problem is particularly relevant for viruses that exhibit significant genetic variation due to an error-prone replication machinery.

This risk might be more severe for RNA viruses and retroviruses than for DNA viruses. The variability of HIV caused by its error-prone reverse transcriptase has been shown to generate mutations in the gene being targeted, thus allowing it to rapidly evade siRNAs (Boden et al. 2003). Similar results were observed for RNAi of a poliovirus infection (Gitlin et al. 2002). Synthetic siRNAs against poliovirus inhibited virus production 100-fold; however, the virus titer increased to high levels upon prolonged incubation. Sequence analysis of the progeny virus demonstrated a single escape mutation in the center of the siRNA target sequence. These findings indicate that the point mutation occurred in the middle of the signal target sequences. Two recent studies have demonstrated that transfection with siRNAs containing mismatches to the target sequence in the middle of the siRNA molecules reduces the efficiency of gene silencing (Brummelkamp et al. 2002b; Amarzguioui et al. 2003). These findings suggest that in order for RNAi to durably suppress HIV-1 replication, more potent shRNAs will need to be designed that can target highly conserved regions of the viral genome (for example, *gag* and *pol*) that are essential for the viral life cycle. Alternatively, RNAi constructs co-expressing multiple shRNAs could be developed that simultaneously target different regions of the viral genome, thereby reducing the probability of generating shRNA escape mutants.

7
Using RNAi to Treat Other Viruses

Although many previous studies on RNAi-mediated inhibition have focused on HIV-1, there is a growing body of data addressing the inhibition of other animal and human viruses. These include RNA viruses such as hepatitis C virus (HCV), poliovirus, Semliki Forest virus (SFV), influenza virus A, rhesus rotavirus (RRV), and Rous sarcoma virus (RSV), and DNA viruses such as human papillomavirus type 16 (HPV-16) and hepatitis B virus (HBV). In most of these studies, the RNAi machinery was directly targeted towards the viral RNA using synthetic siRNAs.

Hepatitis induced by HBV or HCV is a major health problem. At present, hundreds of millions of individuals are infected worldwide. Although there is an effective vaccine against HBV, it is only useful for the prevention of viral infection. There is no vaccine for HCV. Hepatitis caused by these two viruses has therefore been an important target for potential RNAi therapy.

The first demonstration of RNAi efficacy against a virus in vivo involved the hydrodynamic co-delivery of an HBV replicon and an expression unit encoding an anti-HBV shRNA in mice. HBV is a member of the family Hepadnaviridae and has a 3.2-kb circular dsDNA genome. During infection, four RNAs are transcribed, which encode the coat protein (CP), polymerase (P),

surface antigen (S), and transactivator of transcription (X). HBV production in Huh-7 cells was shown to be reduced by up to 20-fold through the transfection of a vector-expressing shRNA against the X mRNA (Shlomai and Shaul 2003).

Inhibition of HBV in the liver of mice was achieved through the co-transfection of HBV DNA and shRNA-expressing plasmids (McCaffrey et al. 2003), which resulted in a six fold decrease in the amount of secreted HBV surface antigen in the serum. This small-animal model of human infectious disease shows that it is possible to use RNAi as a potent antiviral therapy in mammals.

HCV is a major cause of chronic liver disease, which can lead to liver cirrhosis and hepatocellular carcinoma (Reed and Rice 2000). The HCV genome is a positive-strand RNA molecule with a single open reading frame encoding a polyprotein that is processed post-translationally to produce at least 10 proteins. HCV is a member of the family Flaviviridae and has a (+) single-stranded (ss)RNA genome.

Subgenomic and full-length HCV replicons that replicate and express HCV proteins in stably transfected human hepatoma-derived Huh-7 cells have been used to study the effects of various antiviral drugs (Lohmann, et al. 1999; Pietschmann, et al. 2001; Ikeda et al. 2002). Several groups have now tested the efficacy of the siRNA-mediated inhibition of replicon function using these systems (Kapadia et al. 2003; Randall et al. 2003; Wilson et al. 2003). These replicons support HCV RNA transcription and protein synthesis, but do not produce infectious viruses.

siRNAs targeted against sequences in the viral non-structural proteins NS3 and NS5B have been shown to cause profound (up to 100-fold) inhibition of HCV replicon function in cell cultures (Kapadia et al. 2003; Randall et al. 2003; Seo et al. 2003; Wilson et al. 2003). Furthermore, the internal ribosomal-entry site (IRES) in the well-conserved 5′ UTR of the HCV RNA has also been a good target. Both siRNAs and shRNAs have been reported to inhibit HCV replicon function in cells (Seo et al. 2003; Wilson et al. 2003; Yokota et al. 2003; Hamazaki et al. 2005).

