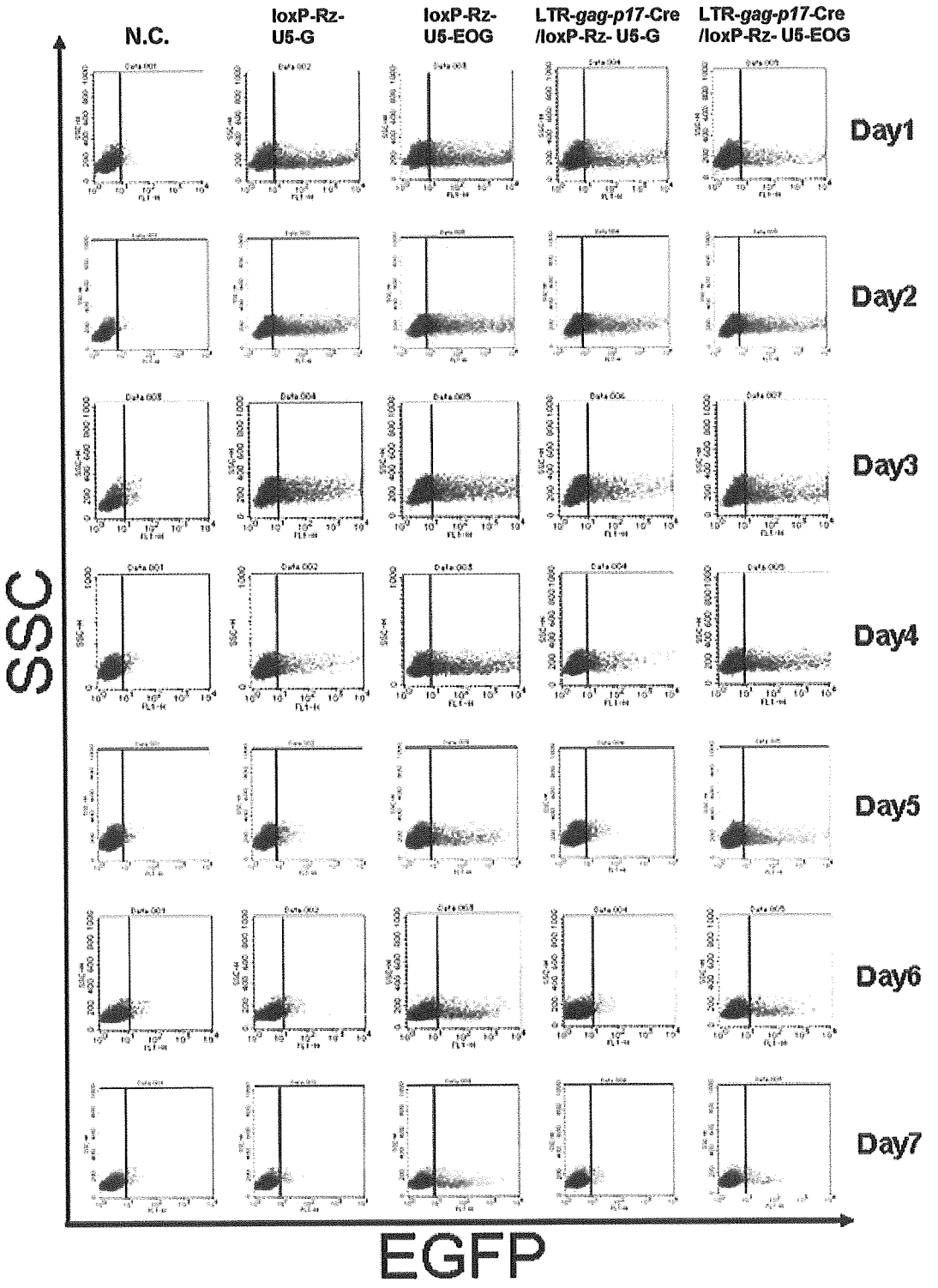

Figure 3. Enhancement of transgene expression by *EBNA-1* and *oriP* in HeLa $CD4^+$ cells. EGFP expression was evaluated on days 1 to 7 post-transfection by flow cytometry.

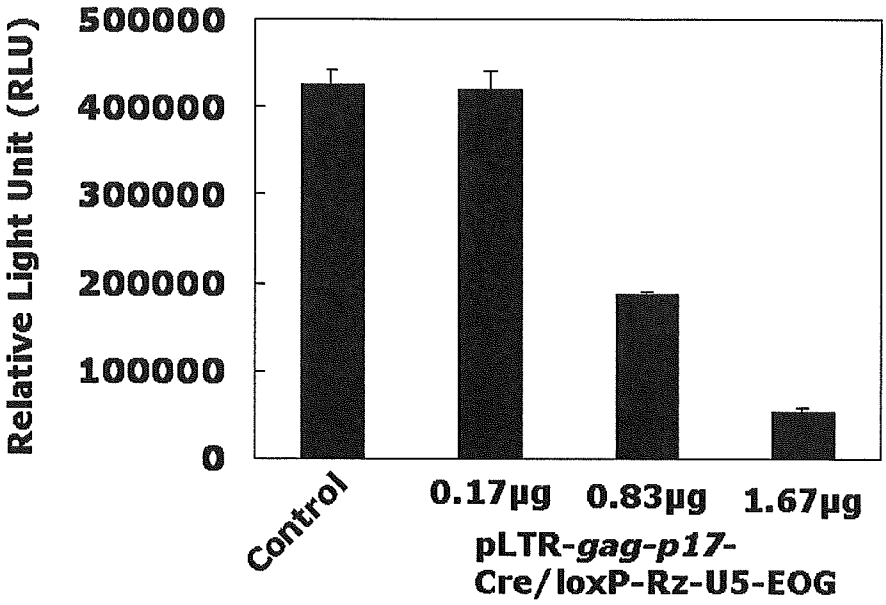

Figure 4. Dose-dependent inhibition of HIV-1 replication by pLTR-*gag-p17*-Cre/loxP-Rz-U5-EOG in HIV-1-transfected cells. Different amounts of pLTR-*gag-p17*-Cre/loxP-Rz-U5-EOG (0.17, 0.83 or 1.67 μg) were co-transfected with HIV-1 (pNL4-3-luc) into HeLa $CD4^+$ cells. At 72 h post-transfection, luciferase activity of the cell lysate was measured as an indirect marker for viral replication.

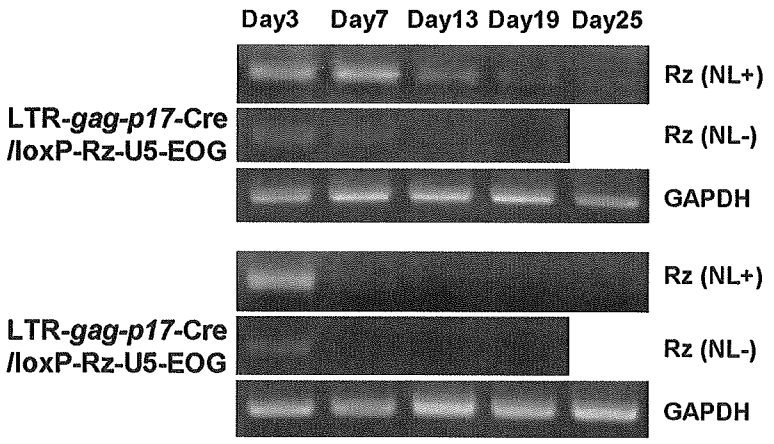

Figure 5. RT-PCR analysis shows persistent ribozyme expression of HeLa $CD4^+$ cells transfected with *EBNA-1/oriP*-containing vector. Total RNA was isolated from confluent pNL4-3 infected cell cultures transfected with pLTR-*gag-p17*-Cre/loxP-Rz-U5-G or pLTR-*gag-p17*-Cre/loxP-Rz-U5-EOG. RT-PCR using ribozyme-specific primers was performed concurrently with amplification of GAPDH mRNA.

the Cre/loxP vector containing EBNA-1 has the potential to confer long-term transgene expression in HIV-1 infected cells. This property therefore puts our vector system in the class of prophylactics, since the vector will function to prevent infection of the target cells.

Long-term inhibition of HIV-1 replication by pLTR-*gag-p17*-Cre/loxP-Rz-U5- EOG in pNL4-3 infected HeLa CD4$^+$ cells

To evaluate further the persistency of the EBNA-1/oriP-dependent ribozyme effect on HIV-1 replication we co-transfected 0.3 µg pNL4-3 with 5.0 µg pLTR-*gag-p17*-Cre/loxP-Rz-U5-EOG, pLTR- *gag-p17*-Cre/loxP-Rz-U5-G or ploxP-Rz-U5-EOG into HeLa CD4$^+$ cells. As shown in Figure 6A, pLTR-*gag-p17*-Cre/loxP-Rz-U5-EOG inhibited HIV-1 replication for 15 days. By contrast, ploxP-Rz-U5-EOG (lacking ribozyme expression) showed little inhibitory activity towards HIV-1 replication compared with the negative control (pNL4-3 only).

EGFP reporter gene expression was monitored as an indicator of transgene expression (Figure 6B). Its persistence throughout the experiment (up to 13 days) confirms our earlier findings, and suggests that the HIV-1-dependent ribozyme-expression vector containing EBNA-1/oriP sequences mediates long-term ribozyme expression, inhibits HIV-1 replication and would be a useful tool for HIV-1 gene-therapy applications.

