

Identification of a Key Target Sequence To Block Human Immunodeficiency Virus Type 1 Replication within the *gag-pol* Transframe Domain

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Although the full sequence of the human immunodeficiency virus type 1 (HIV-1) genome has been known for more than a decade, effective genetic antivirals have yet to be developed. Here we show that, of 22 regions examined, one highly conserved sequence (ACTCTTTGGCAACGA) near the 3' end of the HIV-1 *gag-pol* transframe region, encoding viral protease residues 4 to 8 and a C-terminal Vpr-binding motif of p6^{Gag} protein in two different reading frames, can be successfully targeted by an antisense peptide nucleic acid oligomer named PNA_{PR2}. A disrupted translation of *gag-pol* mRNA induced at the PNA_{PR2}-annealing site resulted in a decreased synthesis of Pr160^{Gag-Pol} polyprotein, hence the viral protease, a predominant expression of Pr55^{Gag} devoid of a fully functional p6^{Gag} protein, and the excessive intracellular cleavage of Gag precursor proteins, hindering the processes of virion assembly. Treatment with PNA_{PR2} abolished virion production by up to 99% in chronically HIV-1-infected H9 cells and in peripheral blood mononuclear cells infected with clinical HIV-1 isolates with the multidrug-resistant phenotype. This particular segment of the *gag-pol* transframe gene appears to offer a distinctive advantage over other regions in invading viral structural genes and restraining HIV-1 replication in infected cells and may potentially be exploited as a novel antiviral genetic target.

The persistence of integrated proviruses in host cells presents formidable challenges to the treatment of human immunodeficiency virus type 1 (HIV-1) infection. Replication-competent HIV-1 can be recovered from resting CD4⁺ T lymphocytes even from individuals receiving potent combination antiretroviral therapy, whose plasma virus levels have remained below the detection limit for a prolonged period (19, 33, 36, 147, 153). The discovery of a long-lived viral reservoir, which is established early in the infection (18, 33, 147), has suggested that HIV-1 cannot be easily eradicated from infected individuals with the current treatments. Another impediment to controlling HIV-1 infection is the emergence of drug-resistant viral strains (21, 47, 50, 61, 62, 67, 78, 90, 107, 110, 111, 130). HIV-1 protease, in particular, seemingly tolerates extensive sequence variations (8, 76, 79), contributing to a rapid emergence of protease inhibitor-resistant strains, which can be cross-resistant to multiple protease inhibitors (21, 47, 90, 107, 110, 111). Indeed, multidrug-resistant (MDR) HIV-1 strains are isolated increasingly from patients who have been extensively treated with various antiretroviral agents of similar classes (151), and the spread of these MDR strains may become a serious threat to the containment of the AIDS epidemic in the future. The identification of novel viral targets is clearly needed to empower anti-HIV-1 therapeutic strategies.

In recent years, viral coreceptors (25, 26, 39, 99, 105, 132), integrase (7, 29, 31, 93, 101, 115, 154, 155), and the viral nucleocapsid protein zinc finger motif (94, 117–120, 137) have emerged as novel antiviral targets. However, substantial progress has yet to be made before any of the candidate compounds can be brought to practical applications.

Another possible antiviral target pursued over the years is the HIV-1 genome itself. Antisense reagents, in particular, have been extensively investigated primarily in the form of nuclease-resistant phosphorothioate oligodeoxynucleotides (PsODN). However, these previous attempts targeting various regions of the HIV-1 genome with antisense PsODN have produced inconsistent results in chronically infected cells (2, 4, 5, 64, 66, 83–86, 92, 141, 148). The reasons for a lack of consistency may vary. Selected target sequences may have been less critical for virion production in chronically HIV-1-infected cells or less accessible to the PsODN molecules because of the RNA-binding proteins or intracellular folding of the target RNA. It is also possible that antisense PsODN molecules were simply ineffective in abating ribosome elongation (9, 14, 139) or that available antisense molecule numbers were insufficient to overcome the enormous amount of viral transcripts expressed in the chronically infected cells (140).

Selection of optimal genetic targets and the use of potent gene-intervening reagents are equally critical elements of a successful antigenic or antisense strategy. Peptide nucleic acid (PNA) (27, 45, 103, 145), initially developed as a reagent for strand invasion of the duplex DNA, is a DNA mimic, consisting of a peptide backbone of *N*-(2-aminoethyl)glycine units in place of a deoxyribose backbone. Although unmodified PNA has a relatively poor cellular uptake compared to that of ODN (104, 144), it has unique molecular characteristics which may enhance its utility as a genome-intervening tool, such as resis-

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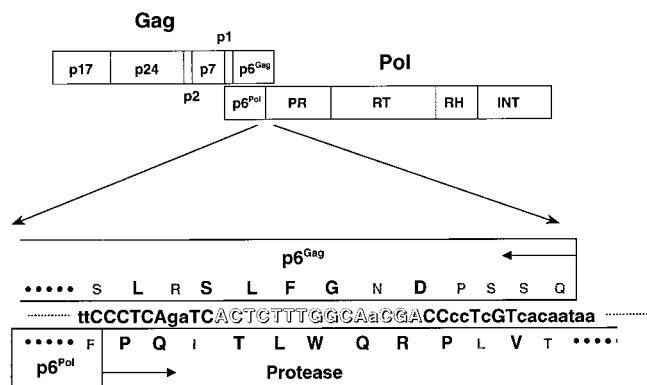


FIG. 1. Schematic representation of the *gag* and *pol* regions of HIV-1 (top) and the amino acid sequences of portions of p6^{Gag} protein and viral protease encoded by two different reading frames (bottom). The amino acid residues conserved in >98% of the majority HIV-1 subtypes (group M), which include subtypes A, B, C, D, F, G, H, and J and circulating recombinant forms (AE, AG, AGI, and AB) (HIV Sequence Database [http://hiv-web.lanl.gov]), are shown in large capital letters. The B subtype consensus sequences are shown in small capital letters. The nucleotide sequence of our interest is shown in open letters. PR, protease; RH, RNase H; INT, integrase.

tance to nucleases and proteases (24) and sequence-specific hybridization to DNA or RNA targets using Watson-Crick base pair formation (27) with much higher thermal stability than that of ODN (27, 28, 51).

Using a PNA oligomer as a prototype molecular tool, we explored viral sequences that were susceptible to PNA-mediated inhibition of gene expression and asked whether such sequences might be considered potential anti-HIV-1 genetic targets in the current study. Target sequences were selected from the previously less explored *gag-pol* gene, with a particular focus on the *pol* gene, as few studies have tried to directly block the expression of viral enzymes. In particular, we were interested in the protease-encoding sequence that begins upstream of the 3' end of the *gag-pol* transframe gene. Despite its extensive sequence variations, a short segment of sequence toward the 5' end of the viral protease-encoding gene, ACTC TTTGGCAACGA, which also encodes the C-terminal Vpr-binding motif of p6^{Gag} protein, LXXLFG, by a different reading frame (17, 68, 88), is highly conserved among various HIV-1 subtypes (Fig. 1). We hypothesized that nucleotide sequences of certain segments of the transframe domain must be invariably conserved if a single transcript has to encode critical amino acid sequences of two different proteins by a ribosomal frameshift, thus reducing the probability of escape mutants, and considered this particular sequence as one of the prime targets.

MATERIALS AND METHODS

PNA oligomers. Because of the propensity of PNA molecules to be confined within the cytoplasm (104) (also see below), we decided to focus on the antisense intervention, primarily targeting the translation of viral RNA, and designed 22 PNA oligomers, 14- to 15-mers in length, complementary to the site of our interest within the *gag-pol* transframe domain or other highly conserved regions within the *gag* and *pol* genes for the initial screening (Table 1). PNA oligomers were synthesized on the Expedite Nucleic Acid Synthesis System (PerSeptive Biosystems, Inc., Framingham, Mass.) by Research Genetics, Inc., Huntsville, Ala. Although all these PNA oligomers were easily dissolved in water, some oligomers, including PNA_{GAG1}, PNA_{GAG2}, PNA_{PR1}, PNA_{PR2}, PNA_{RT1}, PNA_{RT5}, PNA_{RT8}, and PNA_{INT3}, formed fine precipitates when added to the culture medium at higher concentrations, as has previously been reported (104). There was no discernible relationship between the precipitate formation and effects on cell growth or HIV-1 production (see below).