In another in vivo study, siRNAs were used to treat fulminant hepatitis induced by an agonistic Fas-specific antibody in mice (Song et al. 2003b). Fas-mediated apoptosis of hepatocytes can be triggered by HBV and HCV infection. Infusing siRNAs targeting Fas mRNAs into the tails of the mice blocked this self-destructive inflammatory response of the liver. These findings indicate that major hurdles remain before this therapy can be applied to humans.

As with HIV therapeutics, delivery of the siRNAs or shRNA vectors is the main challenge for the successful treatment of HCV.

Generally, human influenzal lesions are local infections that remain in the upper portion of the respiratory tract and do not proceed to pneumonia. Nevertheless, in high-risk patients, cases of influenzal pneumonia have been reported in which expansion of the virally infectious focus is observed in a pulmonary lesion. Furthermore, such cases are often accompanied by a secondary bacterial pneumonia. The influenza virus belongs to the family Orthomyxoviridae and

has a (–) ssRNA genome. Its genome is composed of eight separate segments. The proteins encoded by the eight segmented genes include HA and NA, as well as the M1 and M2 membrane proteins, which are located on the surface of the envelope. Furthermore, a nucleoprotein complex (RNP) is located at the center of the virus and is composed of the gene RNA, three RNA polymerase subunits (PB1, PB2, and PA) and a nucleoprotein (NP). A non-structural protein (NS) is synthesized from the eighth segmented gene. Amantadine and rimantadine are known antiviral agents for the influenza A virus; however, neither drug can cope with mutants and both have strong side effects (Atmar et al. 1990; Wang et al. 1993). Treatment by an inactivated vaccine has also been attempted; however, the vaccine cannot sustain antibody productivity for a long period and, thus, cannot completely prevent the spread of infection (Hirota et al. 1996).

Ge et al. (2003) showed that siRNAs targeting conserved regions (PA and NP) of the influenza genome inhibited virus production in cell culture and in embryonated chicken eggs. Furthermore, RNAi mediated by PA-, NP-, and PB1-specific siRNAs or shRNAs expressed from DNA vectors prevented and treated influenza A virus infection in mice (Ge et al. 2004). In addition, Tompkins et al. (2004) showed that the administration of influenza-specific siRNAs decreased lung virus titers and protected mice from lethal challenge by a variety of influenza A viruses, including the potential pandemic subtypes H5 and H7. This specific inhibition of influenza virus replication requires homology between the siRNAs and gene targets, and is not the result of IFN induction by dsRNAs. For therapeutic applications against the influenza A virus, the siRNAs can be administered via intranasal or pulmonary routes. RNAi is more potent than the antisense approach (Mizuta et al. 1999), and the evaluation of this technology as a treatment for the influenza virus through human clinical trials is expected to take place in the near future.

8 Concluding Remarks

While the results obtained to date should be considered preliminary in terms of their application to humans, they do provide strong justification for further investigations into the use of RNAi for the treatment of viruses in a clinical setting. The major problem with using RNAi as a tool to inhibit viral replication is the fact that it is still difficult to predict the effectiveness of specific siRNAs. It is clear from numerous studies that not all siRNAs are equally effective at generating an RNAi response. It has generally been assumed that siRNAs are under the control of the host interference-response mechanism. Recently, some expressed shRNAs have been shown to activate at least one of the arms of the human IFN-response mechanism. In addition, viral escape from RNA silencing is clearly a problem for developing effective RNAi-based antiviral therapy. Furthermore, some viral RNA sequences might be buried within

secondary structures or highly folded regions. Clearly, difficulties concerning the delivery, specificity, and effectiveness of siRNAs remain. However, once these fundamental questions have been addressed, it seems likely that RNAi therapy against viral infections will progress towards clinical trials.