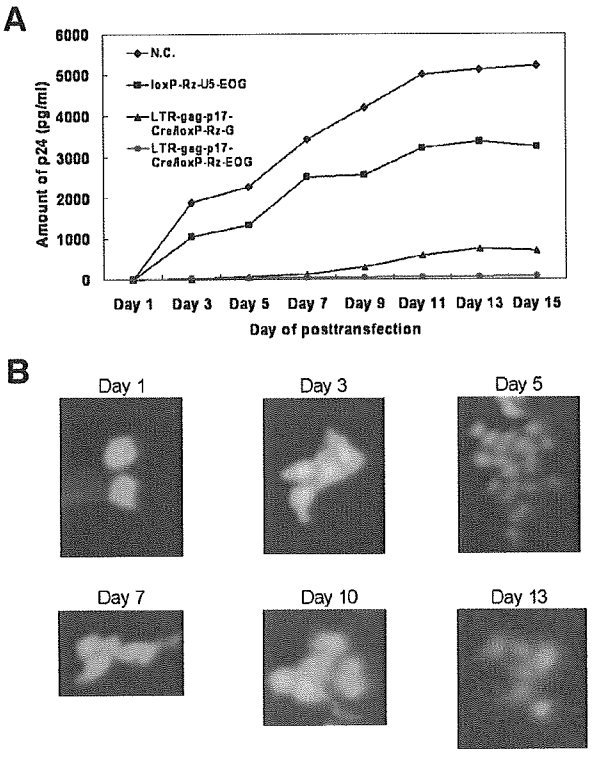

Figure 6. Inhibitory effects on HIV-1 p24 antigen production by pLTR-*gag-p17*-Cre/loxP-Rz-U5-EOG. **(A)** HeLa CD4$^+$ cells were co-transfected with HIV-1 pNL4-3 and either control vector (diamonds), ploxP-Rz-U5-EOG (squares), pLTR-*gag-p17*-Cre/loxP-Rz-U5-G (triangles), or pLTR-*gag-p17*-Cre/loxP-Rz-U5- EOG (circles). HIV-1-virus production was measured by p24 ELISA at the indicated times post-transfection. **(B)** Transgene replication in dividing cells. Cells were passaged every 2 days, and monitored for transgene replication by way of EGFP expression in singly dividing cells.

CONCLUSIONS

- Ribozyme expression is HIV-1 Tat dependent, as we were only able to detect it in the presence of pNL4-3.
- Transgene expression is long-term and is extended by the presence of oriP and EBNA-1. Hence, inhibition is also shown to be long-term.
- The Cre/loxP system induces ribozyme-mediated inhibition of HIV-1 replication in a dose-dependent manner.
- These results demonstrate the anti-HIV-1 effect of the expressed ribozyme from the Cre/loxP system, clearly illustrating the potential of the Cre/loxP-oriP/EBNA-1 system as a gene-therapy tool for controlling HIV-1 infection.

ACKNOWLEDGEMENTS

This work was supported by a Grant-in-Aid for High Technology Research (HTR) from the Ministry of Education, Science, Sports, and Culture, Japan, by research grants from the Human Science Foundation (HIV-K-14719), by a Grant-in-Aid for AIDS research from the Ministry of Health, Labor, and Welfare, Japan (H17-AIDS-002), and by the Sasakawa Scientific Research Grant from The Japan Science Society. Y. H. was a Research Fellow of the HTR until June 2005 and has been a Research Fellow of the Japanese Foundation for AIDS Prevention since July 2005.

STATEMENT OF COMPETING INTERESTS

The authors declared no competing interests.

LIST OF ABBREVIATIONS

EBV; Epstein-Barr virus
EBNA-1; EBV nuclear antigen 1
EOG; EBNA-1/OriP/EGFP
MFI; Mean fluorescence intensity
OriP; EBV latent origin of replication

REFERENCES

Adachi A, Gendelman HE, Koenig S et al. 1986. Production of acquired immunodeficiency syndrome-associated retrovirus in human and nonhuman cells transfected with an infectious molecular clone. J Virol, 59, 284-291.

Akkina RK, Walton RM, Chen ML, Li Q-X, Planelles V and Chen ISY. 1996. High-efficiency gene transfer into CD341 Cells with a human immunodeficiency virus type 1-based retroviral vector pseudotyped with vesicular stomatitis virus envelope glycoprotein G. J Virol, 70, 2581-2585.

Banerjea A, Li MJ, Bauer G et al. 2003. Inhibition of HIV-1 by lentiviral vector transduced siRNAs in T lymphocytes

deferentiated in SCID-hu mice and CD34+ progenitor cell-derived macrophages. Mol Ther, 8, 62-71.
Barnor JS, Miyano-Kurosaki N, Yamaguchi K et al. 2004. Intracellular expression of antisense RNA transcripts complementary to the human immunodeficiency virus type-1 vif gene inhibits viral replication in infected T-lymphoblastoid cells. Biochem Biophys Res Commun, 320, 544-550.
Boden D, Pusch O and Ramratnam B. 2004. HIV-1-specific RNA interference. Curr Opin Mol Ther, 6, 373-380.
Boden D, Pusch O, Lee F, Tucker L, Shank PR and Ramratnam B. 2003. Promoter choice affects the potency of HIV-1 specific RNA interference. Nucleic Acids Res, 31, 5033-5038.
Chang Z, Westaway S, Li S, Zaia JA, Rossi JJ and Scherer LJ. 2002. Enhanced expression and HIV-1 inhibition of chimeric tRNA(Lys3)-ribozymes under dual U6 snRNA and tRNA promoters. Mol Ther, 481-189.
Cordelier P, Kulkowsky JW, Ko C et al. 2004. Protecting from R5-tropic HIV: individual and combined effectiveness of a hammerhead ribozyme and a single-chain Fv antibody that targets CCR5. Gene Ther, 11, 1627-1637.
Daikoku T, Kudoh A, Fujita M, Sugaya Y, Isomura H and Tsurumi T. 2004. In vivo dynamics of EBNA1-oriP interaction during latent and lytic replication of Epstein-Barr virus. J Biol Chem, 279, 54817-54825.
Davis JR and McNeilly AS. 2001. Is pituitary gene therapy realistic? Clin Endocrinol, 55, 427-433.
Habu Y, Miyano-Kurosaki N, Kitano M et al. 2005. Inhibition of HIV-1 gene expression by retroviral vector-mediated small-guide RNAs that direct specific RNA cleavage by tRNase ZL. Nucleic Acids Res, 33, 235-243.
Habu Y, Miyano-Kurosaki N, Matsumoto N, Takeuchi H and Takaku H. 2002. Inhibition of HIV-1 replication by an HIV-1 dependent ribozyme expression vector with the Cre/loxP (ON/OFF) system. Antiviral Chem Chemother, 13, 273-281.
Habu Y, Nagawa T, Matsumoto N, Takeuchi H, Miyano-Kurosaki N and Takaku H. Suppression of human immunodeficiency virus type 1 (HIV-1) replication by an HIV-1-dependent double locked vector with the Cre/loxP system. Nucleosides Nucleotides Nucleic Acids, in press.
Hirai K and Shirakata M. 2001. Replication licensing of the EBV oriP minichromosome. Curr Top Microbiol Immunol, 258, 13-33.
Lee MA, Diamond ME and Yates JL. 1999. Genetic evidence that EBNA-1 is needed for efficient, stable latent infection by Epstein-Barr virus. J Virol, 73, 2974-2982.
Li MJ, Bauer G and Michienzi A. 2003. Inhibition of HIV-1 infection by lentiviral vectors expressing Pol III-promoted anti-HIV RNAs. Mol Ther, 8, 196-206.
Mackey D and Sugden B. 1999. The linking regions of EBNA-1 are essential for its support of replication and transcription. Mol Cell Biol, 19, 3349-3359.
Marechal V, Dehee A, Chikhi-Brachet R, Piolot T, Coppey-Moisan M and Nicolas JC. 1999. Mapping EBNA-1 domains involved in binding to metaphase chromosomes. J Virol, 73, 4385-4392.
Mautino MR and Morgan RA. 2002. Enhanced inhibition of human immunodeficiency virus type 1 replication by novel lentiviral vectors expressing human immunodeficiency virus type 1 envelope antisense RNA. Hum Gene Ther, 13, 1027-1037.
Otomo T, Yamamoto S, Morishita R and Kaneda Y. 2001. EBV replicon vector system enhances transgene expression in vivo: applications to cancer gene therapy. J Gene Med, 3, 345-352.
Sakai A, Hirabayashi Y, Aizawa S, Tanaka M, Ida S and Oka S. 1999. Investigation of a new p24 antigen detection system by thechemiluminescence-enzyme-immuno-assay. Kansenshogaku Zasshi, 73, 205-212.
Takaku H. 2004. Gene silencing of HIV-1 by RNA interference. Antivir Chem Chemother, 15, 57-65.
Tsujie M, Isaka Y, Nakamura H, Kaneda Y, Imai E and Hori M. 2001. Prolonged transgene expression in glomeruli using an EBV replicon vector system combined with HVJ liposomes. Kidney Int, 59, 1390-1396.