Evaluation of cellular uptake of PNA oligomers. H9 cells chronically infected with HIV-1_{LAI} (H9_{LAI}) were incubated with fluorescein-tagged PNA_{PR2},

PNA_{PR4}, or PNA_{RT2} at 10, 30, and 100 μ M in fresh RPMI 1640 complete medium supplemented with 13% fetal bovine serum (HyClone, Logan, Utah), 4 mM L-glutamine, 100 U of penicillin per ml, and 100 μ g of streptomycin per ml at 37°C in 5% CO₂-containing humidified air overnight. The cells were fixed with 2% paraformaldehyde and examined by fluorescence microscopy or by fluorescence-activated cell sorter analysis.

Assessment of effects of PNA oligomers on HIV-1 infection in various cell culture systems. H9_{LAI} cells or H9 cells chronically infected with another HIV-1 strain, HIV-1_{RF} (H9_{RF}), were extensively washed to remove previously produced virions and incubated in a 96-well culture plate at 10⁴ cells/well in 200 μ l of RPMI 1640 complete medium in the absence or presence of PNA oligomers at various concentrations. After 4 days in culture, supernatant was collected from each well and the level of p24 Gag antigen was determined by radioimmunoassay (RIA) (HIV-1 p24 RIA kit; NEN Life Science Products, Boston, Mass.). To compare the antiviral effects of PNA_{PR2} and PNA oligomers targeting the sequences proximate to the PNA_{PR2}-annealing site, H9_{LAI} cells were cultured as described above in the absence or presence of 100 μ M PNA_{PR2} or other PNA oligomers tested. The relative antiviral effects were computed from the following formula: (% p24 antigen suppression by a given PNA oligomer)/(% p24 antigen suppression by PNA_{PR2}). Each PNA oligomer was tested in triplicate. H9_{LAI} and H9_{RF} cells were also cultured in a six-well culture plate at 10⁵ cells/ml in the absence or presence of 30 to 100 μ M PNA_{PR2}. After 4 days, cells were counted by the trypan blue dye exclusion method and lysed at 10⁶ cells/ml in phosphate-buffered saline (PBS) containing 0.5% Triton X-100. The amounts of p24 antigen in the culture supernatant and cell lysate were measured by RIA. The experiments were repeated at least three times.

Phytohemagglutinin (PHA)-activated peripheral blood mononuclear cells (PBMC) obtained from healthy blood bank donors (2 \times 10⁶ cells/ml) were infected with seven MDR HIV-1 clinical isolates (151) in RPMI 1640 complete medium supplemented with 2.5 ng of recombinant human interleukin-2 (R&D Systems, Minneapolis, Minn.) per ml and cultured for at least 2 weeks or until the p24 antigen levels in the culture medium persistently exceeded 30 ng/ml. The PNA_{PR2}-targeting nucleotide sequence of the transframe domain of each isolate was consistent with the consensus B sequence. Freshly PHA-stimulated PBMC from healthy donors (2 \times 10⁶ cells/ml) were added to each culture flask every 3 to 4 days. PBMC (10⁶ cells/ml) infected with each MDR isolate were vigorously washed and cocultured with PHA-stimulated PBMC (10⁶ cells/ml) in 200 μ l of recombinant human interleukin-2-containing complete medium in the absence or presence of 10 to 60 μ M PNA_{PR2}. The number of infectious virions released after 7 days in culture was determined by an assay with multinuclear activation of a galactosidase indicator (MAGI assay) (see below) using an indicator cell line, MAGI-CCR5 cells (16) (AIDS Research and Reference Reagent Program, Division of AIDS, National Institute of Allergy and Infectious Diseases, contributed by Julie Overbaugh). All assays were performed in triplicate.

MT2 cells (10⁴ cells/ml) were exposed to 64 50% tissue culture infectious doses of HIV-1_{NL4.3} at 37°C for 1 h. After a vigorous virus washout, the cells were cultured in 200 μ l of RPMI 1640 complete medium at 37°C in 5% CO₂-containing humidified air in the absence or presence of various PNA oligomers at 100

TABLE 1. Sequences of PNA oligomers and locations of targeted genes relative to the HXB2 numbering system

PNA oligomer	Sequence (5'-3')	Position in HIV-1 genome
PNA _{Gag1}	CGCTCTCGACCCAT	790-804
PNA _{Gag2}	TCCTTGCTTGCCCAT	894-908
PNA _{Gag3}	TCATCATTTCTTCT	1818-1831
PNA _{PR1}	CCAAAGAGTGATTTT	2256-2270
PNA _{PR2}	TCGTTGCCAAAGAGT	2262-2276
PNA _{PR3}	ATCATCTGCTCCTGT	2328-2342
PNA _{PR4}	CCCCCTATCATTTT	2384-2398
PNA _{RT1}	TTTTACTGGTACAGT	2568-2582
PNA _{RT2}	CTGTCAATGGCCATT	2617-2631
PNA _{RT3}	ATTTTCAGGCCCAA	2698-2711
PNA _{RT4}	CTGTCTTTTTTCTTT	2738-2752
PNA _{RT5}	ATTGTAAGTATATCT	2976-2990
PNA _{RT6}	AATCATCCATGTATT	3094-3108
PNA _{RT7}	TGCTGCCCTATTCT	3128-3142
PNA _{RT8}	ATTGACAGTCCAGCT	3300-3314
PNA _{RH1}	TGTGCTGTACCCAT	4151-4165
PNA _{INT1}	TAGCCATTGCTCTCC	4285-4299
PNA _{INT2}	TCTACTTGTCCATGC	4379-4393
PNA _{INT3}	CTTCTGCTCAATTTT	4535-4549
PNA _{INT4}	CCCCCAATCCCTTT	4793-4807
PNA _{INT5}	AATTTTGAATTTT	4883-4896
PNA _{INT6}	TTGCTGGTCCCTTCC	4933-4947

μM . The amount of p24 antigen produced by the MT2 cells was determined by RIA on day 7. All assays were performed in triplicate.

COS-7 cells were transfected with 1 μg of pNL4-3 by FuGENE 6 transfection reagent (Boehringer Mannheim, Indianapolis, Ind.) in a six-well culture plate (35-mm diameter) for 5 h, immediately followed by incubation in Dulbecco's modified Eagle medium (DMEM) supplemented with 13% fetal bovine serum (HyClone), 4 mM L-glutamine, 100 U of penicillin per ml, and 100 μg of streptomycin per ml in the absence or presence of 100 μM PNA_{PR2}. After 48 h, cells and supernatants were harvested from each sample and evaluated for viral protein expression and virion production. HLTat cells (AIDS Research and Reference Reagent Program; contributed by Barbara K. Felber and George Pavlakis) were transfected with 1 μg of p55M1-10 (kindly provided by George Pavlakis, National Cancer Institute-Frederick Cancer Research and Development Center) by FuGENE 6 transfection reagent (Boehringer Mannheim) for 5 h, immediately followed by incubation in complete DMEM in the absence or presence of 100 μM PNA_{PR2}. After 24 h, HLTat cells were lysed for Western blot analysis.

MAGI assay. The MAGI assay was employed to determine the number of newly produced virion particles in the culture supernatant of HIV-1-infected cells as described previously (65). Briefly, the HeLa-CD4-long terminal repeat- β -galactosidase indicator cells were plated in a 96-well tissue culture plate at 10^4 cells per well, each well containing 125 μl of complete DMEM, 24 h prior to the assay. On the following day, the cells were generally 20 to 30% confluent. The cells were washed with 200 μl of Opti-MEM (Life Technologies, Inc., Rockville, Md.) twice and then exposed to serially diluted infectious culture supernatants in a total volume of 30 μl per well in the presence of 20 μg of DEAE-dextran (Sigma, St. Louis, Mo.) per ml. The infectious titers of the supernatants from PHA-PBMC infected with MDR isolates were examined with the MAGI-CCR5 indicator cell line (16), using 30 or 60 μl of inoculum. After the plates were incubated at 37°C in 5% CO₂-containing humidified air for 2 h, 140 μl of complete DMEM was added to each well. The plates were incubated for another 46 h, followed by fixation at room temperature with 1% formaldehyde and 0.2% glutaraldehyde in PBS for 5 min. The cells were then washed with PBS and incubated in 100 μl (per well) of staining solution containing 4 mM potassium ferrocyanide, 4 mM potassium ferricyanide, 2 mM MgCl₂, and 0.4 mg of X-Gal (5-bromo-4-chloro-3-indolyl- β -D-galactopyranoside) per ml. The blue cells were counted under a microscope.

Electron microscopy. Electron microscopic examination was performed as previously described (38). Briefly, the harvested cells were centrifuged at 1,500 \times g for 5 min. The cell pellets were fixed in 1.25% glutaraldehyde and then in 1% osmium, dehydrated in graded alcohol, and embedded in pure epoxy resins. Thin sections (60 nm) were stained with uranyl acetate and lead citrate and stabilized by carbon evaporation for an examination.

