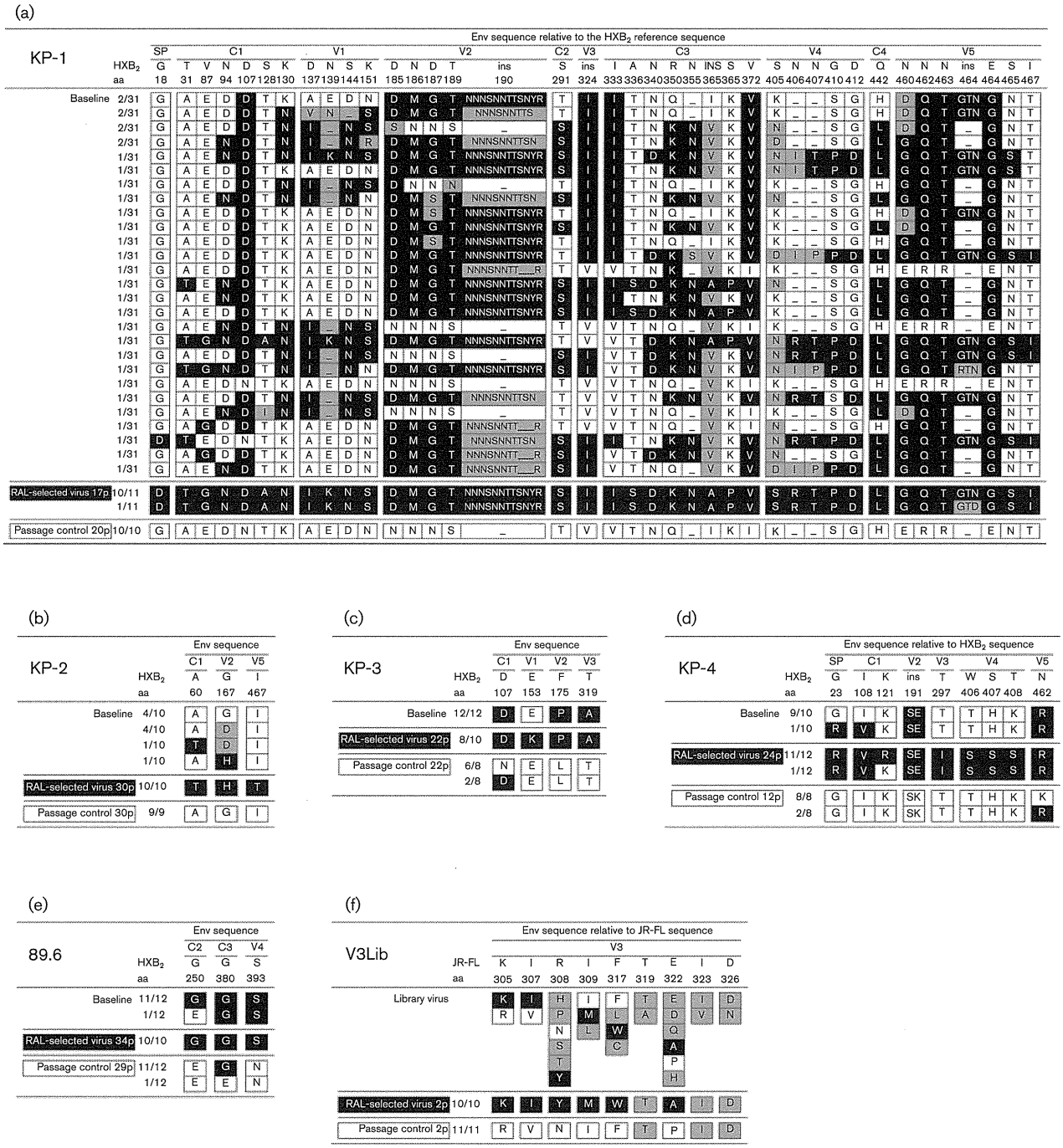


Fig. 1. Comparison of the gp120 sequences between RAL-selected and control-passaged viruses. The gp120 sequences of baseline, RAL-selected and the passage-control viruses were aligned for KP-1 (a), KP-2 (b), KP-3 (c), KP-4 (d) and strain 89.6 (e). Each amino acid in (a)–(e) is numbered relative to the HIV-1 HXB_2 reference sequence. The V3 sequences from the JR-FL-V3Lib baseline library, RAL-selected and passage-control viruses were aligned (f). Filled cells denote the most dominant amino acids observed in RAL-selected variants at the latest passage, open cells denote the most dominant amino acids observed in the passage-control variants at the latest passage and shaded cells show amino acids deleted by the end of both passages, whilst '–' indicates a deletion mutation. The number of passages is indicated, e.g. 17p for passage 17.

In vitro selection of KP-1 variants by 3TC, SQV and MVC

To determine whether other HIV drugs also changed the route of adaptation to the target cells, we attempted to select KP-1 variants using a reverse transcriptase inhibitor (3TC), a protease inhibitor (SQV) and a CCR5 inhibitor (MVC). As shown in Fig. 2(f), the pattern of clustering at distinct positions between the selected isolates and the passage-control variants was similar to that observed for the RAL-selected variants. The selected variants showed decreased diversity in the gp120 sequences; however, the length of the gp120, V1/V2 and V4 sequences increased (apart from in the MVC-selected variants). In addition, the number of PNGs within gp120 was higher than that in the control (Table 3). We also compared the V3 sequences between the passage-control and each of the drug-selected variants. The V3 sequences in all the SQV-selected variants and 83.3 % of those in the 3TC-selected variants, were comparable with those in the RAL-selected variants. This was not the case for the passage controls. Comparison of variants passaged with RAL and 3TC showed that the length of the V1/V2 and V4 regions and the number of PNGs was similar; however, these parameters were different in the SQV-selected variants (Table 3). This indicated that the time at which a drug acts (e.g. during the early or late phase of the HIV life cycle) influences the selection of Env sequences. During selection with MVC, CXCR4-tropic variants were selected from the baseline mixture after seven passages.

Taken together, these results suggested that, in treated cells, different classes of anti-HIV drugs may suppress the variability of quasi-species during *in vitro* selection via a route different from that in untreated cells.

DISCUSSION

This study evaluated the impact of anti-HIV drugs on the Env bottleneck in bulk HIV-1 primary isolates during selection *in vitro*. RAL-, 3TC- and SQV-selected variants of the unique viral isolate, KP-1, harbouring both X4 and R5 variants and with a very high level of baseline viral diversity, were used to study the final destination (genetic bottleneck) of a large variety of Env sequences. Interestingly, the phylogenetic clustering of RAL-selected KP-1 variants was completely different from that of non-drug-treated controls (Fig. 2). Our results also confirmed differences in the length of the gp120, V1/V2 and V4-loop regions and in the number of PNGs (Tables 2 and 3).

It is not clear why viruses cultured under pressure from the non-Env-directed drug RAL result in different *env* genotypes compared with those without the drug. Thus, we cloned the *IN–env* region of the proviral genome from passaged viruses and sequenced the *env* and *IN* regions on the same cloned plasmid, and compared them among the baseline and passages 1, 2, 8 and 17 of the KP-1 virus. Under low concentrations of the IN inhibitor RAL, K7 was selected for at a late passage after accumulation of the other three amino acids, K111, D278 and H216, in IN. During the sequential accumulation of these four amino acids (K111, D278, H216 and K7), the RAL-selected Env sequences at passage 17 (the Env sequences shown as filled boxes in Fig. 1) sequentially accumulated mutations in the same proviral genome (Fig. S1, available in JGV Online). However, we did not find a clone including both the RAL-selected Env at passage 17 and RAL-selected IN at passage 17 in the baseline or each passaged virus, except for in the last passage. We also examined the gp120 and IN sequences of the 3TC- and SQV-selected KP-1 variants. Compared with the RAL-selected region, the variable regions of gp120 in these selected variants were very similar to each other, except for the V1/V2 region (Fig. S2). However, the passage-control variant was very different from the drug-selected variants (Fig. 1a). Furthermore, the IN sequences were different in each passaged virus: K111/D278/H216/K7 in RAL-selected, R111/D278/Q216/R7 in 3TC-selected, K111/D278/H216/R7 in SQV-selected and R111/N278/Q216/R7 in virus without drug treatment (underlined residues indicate amino acids different from those in viruses without drug treatment). To explain these results, we believe that, under pressure from anti-HIV drugs (non-entry ARVs), the virus might show a primitive reaction to select for the Env sequence and recombine from quasi-species to gain advantage for entry and/or enhance replication in target cells. Meanwhile, IN was selected from quasi-species by a direct and/or indirect effect of RAL-induced pressure. The combination of both selective pressures may affect the selection for Env and IN during adaptation in drug-treated conditions (Figs 1a and S2). These results suggest that non-entry inhibitors, such as RAL, 3TC and SQV, might also affect cell adaptation to PM1/CCR5 cells.

Many *in vivo* studies have reported the effects of the anti-HIV drug-induced bottleneck on the *env* gene (Charpentier *et al.*, 2006; Delwart *et al.*, 1998; Ibáñez *et al.*, 2000; Kitrinos *et al.*, 2005; Nijhuis *et al.*, 1998; Nora *et al.*, 2007; Sheehy *et al.*, 1996; Zhang *et al.*, 1994). However, these studies had several limitations. Because viruses were placed under *in vivo* selective pressure using at least two anti-HIV drugs and by the host immune response, it is difficult to separate the different effects and to draw clear conclusions, particularly *in vivo*. Delwart *et al.* (1998) and Kitrinos *et al.* (2005) avoided some of these limitations by employing a heteroduplex tracking assay, although *in vivo* peculiarities still remained. Therefore, we used an *in vitro* selection system using unique bulk primary isolates established in our laboratory (Hatada *et al.*, 2010; Shibata *et al.*, 2007; Yoshimura *et al.*, 2006, 2010b) to observe the effects of the anti-retroviral drug-induced bottleneck on the *IN* and *env* genes.

This selection provides a sensitive approach for analysing virus population dynamics. The effectiveness of ARV drugs can be examined during the *in vitro* passage of a single variant or mixture of variants without being affected by many of the factors encountered *in vivo*. In addition,