Nucleosides, Nucleotides, and Nucleic Acids, 24:1745–1761, 2005

ISSN: 1525-7770 print/1532-2335 online
DOI: 10.1080/10810730500265823

Taylor & Francis
Taylor & Francis Group

THE MIDDLE TO 3′ END OF THE HIV-1 VIF GENE SEQUENCE IS IMPORTANT FOR VIF BIOLOGICAL ACTIVITY AND COULD BE USED FOR ANTISENSE OLIGONUCLEOTIDE TARGETS

Jacob Samson Barnor □ *Department of Life and Environmental Science, Chiba Institute of Technology, Tsudanuma, Narashino, Chiba, Japan; and Noguchi Memorial Institute for Medical Research, Department of Virology, Legon, Accra-Ghana*

Naoko Miyano-Kurosaki and Hiroshi Takaku □ *Department of Life and Environmental Science and High Technology Research Center, Chiba Institute of Technology, Tsudanuma, Narashino, Chiba, Japan*

Kazuya Yamaguchi and Atsushi Sakamoto □ *Department of Life and Environmental Science, Chiba Institute of Technology, Tsudanuma, Narashino, Chiba, Japan*

Koichi Ishikawa and Naoki Yamamoto □ *National Institute of Infectious Diseases, AIDS Research Center, Toyama, Shinjyuku-ku, Tokyo, Japan*

Mubarak Osei-Kwasi and David Ofori-Adjei □ *Noguchi Memorial Institute for Medical Research, Department of Virology, Legon, Accra-Ghana*

□ *The human immunodeficiency virus type-1 (HIV-1)-encoded Vif protein is essential for viral replication, virion production, and pathogenicity. HIV-1 Vif interacts with the endogenous human APOBEC3G protein (an mRNA editor) in target cells to prevent its encapsidation into virions. Some studies have established targets within the HIV-1 vif gene that are important for its biologic function; however, it is important to determine effective therapeutic targets in vif because of its critical role in HIV-1 infectivity and pathogenicity. The present study demonstrates that virions generated in transfected HeLa-CD4$^+$ cells, especially from HIV-1 vif frame-shift mutant (3′-Δvif; 5561-5849), were affected in splicing and had low infectivity in MT-4 cells. In addition, HIV-1 vif antisense RNA fragments constructed within the same region, notably the region spanning*

In honor and blessed memory of the life and career of John A. Montgomery.

Received 19 January 2005; accepted 28 April 2005.

This work was supported in part by a Grant-in-Aid for High Technology Research, No. 09309011, from the Ministry of Education, Science, Sports, and Culture, Japan, by the Research Grant from the Human Science Foundation (HIV-SA-14719). This work was also partially supported by the Ministry of Education, Science, Sports and Culture, Grant-in-Aid for Scientific Research and partly by the Sasakawa Scientific Research Grant from the Japan Science Society.

Address correspondence to Hiroshi Takaku, Department of Life and Environmental Science and High Technology Research Center, Chiba Institute of Technology, Tsudanuma, Narashino, Chiba 275-0016, Japan. Fax: +81-47-471-8764; E-mail: hiroshi.takaku@it-chiba.ac.jp

nucleic acid positions 5561-5705 (M-3′-AS), which corresponds to amino acid residues 96–144, significantly inhibited HIV-1 replication in MT-4 and reduced the HIV-1 vif mRNA transcripts and reporter gene (EGFP) expression. The generated virions showed low secondary infection in H9 cells. These data therefore suggest that the middle to the 3′ end of vif is important for its biological activity in the target cells.

Keywords HIV-1 vif gene; Antisense RNA; Oligonucleotides; Inhibition of HIV-1 replication; Vif biological activity

INTRODUCTION

Human Immunodeficiency Virus Type-1 (HIV-1) encodes six accessory proteins, Vpr, Vpu, Nef, Rev, Tat, and Vif, apart from its major structural Gag-Pol and Env proteins. The Vif protein is well conserved in all lentiviruses, except for the equine infectious anemia virus.[1] The Vif-conserved lentiviruses include feline immunodeficiency virus, caprine arthritis encephalitis virus, bovine immunodeficiency virus, and simian immunodeficiency virus.[2–4] The HIV-1 *vif* gene encodes a highly basic, 23000-M_r phosphoprotein that collapses intermediate filaments, localizes in the cytoplasm of its infected target cells, and acts during virus assembly by an unknown mechanism to enhance viral infectivity.[5–9] HIV-1 Vif is viral- and cellular-specific,[10,11] and is therefore critically essential for cells designated as non-permissive, such as H9, CEM, and U38, and is non-critical for cells classified as permissive, such as HeLa-CD4$^+$, SupT1, COS, and Jurkart cells.[12–16] HIV-1 Vif does not influence the expression or incorporation of the major encoded structural proteins.[17] Hence, various studies have demonstrated that components such as viral proteins and nucleic acids were not changed in virions generated in non-permissive cells.[13] On the other hand, deletions in the *vif* gene alter virion morphology in the same virus-producing cells.[18–20] The HIV-1 Vif protein binds directly to the protease domain of the *pol* precursor, and thereby prevents improper cleavage of the *gag* precursor before viral assembly.[21] Naturally occurring and C-terminally truncated variant HIV-1 Vif proteins lose this ability to bind Pol and affect Gag processing.[8] Furthermore, Vif is an RNA-binding protein and is an integral component of the mRNP complex of viral RNA.[22]

It has been hypothesized that the Vif protein functions by counteracting an unknown endogenous HIV inhibitor(s) in its target cells.[10] It was recently demonstrated that CEM 15, now known as APOBEC3G, which is only expressed in non-permissive cells,[23,24] is that endogenous inhibitor. When expressed in permissive cells, APOBEC3G makes the cells non-permissive. It is proposed to act in concert with other cellular factors such as sp140.[25] The function of APOBEC3G is similar to that of APOBEC-1 (apoB mRNA editing catalytic subunit 1), a cytidine deaminase that converts cytidine into uridine in the mRNA of apolipoprotein B.[26]

Simon and coworkers determined that every amino acid position dispersed throughout the linear sequence of Vif is important for Vif function, because all the amino acid positions analyzed in their scanning mutation studies of the Vif protein either decreased or increased infectivity.[27] Therefore, we hypothesized that combining targets that together either enhanced or decreased HIV-1 infectivity, in mass block in-frame shift mutants in HIV-1 vectors, could result in novel target sites that might be useful for HIV gene therapy applications. Gene therapy has recently emerged as a promising therapeutic tool for the treatment of genetic diseases, cancers, and chronic infectious conditions, such as AIDS.[28–32] These include the intracellular expression of decoy RNAs, ribozymes, single-chain antibodies, trans-dominant proteins, and antisense RNAs.[33–45] Antisense RNAs targeted to various HIV-1 major structural genes, accessory genes, and receptors, successfully inhibited viral replication in the target cells.[46,47]

In the present study, we initially constructed HIV-1 Vif mutants as the basis for determining the effective HIV-1 Vif target domain(s) that would directly attenuate the Vif-dependent infectivity in the cells. HIV-1 *vif* antisense RNA expression vectors of various sizes were subsequently constructed within the established effective target domains of the HIV-1 *vif* gene. Thus, we used antisense RNA to indirectly block at the transcriptional level, targets within the same region as in the mutant constructs that mediated the downregulation of HIV-1 Vif-dependent infectivity in the cells. The potential anti-HIV-1 activity of these HIV-1 *vif* antisense RNAs was evaluated with the view of establishing highly effective therapeutic target(s) in the HIV-1 *vif* gene, which could be further developed for HIV gene therapy applications for the control and management of HIV-AIDS.

RESULTS

Vector Design Strategy and PCR-Mediated Site-directed Mutagenesis

The target sites used in this study for the construction of both HIV-1 *vif* deletion mutants and the HIV-1 *vif* antisense RNA expression vectors are schematically represented in Figures 1B and 1C, and were based on the HIV-1pNLE genome (Figure 1A). The nucleotide deletions extended from the 5′ end to the middle of *vif* (5′-Δ*vif*; 5271-5560), and from the middle to the 3′ end of *vif* (3′-Δ*vif*; 5561-5849) and were each approximately 288 bp. The ORF-Δ*vif* mutant deletion was approximately 589 bp, extending from the start codon to the stop codon (Figure 1B). The HIV-1 *vif* antisense RNA expression vectors, hereafter referred to as the M-5-AS (5417-5560), M-M-AS (5488-5632), M-3′-AS (5561-5705), 3′-M-AS (5633-5778), and 3′-3′-AS (5706-5849) vectors, were designated as short *vif* antisense RNA expression vectors and were approximately 145 bp each (Figure 1C).