RNA analysis. The culture supernatant was subjected to microcentrifugation at 32,800 \times g for 2 h to pellet virions (35, 142). Pelleted virion particles were subjected to RNA extraction as previously described (6), followed by reverse transcriptase PCR (RT-PCR) with a primer pair, SK38-SK39 (128, 129), to estimate the amount of virion-derived RNA. The harvested cells were subjected to RNA extraction as previously described (129) followed by RT-PCR using two primer pairs, SK38-SK39 (128, 129) and BSS-KPNA (102, 124), in order to evaluate the levels of unspliced and singly spliced HIV-1 RNA, respectively.

Western blot analysis. The virion particles pelleted from the culture supernatant (see above) were lysed in viral lysis buffer (10 mM Tris [pH 7.4], 1 μM EDTA, 0.02% NP-40). The harvested cells were washed in PBS and lysed in cell lysis buffer (10 mM Tris [pH 7.4], 50 mM NaCl, 100 mM KCl, 1 mM EDTA, 1% NP-40, 1 mM phenylmethanesulfonyl fluoride) at 2×10^7 cells/ml at 4°C for 30 min, followed by centrifugation at 13,800 \times g to remove cell debris. Protein concentrations of the cell lysates were determined with the bicinchoninic acid protein assay kit (Pierce, Rockford, Ill.). Virion-associated protein derived from 100 μl of supernatant and 2 to 25 μg of cellular protein were resolved by electrophoresis on sodium dodecyl sulfate-4 to 12% polyacrylamide gradient gels (Novex, San Diego, Calif.) under reducing conditions, followed by electrophoretic transfer onto a polyvinylidene difluoride membrane (Novex). The HIV-1 Gag proteins were visualized by a chemiluminescence detection system (Amersham Pharmacia Biotech, Inc., Piscataway, N.J.) using anti-p24^{Gag} antiserum (Advanced Biotechnologies, Inc., Columbia, Md.) (2 μg of cellular protein per lane loaded for this antibody), anti-p17^{Gag} monoclonal antibody (Advanced Biotechnologies, Inc.) (2 μg of protein per lane), and anti-p6^{Gag} antiserum (kindly provided by Louis E. Henderson, National Cancer Institute-Frederick Cancer Research and Development Center) (5 μg of protein per lane). For the evaluations of *pol* gene products, antiprotease antiserum (kindly provided by Louis E. Henderson), (25 μg of protein loaded per lane) and anti-p66^{RT} monoclonal antibody (AIDS Research and Reference Reagent Program; contributed by Paul Yoshihara) (15 μg of protein per lane) were employed. For a resolution of anti-p66^{RT} antibody-reactive proteins, sodium dodecyl sulfate-10% polyacrylamide gel electrophoresis was used instead of a 4 to 12% gradient gel. The anti-p66^{RT} antibody is reactive with the p66^{RT} but not the p51^{RT} band by Western blot analysis (NIH AIDS Research and Reference Reagent Program Catalog). Anti-gp120 antiserum (AIDS Research and Reference Reagent Program; contributed by Margarita Quiroga) (10 μg of protein loaded per lane) was used to evaluate the amount of *env* gene product expressed in HIV-1-infected cells.

Peptide ELISA. The affinity of rabbit anti-p6^{Gag} antiserum (kindly provided by Louis E. Henderson) for a series of HIV-1 HXB2 (subtype B) Gag synthetic peptides, 441–458 (YKGRPGNLFQSRPEPTAP), 451–470 (SRPEPTAPPEESF RSGVETT), 459–479 (PEESFRSGVETTPPKQOEPI), 470–489 (TTPPKQK EPIDKELYPLTSL), and 480–500 (DKELYPLTSLRSLFGNDPSSQ) (obtained through AIDS Research and Reference Reagent Program), which encompassed the entire p6^{Gag} domain, was determined by enzyme-linked immunosorbent assay (peptide ELISA). Briefly, 96-well plates were coated with serially diluted Gag peptides (9.8 to 2,500 ng/well) in triplicate. Anti-p6^{Gag} antiserum diluted 1:500 was incubated in the peptide-coated plates for 90 min at room temperature. After washing, horseradish peroxidase-labeled anti-rabbit secondary antibody was added to each well, followed by the peroxidase substrate. The antibody affinity for each peptide was determined by the optical density (OD) at 405 nm.

RESULTS

Cellular uptake of PNA and its intracellular localization.

First, in order to determine concentrations of PNAs required to achieve a sufficient cellular delivery in tissue culture, H9_{LAI} cells were incubated with fluorescein-tagged PNA at 10 to 100 μM . We elected to deliver PNA by simply adding it to the culture medium, thus relying on endocytosis (42, 104, 131) rather than the microinjection technique commonly adopted in the previous studies (10, 45, 104). After an overnight incubation, H9_{LAI} cells were examined under a fluorescence microscope. A clear fluorescent signal was demonstrated in the majority of cells incubated with PNA at ≥ 30 μM compared to untreated H9_{LAI} cells (Fig. 2A to C), albeit the signal was virtually confined to the cytoplasm, as has previously been reported (104) (Fig. 2D). The fluorescence intensity increased in a dose-dependent manner as demonstrated by fluorescence-activated cell sorter analysis regardless of the sequences tested (Fig. 2E).

PNA_{PR2} targeting the 3' end of the transframe domain, decreases extracellular virion production while increasing intracellular concentration of Gag protein in HIV-1-infected cells. Preliminary effects of various PNA oligomers were evaluated in chronically HIV-1-infected H9_{LAI} cells. While the majority of PNA oligomers, all tested at 100 μM , exhibited virtually no antiviral effect, PNA_{PR2} reduced the HIV-1 p24 antigen production in the culture supernatant by up to 98.4% (Fig. 3A). This p24-inhibitory effect of PNA_{PR2} appeared to be dose dependent in H9_{LAI} as well as in H9_{RF} cells (Fig. 3B) and specific to the PNA_{PR2}-targeting region, as shifting the target sequence by two or more nucleotides upstream or downstream resulted in a more than 50% decrease in the inhibitory effect (Fig. 3C). Significant inhibition of p24 by PNA_{PR2} was also observed in MT2 cells acutely infected with HIV-1_{NL4-3} (inhibition of $[99.6 \pm 0.4] \%$ [mean \pm standard deviation (SD) of triplicate values]) compared to untreated HIV-1-infected MT2 cells. Similarly, PNA_{PR2} reduced infectious virion production from PBMC infected with clinical MDR isolates, originally isolated from extensively pretreated patients (151), by 97.3 to 99.4% (Table 2). These data suggested a potential antiviral effect of PNA_{PR2} against a broad spectrum of HIV-1 strains.

In contrast to a marked decrease in the supernatant p24 antigen levels, the amount of intracellular p24 antigen was increased in H9_{LAI} cells treated with 30 or 60 μM PNA_{PR2} (Fig. 3D) with moderately reduced cell numbers at the time of harvest. Comparable results were obtained in other experiments, in which PNA_{PR2} was tested up to 100 μM . Percent cell growth of H9_{LAI} cells incubated with 60 to 100 μM PNA_{PR2} ranged from 68.3 to 78.1% (mean \pm SD, $[73.9 \pm 5.1] \%$). Similar degrees of impaired cell growth were observed in H9_{RF} as well as uninfected H9 cells incubated with up to 100 μM PNA_{PR2}, while other PNA oligomers had no effect on cell proliferation in H9_{LAI}, H9_{RF}, or uninfected H9 cells (data not shown). These findings suggested that the impaired cell growth