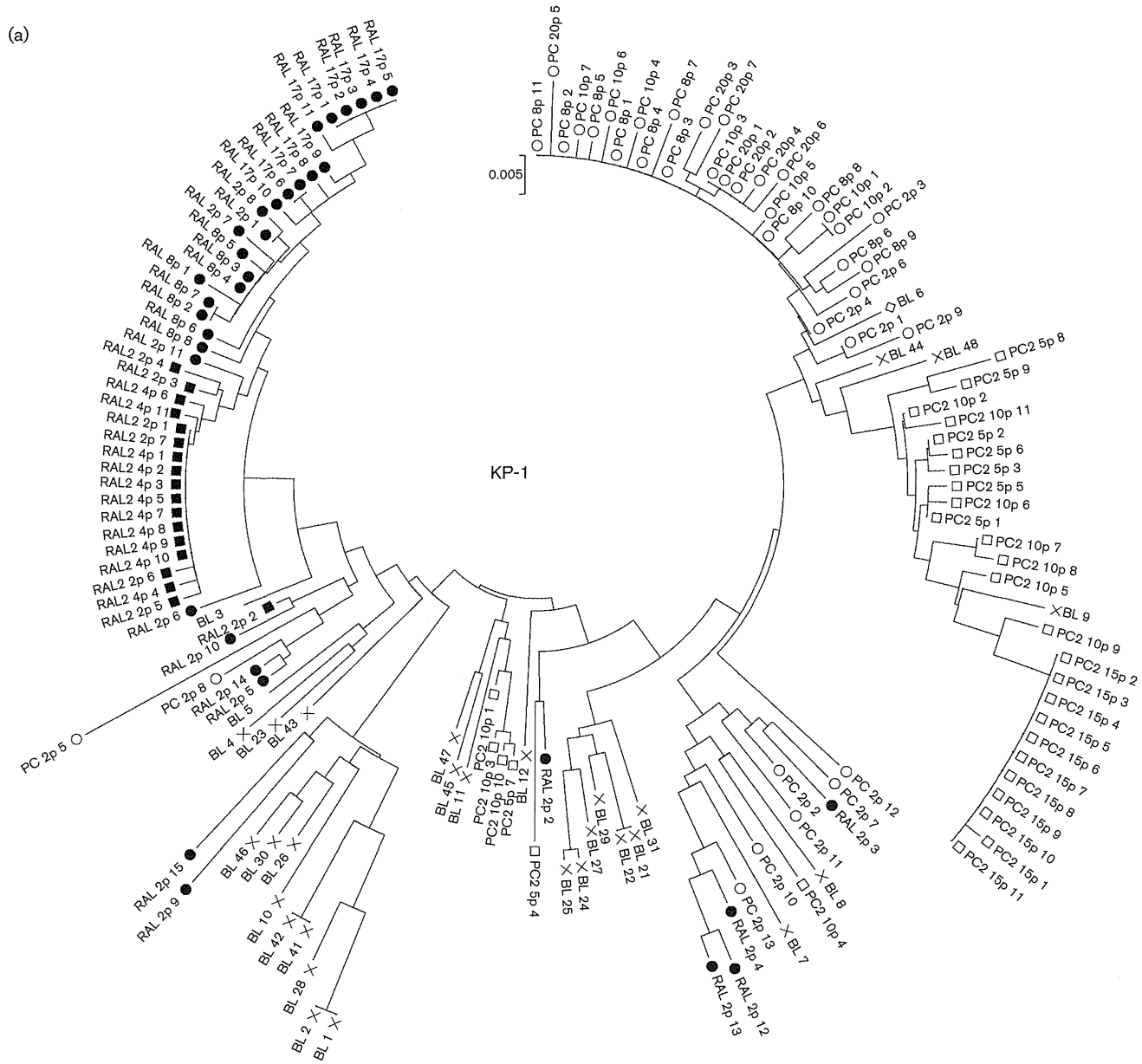
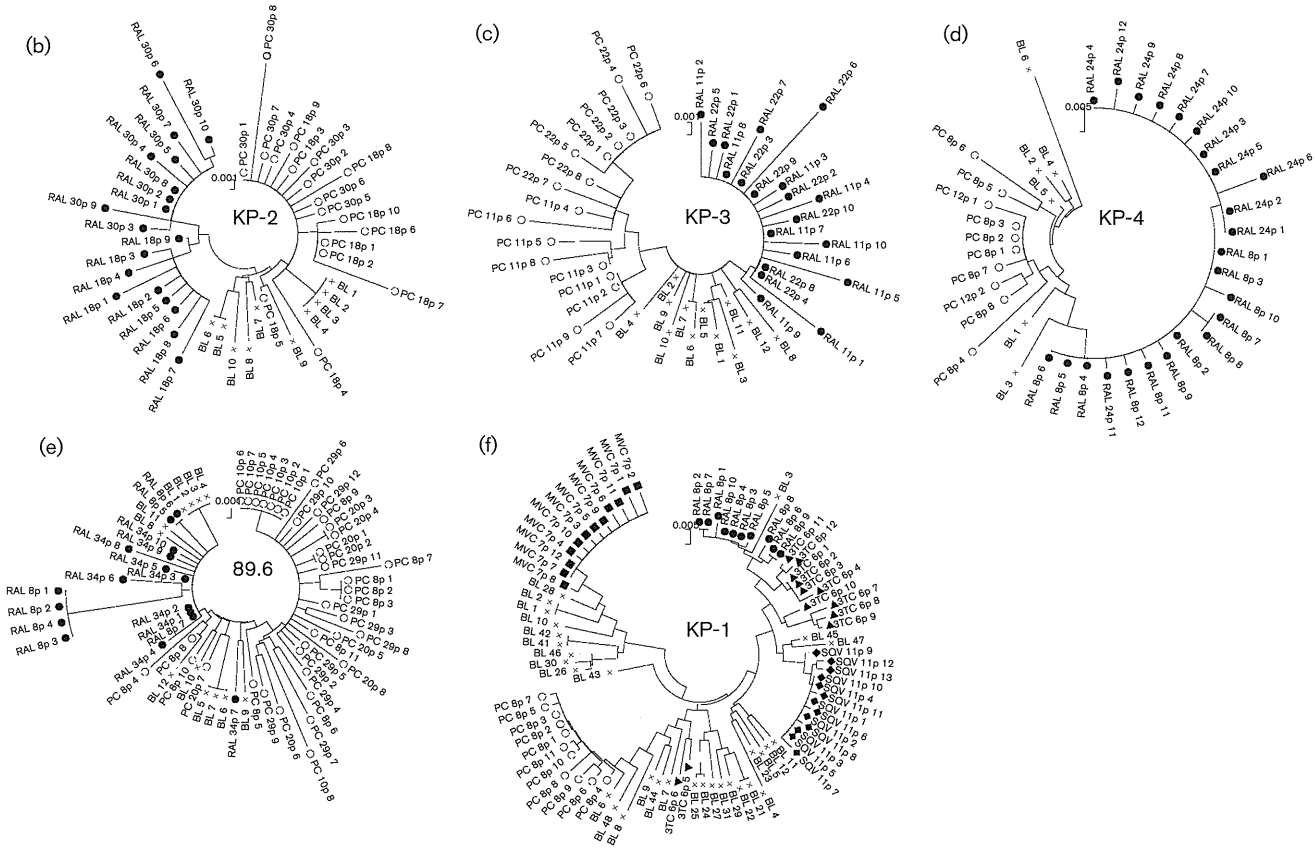


Fig. 2. Phylogenetic analyses of the Env regions from *in vitro*-passaged viruses selected with or without ARV drugs. (a–e) Phylogenetic trees were constructed using gp120 SP–V5 sequences from RAL-selected and passage-control variants of KP-1 (a), KP-2 (b), KP-3 (c), KP-4 (d) and strain 89.6 (e). An '×' represents baseline (BL) variants, and closed and open symbols represent RAL-selected (RAL) and passage-control (PC) variants, respectively. In (a), the results of the second experiment are indicated as RAL2 and PC2, respectively. (f) A phylogenetic tree was constructed using gp120 SP–V5 sequences from RAL-, 3TC-, SQV-, MVC-selected and control-passaged variants of KP-1. ○, Control variants after eight passages; ●, RAL-selected variants after eight passages; ▲, 3TC-selected variants after six passages; ◆, SQV-selected variants after 11 passages; ■, MVC-selected variants after seven passages. The trees were constructed using the neighbour-joining algorithm embedded within the MEGA software.

differences in the Env sequences between the baseline and selected variants can be compared after any number of passages. The results of the present study provide important information that will enhance our understanding of the drug-induced genetic bottleneck. This phenomenon can be examined *in vitro* using bulk primary isolates treated with or without drugs.

Recently, several new ARV drugs have been licensed for use in HIV-1-infected patients. MVC, approved in 2006, is the



first CCR5 inhibitor (Gulick *et al.*, 2008). One important advantage associated with this drug is the absence of cross-resistance with previously available ARV compounds (Gulick *et al.*, 2008; Steigbigel *et al.*, 2008). However, as is usual with anti-HIV drugs, resistant variants with mutations in the Env, gp120 and gp41 sequences are induced both *in vivo* and *in vitro* (Anastassopoulou *et al.*, 2009; Berro *et al.*, 2009; Tilton *et al.*, 2010; Yoshimura *et al.*, 2009, 2010a). As shown in the present study, distinct Env sequences from each quasispecies might be selected by the different anti-HIV drugs (e.g. length of the V1/2 and/or V4 regions, V3 region depletion and the number of PNGs). Moreover, many of the novel anti-retroviral drugs in pre-clinical trials are viral entry inhibitors (e.g. PRO140, ibalizumab, BMS-663068 and PF-232798; Jacobson *et al.*, 2010; McNicholas *et al.*, 2010; Nettles *et al.*, 2011; Stupple *et al.*, 2011; Toma *et al.*, 2011). Therefore, it is necessary to examine whether such entry inhibitors are effective when used alongside conventional drugs.

In conclusion, we studied the genetic bottleneck in bulk primary HIV-1 isolates from untreated patients and drugs targeting the Env (and other) regions. The results showed, for the first time, the presence of drug-selected Env sequences in these isolates. Although our observations were based on a limited number of HIV-1 isolates and need to be confirmed by independent studies, we believe that they provide a new paradigm for HIV-1 evolution in the new combination ARV therapy era.

METHODS

Patients and isolates. Primary HIV-1 isolates were isolated from four drug-naïve patients in our laboratory (KP-1–4) and passaged in phytohaemagglutinin-activated PBMCs. Infected PBMCs were then co-cultured for 5 days with PM1/CCR5 cells (a kind gift from Dr Y. Maeda; Maeda *et al.*, 2008; Yusa *et al.*, 2005) and the culture supernatants were stored at −150 °C (Hatada *et al.*, 2010; Shibata *et al.*, 2007; Yoshimura *et al.*, 2006, 2010b).

After isolation of the primary viruses, we checked the sensitivity of each primary isolate to MVC. The KP-1 isolate was relatively MVC-resistant compared with KP-2 and KP-3 (54 vs 5.9 and 8.7 nM, respectively). KP-1 became MVC sensitive after eight passages in PM1/CCR5 cells [IC_{50}, 3.4 nM; Geno2pheno value (see below), 41.2 %], whilst under the pressure of MVC, KP-1 became highly resistant to MVC after eight passages (IC_{50}, >1000 nM; Geno2pheno value, 1.7 %). These results indicated that the bulk KP-1 isolate used in this study harboured primarily R5 viruses with X4- or dual-tropic viruses as a minor population.

Cells, culture conditions and reagents. PM1/CCR5 cells were maintained in RPMI 1640 (Sigma) supplemented with 10 % heat-inactivated FCS (HyClone Laboratories), 50 U penicillin ml^{-1}, 50 μg streptomycin ml^{-1} and 0.1 mg G418 (Nacalai Tesque) ml^{-1}. MVC, RAL and SQV were kindly provided by Pfizer, Merck & Co. and Roche Products, respectively. 3TC was purchased from Wako Pure Chemical Industries.

The laboratory-adapted HIV-1 strain 89.6, which was obtained through the NIH AIDS Research and Reference Reagent Program, was propagated in phytohaemagglutinin-activated PBMCs. The viral-competent library pJR-FL-V3Lib, which contains 176 bp V3–loop DNA fragments with 0–10 random combinations of amino acid substitutions, was introduced into pJR-FL, as described previously (Yusa *et al.*, 2005).

***In vitro* selection of HIV-1 variants using anti-HIV drugs.** The four primary HIV isolates (KP-1–4), strain 89.6 and JR-FL-V3Lib were treated with various concentrations of RAL and used to infect PM1/CCR5 cells to induce the production of RAL-selected HIV-1 variants, as described previously, with minor modifications (Hatada *et al.*, 2010; Shibata *et al.*, 2007; Yoshimura *et al.*, 2006, 2010b). Briefly, PM1/CCR5 cells (4×10^4 cells) were exposed to 500 $TCID_{50}$ HIV-1 isolates and cultured in the presence of RAL. Virus replication in PM1/CCR5 cells was monitored by observing the cytopathic effects. The culture supernatant was harvested on day 7 and used to infect fresh PM1/CCR5 cells for the next round of culture in the presence of increasing concentrations of RAL. When the virus began to propagate in the presence of the drug, the compound concentration was increased further. Proviral DNA was extracted from lysates of infected cells at different passages using a QIAamp DNA Blood Mini kit (Qiagen). The proviral DNAs obtained were then subjected to nucleotide sequencing. *In vitro* selection of the KP-1 isolate using SQV, 3TC and MVC was also performed using the procedure described above.

