CHMP2A rescue construct pCMV(WT)-CHMP2A were transfected: 500 ng (lane 3), 170 ng (lane 4), 56 ng (lane 5), 19 ng (lane 6), 6.2 ng (lane 7), 2.1 ng (lane 8), and 0.69 ng (lane 9). In the experiments shown in lanes 4–9, total expression vector levels were adjusted to 500 ng with pCMV(WT) empty vector. The sample shown in lane 10 was transfected with 500 ng of the pCMV(Δ4)-CHMP2A expression vector (positive control).

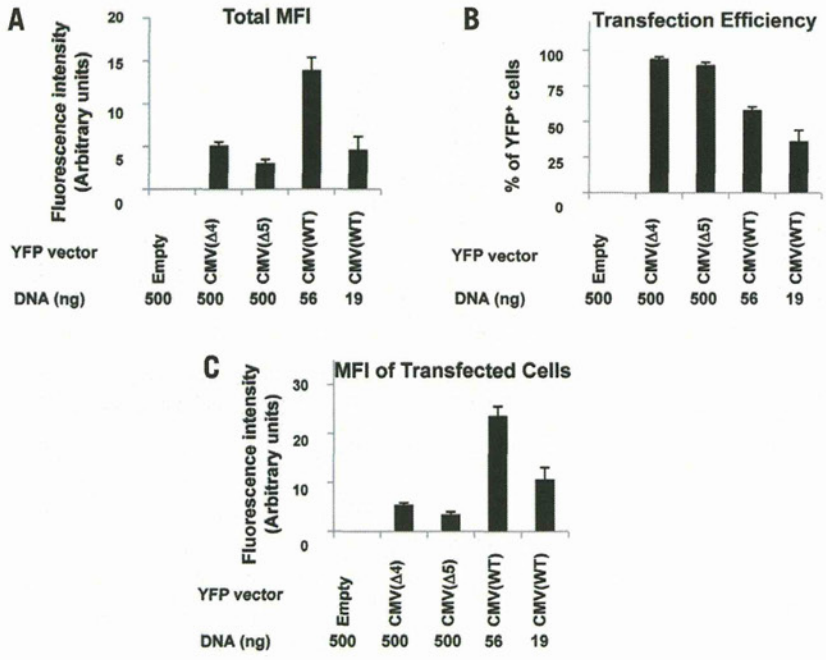

Figure 3. Comparison of transfection efficiencies and protein expression levels for the pCMV(WT)-YFP, pCMV(Δ4)-YFP, and pCMV(Δ5)-YFP vectors. (A) Total mean fluorescence intensity of YFP (MFI, in arbitrary units) for all cells in each of the cultures following transfection with 500 ng empty pCMV(WT) (negative control, lane 1), 500 ng pCMV(Δ4)-YFP (lane 2), 500 ng pCMV(Δ5)-YFP (lane 3), 56 ng pCMV(WT)-YFP (lane 4), or 19 ng pCMV(WT)-YFP (lane 5). The YFP expression vectors were created by PCR amplification of the *yfp* gene and subcloned into the *KpnI*/*XhoI* sites of the custom multiple cloning site of the pcDNA 3.1/myc-His(-)A expression vector. 293T cells were seeded (t = 0, 2×10^5 cells/well, 6-well plates) and transfected (t = 24h) with the designated pCMV-YFP constructs (adjusted to 500 ng total DNA with pCMV(WT) empty vector where necessary), 10 µl Lipofectamine 2000). At t = 72h, cells were trypsinized and analyzed by flow cytometry. YFP-positive cells were scored using a control-transfected sample to set the negative background level (BD CellQuest Pro software). YFP intensity was determined after subtracting control-transfected samples (FL1). Values here and in panels B and C show the average of five independent repetitions with standard errors. (B) Percentages of cells with detectable YFP fluorescence in each of the cultures described in (A). (C) Mean YFP fluorescence intensity (arbitrary units) for the subsets of cells that were transfected (as judged by detectable YFP expression) in each of the cultures described in (A).