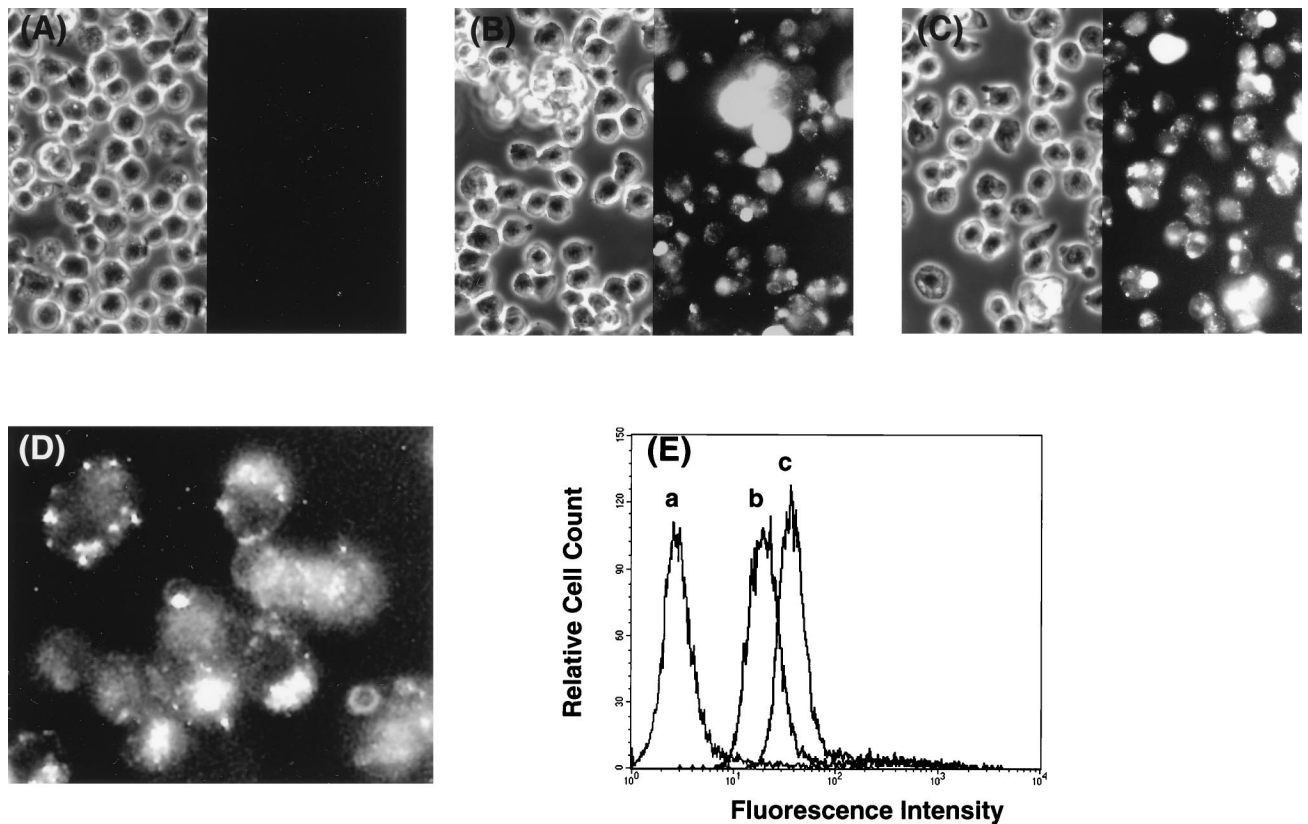


FIG. 2. Cellular uptake of PNA. (A to C) Chronically HIV-1-infected H9_{LAI} cells were incubated with fluorescein-tagged PNA at various concentrations overnight, fixed with 3.7% formaldehyde for 20 min, washed and resuspended in PBS, and examined by fluorescence microscopy. Shown are the cells incubated with 0 (A), 30 (B), and 60 (C) μ M fluorescein-tagged PNA_{PR2}. Note that the cells treated with fluorescein-tagged PNA_{PR2} were resuspended in a slightly larger volume of PBS than was the untreated control so that each cell could be clearly visualized. The panel on the right-hand side is the fluorescence image, and that on the left is the phase-contrast image of the same field. The discernible fluorescent signal was seen in the majority of cells at 30 μ M PNA or greater. (D) Shown at a higher magnification are the cells incubated with 30 μ M PNA_{PR2}. Note that the fluorescent signal is virtually confined to the cytoplasm. (E) H9_{LAI} cells incubated with fluorescein-tagged PNA were also evaluated by fluorescence-activated cell sorter analysis. Curves a, b, and c represent H9_{LAI} cells incubated with 0, 30, and 60 μ M fluorescein-tagged PNA_{PR2}, respectively. Similar results were obtained with fluorescein-tagged PNA_{PR4} and PNA_{RT2}.

was specific to PNA_{PR2}-targeted sequence intervention and may have resulted from an accumulation of p24 Gag protein within the cytoplasm and/or a down-modulation of certain host proteins that have yet to be identified, rather than from general toxicity of the PNA molecules.

Next, the processes of virion morphogenesis and virion release from the cell surface were examined by electron microscopy. Treatment with PNA_{PR2} appeared to hinder the steps of virion assembly, unlike protease inhibitors, which halt the process of virion morphological maturation. For 100 cells surveyed within one 60-nm thin section, the estimated average number of HIV-1 virions formed and released from the cells was reduced to less than two per sectioned cell (62 cells with no virion and 38 cells with less than five virions per cell) in PNA_{PR2}-treated H9_{LAI} cells compared to 10 to 15 virions per sectioned cell in untreated H9_{LAI} cells, while there were no apparent changes in virion morphology (Fig. 4).

PNA_{PR2} blocks production of Pr160^{Gag-Pol} polyprotein and induces excessive intracellular cleavage of Pr55^{Gag}. To determine the mechanism(s) of virion assembly inhibition by PNA_{PR2}, H9_{LAI} cells cultured in the presence of 30 to 100 μ M PNA_{PR2} were evaluated for viral protein expression and virion production. Consistent with the preliminary results, the level of p24 antigen production and the amount of pelletable virions were significantly reduced in the supernatant of PNA_{PR2}-treated cells compared to the untreated control (Fig. 5A). The

amounts of intracellular HIV-1 unspliced and singly spliced RNA transcripts were comparable between PNA_{PR2}-treated and untreated cells (Fig. 5A), indicating that PNA_{PR2} did not interfere with the transcription of the HIV-1 genome. Strikingly, Western blot analysis with anti-p24^{Gag} antibody demonstrated that PNA_{PR2}-treated H9_{LAI} cells contained predominantly p24 Gag protein with Gag precursor Pr55^{Gag} markedly reduced and Pr160^{Gag-Pol} virtually undetectable within the cells (Fig. 5A).

In order to further examine the expression and subsequent proteolytic processing of Gag protein in PNA_{PR2}-treated cells, H9_{LAI} cells were cultured with an HIV-1 protease inhibitor, indinavir, in addition to PNA_{PR2}. The combination of indinavir and PNA_{PR2} resulted in a reduction of intracellular p24 and p17 Gag proteins and the reappearance of Pr55^{Gag} protein, but not Pr160^{Gag-Pol} (Fig. 5B). Because the PNA_{PR2}-targeting site was near the 3' end of the p6^{Gag}-encoding region, the proteolytic processing of Pr55^{Gag}, also a precursor of p6^{Gag} protein, was examined by Western blot analysis with anti-p6^{Gag} antibody. The peptide ELISA demonstrated that the anti-p6^{Gag} antibody was most reactive to the peptide 480–500, which corresponds to the C-terminal domain of p6^{Gag} protein, with the ODs linearly increasing from 0.303 ± 0.095 to 1.468 ± 0.052 (mean \pm SD of triplicate values) in detecting 9.8 to 625 ng of the peptide per well, followed by the peptide 451–470, with ODs ranging from 0.212 ± 0.064 to 0.595 ± 0.067 . The affin-