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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

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□ *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.

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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).

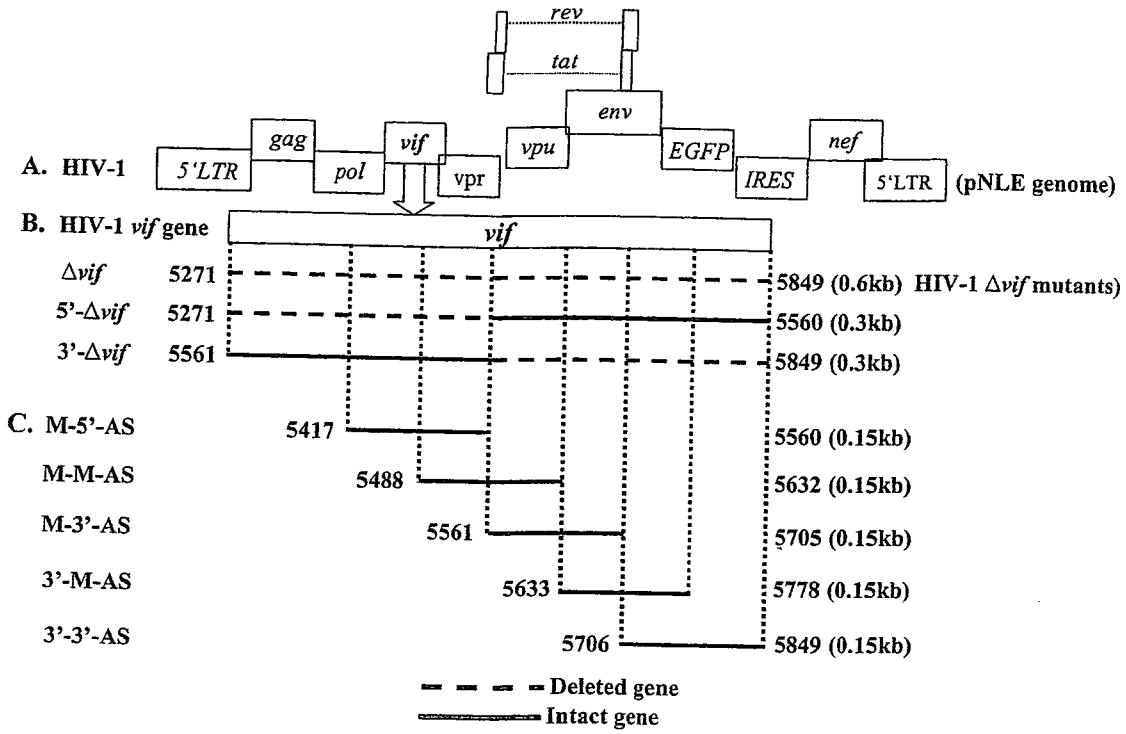

FIGURE 1 Scheme for the construction of both HIV-1 *vif* mutants and the HIV-1 *vif* antisense RNA expression vectors. (A) Schematic representation of the HIV-1pNLE genome, showing the open reading frames, and the 5′and 3′ long terminal repeats. (B) The HIV-1 mutants were constructed by PCR-mediated 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

