X = Cl, Br, Me
Y = H, F

Figure 1. CD4 mimics.

Asp368 and a hydrophobic interaction with Val430, are critical for biological activity. LaLonde et al. focused on modifications of the piperidine moiety using computational approaches, adducing evidence for the importance of these interactions to the binding affinity against gp120.[13] Based on these results, we envisioned that an enhancement of the interaction of CD4 mimics with residues associated with the Phe43 cavity in gp120 would lead to the increase of their potency and CD4 mimicry inducing the conformational changes of gp120, and the decrease of their cytotoxicity. Thus, in this study a series of CD4 mimics, which were designed to interact with the conserved residues in the Phe43 cavity, were synthesized to increase binding affinity for gp120, and the appropriate SAR studies were performed.

2. Results and discussion

Two types of CD4 mimic analogs were designed: (1) CD4 mimics with the ability to interact electrostatically with Asp368, and (2) CD4 mimics with the ability to interact hydrophobically with Val430 (Fig. 2). The X-ray structure of gp120 bound to soluble CD4 (PDB: 1RZJ) revealed that the guanidino group of Arg59 of CD4 is involved in a hydrogen bond with Asp368 of gp120. In order to mimic this interaction, a guanidino and related groups such as thiourea and urea were introduced to the piperidine moiety of the CD4 mimic derivative COC-021, which was developed in order to modify the nitrogen of the piperidine moiety and which showed

biological activity, including anti-HIV activity and CD4 mimicry, similar to that of the parent compound NBD-556.[12] Furthermore, to interact with Val430 by hydrophobic interaction, the methyl groups on the piperidine ring were replaced with cyclohexyl groups to prepare a novel CD4 mimic analog with enhanced hydrophobicity.

2.1. Chemistry

The syntheses of CD4 mimics are outlined in Scheme 1. CD4 mimics with guanidine, thiourea, and urea groups on the piperidine moiety were prepared using our previously reported method.[12] Coupling of p-chloroaniline with ethyl chloroglyoxylate followed by aminolysis of the ethyl ester with 4-amino-N-benzylpiperidine under microwave conditions (150 °C, 3 h) gave the corresponding amide. Removal of the benzyl group with 1-chloroethyl chloroformate[14] gave the free piperidine moiety, which was modified to produce the desired compounds 4-8 (Scheme 1).

For synthesis of a CD4 mimic derivative with two cyclohexyl groups, treatment of 2,2,6,6-tetramethylpiperidin-4-one 9 with cyclohexanone in the presence of ammonium chloride furnished a 2,6-substituted piperidin-4-one derivative,[15] and reductive amination with benzylamine and subsequent removal of benzyl group provided a primary amine 10. Microwave-assisted aminolysis of ester 2 with amine 10 yielded the desired dicyclohexyl-substituted analog 11 (Scheme 2). The synthesis of the other compounds is described in Supplementary data.