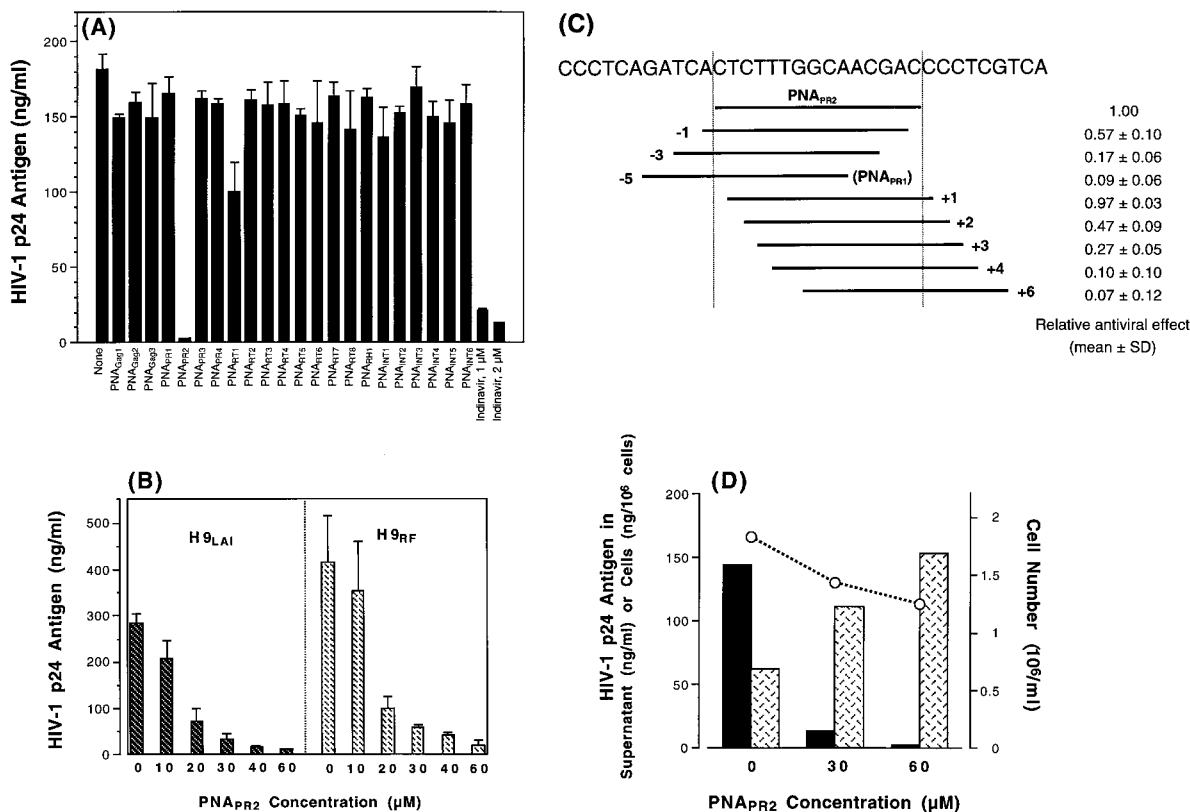


FIG. 3. Effects of PNA oligomers on HIV-1 production in chronically HIV-1-infected cells. (A) Levels of p24 antigen in the supernatants of H9_{LAI} cells cultured in the absence or presence of various PNA oligomers used at a 100 µM concentration. All compounds were tested in triplicate, and the values shown are means with SDs. The p24 antigen level in a supernatant of H9_{LAI} treated with an HIV-1 protease inhibitor, indinavir, is shown as a reference. (B) Levels of p24 antigen in the supernatants of H9_{LAI} and H9_{RF} cells cultured in the absence or presence of various concentrations of PNA_{PR2}. Each dose was tested in triplicate. The values shown are means with SDs. (C) The degrees of inhibition of p24 antigen production in H9_{LAI} cells cultured with 100 µM PNA_{PR2} or other PNA oligomers targeting the sequences proximate to the PNA_{PR2}-annealing site were compared. Each PNA oligomer was tested in triplicate. The values shown are relative antiviral effects (means ± SDs). (D) Amounts of p24 antigen in the supernatant (solid bars) and cell lysate (crosshatched bars) of H9_{LAI} cells cultured in the absence or presence of 30 and 60 µM PNA_{PR2}. The cell numbers are indicated by circles. The experimental results shown are representative of three separate experiments.

ities to the other three peptides were negligible. Western blot analysis with the anti-p6^{Gag} antibody could detect p6^{Gag} protein in the HIV-1 virions (data not shown and reference 106) as well as its precursor (Pr55^{Gag}) in the cell lysate of untreated H9_{LAI} cells (Fig. 5B). This p6^{Gag} antibody also demonstrated the p6^{Gag}-containing intermediate (p15) in the lysate of untreated H9_{RF} cells (data not shown). Notably, the cell lysate of H9_{LAI} treated with 60 µM PNA_{PR2} contained virtually no Pr55^{Gag} protein which could be detected by the anti-p6^{Gag} antibody, even with the addition of a protease inhibitor, indinavir, while the anti-p24 antibody readily recognized Pr55^{Gag} in the same lysate (Fig. 5B), indicating that the Pr55^{Gag} expressed in PNA_{PR2}-treated cells had insufficient binding determinants for the anti-p6^{Gag} antibody. We then examined the effects of PNA_{PR2} on the expression of Pr55^{Gag} protein in HLTat cells (32, 127) transfected with the Gag expression plasmid p55M1-10, in which Pr55^{Gag} was not expected to be cleaved by the viral protease, as p55M1-10 contained solely the *gag* reading frame (126). While Western blot analysis with anti-p24^{Gag} antibody demonstrated Pr55^{Gag} protein in both untreated and PNA_{PR2}-treated cells, the band intensity of anti-p6^{Gag} antibody-reactive Pr55^{Gag} was significantly diminished in PNA_{PR2}-treated HLTat cells (Fig. 5C).

These data suggested that PNA_{PR2} treatment could induce the truncation of Pr55^{Gag} toward the C terminus of p6^{Gag},

presumably by disrupting a translation of the *gag* reading frame at its site of binding to the target mRNA in HIV-1-infected cells. It is also possible that PNA_{PR2} effectively blocked the translation of the *gag-pol* reading frame, resulting in generation of truncated Pr160^{Gag-Pol}, namely, Pr55^{Gag} with p6^{Pol} which could not be detected by the anti-p6^{Gag} antibody. Thus, the intracellular Gag precursor protein in PNA_{PR2}-treated

TABLE 2. HIV-1 virion production from PHA-PBMC infected with clinical MDR isolates and cultured in the absence or presence of 60 µM PNA_{PR2}

MDR isolate no.	Result of MAGI-CCR5 assay ^a	
	No PNA _{PR2}	60 µM PNA _{PR2}
1	467.7 ± 138.6	12.7 ± 4.2 (97.3)
2	486.7 ± 112.0	4.7 ± 5.5 (99.0)
3	210.0 ± 16.10	1.3 ± 0.6 (99.4)
4	589.7 ± 32.10	7.7 ± 4.2 (98.7)
5	214.0 ± 142.6	5.7 ± 1.5 (97.4)
6	219.7 ± 25.20	3.7 ± 1.5 (98.3)
7	208.3 ± 96.70	2.0 ± 1.0 (99.0)

^a Results are shown as the mean numbers ± SDs of blue cells per well. Values in parentheses are the mean percent reductions.