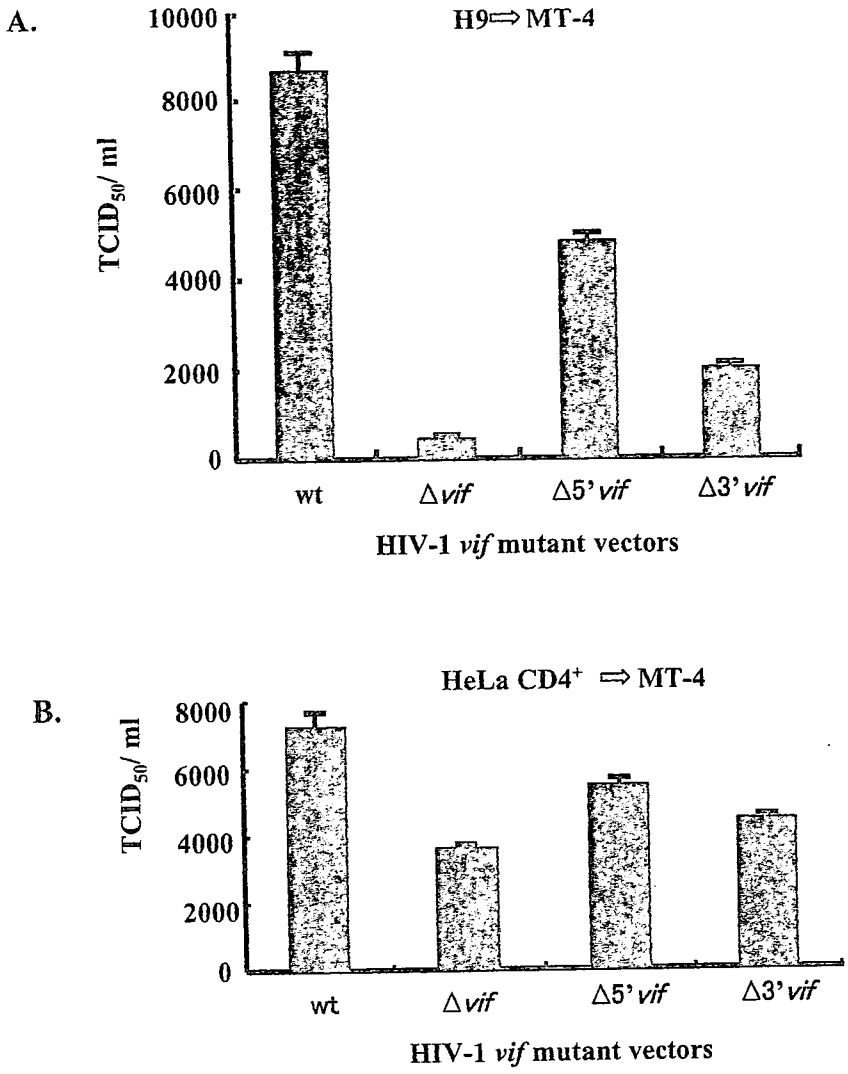

FIGURE 2 Infectivity of wt and mutant viruses. Mutant viruses generated from the co-transfected HeLa-CD4$^+$ and H9 cells were normalized at 100 pg of HIV-1 Gag p24 antigen, and titrated in fivefold serial dilution steps in MT-4 cells. Cell-free culture supernatants were harvested at 6 d posttransfection, 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