2.2. Biological studies

The anti-HIV activity of synthetic CD4 mimics was evaluated in a single-round viral infective assay. Inhibition of HIV-1 infection was measured as reduction in β-galactosidase gene expression after a single-round of virus infection of TZM-bl cells as described previously.[9] IC$_{50}$ was defined as the concentration that caused a 50% reduction in the β-galactosidase activity (relative light units [RLU]) compared to virus control wells. Cytotoxicity
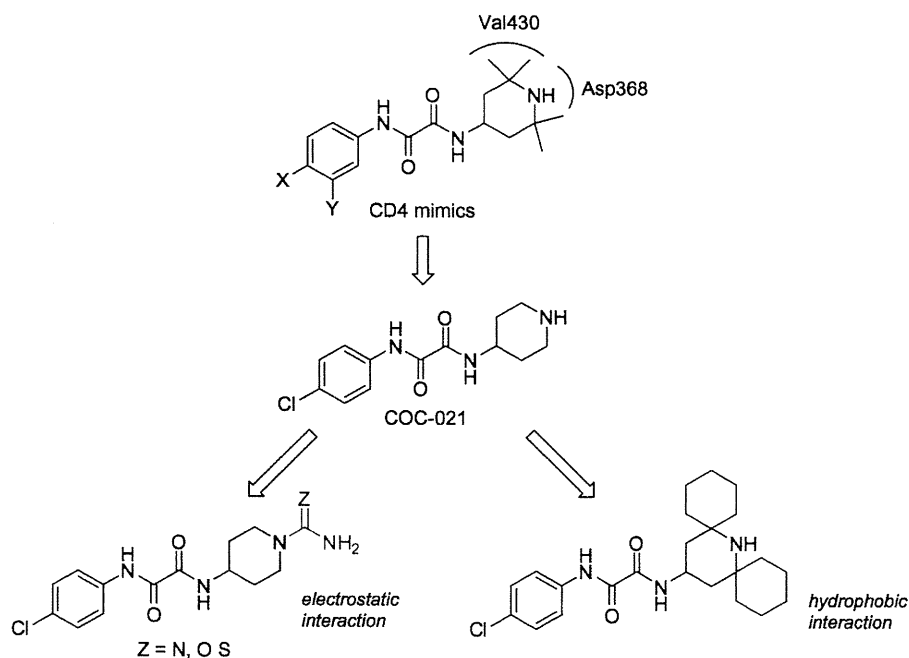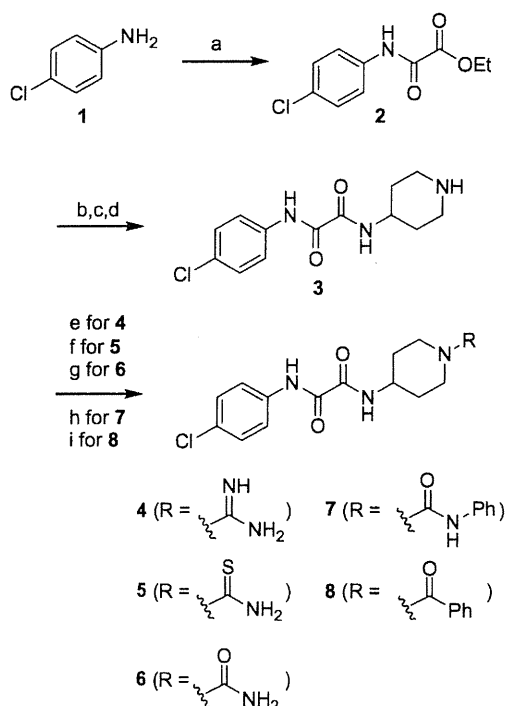

Figure 2. Design strategy for novel CD4 mimics with enhanced electrostatic/hydrophobic interaction.
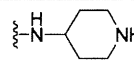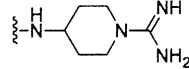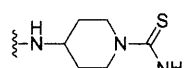
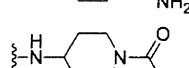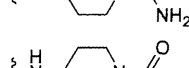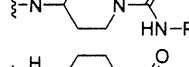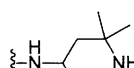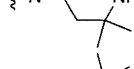**Scheme 1.** Synthesis of N-modified piperidine derivatives **4–8**. Reagents and conditions: (a) Ethyl chloroglyoxylate, Et$_3$N, THF, quant.; (b) 1-benzyl-4-aminopiperidine, Et$_3$N, EtOH, 150 °C, microwave, 78%; (c) 1-chloroethyl chloroformate, CH$_2$Cl$_2$; (d) MeOH, reflux, 64% in two steps; (e) 1H-pyrazole-1-carboxamidine hydrochloride, Et$_3$N, DMF, 61%; (f) (trimethylsilyl)isothiocyanate, CHCl$_3$, 36%; (g) (trimethylsilyl)isocyanate, CHCl$_3$, 30%; (h) phenyl isocyanate, CHCl$_3$, 32%, (i) benzoyl chloride, Et$_3$N, CH$_2$Cl$_2$, 68%.
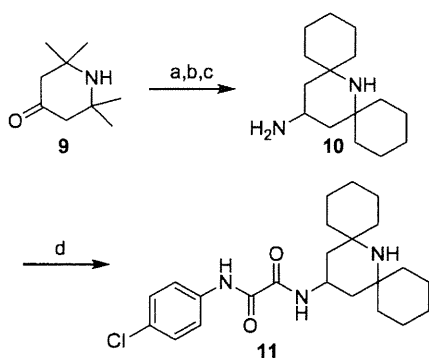
Scheme 2. Synthesis of dicyclohexyl derivative **11**. Reagents and conditions: (a) Cyclohexanone, NH$_4$Cl, DMSO, 60 °C; (b) benzylamine, NaBH$_4$, MeOH; (c) 10% Pd/C, H$_2$, MeOH, 7% from 9; (d) 2, Et$_3$N, EtOH, 150 °C, microwave, 17%.