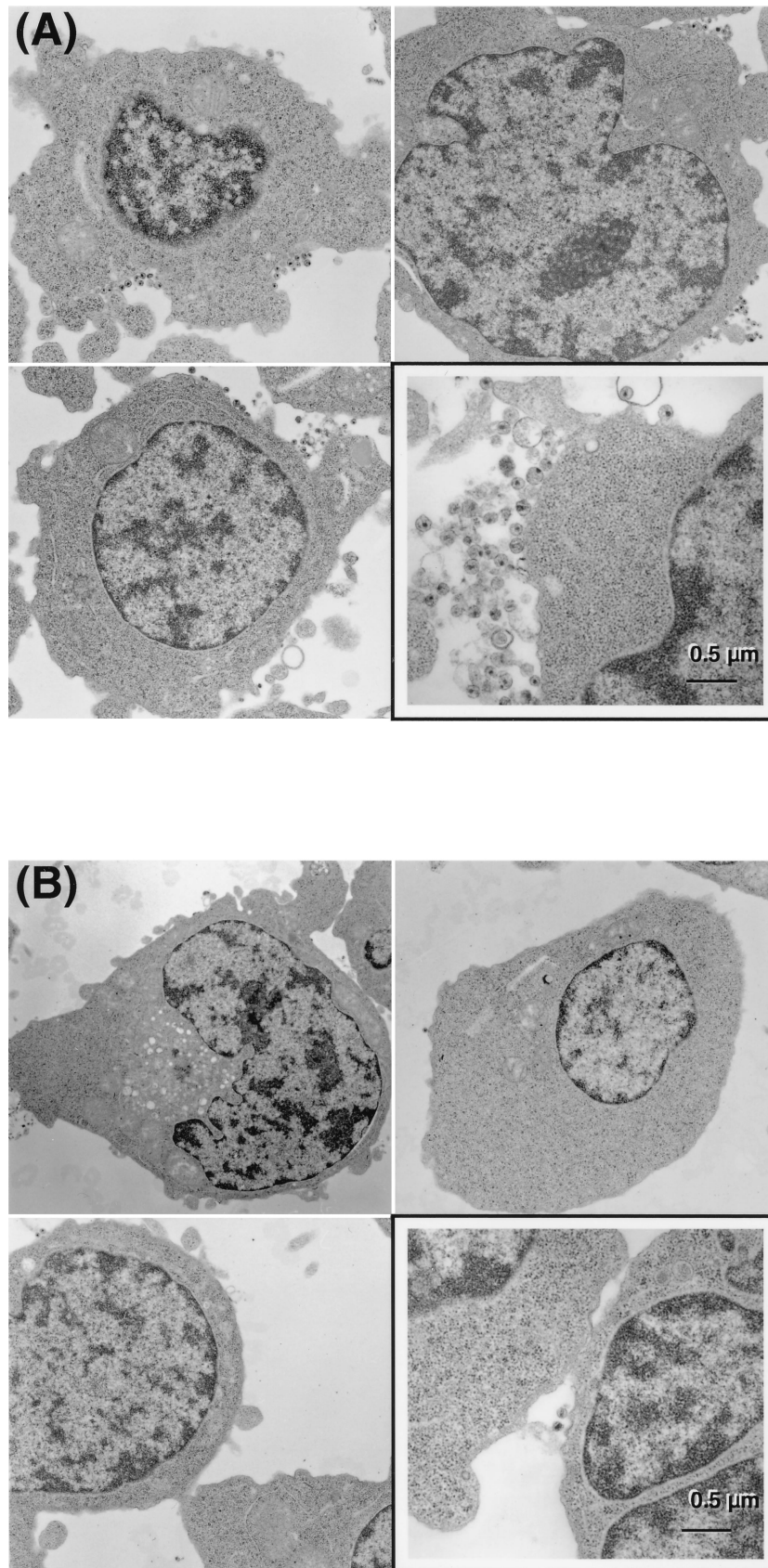


FIG. 4. Electron microscopy of H9_{LAI} cells cultured in the absence (A) or presence (B) of 60 μM PNA_{PR2}. Shown are representatives of 100 cells surveyed in each sample (magnification, ×13,500). Virions are shown at a higher magnification (×54,000) in each inset on the right-hand side at the bottom.

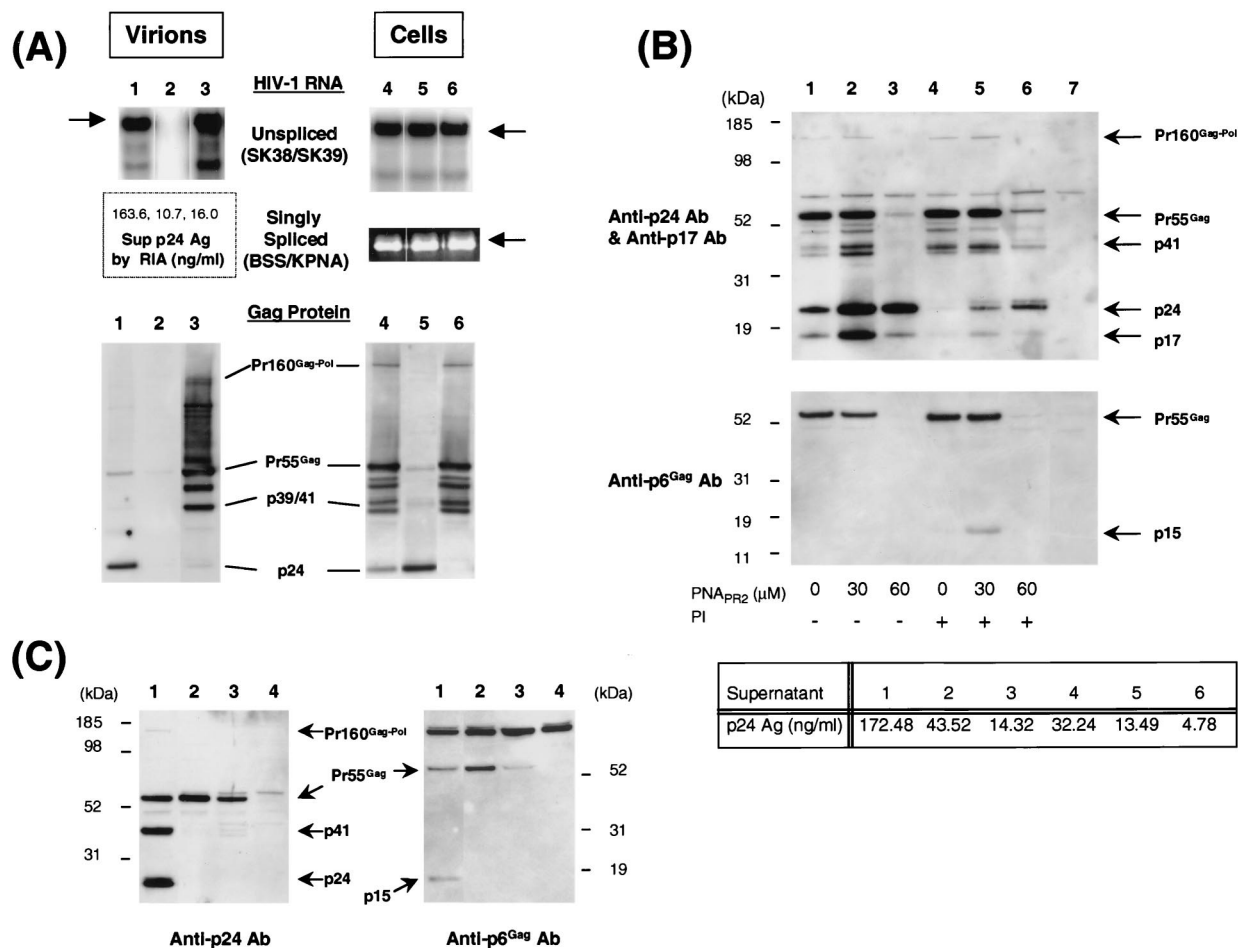


FIG. 5. Effects of PNA_{PR2} on Gag-Pol expression and virion production in HIV-1-infected cells (A and B) and on Gag protein expression in HLTat cells transfected with the Gag expression plasmid p55M1-10 (C). (A) The amounts of viral RNA in the culture supernatant (pelleted virion derived) (lanes 1 to 3) and in the cells (lanes 4 to 6) were evaluated by RT-PCR (top). Arrows indicate the pertinent PCR products for each primer pair. The virion-derived Gag protein in the culture supernatant (lanes 1 to 3) and intracellular Gag protein processing (lanes 4 to 6) were evaluated by Western blot analysis using anti-p24^{Gag} antibody (bottom). Shown are the positions of Pr160^{Gag-Pol}, Pr55^{Gag}, p41, and p24 Gag proteins. Lanes of each gel represent H9_{LAI} cells cultured alone (lanes 1 and 4) or incubated with 100 μM PNA_{PR2} (lanes 2 and 5) and 2 μM indinavir (lanes 3 and 6). (B) Western blot analyses with anti-p24^{Gag} antibody and anti-p17^{Gag} antibody (top) and with anti-p6^{Gag} antibody (bottom) of cell lysates processed from H9_{LAI} cells cultured alone (lane 1) or in the presence of 30 μM PNA_{PR2} (lane 2), 60 μM PNA_{PR2} (lane 3), 2 μM indinavir alone (lane 4), 30 μM PNA_{PR2} plus 2 μM indinavir (lane 5), or 60 μM PNA_{PR2} plus 2 μM indinavir (lane 6). Cell lysate of uninfected H9 cells is shown in lane 7. PI - or + represents the absence or presence of a protease inhibitor, indinavir, respectively. The level of p24 antigen in each culture supernatant is indicated at the bottom. (C) Western blot analyses with anti-p24^{Gag} antibody (left) and anti-p6^{Gag} antibody (right) of cell lysates processed from HLTat cells transfected with pHXB2-based plasmid pSUM9 (136) (lanes 1) or with p55M1-10 and cultured alone (lanes 2) or in the presence of 100 μM PNA_{PR2} (lanes 3). The cell lysate of mock-transfected HLTat cells is included as a reference (lanes 4). Sup, supernatant; Ag, antigen; Ab, antibody.

cells appeared to be predominantly Pr55^{Gag} lacking the full-size p6^{Gag} protein, which was excessively cleaved to the final products by a certain amount of viral protease.