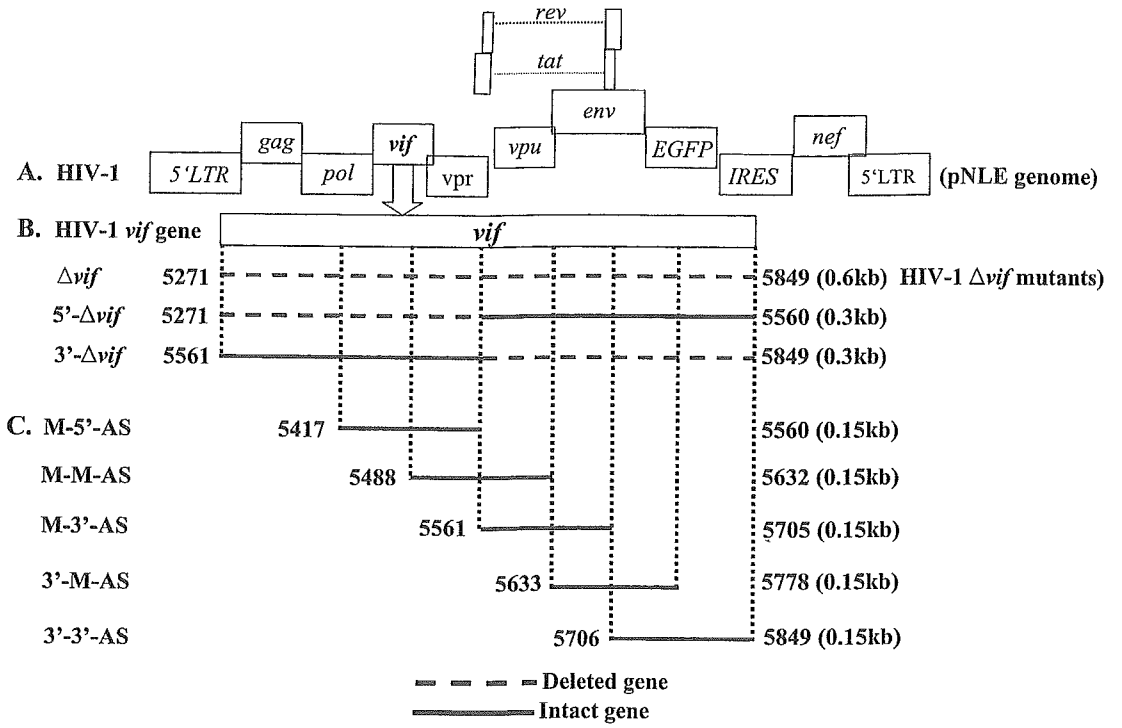

FIGURE 1 Scheme for the construction of both HIV-1 *vif* mutants and the HIV-1 *vif* antisense RNA expression vectors. (A) Schematic representation of the HIV-1pNLE genome, showing the open reading frames, and the 5′and 3′ long terminal repeats. (B) The HIV-1 mutants were constructed by PCR-mediated site-directed mutagenesis. The final amplified fragments were cloned back into the AgeI and EcoRI sites in HIV-1pNLE. The horizontal broken lines represent the deleted portion of the *vif* gene. (C) The selected *vif* targets were amplified by PCR, with EcoRV and XhoI cloning sites added to the fragments, which were then cloned into the EcoRV and XhoI sites in the pcDNA3.1 vector in both the antisense and sense orientations.

H9 Cell-derived Virions Exhibited a Defective Phenotype in MT-4 Cells

To predetermine the target sites for the construction of the HIV-1 *vif* antisense RNA expression vectors, HIV-1 mutant vectors carrying the various extensive deletions in the *vif* gene were generated (Figure 1B), and the intracellular HIV-1 Gag p24 antigen production level for each vector was measured by CLEIA,[48] using the cell-free culture supernatants of the transfected COS, H9, and HeLa-CD4$^+$ cells. The generated virions were normalized at 100 pg of HIV-1 *gag* p24 antigen equivalents, and were then titrated for their relative infectivity in MT-4 cells and H9 cells. The results indicated significant differences in the replication competencies of the H9 and HeLa-CD4$^+$ derived virions on MT-4 cells (Figure 2). The virions generated from H9 cells exhibited significantly lower infectivity in the MT-4 cells compared to those generated from the HeLa-CD4$^+$ cells. The infectivity of the ORF *vif* mutant was twofold lower than that of the 3′*vif* deleted mutant and both were low-titer viruses, while there was no significant difference in the titers of the wt (positive control) and

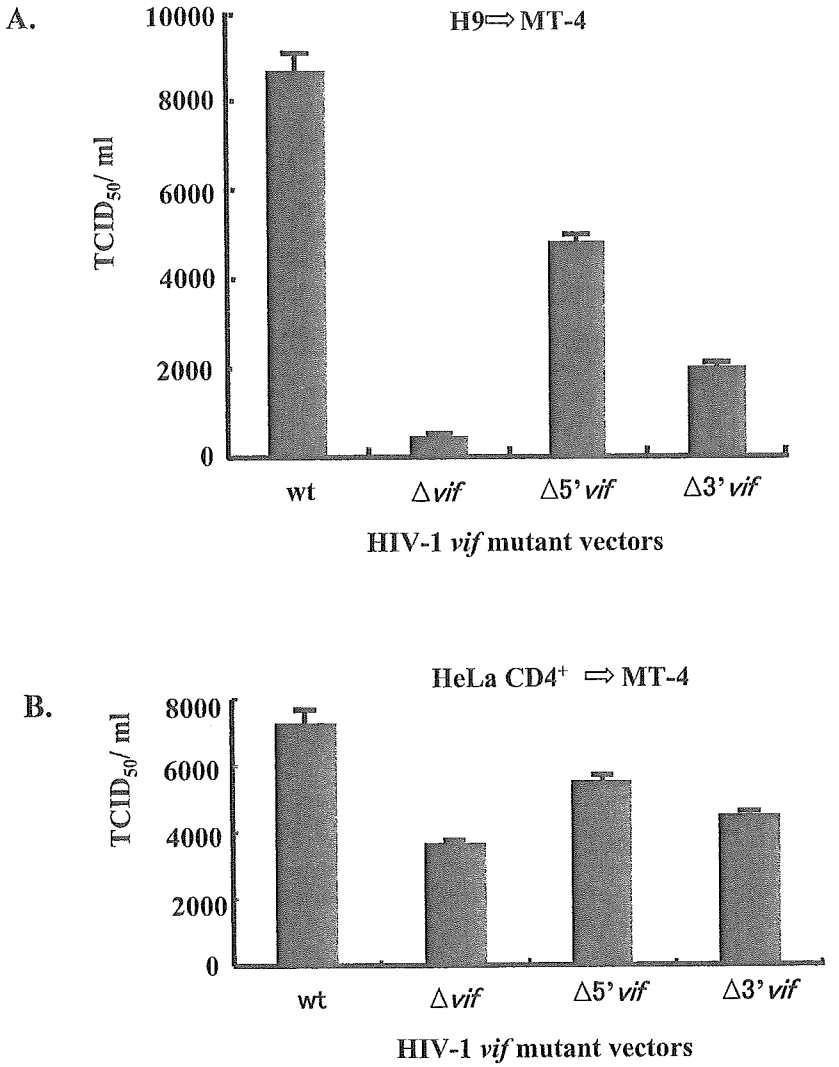

FIGURE 2 Infectivity of wt and mutant viruses. Mutant viruses generated from the co-transfected HeLa-CD4$^+$ and H9 cells were normalized at 100 pg of HIV-1 Gag p24 antigen, and titrated in fivefold serial dilution steps in MT-4 cells. Cell-free culture supernatants were harvested at 6 d posttransfection, and the HIV-1 Gag p24 antigen was measured by ELISA and expressed as $TCID_{50}$/mL. Average and standard deviation of three independent experiments are shown.

5′ *vif* deleted mutants (2A). Generally, there was no significant difference in the titers of the virions generated from the HeLa-CD4$^+$ cells (2B). Results presented as the mean ±SD of three independent experiments.

Growth Kinetics of HIV-1 *vif* Mutants

Transfecting HeLa-CD4$^+$ cells (1×10^6) generated input viruses to further study the growth characteristics of these mutants. H9 and MT-4 cells were infected with HeLa-CD4$^+$-derived viruses at an equal concentration of HIV-1 p24 (100 pg) and cultured for 10 days. All the mutants exhibited a similar growth pattern in MT-4 cells in relation to the wt as they all peaked

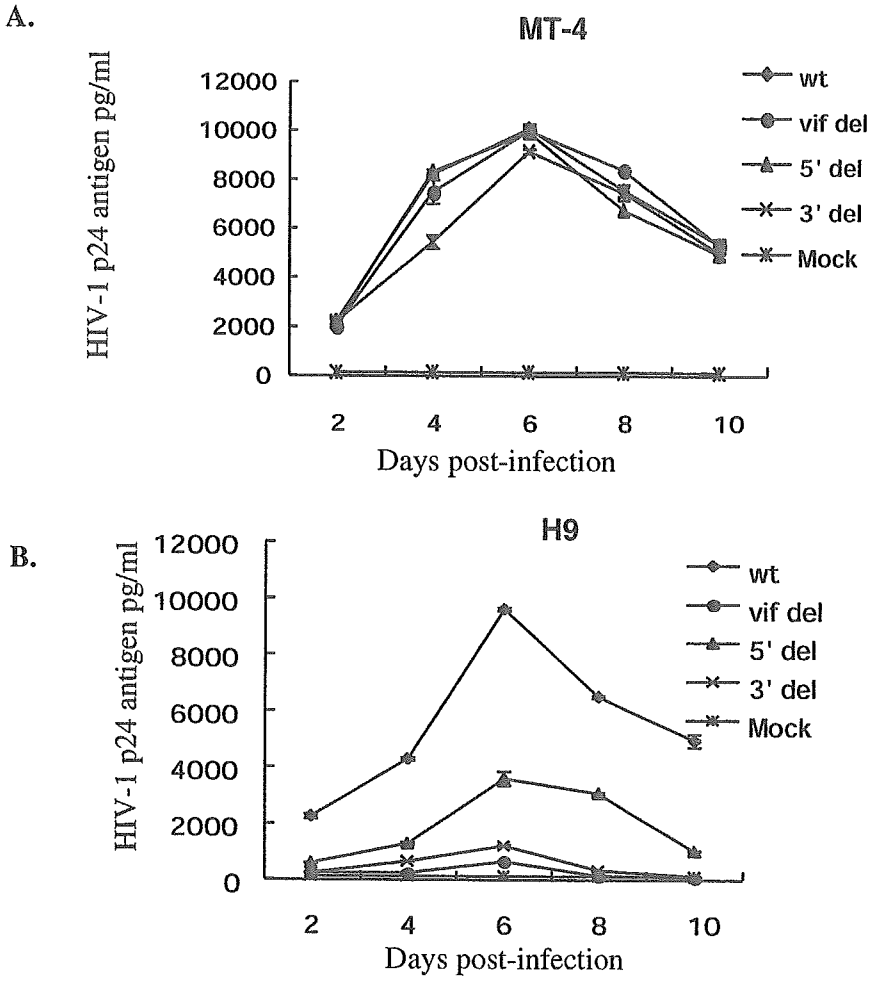

FIGURE 3 Growth kinetics of wt and mutant viruses in H9 and MT-4 cells. Viruses were generated in HeLa-CD4$^+$ cells (1×10^6), normalized at 100 pg p24 antigen and used to infect H9 and MT-4 cells, with the residual virus removed by washing. Subsequently, HIV-1 p24 antigen production was monitored at the indicated time intervals. Average and standard deviation of three independent experiments are shown. (The error bars are shown, but are very small.)

on day 6 (Figure 3A). Significantly, these same virions grew poorly in the H9 cells as compared to the wt. Nevertheless, the 5′ end *vif* mutant grew slightly more than the ORF and the 3′*vif*-deletion mutants, thus indicating that these mutants are defective in the H9 cells (Figure 3B). Results are shown as the mean ±SD of three independent experiments.