Amplification of proviral DNA and nucleotide sequencing. Proviral DNA was subjected to PCR amplification using PrimeSTAR GXL DNA polymerase and Ex-*Taq* polymerase (Takara), as described previously (Hatada *et al.*, 2010; Shibata *et al.*, 2007; Yoshimura *et al.*, 2006, 2010b). The primers used were 1B and H for the gp120 region (Hatada *et al.*, 2010; Shibata *et al.*, 2007; Yoshimura *et al.*, 2006, 2010b), IN 1F (5′-CAGACTCACAATATGCATTAGG-3′) and IN 1R (5′-CCTGTATGCAGACCCCAATATG-3′) for the *IN* region, and IN 1F and H for the *IN*–gp120 region. The first-round PCR products were used directly in a second round of PCR using primers 2B and F (Hatada *et al.*, 2010; Shibata *et al.*, 2007; Yoshimura *et al.*, 2006, 2010b) for gp120, IN 2F (5′-CTGGCATGGGTACCAGCACACAA-3′) and IN 2R (3′-CCTAGTGGGATGTGTACTTCTGAACTTA-3′) for *IN*, and IN 2F and F for *IN*–gp120. The PCR conditions used were as described above. The second-round PCR products were purified and cloned into a pGEM-T Easy Vector (Promega) or pCR-XL-TOPO Vector (Invitrogen), and the *env* and *IN* regions in both the passaged and selected viruses were sequenced using an Applied Biosystems 3500xL Genetic Analyzer and a BigDye Terminator v3.1 Cycle Sequencing kit (Applied Biosystems). Phylogenetic reconstructions were generated using the neighbour-joining method embedded in the MEGA software (http://www.megasoftware.net) (Tamura *et al.*, 2007). Overall, mean distances for viral diversity were also calculated using MEGA software. The number and location of putative PNGs were estimated using *N*-GlycoSite (http://www.hiv.lanl.gov/content/sequence/GLYCOSITE/glycosite.html) from the Los Alamos National Laboratory database.

Susceptibility assay. The sensitivity of the passaged viruses to various drugs was determined as described previously with minor modifications (Hatada *et al.*, 2010; Shibata *et al.*, 2007; Yoshimura *et al.*, 2006, 2010b). Briefly, PM1/CCR5 cells (2×10^3 cells per well) in 96-well round-bottomed plates were exposed to 100 $TCID_{50}$ of the viruses in the presence of various concentrations of drugs and incubated at 37 °C for 7 days. The IC_{50} values were then determined using a Cell Counting Kit-8 assay (Dojindo Laboratories). All assays were performed in duplicate or triplicate.

Predicting co-receptor usage by the V3 sequence. HIV-1 tropism was inferred using Geno2pheno [coreceptor] program, with a false rate positive (FPR) value of 5.0 %, which is freely available (http://coreceptor.bioinf.mpi-inf.mpg.de/index.php). This genotyping tool more accurately predicts virological responses to the CCR5 antagonist MVC in ARV-naïve patients than a reference phenotypic tropism test (Sing *et al.*, 2007).

Statistical analyses. Pairwise comparisons of the different parameters between variants in the two groups was calculated using the homoscedastic *t*-test. A P value of <0.05 was considered statistically significant.

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Conformational Epitope Consisting of the V3 and V4 Loops as a Target for Potent and Broad Neutralization of Simian Immunodeficiency Viruses

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Inducing neutralizing antibodies (NAb) is the key to developing a protective vaccine against human immunodeficiency virus type 1 (HIV-1). To clarify the neutralization mechanism of simian immunodeficiency virus (SIV), we analyzed NAb B404, which showed potent and broad neutralizing activity against various SIV strains. In 4 SIVsmH635FC-infected macaques, B404-like antibodies using the specific VH3 gene with a long complementarity-determining region 3 loop and λ light chain were the major NAbs in terms of the number and neutralizing potency. This biased NAb induction was observed in all 4 SIVsmH635FC-infected macaques but not in 2 macaques infected with a SIV mix, suggesting that induction of B404-like NAbs depended on the inoculated virus. Analysis using Env mutants revealed that the V3 and V4 loops were critical for B404 binding. The reactivity to the B404 epitope on trimeric, but not monomeric, Env was enhanced by CD4 ligation. The B404-resistant variant, which was induced by passages with increasing concentrations of B404, accumulated amino acid substitutions in the C2 region of gp120. Molecular dynamics simulations of the gp120 outer domains indicated that the C2 mutations could effectively alter the structural dynamics of the V3/V4 loops and their neighboring regions. These results suggest that a conformational epitope consisting of the V3 and V4 loops is the target for potent and broad neutralization of SIV. Identifying the new neutralizing epitope, as well as specifying the VH3 gene used for epitope recognition, will help to develop HIV-1 vaccines.

Neutralizing antibodies (NAb) against human immunodeficiency virus type 1 (HIV-1) protect against viral challenge in nonhuman primate models (1–5), suggesting that NAb induction may be an important key to the development of vaccines against HIV-1. The role of NAbs in prevention of infection and control of viral replication has been suggested in several studies using candidate vaccines (6–8). However, the difficulties in inducing NAbs, especially those that are broadly reactive to various HIV-1 strains, have hampered the development of such vaccines (9–11). Monoclonal antibodies (MAb) with broad neutralizing activity that were recently isolated from HIV-1-infected patients have been characterized to understand the specificities and mechanisms of broad neutralization (12–16). The epitopes of these potent and broad NAbs, such as PG9, PGT128, VRC01, and 10E8, have been determined precisely (17–19) and provide an opportunity for structure-based vaccine design to develop antibody-based vaccines for HIV-1 (11, 20–23).

Nonhuman primate models of simian immunodeficiency virus (SIV) infection are commonly used to develop vaccines against HIV-1 (6, 8, 24). Various immunogens, vectors, and regimens have been evaluated by challenge infection with SIV. Moreover, immune factors associated with prevention of infection have been explored in the SIV model. However, epitopes for potent and broad neutralization of SIV remain unclear because few MAbs that neutralize a wide range of SIV strains have been available. Recently, we isolated MAbs from a rhesus macaque infected with SIVsmH635FC, which was isolated from a rapid progressor macaque (25). Infection with SIVsmH635FC, a highly neutralization-sensitive molecular clone, resulted in a vigorous and potent antibody response in all the infected macaques together with viral mutations to escape antibody recognition (26, 27). MAb B404 bound to a conformational epitope on gp120 of various SIV strains and did not react to overlapping peptides of SIV Env. The V3 region was shown to be important by competition enzyme-linked immunosorbent assay (ELISA) with anti-V3 antibodies (25). The neutralizing activity of B404 against homologous neutralization-sensitive SIVsmH635FC, genetically divergent SIVmac316, and neutralization-resistant SIVsmE543-3 was observed.

In this study, we analyzed the epitope of B404 and the induction of B404-like NAbs in SIV-infected macaques. Analysis of more than 400 anti-Env MAbs demonstrated that B404-like NAbs with the same gene usage and specificity were mainly induced in 4 SIVsmH635FC-infected macaques. The B404 epitope was mapped to a conformational epitope consisting of the V3 and V4 loops exposed on a trimeric Env structure after CD4 binding. The identification of the new neutralizing epitope and vigorous antibody response to this epitope in SIV-infected macaques will help us to understand broad neutralization in a macaque model of SIV infection.

MATERIALS AND METHODS

Cells and viruses. PM1 (28) and PM1/CCR5 (29) cells were maintained in RPMI 1640 medium containing 10% fetal bovine serum (FBS). TZM-bl

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(30–33) and 293T (34) cells were maintained in Dulbecco's modified Eagle medium containing 10% FBS. Infectious molecular clones, SIVsmE543-3 (35), SIVsmH635FC (27), SIVmac239 (36), SIVmac316 (37), SIVsmE660FL14, SIVsmH805-24w-3, and SIVsmH807-24w-4 (38) were transfected into 293T cells. After 2 days, the supernatants were filtered (0.45 μm) and stored at −80°C as virus stocks.

Construction of Fab libraries from SIV-infected macaques. The Fab library from SIVsmH635FC-infected rhesus macaque H723 was described previously (25). The Fab libraries from SIV-infected rhesus macaques H704, H709, H714, H711, and H725 (26, 27, 39) were similarly constructed using the pComb3X system according to the instructions of Barbas et al. (40). Four macaques, H723, H704, H709, and H714, were infected with SIVsmH635FC. H711 was infected with a combination of SIVsmE543-3 and SIVsmH635FC. H725 was infected with plasma samples from 2 SIVsmH445-infected macaques, H631 and H635. Rhesus macaques of Indian origin were used in this study. RNA was extracted from lymphocytes from the lymph nodes of these macaques using an RNeasy minikit (Qiagen, Hilden, Germany) and used for subsequent RT-PCR using oligo(dT)20 primer, ReverTra Ace (Toyobo, Osaka, Japan), and Platinum high-fidelity *Taq* DNA polymerase (Invitrogen, Carlsbad, CA). Two libraries, κ and λ light chains, were constructed for each macaque to examine the frequency of NAbs in each population, although only one library, containing both κ and λ light chains, was constructed for H723. Immunoglobulin (Ig) genes were inserted into pComb3X, and the ligation mix was used for transformation of XL1-Blue (Stratagene, La Jolla, CA) by electroporation. Transformed cultures were incubated in superbroth medium with 50 μg/ml carbenicillin, 10 μg/ml tetracycline, and 1.4 μg/ml kanamycin overnight at 37°C after addition of VCSM13 helper phage (Stratagene). Library phage stock was obtained from the culture medium by polyethylene glycol 8000–NaCl precipitation. Library size was determined by assessing the number of CFU after infection of XL1-Blue with a diluted phage sample.

Biopanning to obtain anti-Env antibodies. Biopanning was performed using SIV antigen (Ag), which was prepared by infection of PM1 cells with SIVsmE543-3 as previously described (25). To obtain Fab clones against Env, we selected Fab clones from the H723 library using a 96-well plate in which Env was conjugated with anti-Env Fab clones B404, B408, and H301, which recognize gp120 (conformational), gp41 cluster I and gp120 V1, respectively (25). A MaxiSoap 96-well plate (Thermo Fisher Scientific, Waltham, MA) was incubated with 100 μl of 1.25 μg/ml B404, 0.625 μg/ml B408, and 10 μg/ml H301 for 1 h at 37°C. The wells were washed with phosphate-buffered saline (PBS) containing 0.05% Tween 20 (PBS-T) and blocked with 5% skim milk (Wako Pure Chemical Industries, Osaka, Japan) in PBS (MPBS) for 1 h at 37°C. After the blocking solution was discarded, the wells were incubated with 100 μl 40-fold-diluted SIV Ag for 1 h at 37°C, washed with PBS-T, and used for panning. After incubation with 50 μl of phage library for 2 h at 37°C, the wells were washed 5 times with PBS-T, and bound phage was eluted with 50 μl 100 mM glycine (pH 2.2). Amplified phage was used for the next round of panning, and 3 or 4 rounds of panning were performed. To isolate Fab clones specific to Env, we transformed phagemid DNA into TOP10F′ *Escherichia coli* cells (Invitrogen), and supernatants from isopropyl-β-D-thiogalactopyranoside (IPTG; Wako Pure Chemical Industries)-induced cultures were screened for reactivity to SIV Env using ELISA. Fab clones were purified using a His GraviTrap column (GE Healthcare, Buckinghamshire, United Kingdom), as described previously (25).

Construction of a single-chain variable fragment (scFv) form of B404. B404 Fab was previously converted into complete rhesus IgG produced from a stable cell line carrying heavy- and light-chain plasmids pHCG-B404 and pLL-B404 (25). From these plasmids, B404 scFv was constructed using the pComb3X system (40). The heavy-chain variable region (VH) was amplified using pHCG-B404 as a template and primers HSCVH35-FL (5′-GGT GGT TCC TCT AGA TCT TCC TCC TCT GGT GGC GGT GGC TCG GGC GGT GGT GGG GAG GTG CAG CTG GTG SAG TCT GG-3′) and RhSCG404-B (5′-CCT GGC CGG CCT GGC CAC TAG TGA CCG ATG GGC CCT TGG TGG AGC C-3′). The light-chain λ variable region (VL) was amplified from pLL-B404 using primers HSCLam3 (5′-GGG CCC AGG CGG CCG AGC TCG AGC TGA CTC AGC CAC CCT CAG TGT C-3′) and RhSCJLam404 (5′-GGA AGA TCT AGA GGA ACC ACC GCC TAG GAC GGT CAG CCG GGT CCC-3′). The amplified products were combined by overlapping PCR using primers RSC-F (5′-GAG GAG GAG GAG GAG GAG GCG GGG CCC AGG CGG CCG AGC TC-3′) and RSC-B (5′-GAG GAG GAG GAG GAG GAG GAG CCT GGC CGG CCT GGC CAC TAG TG-3′), digested with SfiI, and inserted into pComb3X in a manner similar to that of Fab construction. The resultant plasmid had the B404 VL and VH regions, which were connected with an 18-amino-acid linker, a histidine tag, and a hemagglutinin (HA) tag. This plasmid was transformed into Rosetta 2 (Merck, Darmstadt, Germany), and B404 scFv was purified from the cell pellet using a His GraviTrap column.