PNA_{PR2} reduces synthesis of viral protease as well as triggering its premature activation. We then asked whether preexisting viral protease at the beginning of H9_{LAI} cell culture subsequently influenced the proteolytic processing of the viral protein. To this end, nonpermissive COS-7 cells were transfected with an infectious HIV-1 molecular clone, pNL4-3, immediately followed by incubation with 100 μM PNA_{PR2} in tissue culture. Virion production was significantly suppressed in PNA_{PR2}-treated COS-7 cells as demonstrated by the reduced p24 antigen level and the decreased number of infectious virion particles in the culture supernatant determined by the MAGI assay (65). The intracellular Gag protein was predominantly p24 and p17 with significantly decreased amounts of Pr55^{Gag} and virtually undetectable Pr160^{Gag-Pol} as

observed in chronically HIV-1-infected H9 cells (Fig. 6A). Consistent with the decreased quantity of full-size Pr160^{Gag-Pol}, the amount of intracellular viral protease was reduced in PNA_{PR2}-treated cells compared to untreated control (Fig. 6B). It should be noted that the antiprotease antibody that we employed in the current study detected a monomeric form of viral protease, not a homodimer, an active form of viral protease (112, 146). The latter is known to continually undergo autodegradation as it is being activated (123, 135). Thus, the amount of intracellular monomeric viral protease may not necessarily reflect the total amount of active viral protease within the cytoplasm but may simply correlate with the amount of precursor polyprotein. These results strongly suggested that the disrupted translation of *gag-pol* mRNA induced by PNA_{PR2} subsequently led to a premature activation of viral protease, albeit synthesized in probably a much smaller quantity than untreated control, resulting in an excessive intracel-

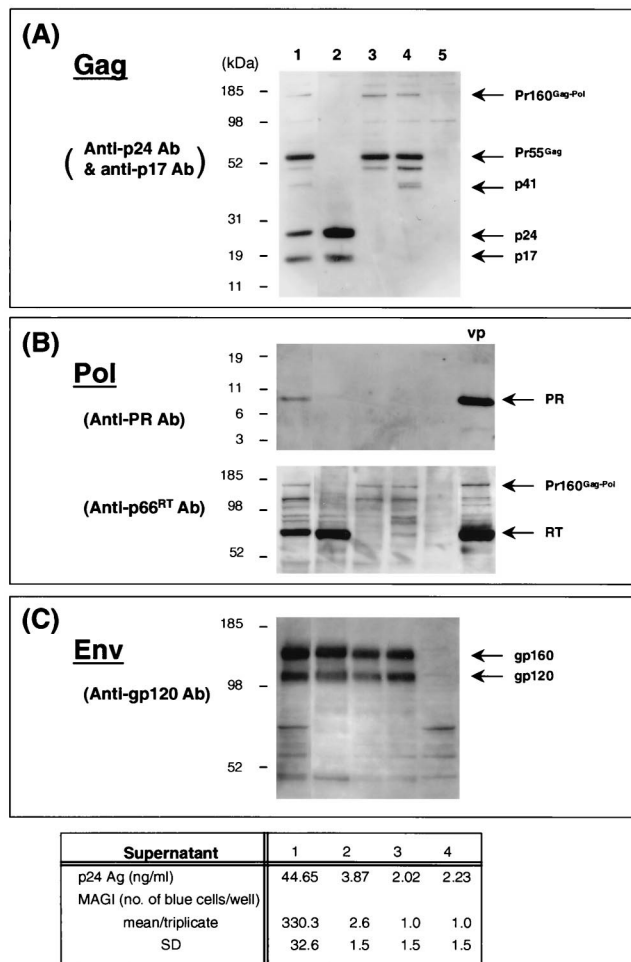


FIG. 6. Effects of PNA_{PR2} on *gag*, *pol*, and *env* gene expression and virion production in COS-7 cells transfected with an infectious HIV-1 molecular clone, pNL4-3. Shown are results of Western blot analyses with anti-p24^{Gag} antibody and anti-p17^{Gag} antibody (A), antiprotease antibody and anti-p66^{RT} antibody (B), and anti-gp120 antibody (C) of pNL4-3-transfected COS-7 cells cultured with no drug (lanes 1), 100 μ M PNA_{PR2} (lanes 2), 1 μ M saquinavir (also a protease inhibitor) (lanes 3), or 3 μ M indinavir (lanes 4). The cell lysate of mock-transfected COS-7 cells is shown in lanes 5. Viral lysate from pelleted virion particles (vp) is included in the Western blot analyses for the *pol* gene products as a reference. The levels of p24 antigen in supernatant and the infectious titers determined by MAGI assay are shown at the bottom. Ab, antibody; Ag, antigen.

lular cleavage of the Gag protein and an impairment of HIV-1 virion morphogenesis.

Interestingly, the amount of another *pol* gene product, RT, appeared to be disproportionately high compared to the low-level expression of its precursor, Pr160^{Gag-Pol} polyprotein, in PNA_{PR2}-treated cells. Western blot analysis using a monoclonal antibody against p66^{RT}, which also recognizes the precursor (p160) and several intermediates, but not p51^{RT} (NIH AIDS Research and Reference Reagent Program Catalog, 1998), clearly demonstrated p66^{RT} in both untreated and PNA_{PR2}-treated cells (Fig. 6B). However, the cell lysate of PNA_{PR2}-treated COS-7 cells contained fewer precursor intermediates, smaller than 100 kDa in size (Fig. 6B). These data suggested that, in PNA_{PR2}-treated cells, the translation of *gag-pol* mRNA may have been reinitiated at the appropriate AUG codon located downstream of the PNA_{PR2}-targeting site by the mechanism described previously as ribosomal leaky scanning (71, 74, 75). A consensus sequence for the efficient initiation of

translation by eukaryotic ribosomes has been reported as xx-PuuxAUGG with a purine (Pu) in the -3 position (three nucleotides upstream of the AUG codon) having a dominant effect (70, 72, 73). The potential AUG codons downstream of the PNA_{PR2}-annealing site were identified at various positions, including 2358 to 2360 (GAAAUGA), 2388 to 2390 (AAAAUGA), 2595 to 2597 (GGAAUGG), and 2670 to 2672 (GAG AUGG) of the HIV-1 HXB2 genome, preserving the amino acid sequence of the remaining Pol. If the translation is internally initiated at the sites listed above, resulting Pol proteins will be approximately 103.7, 102.5, 95.2, and 92.3 kDa, respectively. These Pol proteins may be cleaved by viral protease expressed in *trans* or by host proteases (34, 87). A similar pattern of p66^{RT} expression was also observed in chronically infected H9 cells, and the addition of a viral protease inhibitor, indinavir, to PNA_{PR2} did not restore detection of the full-size precursor p160 (data not shown). Expression of HIV-1 Env was not affected by PNA_{PR2} in either COS-7 cells transfected with pNL4-3 (Fig. 6C) or chronically infected H9 cells (data not shown).

DISCUSSION

The introduction of protease inhibitors (55–57, 63, 77, 121) to conventional RT inhibitor-based antiretroviral therapy (23, 46, 95–97, 149, 150) has induced unprecedented degrees of viral load reduction and a recovery of CD4⁺ T-lymphocyte counts even in patients with advanced HIV-1 disease (20, 22, 43, 44, 91, 125). Substantial declines in AIDS incidence and death observed in the United States and other industrialized countries for the past 2 years have also been attributed to this improved treatment regimen (1, 15), often referred to as highly active antiretroviral therapy. While RT inhibitors, which block *de novo* HIV-1 infection of uninfected cells, have no control over production of virions from HIV-1-infected cells, protease inhibitors actively exert their effect in infected cells, driving them to release noninfectious immature virions and thereby preventing the spread of HIV-1. Dramatic effects of highly active antiretroviral therapy on individual cases of HIV-1 infection as well as on the global AIDS epidemic, although they may possibly be short-lived, underscore the importance of targeting the existing HIV-1 reservoir (HIV-1-infected cells) to better control HIV-1 disease, rather than simply providing protective shields for uninfected cells.

In the current study, we attempted to identify the viral gene sequences that were not only critical for the virion production but also accessible to gene-intervening molecules in chronically HIV-1-infected, provirus-laden cells. We showed that PNA_{PR2}, which is complementary to a region of the viral *gag-pol* mRNA sequence near the 3' end of the transframe domain, encoding protease residues 4 to 8 and the C-terminal Vpr binding motif of p6^{Gag} protein, can effectively interrupt a translation of *gag-pol* mRNA. The disrupted translation of *gag-pol* mRNA at the PNA_{PR2}-annealing site gave rise to Pr55^{Gag} as a predominant Gag precursor, which lacked a full-length p6^{Gag} protein due to a C-terminal truncation of p6^{Gag} and/or production of Pr55^{Gag} containing p6^{Pol} protein. The arrest of *gag-pol* mRNA translation by PNA_{PR2} was not complete, thereby permitting a synthesis of a small quantity of full-size Pr160^{Gag-Pol} polyprotein, which was presumably processed to viral protease.