Mutation Affected HIV-1 Splicing in Transiently Transfected HeLa-CD4$^+$ Cells

To further determine the extent of the mutant defects, HIV-1 splicing was observed in HeLa-CD4$^+$ cells transiently transfected with the vectors. Total RNA was extracted 48 h posttransfection and RT-PCR amplified with

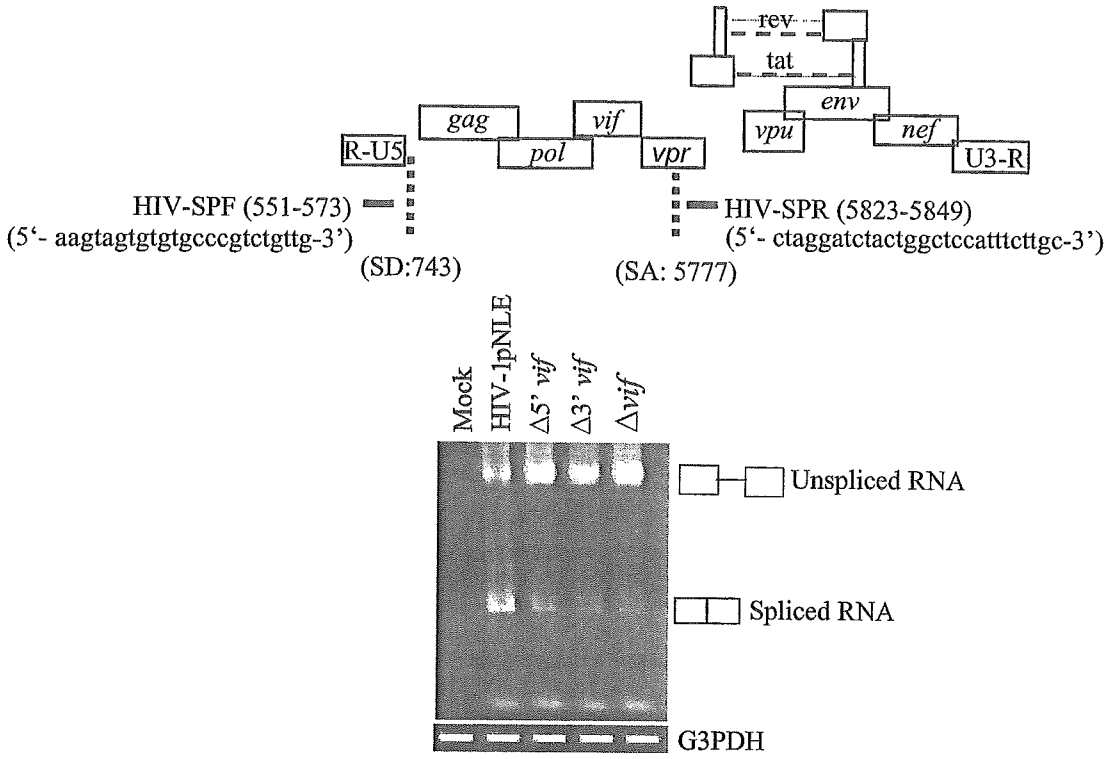

FIGURE 4 HIV-1 mutant splicing in transfected-HeLa-CD4$^+$ cells. (A) HIV-1 genome and RT-PCR primers were positioned around the splicing donor site (SD) and the splicing acceptor (SA) region as forward and reverse primers, respectively. (B) Total and nuclear RNA extracted from transiently transfected HeLa-CD4$^+$ cells with mutants after 48 h was subjected to RT-PCR and fractionated on 8% polyacrylamide gels stained with ethidium bromide. Lane 1: mock-transfected HeLa-CD4$^+$ cells; Lane 2: HIV-1pNLE-transfected HeLa-CD4$^+$ cells; Lane 3: 5′ *vif*-deletion mutant-transfected HeLa-CD4$^+$ cells; Lane 4: 3′ *vif*-deletion mutant transfected HeLa-CD4$^+$ cells; and Lane 5: ORF *vif* deletion mutant-transfected HeLa-CD4$^+$ cells.

the specific forward primer that was positioned in the splicing donor region, while the reverse primer was positioned in the splicing acceptor region of the *vpr* gene (Figure 4A). The resultant products were analyzed on polyacrylamide gels and the wt had more spliced pre-mRNA than unspliced pre-mRNA. In contrast, the mutants had more unspliced pre-mRNA than spliced pre-mRNA. Therefore, the deletions affected HIV-1 splicing in the HeLa-CD4$^+$ cells (Figure 4B).

Intracellular Expression Level of Antisense RNA in the Cells

Because the antisense mechanism is partly dependent on the expressed antisense RNA in the cells, we determined the level of mRNA expression for all the antisense RNA constructs in transiently transfected HeLa-CD4$^+$ and COS cells. The following primer pair was used to amplify total RNA from co-transfected cells; forward primer vmRNA-F, (5′-CAA GAA GAA AAG CAA AGA TCA TCA G-3′) and reverse primer vmRNA-R, (5′-CTA GTG TCC ATT

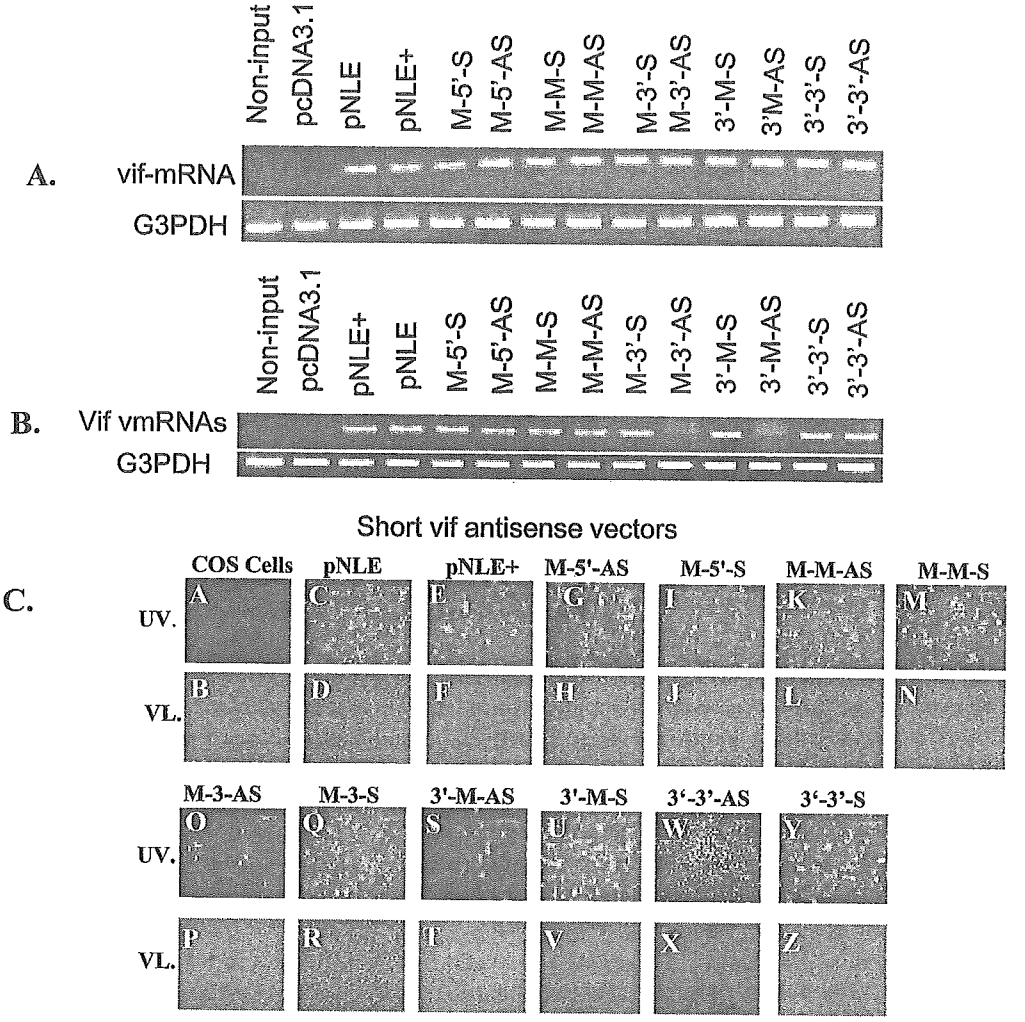

FIGURE 5 RT-PCR analysis of the *vif* antisense and the control RNA expression in COS cells. (A) The expressed short *vif* antisense RNA transcripts from the COS cells was concurrently amplified by RT-PCR with the controls, including the G3PDH RNA, and were resolved on an agarose gel. Lane 1: control G3PDH RNA; lane 2: empty vector (pcDNA3.1); lane 3: pNLE; lane 4: (pNLE + pcDNA 3.1); lane 5: M-5′-S; lane 6: M-5′-AS; lane 7: M-M-S; lane 8: M-M-AS; lane 9: M-3′-S; lane 10: M-3′-AS; lane 11: 3′-M-S; lane 12: 3′-M-AS; lane 13: 3′-3′-S; and lane 14: 3′-3′-AS. Inhibition of the HIV-1 viral *vif* mRNA and reporter gene expression. (B) RNA extracted from COS cells co-transfected with the short *vif* antisense RNA and pNLE was subjected to RT-PCR and separated on an agarose gel. Lane 1: control G3PDH RNA; lane 2: blank vector (pcDNA3.1); lane 3: (pNLE + pcDNA 3.1); lane 4: wt (pNLE); lane 5: M-5′-S; lane 6: M-5′-AS; lane 7: M-M-S; lane 8: M-M-AS; lane 9: M-3′-S; lane 10: M-3′-AS; lane 11: 3′-M-S; lane 12: 3′-M-AS; lane 13: 3′-3′-S; and lane 14: 3′-3′-AS. (C) The expressed antisense RNA transcripts mediated downregulation of the EGFP in COS cells. Notable, the panels representing M-3′-AS (Panel O), and 3′-M-AS (Panel S) showed >98% and >90%, respectively, downmodulation of the gene expression as compared to the HIV-1pNLE (Panel C).