ELISA. ELISA was performed to detect antibodies specific to SIV Ag as previously described (25, 41). Briefly, a MaxiSoap 96-well plate was coated with PBS containing 50 ng/ml concanavalin A (Sigma, St. Louis, MO) for 1 h at 37°C, and SIV Env was conjugated by incubation with 50 μl/well 10-fold diluted SIV Ag for 1 h at 37°C. Samples were added to each well at 50 μl/well with 50 μl of MPBS, and the plate was incubated for 1 h at 37°C. When the enhancement effect of soluble CD4 (sCD4) was examined, 25 μl of sample, 25 μl of sCD4, and 50 μl MPBS were added to each well. Fabs specific to SIV Env were detected with anti-HA–peroxidase (1:1,000 dilution; 3F10, Roche Molecular Biochemicals, Mannheim, Germany) and ABTS [2,2′-azinobis(3-ethylbenzthiazolinesulfonic acid)] solution (Roche Molecular Biochemicals).

Competition ELISA was performed similarly using B404 IgG as a competitor. Ag-coated wells were incubated with 50 μl MPBS and 25 μl serial dilutions of B404 IgG for 1 h at 37°C. After incubation with 25 μl subsaturating concentrations of Fab clones, Fab clone binding was detected by anti-HA–peroxidase (1:1,000) and ABTS solution.

Analysis of neutralizing antibody titers. The neutralizing capability of Fab samples was measured as the reduction in luciferase activity after infection of TZM-bl cells with various SIV strains (6, 25). In addition to Fab samples, plasma samples from SIVsmH635FC-infected macaque H704 (26) and SIVmac239-infected macaque MM324 (42) and MAb M318T (43), which recognizes the V2 region of SIV Env, were used to examine the sensitivity of SIV variants to antibody-mediated neutralization. Briefly, 100-μl portions of serially diluted samples in duplicate were incubated with 50 μl containing 200 50% tissue culture infectious doses ($TCID_{50}$) of virus in a 96-well plate. After incubation for 1 h at 37°C, 100 μl containing 1×10^5 TZM-bl cells/ml with 37.5 μg/ml DEAE dextran was added. Infected cultures were incubated for 2 days, but cultures infected with SIVsmH635FC were incubated for 3 days. After incubation, cells were lysed with 30 μl cell lysing buffer (Promega, Madison, WI) for 15 min at room temperature (RT), and 10 μl cell lysate was transferred to a 96-well black solid plate (OptiPlates-96F; Perkin-Elmer, Boston, MA) for measurements of luminescence using a GloMax 96 microplate luminometer (Promega) and a luciferase assay system (Promega). The 50 and 90% inhibitory concentrations (IC_{50} and IC_{90}, respectively) were calculated with nonlinear regression using PRISM5 and defined as the concentration that caused 50 and 90% reductions in luciferase activity, respectively, compared to that in virus control wells after the subtraction of background.

Construction of Env mutants. The *env* gene was amplified by PCR using primers SRev-F (5′-GGT TTG GGA ATA TGC TAT GAG-3′) and SEnv-R (5′-CCT ACT AAG TCA TCA TCT T-3′) and SIVsmE543-3 plasmid as a template. The PCR product was inserted into pcDNA3.1/V5-His-TOPO vector (Invitrogen). After XbaI digestion, the plasmid was ligated with an NheI-XbaI fragment from pLP-IRES2-EGFP (Clontech Laboratories Inc., Mountain View, CA) to generate a plasmid designated RE543-EGFP that expressed both enhanced green fluorescent protein (EGFP) and Env. Mutants were constructed from RE543-EGFP using PCR mutagenesis. Deletion mutants ΔV1, ΔV2, ΔV3, and ΔV4 were created by

deleting amino acid residues 115 to 149 in the V1 loop, 153 to 209 in the V2 loop, 313 to 342 in the V3 loop, and 404 to 430 in the V4 loop and replacing them with Gly-Ala-Gly, Gly, Gly-Ala, and Gly-Ala-Gly, respectively. These mutations were introduced into RE543-EGFP using primers DV1F (5′-ATG TAA TGG AGC CGG CTC TTG CAT AAA AAA-3′) and DV1R (5′-AAG AGC CGG CTC CAT TAC ATC TCA TTG CTA-3′) for ΔV1, DV2F (5′-ATA GGA GCC GGC CAT TGT AAC ACC AGT-3′) and DV2R (5′-ACA ATG GCC GGC TCC TAT GCA AGA ATC ACC-3′) for ΔV2, DV3F (5′-TGT AGA GGA GCC GGC TGG TGC CGG TTT GGA-3′) and DV3R (5′-GCA CCA GCC GGC TCC TCT ACA TTT CAT TGT-3′) for ΔV3, and DV4F (5′-AAG AAT TCT TAT ACT GCA AAG GAG CCG GCC CAT GTC ATA TTA GAC AAA-3′) for ΔV4. Mutant ΔGly was constructed using primers N306AFw2 (5′-TAT TAT GCT CTA ACA ATG AAA TGT AG-3′), N306ARv (5′-CAT TGT TAG AGC ATA ATA CTT-3′), N316AFw (5′-AGA CCA GGA GCT AAG ACA GTT-3′), N316ARv (5′-AAC TGT CTT AGC TCC TGG TCT-3′), N349AFw (5′-GGT TTG GAG GAG CCT GGA GCG-3′), and N349ARv (5′-CGC TCC AGG CTC CTC CAA ACC G-3′) to introduce the mutations N306A, N316A, and N349A at potential N-linked glycosylation sites. Mutant D385R was constructed using primers S-D368RFw (5′-CCA GCA GGA GGA CGT CCA GAA GTC AC-3′) and S-D368RRv (5′-TTC TGG ACG TCC TCC TGC TGG AGC TGT-3′). The D385R substitution in SIVsmE543-3 corresponds to D368R in HIV-1, which interferes with CD4 binding site (CD4bs) antibodies (13, 44, 45). Mutant I434R was constructed using primers S-I420RFw (5′-GCC ATG TCA TCG TAG ACA AAT AAT CAA C −3′) and S-I420RRv (5′-GAT TAT TTG TCT ACG ATG ACA TGG CAC −3′). The I434R substitution in SIVsmE543-3 corresponds to I420R in HIV-1, which interferes with CD4-induced (CD4i) antibodies (13, 45, 46). Amino acid numbering of Env was based on that of SIVmac239, the reference sequence of SIV, and the HIV-2 sequence in the Los Alamos HIV databases (http://www.hiv.lanl.gov/).

Flow-cytometric analysis. Plasmids to express wild-type and mutant Env were transfected into 293T cells using X-tremeGENE 9 DNA transfection reagent (Roche Molecular Biochemicals) according to the manufacturer's instructions. After incubation for 2 days, the transfected cells were detached with PBS containing 0.05% trypsin and 0.53 mM EDTA and adjusted to 1×10^7 cells/ml in PBS containing 0.2% bovine serum albumin (BSA). To examine the reactivity of Fab, we incubated 50 μl cells with 10 μl 50 ng/μl Fab for 40 min at RT. After washing with PBS containing 0.2% BSA, the cells were incubated with 50 μl anti-HA antibody (1:200; 3F10; Roche Molecular Biochemicals) for 20 min at RT, followed by incubation with 50 μl allophycocyanin (APC)-conjugated AffiniPure goat anti-rat IgG (H+L) $F(ab')_2$ fragment (1:200; Jackson ImmunoResearch Laboratories, Inc., West Grove, PA) for 20 min at RT. When enhancement with sCD4 was examined, cells were resuspended in PBS containing 0.2% BSA in the presence or absence of 2 μg/ml sCD4 at 1×10^7 cells/ml before staining. After incubation with sCD4 for 15 min at RT, 20 μl of cells was mixed with 10 μl 25 ng/μl Fab and stained with anti-HA and anti-rat antibodies. Murine MAb KK46 (1:200) was used as a control antibody against the linear V3 epitope (47). KK46-incubated cells were stained by APC-conjugated goat anti-mouse Ig (1:200; BD Biosciences, Franklin Lakes, NJ). The stained cells were analyzed using a FACSCalibur flow cytometer (BD Biosciences). The reactivity of Fab to Env was determined by comparison with an unstained control after gating $EGFP^+$ cells. Data analysis was performed using FlowJo (TreeStar, San Carlos, CA).

Isolation of B404-resistant variants from SIVmac316. The selection of B404-resistant variants from SIVmac316 was performed as described previously (48, 49). Briefly, 5,000 $TCID_{50}$ SIVmac316 was incubated with 5 ng/ml Fab B404 for 30 min at 37°C. Then, 5×10^4 PM1/CCR5 cells were added to the virus-Fab mixture. After incubation for 5 h, cells were washed with PBS and resuspended in RPMI 1640 medium supplemented with 10% FBS without Fab B404. The culture supernatant was harvested on day 7 and used to infect fresh PM1/CCR5 cells for the next round of culture in the presence of increasing concentrations of Fab B404. A B404-resistant virus, P26B404, was recovered from the cell culture supernatant at passage 26 at 400 μg/ml Fab B404. SIVmac316 was also passaged for the same period in PM1/CCR5 cells in the absence of Fab B404, and the resulting virus was designated P26C. Proviral DNA samples were extracted from PM1/CCR5 cells infected with P26B404 and P26C using a QIAamp DNA blood minikit (Qiagen). The gp120 region was amplified by PCR using primers SEnv-F (5′-ATG GGA TGT CTT GGG AAT CAG C-3′) and SER1 (5′-CCA AGA ACC CTA GCA CAA AGA CCC-3′), cloned using a TA cloning kit (Invitrogen), and subjected to sequencing.

Nucleic acid sequence analysis. The Ig variable regions were sequenced using the primers ompseq and pelseq (40), and analyzed with V-QUEST in the International Immunogenetics Database (IMGT; http://www.imgt.org/) (50). The germ line sequence of the VH gene, from which B404 originated, was determined using the genome database of rhesus macaque (51). Sequences were aligned and phylogenetically analyzed using Molecular Evolutionary Genetics Analysis version 5 (MEGA5) (52).

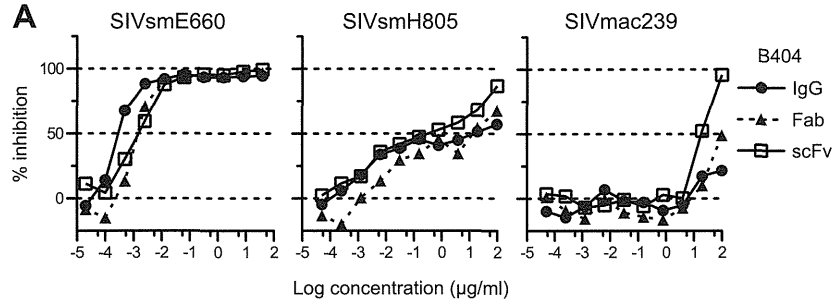
The gp120 region from P26B404 and P26C was sequenced using primers M13F and M13R in the vector and SE1 (5′-ATA ATA CAG TCA CAG AAC A-3′). Predicted amino acid sequences were aligned using CLC Sequence Viewer 6 (CLC Bio, Aarhus, Denmark), together with other SIV sequences.