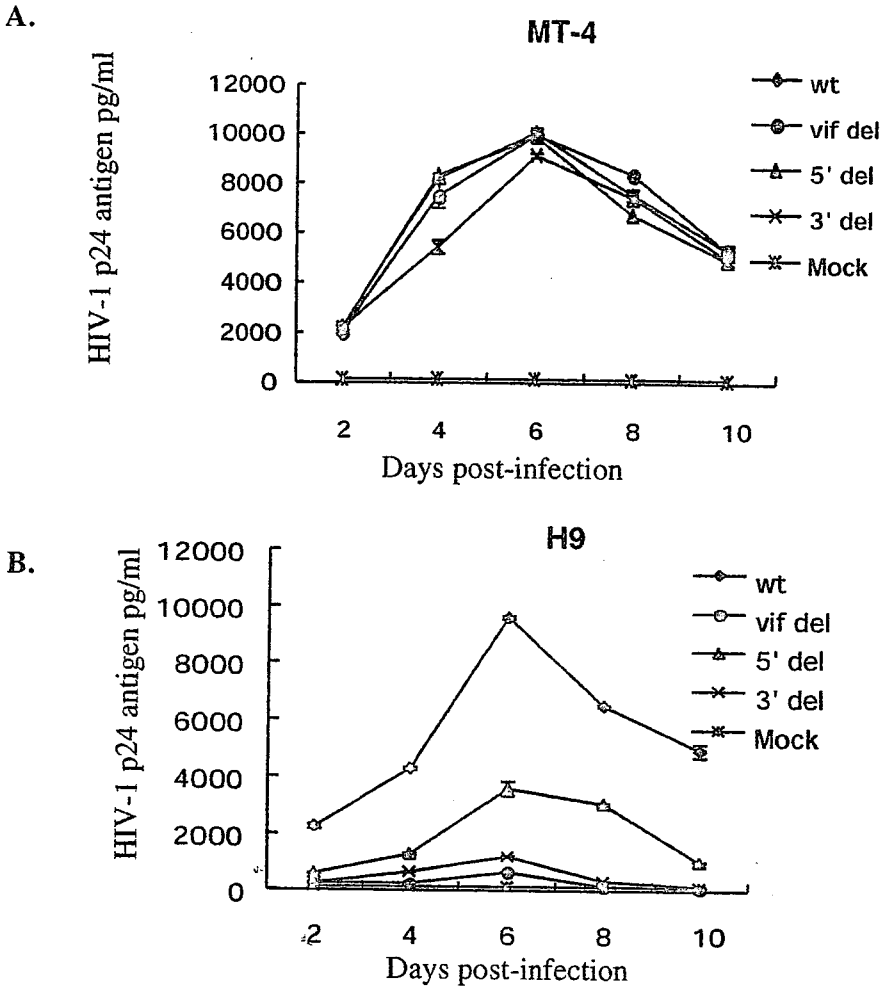

FIGURE 3 Growth kinetics of wt and mutant viruses in H9 and MT-4 cells. Viruses were generated in HeLa-CD4$^+$ cells (1×10^6), normalized at 100 pg p24 antigen and used to infect H9 and MT-4 cells, with the residual virus removed by washing. Subsequently, HIV-1 p24 antigen production was monitored at 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

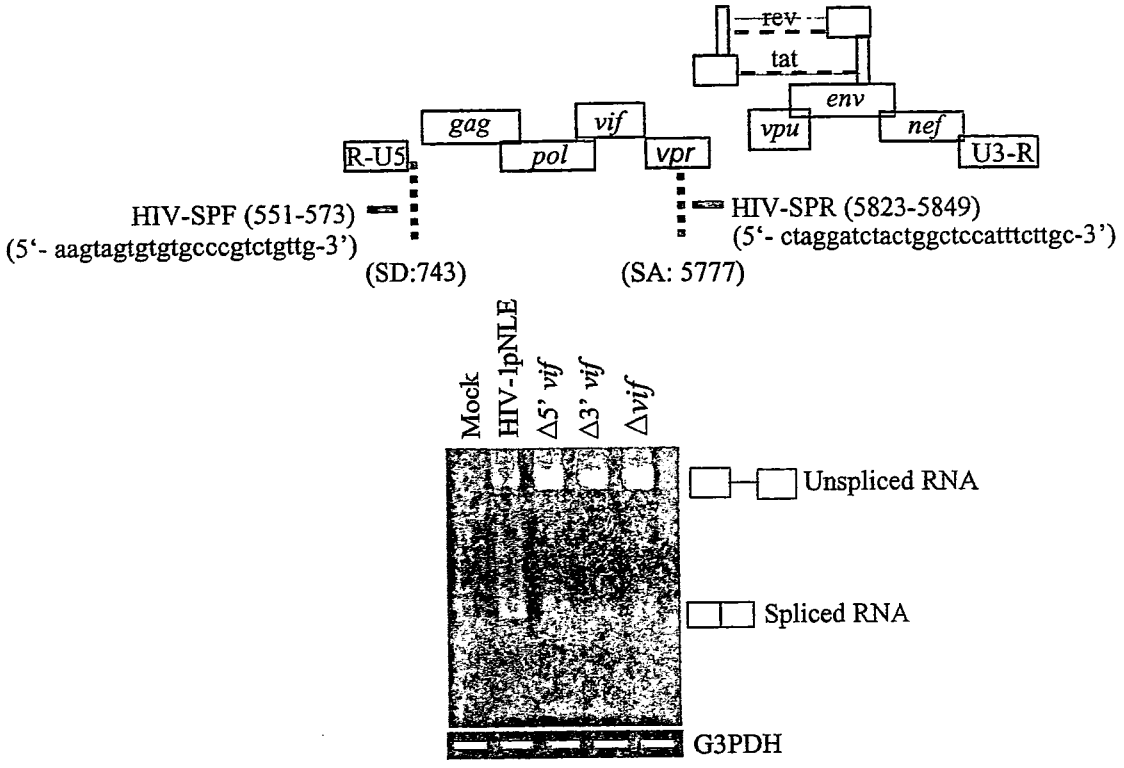

FIGURE 4 HIV-1 mutant splicing in transfected-HeLa-CD4$^+$ cells. (A) HIV-1 genome and RT-PCR primers were positioned around the splicing donor site (SD) and the splicing acceptor (SA) region as forward and reverse primers, respectively. (B) Total and nuclear RNA extracted from transiently transfected 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