11 ± 2, whereas transfected cells in the 500 ng pCMV(Δ4)-YFP and pCMV(Δ5)-YFP reactions had MFI of 5.4 ± 0.4 and 3.4 ± 0.6. These data demonstrate that although bulk YFP expression levels were comparable for the three conditions, this was achieved in different ways: the pCMV(Δ4)-YFP and pCMV(Δ5)-YFP vectors supported low-level YFP expression in nearly all of the cells, whereas the pCMV(WT)-YFP vector supported higher expression levels per cell, but in fewer than half of the cells. Thus, the attenuated vectors appear to work better in rescue experiments because, unlike the wild type pCMV(WT) vector, they can be used at sufficiently high concentrations to maintain high overall transfection efficiencies, yet they express low levels of the target protein in each cell. It is possible that varying HIV-1 vector levels could also affect the degree of rescue, but our experiments did not test this parameter.

In summary, we have created mammalian expression vectors that allow tunable expression of siRNA-resistant constructs and demonstrated their utility in rescuing HIV-1 budding from cells that lacked endogenous CHMP2 proteins. We have also used this system successfully in other experiments, for example to achieve high-level rescue of retrovirus budding from cells depleted of endogenous ALIX and CHMP4 proteins (although the relative advantages of using the attenuated CMV vector system were somewhat less pronounced in these two cases, data not shown). The optimal CMV vector must, of course, be determined empirically for each new system because the correct choice will be influenced by differences in endogenous protein levels, protein expression efficiencies, and the degree to which the specific pathway and cell type can tolerate protein overexpression. Although, we are not aware of previous studies that have employed the approach described here, related approaches such as the use of inducible promoters to optimize the expression of siRNA-resistant rescue constructs have been described (21). In principle, this is an elegant approach that can also be used to maximize phenotypic rescue, but it requires the creation of stable cell lines and is therefore less convenient than transient transfection, particularly when the functions of multiple mutant proteins are being screened. Hence, our system is likely to be most useful in cases where levels of the rescue protein must be tightly controlled and where the creation of stable cell lines is overly time consuming or problematic. Our vectors should also be useful in other applications where it is desirable to attenuate protein expression while maintaining high transfection levels.

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Competing interests

The authors declare no competing interests.

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Proteomic Analysis of Hepatitis C Virus (HCV) Core Protein Transfection and Host Regulator PA28γ Knockout in HCV Pathogenesis: A Network-Based Study

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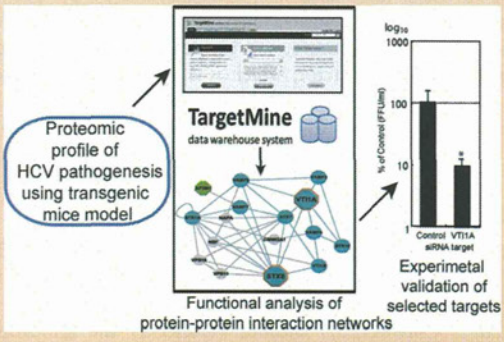
Supporting Information

ABSTRACT: Hepatitis C virus (HCV) causes chronic liver disease worldwide. HCV Core protein (Core) forms the viral capsid and is crucial for HCV pathogenesis and HCV-induced hepatocellular carcinoma, through its interaction with the host factor proteasome activator PA28γ. Here, using BD-PowerBlot high-throughput Western array, we attempt to further investigate HCV pathogenesis by comparing the protein levels in liver samples from Core-transgenic mice with or without the knockout of PA28γ expression (abbreviated PA28$\gamma^{-/-}$CoreTG and CoreTG, respectively) against the wild-type (WT). The differentially expressed proteins integrated into the human interactome were shown to participate in compact and well-connected cellular networks. Functional analysis of the interaction networks using a newly developed data warehouse system highlighted cellular pathways associated with vesicular transport, immune system, cellular adhesion, and cell growth and death among others that were prominently influenced by Core and PA28γ in HCV infection. Follow-up assays with *in vitro* HCV cell culture systems validated VTI1A, a vesicular transport associated factor, which was upregulated in CoreTG but not in PA28$\gamma^{-/-}$CoreTG, as a novel regulator of HCV release but not replication. Our analysis provided novel insights into the Core-PA28γ interplay in HCV pathogenesis and identified potential targets for better anti-HCV therapy and potentially novel biomarkers of HCV infection.