Molecular dynamics (MD) simulation of gp120 from B404-resistant variants. MD simulations of the gp120 outer domain of SIVmac316 and the mutants with a F277V or N295S substitution were performed essentially as described for MD simulations of the HIV-1 gp120 outer domain (53). SIV gp120 outer domain structures with various V3 regions were constructed using the homology modeling technique with the Molecular Operating Environment (MOE) 2011.10 (Chemical Computing Group Inc., Montreal, Quebec, Canada). The modeling template was the crystal structure of HIV-1 gp120 containing the entire V3 region at a resolution of 3.30 Å (PDB code, 2QAD [54]) and the SIV gp120 core at a resolution of 4.00 Å (PDB code, 3FUS [55]). The 195 amino-terminal and 7 carboxyl-terminal residues were deleted to construct the gp120 outer domain structures. Glycans were added to the gp120 outer domain structures using Online Glycoprotein Builder (56). MD simulations were performed using the SANDER module in the AMBER 10 program package (57, 58) and the AMBER force field (59) and GLYCAM06 (60) with the TIP3P water model (61). Bond lengths involving hydrogen were constrained with SHAKE (62), and the time step for all MD simulations was set to 2 fs. A nonbonded cutoff of 12 Å was used. After heating calculations for 20 ps until 310 K using the NVT ensemble, the simulations were executed using the NPT ensemble at 1 atm and at 310 K for 50 ns. To map structurally fluctuating sites in the gp120 outer domain, we calculated the root mean square fluctuation (RMSF) of the main chains of individual amino acid residues as described previously (53). Briefly, the RMSF were calculated using the 90,000 snapshots obtained from MD simulations of 5 to 50 ns. The average structures during these MD simulations were used as reference structures for the calculation of the RMSF using the ptraj module in AMBER 10.

Nucleotide sequence accession numbers. Sequence data for Ig clones obtained from SIVsmH635FC-infected macaques were submitted to GenBank under accession numbers JF925337 to JF925378 and JF925380 to JF926116.

RESULTS

Potent and broad neutralizing activity of NAb B404 against various SIV strains. SIV-specific Fab clones were previously isolated from the Fab library from SIVsmH635FC-infected macaque H723 through panning against whole SIV Ag (25). Four Fab clones specific to gp120, represented by B404, showed similar gene usage, epitope specificity, and neutralizing activity that covered homologous and heterologous SIV strains. To define the neutralizing potency of B404 further, IgG, Fab, and scFv with B404 variable regions were constructed and examined for their neutralizing ac-



B

IC_{50} and IC_{90}(μg/ml) of IgG, Fab and scFv of B404 against various SIV strains.

Virus	% aa difference	IgG		Fab		scFv	
		IC50	IC90	IC50	IC90	IC50	IC90
SIVmac316	16.8	2.5E-04	1.9E-03	6.0E-04	4.8E-03	4.5E-04	1.9E-03
SIVsmE660	7.3	3.0E-04	2.5E-03	1.4E-03	7.8E-03	1.6E-03	2.0E-02
SIVsmH635FC	0	1.6E-03	5.8E-03	3.7E-03	1.4E-02	2.1E-03	1.0E-02
SIVsmE543-3	1.1	2.4E-03	>100	2.7E-03	>100	2.6E-03	80
SIVsmH805	7.5	16	>100	5.0	>100	5.2E-01	>100
SIVsmH807	6.9	>100	>100	9.1	>100	2.8	>100
SIVmac239	16.4	>100	>100	>100	>100	19	51
HIV-2_{GH123}	29.3	>100	>100	>100	>100	>100	>100
HIV-1_{NL432}	59.7	>100	>100	>100	>100	>100	>100

< 1.0E-02 | 1.0E-02 - 1.0E+00 | 1 - 100 | > 100 μg/ml

FIG 1 Potent and broad neutralization by monoclonal antibody B404 from a SIVsmH635FC-infected macaque. (A) The neutralizing potencies of IgG, Fab, and scFv of B404 are shown by inhibition kinetics against SIVsmE660FL14, SIVsmH805-24w-3, and SIVmac239. (B) The neutralizing potencies of IgG, Fab and scFv of B404 are shown by IC_{50} and IC_{90} (μg/ml). Seven SIV strains, HIV-2_{GH123} and HIV-1_{NL432} were examined for their neutralizing sensitivities against B404 in TZM-bl cells. The IC_{50} and IC_{90} values are shown in dark gray ($<1.0 \times 10^{-2}$ μg/ml), medium gray (1.0×10^{-2} to 1.0×10^{0} μg/ml), light gray (1 to 100 μg/ml) and white (>100 μg/ml). Percent amino acid differences were calculated by pairwise comparison with SIVsmH635FC.

tivity against 7 SIV strains (Fig. 1). These SIV strains were classified into 2 lineages, lineage 1 (SIVsmE660, SIVsmH635FC, SIVsmE543-3, SIVsmH805, and SIVsmH807) and lineage 8 (SIVmac316 and SIVmac239), according to the phylogenetic analysis by Apetrei et al. (63), which identified nine divergent lineages in SIVsm/mac corresponding to HIV-1 subtypes. Sensitivity to neutralization was known to be high in SIVmac316, SIVsmE660, and SIVsmH635FC (25, 38). Infection with these neutralization-sensitive SIV strains was almost completely blocked by low concentrations of all forms of B404. Although the potency to inhibit infection was similar among IgG, Fab, and scFv, B404 IgG was slightly more effective against these SIV strains, as shown by the neutralizing kinetics of SIVsmE660 (Fig. 1A). Neutralization of SIVsmE543-3, SIVsmH805, and SIVsmH807 reached a plateau at 10 to 100 ng/ml IgG B404 and Fab B404, as represented by neutralization kinetics against SIVsmH805 (Fig. 1A). These viruses were moderately sensitive to B404-mediated neutralization, although the IC_{50}s were variable among these SIV strains (Fig. 1B). Interestingly, B404 scFv was more effective at high concentrations than B404 IgG and B404 Fab in neutralization of these moderately neutralization-sensitive viruses and SIVmac239, which is a highly neutralization-resistant strain (Fig. 1). Infection with SIVmac239 was unaffected by the presence of any form of B404 at a concentration of less than 1 μg/ml but was inhibited more than 90% by 100 μg/ml B404 scFv. Neutralization of 7 of 7 SIV strains, including genetically diverse, neutralization-resistant SIVmac239, by B404 scFv indicates that B404 is a potent and broad NAb against SIVsm/mac strains.

Isolation of Env-specific Fab clones from SIVsmH635FC-infected macaques. To analyze the induction of B404-like antibodies in SIV-infected macaques, Env-specific Fab clones were isolated from 4 SIVsmH635FC-infected macaques: H723, H704, H709, and H714 (26, 39). Env-specific Fab clones from H723 were isolated from the previously constructed phage library (25) through panning against Env, which was conjugated by coating plate wells with the anti-Env Fab clones B404 (anti-gp120 conformational), B408 (anti-gp41 cluster I), and H301 (anti-gp120 V1). Together with anti-Env Fab clones from the previous study, 98 anti-Env Fab clones, including 33 NAbs (33.7%), were obtained from H723. From 3 other SIVsmH635FC-infected macaques, κ and λ light-chain phage libraries were separately constructed, and 2 panning series were performed using B404 and H301 to conjugate Env. After 4 series of panning in each macaque, we obtained 155, 102, and 53 independent Fab clones from H704, H709, and

TABLE 1 Preferential gene usage and competition with B404 of NAbs

Inoculated virus	Animal	Frequency (%) of NAbs[a]	No. of NAbs	% of NAbs with:		Avg CDRH3 length[b]	Competition (%) with B404[c]
				VH3 genes	λ light chains		
SIVsmH635FC	H723	33.7	33	81.8	93.9	20.0	81.8
	H704	30.3	47	95.7	97.9	18.7	100
	H709	7.8	8	75.0	100	17.8	100
	H714	52.8	28	96.4	92.9	18.7	100
SIV mix[d]	H711	17.2	15	26.7	40.0	15.2	86.7
	H725	2.2	1	0.0	100	12	100

[a] Frequencies of Fab clones with the VH3 gene and λ light chain are shown as percentages of NAbs.
[b] Average number of amino acids in CDRH3.
[c] Competition ELISA with 2 μg/ml B404 IgG was performed. The frequency of Fabs showing more than 50% inhibition is shown as a percentage of NAbs.
[d] H711 was inoculated with a mixture of SIVsmE543-3 and SIVsmH635FC. H725 was inoculated with plasma samples from 2 SIVsmH445-infected macaques, H631 and H635.

H714, respectively. Neutralizing activities were observed in 47 clones (30.3%) from H704, 9 clones (8.8%) from H709, and 28 clones (52.8%) from H714 (Table 1). Phylogenetic analysis of VH genes revealed that 105 NAbs formed a major NAb cluster with B404 (Fig. 2). The remaining NAbs were separated into 3 minor clusters containing 3 or 4 NAbs. Fab clones in the major group, designated the B404 group, were isolated from all 4 macaques analyzed.

Although Fab clones in the B404 group were genetically similar to one another, several small clusters were observed in the B404 group, suggesting multiple B cell origins generated by VDJ recombination in these B404-like NAbs. Sequence analysis using the International Immunogenetics Database (50) indicated that the VH genes of Fab clones in the B404 group were close to human pseudogene IGHV3-h (approximately 90% identity), but no functional VH gene showed >90% identity. Analysis using the genome database of the rhesus macaque (51) revealed a significant relationship (>95% identity) between Fab clones in the B404 group and the rhesus macaque VH3 gene in the chromosome 7 scaffold (GenBank accession number NW_001122023). These results suggest that a major group of NAbs in SIVsmH635FC-infected macaques preferentially use the same rhesus VH3 germ line that lacks a human counterpart.

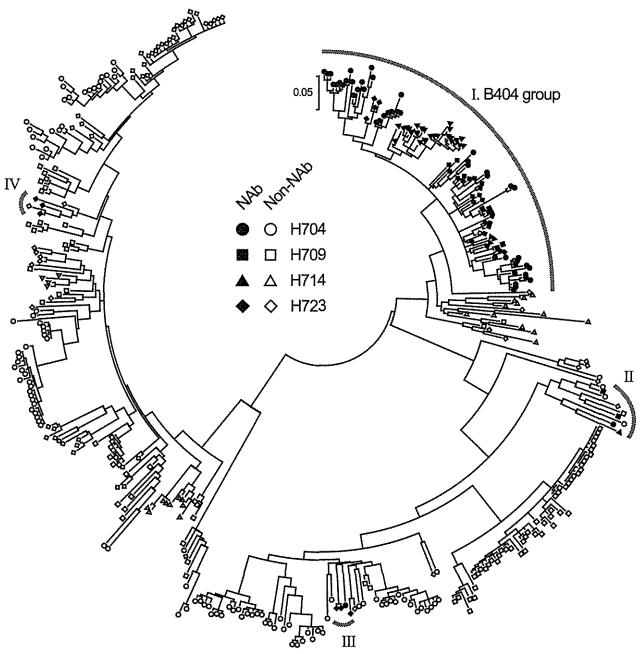


FIG 2 B404-like NAbs formed a major group in anti-Env antibodies from 4 SIVsmH635FC-infected rhesus macaques. NAbs were separated into 4 groups in the phylogenetic tree, which was generated using MEGA5 (70) from heavy-chain genes of 98, 155, 102, and 53 Fab clones from H704, H709, H714, and H723, respectively.

Bias in gene usage of NAbs from SIVsmH635FC-infected macaques. The genetic features of anti-Env Fab clones are summarized in Fig. 3 and Table 1. As mentioned above, a major population of NAbs from SIVsmH635FC-infected macaques used the same VH3 gene as B404, resulting in a high rate of NAbs using the VH3 gene (Fig. 3A and Table 1). A high occupancy of λ light chains was also characteristic of NAbs from SIVsmH635FC-infected macaques (Fig. 3B and Table 1). Moreover, a long complementarity-determining region 3 loop of the heavy chain (CDRH3) was characteristic of the NAbs (Fig. 3C and Table 1). CDRH3 of most NAbs had 19 or more amino acids, although the length of CDRH3 was usually less than 18 amino acids in nonneutralizing Fab clones. These results clearly showed that B404-like NAbs with the VH3 gene-encoded heavy chain with a long CDR3 and λ light chain are the main NAb population in SIVsmH635FC-infected macaques. In contrast, Fab clones from macaques H711 and H725 lacked these remarkable features of B404-like NAbs (Fig. 3, bottom; Table 1). These 2 macaques were inoculated with a mixture of SIVs (SIV mix). H711 was infected with a combination of SIVsmE543-3 and SIVsmH635FC. H725 was infected with plasma samples from 2 SIVsmH445-infected macaques, H631 and H635, which SIVsmH635FC was isolated from. Although anti-Env Fab clones were similarly isolated from these macaques, the frequency of NAbs from H711 (17.2%) and H725 (2.2%) was lower than that from SIVsmH635FC-infected macaques (8.8 to 52%). NAbs from H711 and H725 preferentially used VH1 gene-encoded heavy chains with a short CDRH3 and κ light chains, but NAbs from these macaques showed a genetic variation, similarly to those in HIV-1-infected patients (64). These results suggested that B404-like NAbs are induced exclusively in SIVsmH635FC-infected macaques.