CAT TGT ATG GCT-3′). There were significant levels of expression of both the antisense and sense mRNA in COS cells (Figure 5A), and HeLa-CD4$^+$ cells (data not shown).

RNA Content and HIV-1 *vif* Viral mRNA Reduction

To determine the relative inhibitory efficacies of the short *vif* antisense RNA expression vectors, they were co-transfected with the HIV-1pNLE. The co-transfected vectors were examined for a reduction in the viral *vif* mRNA and the downregulation of the reporter gene expression. Total RNA isolated from the co-transfected HeLa-CD4$^+$ cells, which were concurrently amplified with an internal control RNA (G3PDH) by reverse transcription (RT)-PCR using the specific *vif* viral mRNA detection primers and the following pair of specific primers for the control RNA (G3PDH), the *G3PDH-forward primer* (5′-ACC ACA GTC CAT GCC ATC AC-3′) and the *G3PDH-reverse primer* (5′-TCC ACC ACC CTG TTG CTG TA-3′), demonstrated that the short *vif* antisense RNA expression vectors encoding M-3′-AS and 3′-M-AS equally mediated downregulation of HIV-1pNLE *vif* mRNA expression (Figure 5B) in comparison with the control HIV-1pNLE *vif* mRNA alone (lane 4) and the control HIV-1 plus the empty vector (lane 3). Visualizing the RT-PCR products in ethidium-bromide-stained agarose gels thus provided a quantitative estimate of the degree of the reduction in the expressed HIV-1 *vif* viral mRNA. These reductions in the viral mRNA could be a result of the effective antisense mechanism mediated by the highly expressed *vif* antisense RNA transcripts in the cells (Figure 5A).

Downregulation of EGFP as Markers for HIV-1 Replication

To determine the suppression level of HIV-1 replication, transfected COS cells were examined under a fluorescence microscope to detect EGFP expression for extrapolations. The results exhibited significantly varied levels of reporter gene expression (Figure 5C). Panels O and S representing M-3′-AS and 3′-M-AS showed >98% and >90% inhibition of HIV-1 replication respectively, as compared to Panel C representing HIV-1pNLE (positive control for HIV replication). The others did not mediate any significant inhibitions.

DISCUSSION

In this study, we screened for highly effective therapeutic targets in the HIV-1 *vif* gene that interfered with HIV-1 Vif-dependent infectivity, due to the critical role Vif has in the infectivity and pathogenicity of HIV-1 in the target cells of the host. For this purpose, to determine the target sites for

the construction of the HIV-1 *vif* antisense RNA expression vectors, we used the HIV-1 *vif* mutant scheme (Figure 1). The Δ*vif* and the 3′Δ*vif* virions generated from H9 cells and titrated on MT-4 cells had low infectivity. The 5′Δ*vif* was not significantly affected compared to the ORF Δ*vif* and the 3′Δ*vif* virions, but was still not as potent as the wt. Contrarily, we did not observe any significant differences among the virions generated from HeLa-CD4$^+$ cells (Figure 2), which is consistent with results from others.[49] We further examined the growth characteristics of the HeLa-CD4$^+$-derived virions by comparing the growth kinetics on H9 and MT-4 cells. There was a direct correlation between the level of infectivity and the growth kinetics of the virions in both cell types. The Δ*vif* and 3′Δ*vif* virions grew poorly on the H9 cells, whereas the growth of the 5′Δ*vif* was slightly better, but not as progressive as the wt (Figure 3B). Comparatively, there were no significant differences observed in the growth kinetics of the HeLa-CD4$^+$-derived virions on MT-4 cells (Figure 3A). We further investigated whether the resultant low infectivity and the poor growth kinetics could eventually affect HIV-1 splicing. Pre-mRNA analysis from transiently-transfected HeLa-CD4$^+$ cells by RT-PCR revealed that the block deletions in the *vif* gene affected splicing. In the wt, there was significantly more spliced mRNA than unspliced. In contrast, the mutants demonstrated a significantly higher level of unspliced mRNA than spliced mRNA (Figure 4), which might be the result of the block deletions affecting elements that are crucial for HIV-1 biologic function in the cells. Based on these data, we further investigated whether HIV-1 *vif* antisense RNAs targeting various sites in the *vif* gene would equally attenuate the Vif-mediated infectivity in the target cells. The expression level and fidelity of the mRNA of the constructs were verified from transiently transfected COS cell and HeLa-CD4$^+$ cells, because the key step in the antisense mechanism is the expression of the antisense mRNA in the cells. There was significant mRNA expression in the cells, which might have led to the specific antisense effect on the HIV-1 *vif* mRNA in the co-transfected cells. As shown in Figure 5B, there was an effective reduction in HIV-1 viral *vif* mRNA by vectors encoding fragments within the overlapping sequences between the middle and 3′ ends of *vif*, referred to as (M-3′-AS) lane 10 and (3′-M-AS) lane 12. This correlatively mediated downregulation of the reporter gene (Figure 5C) and inhibited viral replication. In conclusion, M-3′-AS, spanning nucleic acid positions 5561-5705, which correspond to amino acid residues 96-144, significantly inhibited HIV-1 replication in COS cells. This resulted in marked downregulation of the level of the HIV-1 *vif* mRNA transcripts and reporter gene (EGFP) expression. Although not in all cases does the effect of deletions in a gene correspond to antisense effect if the same target is used (depending on the secondary RNA structure of the target), our results have shown that the amino acid residues stretching

from the middle towards the C-terminal end of Vif, especially 96-144, could be developed as an effective therapeutic target for gene therapy applications because both *vif* deletions and antisense RNA designed to target the same domain abrogated the HIV-1-Vif-dependent infectivity in the target cells.

EXPERIMENTAL PROCEDURE

Cell Cultures

COS, HeLa-CD4$^+$, H9, and MT-4 cells were grown in complete culture medium consisting of either RPMI 1640 medium (Sigma Chemical Co., St. Louis, Missouri), or D-MEM (Gibco, Invitrogen Corp., Japan) supplemented with 10% (v/v) heat-inactivated fetal bovine serum (FBS), L-glutamine (2 mM), penicillin (100 U/mL), and streptomycin (100 μg/mL), as previously described.[50] All cultures were maintained at 37°C under a 5% CO_2 atmosphere.

Construction of Plasmid Vectors and Virus

We used the HIV-1pNLE infectious molecular clone,[51] which was based on the previously described HIV-1pNL4-3.[52] Harvesting cell-free virus from the supernatant of transfected HeLa-CD4$^+$ or H9 cells generated the wild-type (wt) HIV-1_{NLE} used in the infection assays. The constructed HIV-1 *vif* antisense RNA expression vectors were based on the eukaryotic vector pcDNA3.1 (+/−) (Invitrogen Co., Carlsbad, California), while the HIV-1 *vif* deletion mutants were based on the HIV-1pNLE infectious molecular clone. The HIV-1 *vif* open reading frame (ORF) and the 5′-*vif* and 3′-*vif* extensive block-in-frame deletion mutants were constructed by polymerase chain reaction (PCR)-mediated site-directed mutagenesis, with primers designed to amplify the AgeI and EcoRI recognition sites on either side of the *vif* gene of the HIV-1pNLE template.

Mutagenic PCR for the Construction of HIV-1 *vif* Mutants

The various fragments of the *vif gene* were amplified by PCR, using KOD plus polymerase (Toyobo, Osaka, Japan) and the following sets of mutagenic primers: (a) For the ORF Δ*vif* mutant (5271-5849), we used *forward primer-1*: 5′ LF (5′-GGAT TAA AGT AAG GCA ATT ATG TAA ACT TC-3′), *reverse primer-1*: 5′ LR-1 (5′-CAG CTT CAC TCT TAA GTT CCT CTA AAA GCT AAT CCC TGA TGA TCT TTG CTT TTC TTC TTG GCA-3′), and *forward primer-2*: 3′ RF-1 (5′-CAA GAA GAA AAG CAA AGA TCA TCA GGG ATT AGC TTT TAG AGG AAC TTA AGA GTG AAG CTG TTA-3′) and *reverse primer-2*: 3′ RR (5′-GGC TGA CTT CCT GGA TGC TTC CAG GGC TCT-3′).