KEYWORDS: *CoreTG, GO, HCC, HCV, KEGG, OMIM, PA28$\gamma^{-/-}$CoreTG, PPI, siRNA, TargetMine*

INTRODUCTION

Hepatitis C virus (HCV) is a prime cause of chronic liver disease frequently characterized by liver inflammation with accompanying steatosis, progressive fibrosis, and hepatocellular carcinoma (HCC) and infects nearly 3% of the world's population. HCV contains a single-stranded RNA genome encoding a 3000-amino-acid polyprotein, which is processed by host and viral factors to yield 10 viral proteins, Core, E1, E2, p7, NS2, NS3, NS4A, NS4B, NS5A, and NS5B.[1−4] HCV variants are classified into six major genotypes with multiple subtypes characterized by phylogenetic heterogeneity, differences in infectivity, and interferon sensitivity.[5,6] The availability of cell-culture-based systems for HCV infection has provided an increased understanding of HCV pathogenesis.[5,7−9] Transgenic mice (preferably C57BL strain) expressing HCV proteins in the liver are also a preferred choice for the investigation of HCV pathogenesis.[10] However, despite considerable research efforts, precise molecular mechanisms underlying HCV pathology remain unclear.

HCV Core protein (hereafter referred to as Core) is spliced from the polyprotein by the signal peptidase and further processed into a highly conserved 21-kDa mature form by the signal peptide peptidase; this processing facilitates its transfer to the detergent-resistant membrane fraction where virus replication and assembly take place. Core is a multifunctional protein implicated in RNA binding and as a pathogenic factor; it induces steatosis and HCC and, thus, liver failure.[1,10] The ubiquitin-proteasome pathway, the premier intracellular protein degradation system in eukaryotes, is a key regulator of cellular processes and is also associated with the evasion of host immune response by many viruses, viral maturation, and progeny release.[11] Core binds to the proteasome activator PA28γ in the nucleus and is degraded via a PA28γ-dependent pathway. PA28γ plays a crucial role in Core-induced insulin resistance, steatogenesis, and hepatocarcinogenesis and in HCV propagation; PA28γ knockout in Core transgenic mice disrupts

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steatosis and HCC, restores insulin sensitivity, and impairs viral particle production, and thus PA28γ is a promising target for anti-HCV therapies with minimal side effects.[2,12−15] However, the exact mechanisms through which PA28γ facilitates Core-induced HCV pathogenesis remain poorly understood.

In this study, we aim to put forth biological networks that describe the differential expression of the host proteins and their likely roles in modulating PA28γ function in HCV pathogenesis. We employed PowerBlot Western Array screening system, a high-throughput Western blotting method, to identify changes at the proteome level in Core expressing transgenic C57BL/6 mice with or without the knockout of PA28γ gene expression (abbreviated PA28$\gamma^{-/-}$CoreTG and CoreTG, respectively). In our analysis, we included human protein interaction data and gene regulatory information for the differentially expressed proteins using TargetMine, an integrated data warehouse that we have developed recently.[16] Our network-based analyses of the proteomic changes from the three data sets (CoreTGvsC57BL/6, PA28$\gamma^{-/-}$CoreTGvsC57BL/6 and PA28$\gamma^{-/-}$CoreTGvsCoreTG) provided novel insights into PA28γ function in Core-induced HCV pathogenesis. Furthermore, we identified VTI1A, a vesicular transport associated factor, which was upregulated in CoreTG but not in PA28$\gamma^{-/-}$CoreTG, as a novel regulator of HCV release and, thus, an attractive target for anti-HCV therapy.

■ MATERIALS AND METHODS

Protein Sample Preparation

Protein samples were prepared from the livers of the C57BL/6 wild-type (hereafter referred to as WT) and the transgenic mice expressing HCV Core protein genotype 1b line C49 with (PA28$\gamma^{-/-}$CoreTG) or without (CoreTG) the knockout of PA28γ expression.[2,12] Livers were harvested from three individuals each of WT, CoreTG, and PA28$\gamma^{-/-}$CoreTG mice, and the harvested samples for each mice type were pooled together prior to protein sample preparation for PowerBlot analysis. The pooled liver samples of each mice type were homogenized in 1x sample buffer of SDS-PAGE on ice and then boiled for 5 min. The boiled sample was sonicated for the viscosity of DNA and employed for PowerBlot analysis.