Potent neutralizing activity and the same specificity of NAbs in the B404 group. To analyze the epitopes recognized by these NAbs, we first separated Fabs with neutralizing activity into 2 groups according to the results of competition ELISA with B404 IgG. All the NAbs in the B404 group and group II (Fig. 2) com-

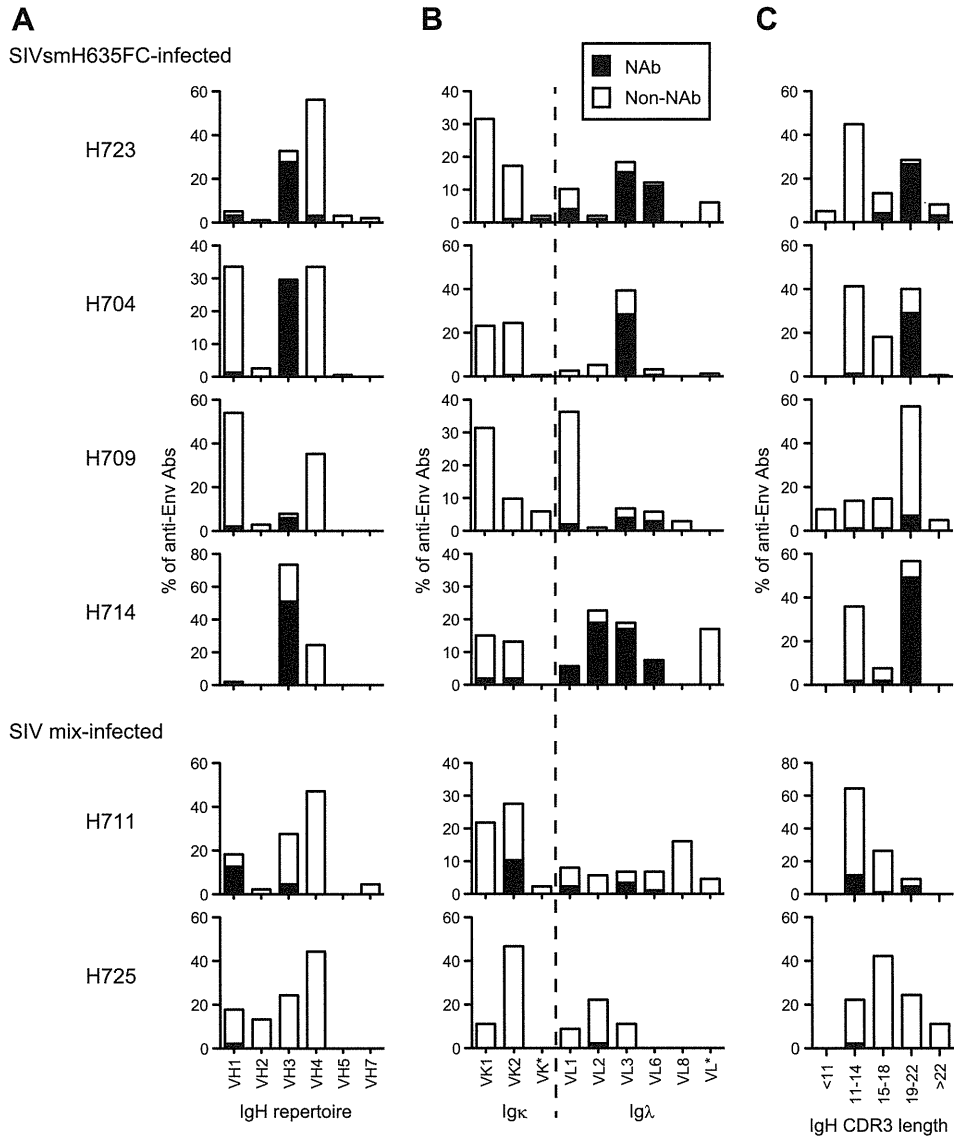


FIG 3 Bias in the Ig gene usage and CDR3 length of neutralizing Fab clones from SIVsmH635FC-infected macaques. The proportions of IgH (A) and Igκ and Igλ (B) repertoires and heavy-chain CDR3 length (C) are shown as percentages of NAbs and non-NAbs. In addition to Fabs isolated from 4 SIVsmH635FC-infected macaques, 87 Fab clones from H711, which was infected with a combination of SIVsmE543-3 and SIVsmH635FC, and 45 Fab clones from H725, which was infected with plasma samples from 2 SIVsmH445-infected macaques, H631 and H635, were similarly analyzed. Usage of Ig genes was analyzed using V-QUEST in the International Immunogenetics Database (44).

peted with B404 IgG (Fig. 4A), suggesting that epitopes for these NAbs overlap or are close to that for B404. Despite the differences in gene usage, competition with B404 IgG was also observed in most NAbs from macaques infected with SIV mix (Table 1). NAbs belonging to groups III and IV, with the exception of 1 Fab in group III, did not compete with B404 IgG (Fig. 4A). The binding ability of these Fabs was even enhanced by the addition of B404. Competition of the Fabs in groups III and IV with biotinylated K8 in group III suggested that the Fabs in group III and IV share the same epitope (data not shown). The neutralizing activity of these Fabs was examined against the genetically divergent SIVmac316 and the neutralization-resistant SIVsmE543-3 (Fig. 4B). All of the Fabs tested showed at least 50% inhibition against both viruses, and the B404 group included Fabs with potent neutralizing activity that showed efficient inhibition at low concentrations. Accordingly, the IC_{50}s of the 4 Fabs in the B404 group ranged from 0.8 to 316 ng/ml (average IC_{50}, 79 ng/ml) against SIVmac316, indicating the presence of NAbs comparable to B404 (IC_{50} against SIVmac316, 0.6 ng/ml) (Fig. 1). In contrast, IC_{50} against SIVmac316 ranged between 32 and 908 ng/ml (average IC_{50}, 243 ng/ml) in groups III and IV. This result suggests that B404-like NAbs are the main NAb population in terms of number and neutralizing potency.

Epitope mapping of NAb B404. To define the region of the Env targeted by B404, we examined reactivity against mutants of SIVsmE543-3 Env. Because the V3 loop has been shown to be important for B404 binding (25), mutants with deletions in the V1, V2, V3, and V4 loops (ΔV1, ΔV2, ΔV3, and ΔV4) and a mu-

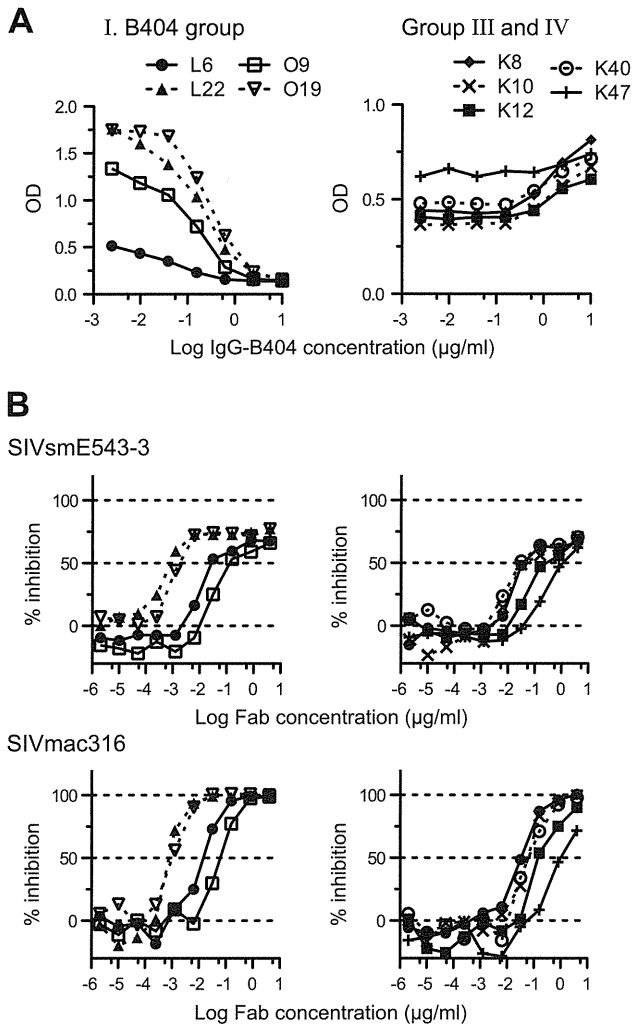


FIG 4 The specificity and potency of Fab clones in the B404 group are similar to those of B404. (A) Competition ELISA was performed using serially diluted B404 IgG as a competitor. B404 IgG significantly inhibited the binding of the Fabs in the B404 group (L6, L22, O9, and O19). In contrast, B404 IgG did not compete with the Fabs in groups III (K8 and K10) and IV (K12, K40, and K47) and even enhanced the binding of these Fabs. (B) Neutralization potencies of Fabs in the B404 group (left) and groups III and IV (right) are shown by inhibition of infection to TZM-bl cells with neutralization-resistant SIVsmE543-3 and genetically divergent SIVmac316.

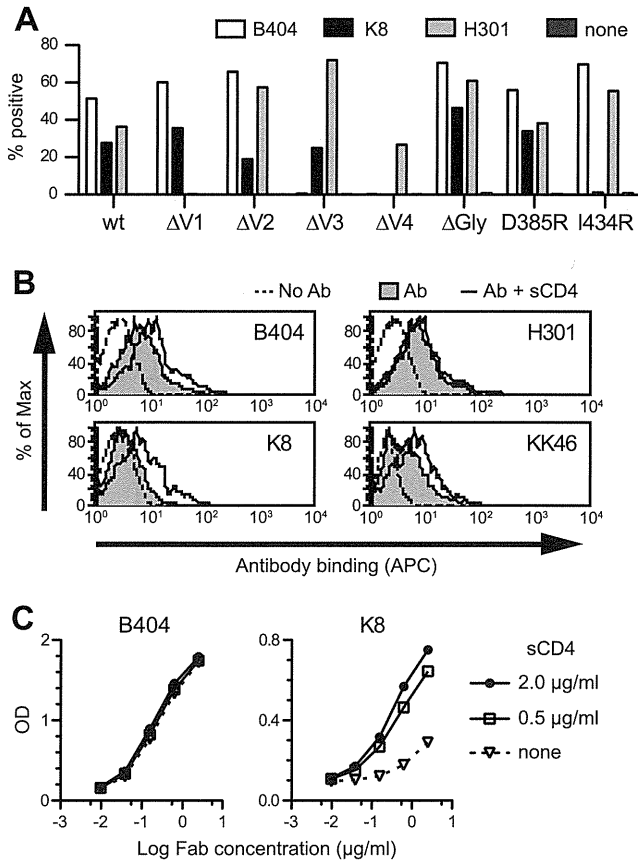
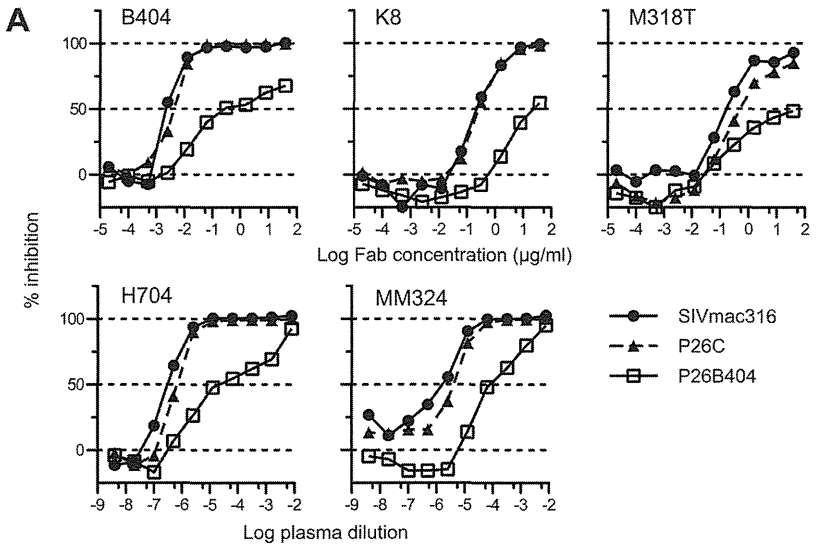