(b) For the 5′-Δ*vif* (5271-5560), we used *forward primer-1*: 5′ LF-1 (5′-CAG CTT CAC TCT TAA GTT CCT CTA AAA GCT AAT CCC TGA TGA TCT TTG CTT TTC TTC TTG GCA-3′), and *reverse primer-3*: 5′ LR-2 (5′-AAT TAG TTG GTC TGC TAG GTC AGG GTC TAC TAA TCC CTG ATC TTT GCT TTT CTT CTT GGC A-3′) and *forward primer-2*: 3′ RF-2 (5′-CAA GAA GAA AAG CAA AGA TCA TCA GGG ATT AGT AGA CCC TGA CCT AGC AGA CCA ACT AAT T-3′), *reverse primer-2*: 3′ RR (5′-GGC TGA CTT CCT GGA TGC TTC CAG GGC TCT-3′). (c) For the 3′-Δ*vif* (5561-5849), we used *forward primer-1*: 5′ LF (5′-GGA TTA AAG TAA GGC AAT TAT GTA AAC TTC-3′), *reverse primer-1*: 5′ LR-3 (5′-CAG CTT CAC TCT TAA GTT CCT CTA AAA GCT TGT GTG CTA TAT CTC TTT TTC CTC CAT TCT-3′), and *forward primer-2*: 3′ RF-3 (5′-AGA ATG GAG GAA AAA GAG ATA TAG CAC AAG CTT TTA GAG GAA CTT AAG AGT GAA GCT GTT A-3′), and *reverse primer-2*: 3′ RR (5′-GGC TGA CTT CCT GGA TGC TTC CAG GGC TCT-3′). The above PCR amplifications were designed to generate fragments with extended ends in the first round of the PCR fusion reaction. Briefly, the resulting pair of fragments with overlapping extensions were then used for further amplification by PCR as primers for the extension of the 3′ ends, subsequently "A-tailed," cloned into the pGEM-T Easy vector (Promega, Japan) using T4-DNA ligase, and designated as pGEM-TΔ*vif*. The AgeI and EcoRI recognition sites in the cloned fragments in pGEM-TΔ*vif* allowed vector recircularization by treating the vector with AgeI and EcoRI. Finally, the purified fragments were cloned into the AgeI and EcoRI sites in HIV-1pNLE to generate the (HIV-1pNLE-Δ*vif*) mutants.

Construction of the HIV-1 *vif* Antisense RNA Expression Vectors

The HIV-1 *vif* antisense and sense RNA vectors were also constructed by amplifying various targets of the *vif* gene from HIV-1pNLE (Figure 1C) by PCR using KOD plus polymerase with the forward and reverse primers containing the EcoRV and XhoI recognition sites, respectively. The short *vif* antisense RNA fragments were generated with the following sets of primers: (a) for the M-5′ *vif* antisense RNA (M-5′-AS), (5417-5560), the *forward primer* was V-4FecoV (5′-GAT ATC CAA AAA TAA GTT CAG AAG TAC ACA TCC C-3′) and the *reverse primer* was V-4Rxho (5′-CTC GAG TGT GTG CTA TAT CTC TTT TTC CTC-3′), (b) for the Mid-Mid *vif* antisense RNA (M-M-AS), (5488-5632), the *forward primer* was V-4MFecoV (5′-GAT ATC ATA CAG GAG AAA GAG ACT GGC AT-3′), and the *reverse primer* was V-4MRXho: (5′-CTC GAG CTT ATA GCA GAT TCT GAA AAA CAA TCA AAA TA-3′). (c) For the Mid-3′ *vif* antisense RNA (M-3′-AS), (5561-5705), the *forward primer* was the same as V-MFecoV and the *reverse primer* was the same as V-4MRXho, (d) while the *forward primer* for the 3′-Mid *vif* antisense

RNA (3′-M-AS), (5633-5778) was V-3′ MFecoV (5′-GAT ATC AAT ACC ATA TTA GGA CGT ATA GTT AGT CC-3′) and the *reverse primer* was V-3MRXho: (5′-CTC GAG TCA GTT TCC TAA CAC TAG GCA AAG GTG GCT-3′). (e) Finally, the set of primers for the 3′-3′ *vif* antisense RNA (3′-3′-AS), (5706-5849) were as follows: the *forward primer* was V-3FecoV: (5′-GAT ATC CAG TAC TTG GCA CTA GCA GCA TTA-3′) and the *reverse primer* was V-Rxho (5′-CTC GAG CTA GTG TCC ATT CAT TGT ATG GCT-3′). The PCRs were performed according to the manufacturers' protocol, and the integrity of the resulting *vif* fragments was confirmed by automated sequencing. These amplified fragments were then cloned into the EcoRV and XhoI sites in the pcDNA3.1 (+/−) vector in both the antisense and sense orientations, to generate the *vif* antisense RNA and the control sense expression vectors.

Transfections and HIV-1 Gag p24 Assay

The HIV-1 Gag p24 antigen production level was used to determine the degree of attenuation in the HIV-1 vif-dependent infectivity mediated by the HIV-1 *vif* mutants and the expressed HIV-1 *vif* antisense RNA transcripts in the transfected cells. In some of the experiments, the infectious molecular clone HIV-1pNLE and the HIV-1 *vif* mutants were separately transfected, while in other experiments, the HIV-1 *vif* antisense RNA vectors were either separately transfected or co-transfected with HIV-1pNLE into COS (3×10^5), HeLa-CD4$^+$ (2×10^5), or H9 at 5×10^5 cells per 60-mm culture dish. The FuGENE^{TM} 6 transfection reagent (Roche Diagnostics, Japan) and Lipofectamine 2000 (Life Technologies, Japan) were used according to the manufacturers' protocols. Briefly, 24 h before transfection, the adherent cells were seeded as described above. COS and HeLa-CD4$^+$ cells were either transfected with 3.0 μg of mutant DNA or antisense vectors or co-transfected with 2 μg antisense DNA and 2 μg HIV-1pNLE DNA using 3 μL of FuGENE 6 reagent. H9 cells were transfected with 3 μL Lipofectamine 2000 transfection reagent, optimized with 50 μL serum-free Opti-MEM. After 72 h of culture, the supernatants were harvested and cleared by centrifugation, and HIV-1 p24 antigen production was measured using an enzyme-linked immunosorbent assay system (CLEIA). The remaining cells were washed and fixed in 1% formaldehyde in phosphate-buffered saline. The co-transfected cells were subsequently monitored for down regulation of the expressed reporter gene (EGFP) using fluorescence microscopy.

Replication Competency of Mutants in H9 and MT-4 Cells

To evaluate the replication competencies of the HIV-1 *vif* mutants, stock virions from multiple samples generated from mutant-transfected

HeLa-CD4$^+$ and H9 cells were further normalized at 100 pg of HIV-1Gag p24 antigen equivalents each, and assayed for replication competency using the terminal dilution micro-assay in susceptible MT-4 cells. Endpoint titration was performed in flat-bottomed micro-titer wells using four parallel series of five-fold dilutions. After 5 to 7 d of incubation, cell-free supernatants were harvested and the presence of the major viral core p24 protein was examined using an HIV-1 p24 CLEIA. The $TCID_{50}$ was calculated by the method of Reed and Muench.[53]

HIV-1 *vif* Mutations Affected Splicing in Transfected Cells

Total RNA was extracted from HeLa-CD4$^+$ cells after 48 h posttransfection with mutant vectors using Trizol (Invitrogen Co.). The RNA was resuspended in 50 μL of RNase-free water, and then contaminating DNA that could interfere with the subsequent amplification experiments was digested with RNase free DNase by treating the sample (10 μL) with 0.2 μg of the enzyme in 10 mM Tris-acetate (ph 7.5), 10 mM magnesium acetate, and 50 mM potassium acetate for 30 min at 37°C, followed by phenol-chloroform and ethanol precipitation. The integrity of the RNA sample was verified by standard agarose gel electrophoresis. Total RNA (2 μg) was concurrently amplified with the human housekeeping gene (G3PDH) using the RT-PCR high plus kit (Toyobo) under the following conditions: One cycle of 60°C for 30 min and 94°C for 2 min, 40 cycles of 94°C for 1 min and at 50°C for 2 min, and 1 cycle of 50°C for 1 min, using the following specific primers within the splicing donor and splicing acceptor sites located in the pNL4-3 DNA; *forward* HIV-SPF (551-573) 5′-AAG TAG TGT GTG CCC GTC TGT TG-3′ and *reverse* HIV-SPR (5823-5849) 5′-CTA GGA TCT ACT GGC TCC ATT TCT TGC-3′. The resultant products were fractionated on 8% native polyacrylamide gels, stained in ethidium bromide, and visualized under an ultraviolet (UV) illuminator.

Growth Kinetics of HIV-1 Virions in H9 and MT-4 Cells

To analyze the growth characteristics of the mutant virions generated from HeLa-CD4$^+$ cells, the growth kinetics was compared in infected H9 and MT-4 cells. Virions harvested from cell-free supernatant of transiently transfected HeLa-CD4$^+$ cells (1×10^6), were further normalized at 100 pg HIV-1 Gag p24 and infected to H9 (2×10^5), and MT-4 (3×10^5) cells in 6-well plates. Briefly, the cells were seeded 24 h prior to infection (100 pg of p24 antigen) and incubated for 6 h at 37°C with intermittent agitation. Cells were then washed three times to remove residual virus. Culture supernatant was sampled on days 2, 4, 6, 8, and 10, and the quantitative levels of HIV-1 Gag p24 measured by CLEIA.

RNA Purification and RT-PCR

Total cellular RNA was isolated from transfected and co-transfected COS cells with the GenElute Mammalian Total RNA Kit (Sigma-Aldrich Co., St. Louis, Missouri), according to the manufacturer's instructions. The isolated RNA samples were pretreated with DNase I (Promega, Madison, Wisconsin) and then subjected to one-step RT-PCR assays (RT-PCR high-plus-kit; Toyobo, Japan) with specific HIV-1 *vif* mRNA primers, *forward primer*: vmRNA-F, (5′-CAA GAA GAA AAG CAA AGA TCA TCA G-3′) and *reverse primer*: vmRNA-R (5′-CTA GTG TCC ATT CAT TGT ATG GCT-3′), according to the manufacturer's instructions. Briefly, the RNA samples were normalized at 1 μg per reaction and concomitantly amplified with G3PDH as a control. To analyze the extent of the RNA expression in the cells, the products from the RT-PCR amplified RNAs were electrophoresed through a non-denaturing 1.8% agarose gel in TAE buffer.