Despite the small amount of viral protease synthesized in PNA_{PR2}-treated cells, Gag precursors were almost entirely cleaved to the final products of p24 and p17 within the cytoplasm. These seemingly counterintuitive findings prompted us to examine the intracellular expression profiles of viral protease. The Western blot analysis of cell lysate with antiprotease

antibody demonstrated a significantly decreased amount of monomeric viral protease in PNA_{PR2}-treated COS-7 cells transfected with an HIV-1 molecular clone compared to untreated control, whereas an active form of homodimeric viral protease (112, 146) could not be visualized in either PNA_{PR2}-treated or untreated cells, probably because the homodimer had undergone autolysis as it was being activated (123, 135). It has previously been reported that the level of viral protease activity required to properly process the precursor proteins may be reduced by 4- to 50-fold, below which a limited amount of proteolytic processing can still be demonstrated (122). Therefore, it would not have been surprising to see some degree of Gag precursor processing in PNA_{PR2}-treated cells even if the actual quantity of active viral protease had been significantly decreased. However, the extent of intracellular Gag precursor cleavage observed in PNA_{PR2}-treated cells notably exceeded that in the untreated control, resulting in a significant accumulation of p24 and p17 within the cells. These data strongly suggested that the rate or timing of protease activation was markedly accelerated within the cytoplasm of PNA_{PR2}-treated cells.

The impact of PNA_{PR2}-mediated translation arrest of *gag-pol* mRNA seems to be severalfold. Not only did it impede the synthesis of full-size Pr160^{Gag-Pol}, leading to decreased production of viral protease, but it also appeared to trigger the premature activation of viral protease, resulting in excessive and untimely intracellular cleavage of Gag proteins and significantly reduced virion production. In HIV-1, approximately 5 to 10% of *gag-pol* mRNA translational events are mediated by -1 ribosomal frameshifting to produce Pr160^{Gag-Pol} precursor polyprotein (52, 143), which is eventually incorporated into viral particles to provide viral protease, RT, and integrase. This delicately balanced synthesis of Pr55^{Gag} and Pr160^{Gag-Pol} and their intermolecular association are believed to play a critical role in coordinating sequential events of virion assembly and release. The final stages of virion morphogenesis begin with the interaction of Pr55^{Gag} and Pr160^{Gag-Pol} polyprotein (80, 81, 108, 133), which then attach to the plasma membrane of host cells (13, 41, 116). Viral protease embedded in Pr160^{Gag-Pol} remains inactive until Gag and Gag-Pol precursors reach the plasma membrane, where precursor protein processing and virion assembly are initiated upon activation of the viral protease, followed by the budding and completion of virion maturation (58). Although viral protease-mediated precursor cleavage may take place within the cytoplasm (13, 41, 59), the membrane-associated precursor processing and assembly events must occur in a regulated sequence in order for the infectious virions to be released (58).

Excessive intracellular processing of Gag precursor proteins without concomitant extracellular production of mature virions as induced by PNA_{PR2} has also been observed in a number of other conditions, including (i) sole expression of Pr160^{Gag-Pol} encoded in a single reading frame and thus lacking p6^{Gag} (60, 109), (ii) p6^{Gag}-deletion or -truncation HIV-1 molecular clones (40, 49, 152), and (iii) HIV-1 molecular clones containing p6^{Gag} with mutated Vpr-binding motifs (49, 152). Notably, inactivation of the viral protease induced by mutational changes could restore the production of virions, albeit immature virions, in the p6^{Gag}-deletion HIV-1 provirus-containing cells (49). These data suggest that the majority of viral protease may be prematurely released from the precursors and activated in the absence of fully functional p6^{Gag}. How p6^{Gag} protein exerts such a regulatory effect on viral protease has yet to be determined. It is possible that p6^{Gag} may actively participate in the process of intermolecular association of Pr55^{Gag} and Pr160^{Gag}, in addition to the major homology domain of capsid protein (48, 134), such that the release of

viral protease occurs in a coordinated fashion at the plasma membrane. Whether the binding of Vpr to p6^{Gag} plays any role in regulating the processes of Gag and Gag-Pol precursor association and subsequent protease activation is unclear, since some studies have shown that a deletion of Vpr had no effect on viral infectivity or replication (3, 37).

In the current study, we could not determine whether the Pr55^{Gag} synthesized in the PNA_{PR2}-treated cells was the product of the *gag* reading frame and thus contained C-terminally truncated p6^{Gag} or was predominantly the product of the *gag-pol* reading frame and had p6^{Pol} protein. It is conceivable that the antisense PNA oligomer targeted downstream of the stem-loop structure within the *gag-pol* overlap region may have enhanced the ribosomal frameshifting, as has been demonstrated with the use of antisense oligonucleotides (138), resulting in increased synthesis of *gag-pol* gene products, most of which were nonetheless truncated toward the N terminus of the viral protease in PNA_{PR2}-treated cells. Regardless, the lack of fully functional p6^{Gag} protein was evidently as important a factor as the reduced synthesis of viral protease, both resulting from the PNA_{PR2}-mediated interference with the translation of *gag-pol* mRNA, in blocking virion production from HIV-1-infected cells. In addition to these posttranscriptional events, it is also possible that the reverse transcription may be inhibited by the PNA oligomers tightly bound to the viral RNA target (69), thus preventing the integration of viral DNA in uninfected cells. This may potentially augment the overall antiviral effect of PNA_{PR2} in the setting of de novo HIV-1 infection.

One of the most challenging aspects of the development of antisense or antigene strategies is, in general, to identify the genetic targets the expression of which is crucial to the pathological process of disease. Targeting various regulatory genes of the HIV-1 genome has not always been effective against diverse HIV-1 strains (2, 64, 66, 83-85, 92, 141). The structural *gag* gene has also been targeted by antisense PsODN at a *gag* translation initiation site or various regions of capsid-encoding domain (4, 5, 66, 86, 141, 148). Such an anti-*gag* antisense strategy, however, exhibited only a modest, at most, antiviral effect in tissue culture. These previous studies have clearly demonstrated that a complete disruption of *gag* gene expression is difficult to achieve and that the moderate suppression of Gag protein production may not be substantially detrimental to HIV-1. Furthermore, even if the anti-*gag* antisense could block the translation of full-length Gag protein, eukaryotic ribosomes would most likely scan the downstream *gag* or *gag-pol* mRNA and identify the optimal initiation codon by leaky scanning as discussed above. The resulting truncated Gag and Gag-Pol may still be sufficient for virion particle assembly and release (11), or compensatory downstream mutations may arise to negate deletional effects and restore replication competency, as has been demonstrated for similar deletion mutants (82). The viral gene sequence identified by the current study appeared to be sufficiently accessible to the PNA oligomers within the living cells and presented a narrow window of opportunity to invade HIV-1 structural genes, as shifting the target by a few nucleotides upstream or downstream resulted in a significant loss of antiviral activity. This sequence, therefore, can be considered a vulnerable spot of the HIV-1 genome. Such genetically vulnerable spots may also be identified in other viruses that adopt a frameshift for the translation of critical proteins (12, 30, 53, 54, 89, 98, 100) and possibly exploited to develop pathogen-specific antiviral genetic intervention.

Development of optimal genome-blocking molecules with an appropriate delivery system is another critical step toward a successful antigene-antisense intervention. Antisense PsODN targeting the same sequence as PNA_{PR2} (PsODN_{PR2}) did not show a substantial antiviral effect in chronically infected H9_{LAI} or

H9_{RF} cells in our laboratory (data not shown). The antiviral effects of antisense PsODN are exhibited through several mechanisms, including sequence-specific suppression of transcription or translation and a sequence-independent inhibition of viral adsorption (83, 85, 148). Moreover, the translational suppression induced by antisense PsODN is predominantly mediated by degradation of target RNA by RNase H (9, 14, 139), unlike PNA, which blocks ribosomal elongation in an RNase H-independent manner (45). Thus, PsODN may not be the best possible agent to efficiently block genes in cells that are already infected with HIV-1, and this may explain the discrepancy between the antiviral effects of PNA_{PR2} and PsODN_{PR2} observed in our laboratory. Although PNA exhibits seemingly superior properties as a DNA-RNA-blocking tool compared with other oligonucleotide analogs, the current unmodified form of PNA cannot immediately be utilized as a therapeutic agent. Because of the poor cellular uptake of PNA, relatively higher concentrations of PNA molecules in tissue culture were required to sufficiently block the expression of the target sequence in our study. A conjugation of certain transporter molecules to the PNA may facilitate its cellular uptake (113, 114) and may prove useful if the gene-blocking ability of such a modified PNA construct is maintained. Innovative and optimal modifications to the existing PNA molecules or development of novel gene-intervening agents will clearly advance the efforts to develop potent antiviral therapeutics targeting viral genes.

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