FIG 5 B404 recognizes a conformational epitope, including the V3 and V4 loops, and sCD4 enhances the exposure of the epitope in trimeric Env. (A) Reactivity of B404, K8, and H301 (anti-V1 Fab) to Env mutants was examined using 293T cells transfected with plasmids to express SIVsmE543-3 Env (wild-type), mutants with deletions in the V1 (ΔV1), V2 (ΔV2), V3 (ΔV3), and V4 (ΔV4) loops, an N306A/N316A/N349A mutant lacking glycosylation sites near the V3 loop (ΔGly), a D385R mutant interfering with CD4bs antibodies (D385R), and an I434R mutant interfering with CD4i antibodies (I434R). The transfected cells were stained with Fabs B404, K8, and H301, and the reactivity of Env mutants was analyzed using flow cytometry. The percentage of Fab^+ cells is shown. (B) Reactivity of Fabs B404, K8, and H301, and murine anti-V3 MAb KK46 to sCD4-treated trimeric Env on the cell surface. Cells transfected with the plasmid to express SIVsmE543-3 Env were incubated with 2 μg/ml sCD4 for 15 min, and the reactivities of antibodies were similarly examined. The tinted histogram represents cells stained by antibody in the absence of sCD4. The dotted line shows the unstained control. (C) Reactivity of Fab clones B404 and K8 to sCD4-treated monomeric Env. The reactivity of serially diluted Fab to Env was examined by ELISA using SIVsmE543-3 as an antigen in the absence or presence of 0.5 or 2.0 μg/ml sCD4.

tant lacking 3 glycosylation sites flanking the V3 loop (ΔGly) were constructed. In addition, mutants carrying single mutations in the CD4bs (D385R) and CD4i (I434R) sites, corresponding to D368R and I420R in HIV-1 gp120 (13, 44–46), were examined to clarify the relationship of the B404 epitope to the CD4bs and CD4i sites. Flow cytometry analysis using cells expressing these Env mutants revealed that the reactivity of B404 was completely lost in ΔV3 and ΔV4 mutants, though B404 bound to other mutants even better than it did to the wild type (Fig. 5A). These results suggested that B404 recognizes a conformational epitope consisting of the V3 and V4 loops.

The reactivity of another Fab, K8, which targets an epitope other than that of B404 (Fig. 4A), was lost in ΔV4 and I434R mutants (Fig. 5A). No reactivity to I434R strongly suggested that K8 is a CD4i antibody. Therefore, the effect of sCD4 ligation on antibody binding to Env trimers and monomers was examined using flow cytometry and ELISA, respectively. The reactivity of B404, K8, and KK46 (murine anti-V3 MAb) to Env on the cell surface was enhanced by the addition of sCD4, although no effect was observed in anti-V1 Fab H301 (Fig. 5B). This suggested that epitopes for B404, K8, and KK46 are exposed in the open conformation of the Env trimer triggered by CD4 binding. Consistent with the analysis of mutant Envs, the reactivity of K8 to Env monomer was enhanced by the addition of sCD4, but B404 showed no enhancement of reactivity (Fig. 5C).



B

N-terminal region

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                    10         20         30
SIVmac316 MGCLGNQLLI AILLLSVYGI YCTLYVTVFY
SIVmac239 .......... .......... ..........
SIVsmE543 .......... .L..V..LE. C.VQ......
SIVsmH635 .......... .L..V..LE. C.VQ......

P26C(5/5) .......... .......... ..........

P26B404
  (13/15) .......... ......L... ..........
   (2/15) .......... ......L... .....A....
```

C2

```
                    280        290        300
          TSTWFGFNGT RAENRTYIYW HGRDNRTIIS
          .......... .......... ..........
          .......... .......... ..NS......
          .......... .......... ..NS......

  (4/5)   .......... .......... ..........
  (1/5)   .......... .......... .D........