REFERENCES

1. Miller, R.J.; Cairns, J.S.; Bridges, S.; Sarver, N. Human immunodeficiency virus and AIDS: Insights from animal lentiviruses. J. Virol. **2000**, 74, 7187–7195.
2. Seroude, V.; Audoly, G.; Gluschankof, P.; Suzan, M. Tryptophan 95, an amino acid residue of the Caprine arthritis encephalitis virus vif protein, which is essential for virus replication. Virology **2001**, 280, 232–242.
3. Metharom, P.; Takyar, S.; Xia, H.Q.; Ellem, K.A.; Wilcot, G.E.; Wei, M.Q. Development of disabled, replication-defective gene transfer vectors from the Jembrana disease virus, a new infectious agent of cattle. Vet. Microbiol. **2001**, 80, 9–22.
4. Chatterji, U.; Grant, C.K.; Elder. J.H. Feline immunodeficiency virus *Vif* localizes to the nucleus. J. Virol. **2000**, 74, 2533–2540.
5. Dettenhofer, M.; Cen, S.; Carlson, B.A.; Kleiman, L.; Yu, X.F. Association of human immunodeficiency virus type-1 Vif with RNA and its role in reverse transcription. J. Virol. **2000**, 74, 8938–8945.
6. Goncalves, J.; Jallepalli, P.; Gabuzda, D.H. Subcellular localization of the *Vif* protein of human immunodeficiency virus type 1. J. Virol. **1994**, 70, 704–712.
7. Goncalves, J.; Silva, F.; Freitas-Vieira, A.; Santa-Marta, M.; Malho, R.; Yang, X.; Gabuzda, D.; Barbas, C., III. Functional neutralization of HIV-1 *Vif* protein by intracellular immunization inhibits reverse transcription and viral replication. J. Biol. Chem. **2002**, 277, 32036–32045.
8. Henzler, T.; Harmache, A.; Herrman, H.; Spring, H.; Suzan, M.; Audoly, G.; Panek, T.; Bosch, V. Fully functional, naturally occurring and C-terminally truncated variant human immunodeficiency virus (HIV) *Vif* does not bind to HIV *Gag* but influences intermediate filament structure. J. Gen. Virol. **2001**, 82, 561–573.
9. Karczewski, M.K.; Strebel, K. Cytoskeleton association and virion incorporation of the human immunodeficiency virus type 1 Vif protein. J. Virol. **1996**, 70, 494–507.
10. Madani, N.; Kabat, D. An endogenous inhibitor of human immunodeficiency virus in human lymphocytes is overcome by the viral Vif protein. J. Virol. **1998**, 72, 10251–10255.
11. Simon, J.H.; Miller, D.L.; Fouchier, R.A.; Soares, M.A.; Peden, K.W.; Malim, M.H. The regulation of primate immunodeficiency virus infectivity by *Vif* is cell species restricted: a role for *Vif* in determining virus host range and cross-species transmission. EMBO J. **1998**, 17, 1259–1267.
12. Fan, L.; Peden, K. Cell-free transmission of *Vif* mutants of HIV-1. Virology **1992**, 190, 19–29.
13. Gabuzda, D.H.; Lawrence, K.; Langhoff, E.; Terwilliger, E.; Dorfman, T.; Haseltine, W.; Sodroski J. Role of *vif* in replication of human immunodeficiency virus type 1 in CD4+ T lymphocytes. J. Virol. **1992**, 66, 6489–6495.

14. Von Schwedler, U.; Song, J.; Aiken, C.; Trono, D. *Vif* is crucial for human immunodeficiency virus type 1 proviral DNA synthesis in infected cells. J. Virol. **1993**, 67, 4945–4955.
15. Sova, P.; Volsky, V. Efficiency of viral DNA synthesis during infection of permissive and nonpermissive cells with *vif*-negative human immunodeficiency virus type 1. J. Virol. **1993**, 67, 6322–6326.
16. Sakai, H.; Shibata, R.; Sakuragi, J.-I.; Sakuragi, S.; Kawamura, M.; Adachi, A. Cell-dependent requirement of human immunodeficiency virus type 1 *Vif* protein for maturation of virus particles. J. Virol. **1993**, 67, 1663–1666.
17. Fouchier, R.A.; Simon, J.H.; Jaffe, A.B.; Malim, M.H. Human immunodeficiency virus type-1 *Vif* does not influence expression or virion incorporation of gag-, pol-, and env-encoded proteins. J. Virol. **1996**, 70, 8263–8269.
18. Borman, A.M.; Quillent, C.; Charneau, P.; Dauguet, C.; Clavel, F. Human immunodeficiency virus type 1 *Vif*-mutant particles from restrictive cells: Role of *Vif* in correct particle assembly and infectivity. J. Virol. **1995**, 69, 2058–2067.
19. Bouyac, M.; Rey, F.; Nascimbeni, M.; Courcoul, M.; Sire, J.; Blanc, D.; Clavel, F.; Vigne, R.; Spire, B. Phenotypically *vif* human immunodeficiency virus type 1 is produced by chronically infected restrictive cells. J. Virol. **1997**, 71, 2473–2477.
20. Hoglund, S.; Ohagen, A.; Lawrence, K.; Gabuzda, D. Role of vif during packing of the core of HIV-1. Virology **1994**, 201, 349–355.
21. Bouyac, M.; Courcoul, M.; Bertonia, G.; Baudat, Y.; Gabuzda, D.; Blanc, D.; Chazal, N.; Boulanger, P.; Sire, J.; Vigne, R.; Spire, B. Human immunodeficiency virus type-1 *Vif* protein binds to the Pr55Gag precursor. J. Virol. **1997**, 71, 9358–9365.
22. Zhang, H.; Pomerantz, R.J.; Dornadla, G.; Sun, Y. Human immunodeficiency virus type 1 *Vif* protein is an integral component of an mRNP complex of viral RNA and could be involved in the viral RNA folding and packaging process. J. Virol. **2000**, 74, 8252–8261.
23. Sheehy, A.M.; Gaddis, N.C.; Choi, J.D.; Malim, M.H. Isolation of a human gene that inhibits HIV-1 infection and is suppressed by the viral *Vif* protein. Nature **2002**, 418, 646–650.
24. Roberto, M.; Chen, D.; Schrofelbauer, B.; Navarro, F.; Konig, R.; Boliman, B.; Munk, C.; Nymark-McMahon, H.; Landau, N.R. Species-specific exclusion of APOBEC3G from HIV-1 virions by vif. Cell **2003**, 114, 21–31.
25. Madani, N.; Millette, R.; Platt, E.J.; Marin, M.; Kozak, S.L.; Bloch, D.B.; Kabat, D. Implication of the lymphocyte-specific nuclear body protein Sp140 in an innate response to human immunodeficiency virus type 1. J. Virol. **2002**, 76, 11133–11138.
26. Simon, J.H.; Gaddis, N.C.; Fouchier, R.A.; Malim, M.H. Evidence for a newly discovered cellular anti-HIV-1 phenotype. Nat. Med. **1998**, 4, 1397–1400.
27. Simon, J.H.; Sheehy, A.M.; Carpenter, E.A.; Fouchier, R.A.; Malim, M.H. Mutational analysis of the human immunodeficiency virus type 1 *Vif* protein. J. Virol. **1999**, 73, 2675–2681.
28. Bordignon, C.; Notarangelo, L.D.; Nobili, N.; Ferrari, G.; Casorati, G.; Panina, P.; Mazzolari, E.; Maggioni, D.; Rossi, C.; Servida, P.; Ugazio, A.G.; Mavilio, F. Gene therapy in peripheral blood lymphocytes and bone marrow for ADA-immunodeficient patients. Science **1995**, 270, 470–475.
29. Bridges, S.H.; Sarver, N. Gene therapy and immune restoration for HIV disease. Lancet **1995**, 345, 427–475.
30. Ojwang, J.O.; Hampel, A.; Looney, D.J.; Wong-Staal, F.; Rappaport, J. Inhibition of human immunodeficiency virus type 1 expression by hairpin ribozyme. Proc. Natl. Acad. Sci. USA **1992**, 89, 10802–10806.
31. Potash, M.J.; Bentsman, G.; Muir, T.; Krachmarov, C.; Sova, P.; Volsky, D.J. Peptide inhibitors of HIV-1 protease and viral infection of peripheral blood lymphocytes based on HIV-1 Vif. Proc. Natl. Acad. Sci. USA **1998**, 95, 13865–13868.
32. Snyder, D.S.; Wu, Y.; Wang, J.L.; Rossi, J.J.; Swiderski, P.; Kaplan, B.E.; Forman, S.J. Ribozyme-mediated inhibition of bcr-abl gene expression in a Philadelphia chromosome-positive cell line. Blood **1993**, 82, 600–605.
33. Cen, S.; Huang, Y.; Khorchid, A.; Darlix, J.L.; Wainberg, M.A.; Kleiman, L. The role of Pr55 (gag) in the annealing of tRNA3Lys to human immunodeficiency virus type 1 genomic RNA. J. Virol. **1999**, 73, 4485–4488.
34. Chang, H.K.; Gendelman, R.; Lisziewicz, J.; Gallo, R.C.; Ensoli, B. Block of HIV-1 infection by a combination of antisense tat RNA and TAR decoys: A strategy for control of HIV-1. Gene Ther. **1994**, 1, 208–216.