PowerBlot Western Array Analysis

The levels of differentially expressed proteins were determined by the PowerBlot assay by BD Biosciences Pharmingen (San Diego, CA, USA). Briefly, samples containing 200 μg of protein was loaded in one big well on top of a 4−15% gradient SDS-polyacrylamide gel and separated by electrophoresis (1.5 h at 150v). The proteins were transferred to Immobilon-FL membrane (Millipore, Billerica, MA, USA) for 2 h at 200 mA. After transfer, the membranes were incubated in the blocking buffer (LI-COR, Lincoln, NE, USA). The membrane was clamped with a Western blotting manifold that isolates 41 channels across the membrane. Each channel was incubated with a complex antibody cocktail for 1 h. The blots were removed from the manifold, washed, and hybridized for 30 min with secondary goat anti-mouse antibody conjugated to Alexa680 fluorescent dye (Molecular Probes, Eugene, OR, USA). Image data were captured using the Odyssey Infrared Imaging System (LI-COR). Data analysis included the raw and normalized signal intensity data from each blot. The results were expressed as fold change that represented the protein changes, either increasing or decreasing in the comparative analysis between the experimental samples and the control. The detected protein expression changes were listed in the order of confidence, 0 through 3, with 3 being the highest level of confidence, based on the signal quality. Only the data from confidence levels 2 and 3 (good quality signals; Supporting Information; Tables S1, S2a, S2b, and S2c) for proteins mapped to valid accessions were considered for further analysis. Proteins that displayed >1.8-fold change in abundance were judged to be differentially expressed, following the manufacturer's recommendation.

Human Orthologues for the Differentially Expressed Proteins

BD PowerBlot assay employs a cocktail of monoclonal antibodies that target human, mouse, and rat proteins, and in a specific study, over 90% were found to cross-react with proteins from human, mouse and rat[17] (Table S1). Human orthologues for the proteins picked up by the antibody cocktail were retrieved from KEGG (Tables S2a, S2b, and S2c).

Construction of Protein−Protein Interaction Networks

PPIs for the human orthologues of each set of differentially expressed proteins were retrieved from BioGRID 3.1.74[18] and iRefIndex 8.0[19] databases along with the interactions between the primary interactors of the differentially expressed proteins using TargetMine.[16] TargetMine is an integrated data warehouse that combines different biological data types and employs an objective protocol to prioritize candidate genes for further experimental investigation.[16] The interactions were merged and filtered for redundancy to infer overall extended PPI networks. Protein identifiers used in the different databases were mapped to Entrez gene IDs and official gene symbols. The official gene symbols are used hereafter, to refer to the differentially expressed proteins (Table 1) and their interacting partners. All the relationships discussed should be interpreted as protein relationships unless otherwise clarified.

PPI Network Topological Analysis

Network components were visualized using Cytoscape 2.6,[20] while network properties such as *node degree distribution* and *shortest path* measures were computed using the Cytoscape NetworkAnalyzer plugin[21] as described previously.[22] In a PPI network, the degree of a node (protein) is defined as the number of nodes directly connected to (interacting with) it, i.e., its first neighbors. *Node degree distribution*, $P(k)$, is the number of nodes with a degree k for $k = 0, 1, 2, \ldots$. The *shortest path length* between two nodes n and m, $L(n,m)$, is the minimal number of interactions that link proteins n and m in a PPI network. The *shortest path length distribution* is the number of node pairs (n,m) with $L(n,m) = x$ for $x = 1, 2, \ldots$. The *average shortest path length*, also known as the *characteristic path length*, gives the expected distance between two connected nodes i.e. the minimal number of interactions that link any two proteins in a PPI network.

Functional Analysis by Characterization of Enriched Biological Associations

Gene ontology (GO) associations retrieved from GO consortium,[23] biological pathway data from KEGG (retrieved on March 1, 2011),[24] and disease phenotype associations from OMIM[25] were used to assign functional annotations to the constituents of the extended PPI networks. The proteins in each of the extended PPI networks were uploaded to TargetMine to create protein lists, and the enrichment of specific biological themes (GO terms, KEGG Pathways, OMIM phenotypes) associated with each PPI network was estimated