(11/15)   ......V... .......... ..........
 (3/15)   .......... .......... ....S.....
 (1/15)   .......... .......... ..........
```

FIG 6 Isolation of variants resistant to B404 and amino acid substitutions in gp120. The B404-resistant variant was induced from SIVmac316 by passages of viruses in PM-1/CCR5 cells with increasing concentrations of B404 Fab. A B404-resistant variant, P26B404, was obtained from the supernatant of passage 26. P26C was obtained after 26 passages without B404. (A) The sensitivities of P26B404, P26C, and parental SIVmac316 to neutralization are shown by inhibition of infection of TZM-bl cells. B404 and K8 Fabs, murine MAb M318T, which recognizes the V2 of gp120, and plasma samples from SIVsmH635FC-infected macaque H704 and SIVmac239-infected macaque MM324 were used for the neutralization assay. (B) Amino acid sequences of the N-terminal and C2 regions of gp120 from P26C and P26B404 are aligned with those of parental SIVmac316 and SIV strains, SIVmac239, SIVsmE543-3 and SIVsmH635FC. The number of clones per total number of clones is given in parentheses. Identical amino acids are shown as dots, and potential glycosylation sites in SIVmac316 are indicated with underlining.

The enhancement by sCD4 of reactivity to both monomeric and trimeric Env and the interference in binding by the I434R (I420R in HIV-1) mutation in Env, which are features of so-called CD4i antibodies against HIV-1 (13, 45, 46), indicate that K8 targets the CD4i epitope. The enhanced reactivity of B404 by sCD4 to trimeric but not monomeric Env is analogous to the reactivity of anti-V3 antibodies (65). These results suggest that B404 recognizes a conformational epitope consisting of the V3 and V4 loops, which are intensely exposed on the Env trimer after CD4 ligation.

Selection of variants resistant to NAb B404. To select B404-resistant variants *in vitro*, we passaged SIVmac316, which is the most sensitive to B404 of the SIV strains tested (Fig. 1), in PM1/CCR5 cells in the presence of increasing concentrations of B404. As a control, passage under the same conditions without B404 was also performed to monitor spontaneous changes during infection in PM1/CCR5 cells. The concentration of B404 was increased from 5 ng/ml to 400 μg/ml at passage 26. Viruses recovered at passage 26 in the presence and absence of B404, which were designated P26B404 and P26C, respectively, were examined for their sensitivity to antibodies and plasma samples from SIV-infected macaques (Fig. 6A). The IC_{50} for B404 against SIVmac316, P26C, and P26B404 were 2.8, 4.1, and 240 ng/ml, respectively, showing an 86-fold resistance of P26B404 to B404 compared with that of wild-type SIVmac316. P26B404 was also resistant to neutralization by MAbs K8 (CD4i) and M318T (V2), which target epitopes other than that of B404, and plasma samples from SIV-infected macaques (Fig. 6A). These results suggested that P26B404 acquired resistance to antibody-mediated neutralization comparable to that observed in neutralization-resistant SIV strains, such as SIVmac239 and SIVsmE543-3. Sequence analysis of gp120 revealed 3 amino acid substitutions specific to P26B404: V17L in the N-terminal region and F277V and N295S in the C2 region (Fig. 6B). Of these substitutions, the two in the C2 region were highly conserved among SIVsm/mac and HIV-2 strains. These substitutions were independently observed, and no variant with both F277V and N295S was found in the 15 clones sequenced.

MD simulation of gp120 outer domains from B404-sensitive and B404-resistant variants. To address structural impacts of the 2 mutations in the C2 region, we performed MD simulation of unliganded gp120 outer domains from B404-sensitive (SIVmac316) and B404-resistant (F277V and N295S) variants. To map the sites at which structural dynamics were influenced by C2 mutations, we calculated the RMSF of the main chains of individual amino acid residues using 90,000 snapshots from 5 to 50 ns of

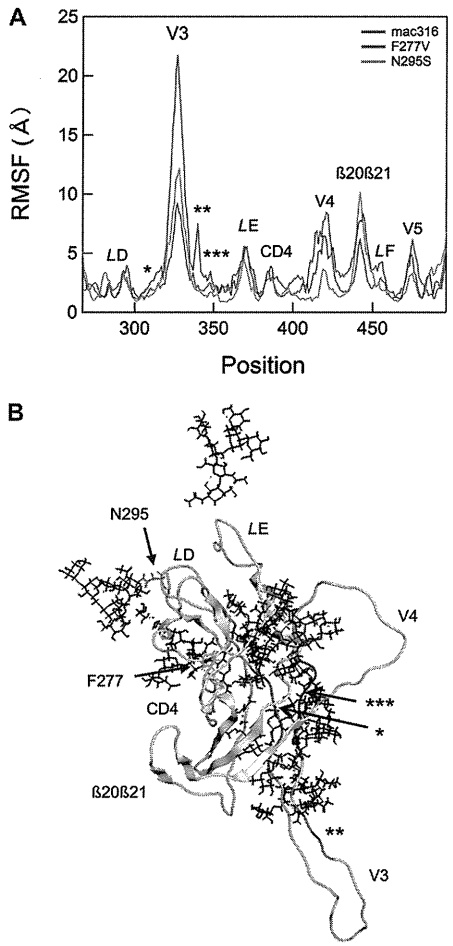

FIG 7 Effects of F277V and N295S mutations on the structural dynamics of the gp120 outer domain. (A) Distribution of RMSF in the gp120 outer domain. MD simulations of gp120 outer domains of SIVmac316, F277V, and N295S were carried out at 1 atm and 310 K for 50 ns as described in Materials and Methods. The RMSF values, which indicate the atomic fluctuations of the main chains of individual amino acids during MD simulations, were calculated using 90,000 snapshots from 9 to 50 ns of each MD simulation. The numbers on the horizontal axes indicate amino acid positions in gp120. The RMSF values of the mutants are significantly different from those of parental SIVmac316 at the V3 loop, the V3 flanking regions (indicated by asterisks), the V4 loop, the β20β21/*LF* loop, and the V5 loop regions. (B) A structure at 50 ns of MD simulation of the SIVmac316 gp120 outer domain is shown as a representative to indicate the steric location of mutation sites and various loops. The regions that are proximal to the V3/V4 loops and displayed fluctuations that differed from those of parental SIVmac316 (Fig. 7A) are highlighted in orange (*), blue (**), and purple (***). Green sticks indicate glycans.

each MD simulation (Fig. 7A). RMSF values provide key information about the atomic fluctuations of the individual amino acids of a protein in solution (57). These values were maximal at the tip of the V3 loop and prominent at other loop regions, including *LD*, *LE*, CD4 binding, V4, β20β21/*LF*, and V5 (Fig. 7A), suggesting that these loops fluctuate in solution. Notably, the F277V and N295S mutations were found to induce changes in RMSF values mainly at the V3, V4, β20β21/*LF*, and V5 loop regions (Fig. 7A, blue and green lines, respectively). Interestingly, these regions are located far from the C2 mutation sites compared with the locations of other loops, such as *LD*, *LE*, and CD4 binding, which had RMSF values that were similar among wild-type and B404-resistant variants (Fig. 7B; F277V in *LD* and N295S in the proximal region of *LD*). In particular, RMSF changes by the C2 mutations were the most prominent at the V3/V4 loops and their neighboring regions (Fig. 7). These results suggested that the F277V and N295S mutations could alter the structural dynamics of V3/V4 loops and their neighboring regions in solution. The structural alterations would lead to changes in entropy of the regions, which affect the binding affinity to B404. The finding is consistent with the results of an epitope mapping study of B404.

DISCUSSION

Potent and broadly neutralizing MAbs have recently been isolated from HIV-1-infected patients and analyzed to understand the mechanism of neutralization against a broad spectrum of HIV-1 strains and to design vaccines against their neutralizing epitopes (12–16). Although the SIV-macaque model has been used as an animal model for HIV-1 infection for vaccine development (6, 8, 24), no potent and broadly neutralizing monoclonal antibody against SIV was available. Therefore, the epitopes and mechanism for broad neutralization of SIV remained uncertain. Many monoclonal antibodies against SIVsm/mac were isolated from SIV-infected macaques (66, 67) and mice immunized with SIV Env (43, 47, 68), but few of them showed neutralizing activity against various SIV strains, including highly neutralization-resistant SIVmac239 (68). In comparison with these monoclonal antibodies against SIV identified so far, B404 apparently has a broadly neutralizing activity, which enables it to neutralize multiple, diverse SIV isolates, and can be defined as the first generation of broadly NAbs against SIV. The broad and potent neutralizing activity of B404 shown in this study indicates that B404 can be used to analyze broad neutralization against SIV. The B404 epitope, the newly identified broadly neutralizing epitope against SIV, will further understanding of the mechanism of broad neutralization effective for protection from SIV infection.

The infection of rhesus macaques with SIVsmH635FC, a highly neutralization-sensitive clone, was chosen for this study because this SIV strain induced a vigorous and potent antibody response in all the infected macaques and acquired many viral mutations to escape antibody recognition (25, 26). The kinetics of B404 neutralization against various SIV strains were similar to those observed in the plasma sample of the macaque from which B404 was isolated, suggesting that B404-like NAbs are representative of the neutralizing activity in SIVsmH635-infected macaque H723 (25). Consistent with this observation, B404-like NAbs were shown to be a major group in NAbs genetically and functionally. Most of the NAbs in the 4 SIVsmH635FC-infected macaques analyzed had the same features, including the use of a specific VH3 germ line and λ light chains, a long CDRH3 loop, and competition with B404. The bias in the specificity and gene usage may be partially enhanced by the screening process, because B404-like NAbs were predominantly isolated from λ light-chain libraries by panning against H301-conjugated Env. In addition, isolating antibodies against quaternary epitopes constituted by the Env trimer through panning using monomeric Env was difficult. However, the presence of many independent B404-like NAbs strongly suggests that B404-like NAbs compose a significant fraction of NAbs in 4 SIVsmH635FC-infected macaques. Moreover, the vigorous induction of B404-like NAbs in SIVsmH635FC-infected macaques was also supported by the multiple B cell origins apparent

from several subgroups in B404-like NAbs (Fig. 1). These subgroups originated from distinct B cell precursors generated by VDJ recombination, because they were often distinguished by the length and nucleotide sequences of CDRH3.

The observation of few B404-like NAbs from macaques infected with the SIV mix clearly indicates that induction of B404-like NAbs depends on infection with SIVsmH635FC. The exclusive induction of B404-like NAbs only in SIVsmH635FC-infected macaques also raises the possibility that Env from SIVsmH635FC is a highly immunogenic protein that induces antibodies against the B404 epitope. The use of Env from SIVsmH635FC for vaccination may be advantageous for the induction of broadly neutralizing antibodies, because the Env from an HIV-1-infected patient with broadly neutralizing antibodies induced cross-reactive anti-HIV-1 NAbs in an animal model (69). The Env in this vaccination study is capable of mediating CD4-independent infection. Since the Env of SIVsmH635FC has a mutation in the CD4-binding region (D385N), NAb induction may be affected by CD4 independency of Env. The development of vaccines aimed at inducing B404-like NAbs in rhesus macaques will be useful in establishing models for development of antibody-based vaccines targeting specific epitopes for broad neutralization.

Biased usage of a specific VH3 germ line gene and λ light chain are remarkable genetic features of B404-like NAbs. The induction of NAbs with specific germ line genes, such as VH1-69 for CD4i (70) and VH5-51 for V3 (64), is frequently observed in HIV-1-infected patients. A close relationship between VH germ line genes and target epitopes suggests the importance of Ig gene usage in the induction of broadly neutralizing antibodies. Therefore, rational design of vaccines has been undertaken based on reactivity to antibodies with the germ line genes used by known broadly neutralizing antibodies (11, 71, 72). Unfortunately, the VH3 germ line gene of B404 is divergent from all human VH3 germ line genes, suggesting the absence of a human counterpart. This may partially explain why B404-like NAbs have not been identified in HIV-infected humans, although the structure of HIV-1 Env, which is different from that of SIV, significantly affects immunogenicity of the B404 epitope. Rhesus macaque-specific germ line genes were also used by NAbs against the quaternary epitope of HIV-1 Env from simian and human immunodeficiency virus (SHIV)-infected macaques, but their germ line genes were different from the VH3 germ line gene used by B404 (73). Even in the presence of a human VH gene counterpart, the antibody response to a neutralizing epitope may differ between rhesus macaques and humans (74). In addition to the genetic diversity of germ line genes, the rhesus macaque CDRH3 repertoire differs from that of humans, resulting in species-specific antibody repertoires (75). This species specificity in antibody induction is a problem in the evaluation of HIV-1 vaccines in animal models, especially those designed for specific neutralizing epitopes of HIV-1. Conversely, K8, the CD4i NAb from a SIV-infected macaque, used the rhesus VH1 germ line gene, an analog of human VH1-69 frequently used by CD4i NAbs in HIV-1-infected humans (70). Thus, the mechanism of induction of CD4i NAbs with VH1-69 may be common in both humans and rhesus macaques. To analyze vaccine candidates properly in nonhuman primates, similarities and differences in antibody response between rhesus macaques and humans should be considered.

B404 recognizes a conformational epitope consisting of the V3 and V4 loops. The enhanced exposure of the epitope in trimeric Env by sCD4 and efficient neutralization of neutralization-resistant SIV strains by the scFv form of B404 suggests that the B404 epitope is sterically masked by the V1/V2 loops and glycans, analogous to CD4i and V3 epitopes (46, 65, 76). Consistent with this interpretation, B404 reacted more intensely to Env mutants lacking the V1 and V2 loops than to the wild-type Env. MD simulation supported these observations by indicating changes in the structural dynamics of V3/V4 loops and their neighboring regions in gp120 of resistant variants with F277V and N295S mutations in the C2 region. The acquisition of resistance to the broadly neutralizing antibodies b12, PG9, and PG16 due to C2 mutations far from the target epitopes was also observed in HIV-1 CRF01_AE (77, 78). MD simulation is a powerful computational method for analyzing structural dynamics of proteins in solution on the basis of theoretical and empirical principles in physical chemistry (79) and has been applied to research on viruses (80). The structural dynamics of protein surfaces in solution plays a key role in protein interactions, and MD simulation is advantageous in speculation about interactions between proteins containing flexible regions, such as V3 and V4 loops. Analysis of fluctuation changes in mutant proteins is useful to identify the regions which affect protein-protein interaction.

Although the V3 and V4 loops are known to contain linear epitopes for antibody-mediated neutralization in SIV infection, no conformational MAb against SIV with characteristics similar to those of B404 has been reported (43, 47, 66–68). Several MAbs to conformational epitopes that include the V3 region, such as PGT antibodies, represented by PGT128 (15, 19), 3BC176, and 3BC315 (81), were isolated from HIV-1-infected patients. The PGT128 epitope consists of the short segment of the V3 loop and 2 neighboring glycans (19), but the binding of B404 is independent of these glycans near the V3 region. The epitope of 3BC176 and 3BC315 is close to the V3 loop, and their binding is partially enhanced by CD4 binding, similar to that of B404 (81). However, in contrast to B404, 3BC176 and 3BC315 do not bind to monomeric Env and compete with CD4i antibodies, suggesting that their epitope is different from that of B404. Although we have not determined the precise B404 epitope, the characteristics of B404 that are similar to those of CD4i and V3 antibodies suggest that B404 recognizes a conserved region important for binding to the CCR5 coreceptor (46, 65, 76, 82).

Despite recent progress in understanding the broad neutralization of HIV-1, epitopes for potent and broad neutralization have not been analyzed in an SIV model because NAb analysis using SIV cannot be directly applied to HIV-1. The main disadvantage of SIV is the antigenicity difference relative to HIV-1, which makes examination of neutralizing epitopes of HIV-1 impossible. Although the use of SHIV expressing HIV-1 Env enables the evaluation of vaccine candidates designed for target epitopes of HIV-1 in nonhuman primates, an SIV model was more predictive of vaccine efficacy than a SHIV model in clinical trials of a T-cell-based vaccine (83, 84). For comprehensive assessment of immunity induced by vaccine candidates, proof-of-concept trials using the SIV model should be considered before further efficacy trials. The identification of B404 with its potent and broad neutralizing activity against SIV will be a useful adjunct for evaluating the mechanism of neutralization in an SIV-macaque model and will contribute to the development of HIV-1 vaccines.

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CD4 mimics as HIV entry inhibitors: Lead optimization studies of the aromatic substituents

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ABSTRACT

Several CD4 mimics have been reported as HIV-1 entry inhibitors that can intervene in the interaction between a viral envelope glycoprotein gp120 and a cell surface protein CD4. Our previous SAR studies led to a finding of a highly potent analogue **3** with bulky hydrophobic groups on a piperidine moiety. In the present study, the aromatic ring of **3** was modified systematically in an attempt to improve its antiviral activity and CD4 mimicry which induces the conformational changes in gp120 that can render the envelope more sensitive to neutralizing antibodies. Biological assays of the synthetic compounds revealed that the introduction of a fluorine group as a *meta*-substituent of the aromatic ring caused an increase of anti-HIV activity and an enhancement of a CD4 mimicry, and led to a novel compound **13a** that showed twice as potent anti-HIV activity compared to **3** and a substantial increase in a CD4 mimicry even at lower concentrations.

1. Introduction

The first step of HIV entry into host cells is the interaction of a viral envelope glycoprotein gp120 with the cell surface protein CD4.[1] Such a viral attachment process is an attractive target for the development of the drugs to prevent the HIV-1 infection of its target cells.[2] Several small molecules including BMS-806,[3] IC-9564[4] and NBDs[5] have been identified that inhibit the viral attachment process by binding to gp120. Recently, we and others have been exploring the potentials of NBDs-derived CD4 mimics as a novel class of HIV entry inhibitors (Fig. 1).[6–8]

Small molecular CD4 mimics identified by an HIV syncytium formation assay showed potent cell fusion and virus cell fusion inhibitory activity against several HIV-1 laboratory and primary isolates.[5] Furthermore, the interaction of CD4 mimics with a highly conserved and functionally important pocket on gp120, known as the 'Phe43 cavity', induces conformational changes in gp120,[9] a process which occurs with unfavorable binding entropy, leading to a favorable enthalpy change similar to those caused by binding of the soluble CD4 binding to gp120. These unique properties render CD4 mimics valuable not only for the development of entry inhibitors, but which also, when combined with neutralizing antibodies function as envelope protein openers-putatively, stimulants.[10]

The structure of the complex formed by NBD-556 (**1**) bound to the gp120 core from an HIV-1 clade C strain (C1086) was recently determined by X-ray analysis (PDB: 3TGS).[11] As expected with molecular modeling by us[8a] and others,[6a] NBD-556 binds with Phe43 cavity with its *p*-chlorophenyl ring inserted into the cavity, and in addition multiple contacts were observed, with Trp112, Val255, Phe382, Ile424, Asn425, Trp427, Gly473, and Val430 of gp120 were observed (Fig. 2). However, no obvious interaction with Arg59 of CD4 was observed, although the salt bridge formation between Arg59 of CD4 and Asp368 of gp120 is a critical interaction of the viral attachment.[12] Based on this binding model, several potent compounds were recently identified.[6c,7]

Prior to those studies, we performed structure–activity relationship (SAR) studies based on the modification of the piperidine moiety of CD4 mimics to interact with Val430 and/or Asp368. These resulted in the discovery of a potent compound **3** which has bulky hydrophobic groups on its piperidine ring, and shows significant anti-HIV activity and lower cytotoxicity than other known CD4 mimics.[8c] Our study of the docking of **3** into the Phe43 cavity of gp120 suggests that the cyclohexyl group of **3** can interact hydrophobically with the isopropyl group of Val430.

We hypothesized that the optimization of the aromatic ring of **3** would lead to an increase of antiviral activity and CD4 mimicry, the latter inducing the conformational changes in gp120. Here, we de-

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