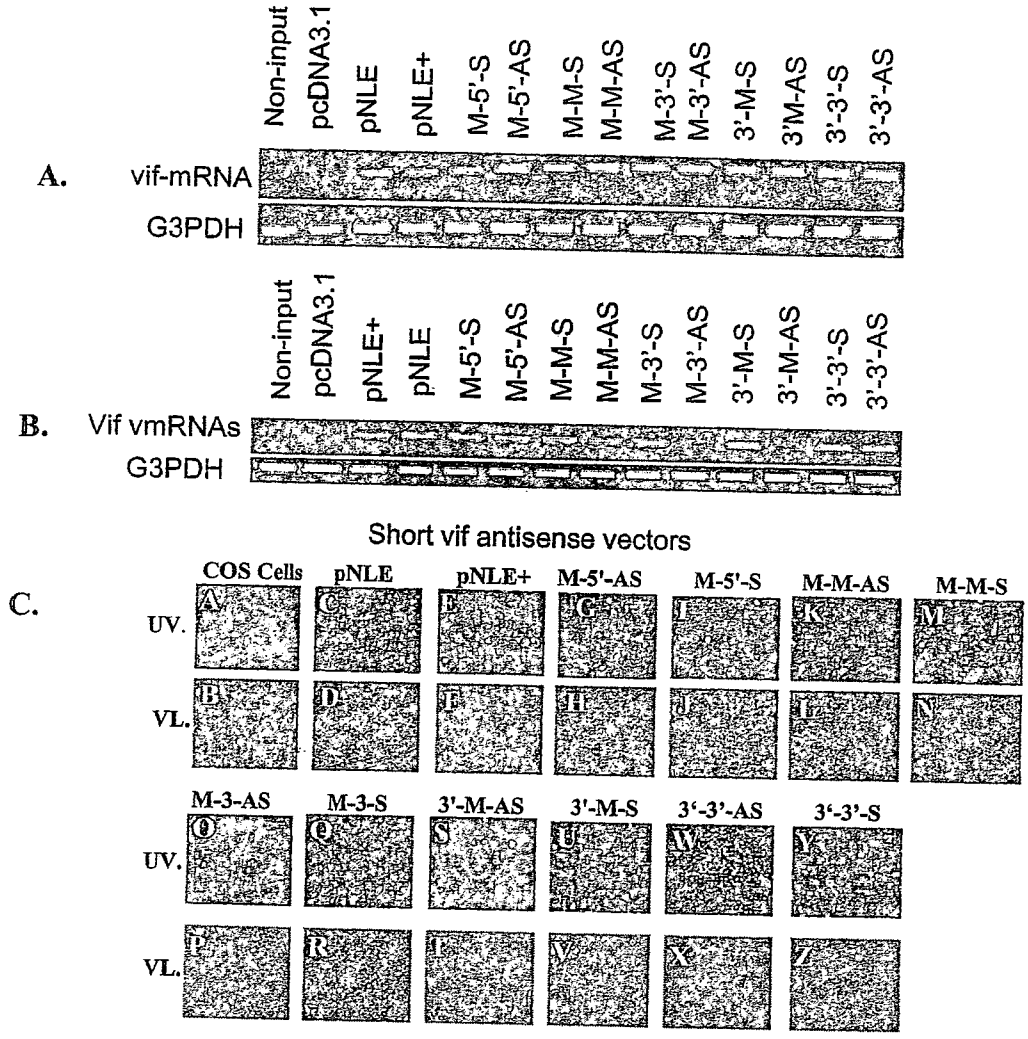

FIGURE 5 RT-PCR analysis of the *vif* antisense and the control RNA expression in COS cells. (A) The expressed short *vif* antisense RNA transcripts from the COS cells was concurrently amplified by RT-PCR with the controls, including the G3PDH RNA, and were resolved on an agarose gel. Lane 1: control 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′).