of the compounds based on the viability of mock-infected PM1/ CCR5 cells was evaluated using WST-8 method. The assay results for the CD4 mimics **3–8** are shown in Table 1. Compound **12** (NBD-556) showed potent anti-HIV activity; its IC$_{50}$ value was 0.61 µM, and it is thus 13–20-fold more potent than the reported values.[11,12] Although previous studies found that compound **13**, with a methyl group at the p-position of the phenyl ring, and compound **3**, with no dimethyl groups on the piperidine ring, showed potent anti-HIV activity, only moderate activities were observed in the current study; this is about 12–14-fold less potency than reported for compound **12** and is probably due to

Table 1
Effects of the nitrogen-substituents on anti-HIV activity and cytotoxicity of CD4 mimic analogs[a]

Compd	X	R	IC$_{50}$[b] (µM)	CC$_{50}$[c] (µM)	SI (CC$_{50}$/IC$_{50}$)
			YTA (R5)		
3[d]	Cl		7.0	51	7.3
4[e]	Cl		6.1	72	12
5	Cl		5.5	42	7.6
6	Cl		8.3	310	37
7	Cl		11	6.2	0.56
8	Cl		5.1	ND	—
12 (NBD-556)	Cl		0.61	35	57
13	Me		8.4	260	31

[a] All data with standard deviation are the mean values for at least three independent experiments (ND = not determined)
[b] IC$_{50}$ values are based on the reduction in the β-galactosidase activity in TZM-bl cells.
[c] CC$_{50}$ values are based on the reduction of the viability of mock-infected PM1/ CCR5 cells.
[d] Desalted by satd NaHCO$_3$ aq.
[e] TFA salts.

the different assay system. All of the synthesized novel derivatives of compound **12** showed moderate to potent anti-HIV activity. A guanidine derivative **4** and thiourea derivative **5** showed potent anti-HIV activities (IC$_{50}$ of **4** = 6.1 µM and IC$_{50}$ of **5** = 5.5 µM) but their potency was approximately 10-fold lower than that of the parent compound **12**. A urea derivative **6** also showed potent anti-HIV activity (IC$_{50}$ = 8.3 µM) and exhibited lower cytotoxicity (CC$_{50}$ = 310 µM). On the other hand, introduction of a phenyl group in the urea derivative **6**, led to an N-phenylurea derivative **7**, with an increase of cytotoxicity (CC$_{50}$ = 6.2 µM). To examine the influence of the N–H group on anti-HIV activity, an N-benzoyl derivative **8** was also tested. The IC$_{50}$ value of **8** was 5.1 µM, which is equipotent with the thioamide derivative **5**. The N-benzoyl derivative **8** was essentially equipotent with **3** and this result suggests the presence of the hydrogen atom of the N–H group does not contribute to an increase in anti-HIV activity. The thiourea derivative **5** and the N-phenylurea derivative **7**, which have more acidic protons (pK$_a$ of thiourea and N-phenylurea; 21.0 and 19.5,[16] respectively) than the urea derivative **6** (pK$_a$ of urea; 26.9[16]), were found to exhibit relatively strong cytotoxicity. This observation indicates that

Table 2
Anti-HIV activity and cytotoxicity of CD4 mimic analogs 11, 12, and 14–17[a]

Compd	R	YTA (R5)		
		IC_{50}^{b} (μM)	CC_{50}^{c} (μM)	SI (CC_{50}/IC_{50})
11		0.68	120	176
14		3.1	>500	>160
15		>100	>500	–
16		>100	>500	–
17		19.8	480	24
12 (NBD-556)		0.61	35	57

[a] All data with standard deviation are the mean values for at least three independent experiments

[b] IC_{50} values are based on the reduction in the β-galactosidase activity in TZM-bl cells.

[c] CC_{50} values are based on the reduction of the viability of mock-infected PM1/CCR5 cells.

Table 3
Anti-HIV activity of CD4 mimic 12 and dicyclohexyl derivative 11[a]

Compd	R	IC_{50}^{b} (μM) Single-round assay	IC_{50}^{c} (μM) Multi-round assay
12 (NBD-556)		0.61	0.90
11		0.68	0.56

[a] All data with standard deviation are the mean values for at least three independent experiments.

[b] IC_{50} values of the single-round assay are based on the reduction in the β-galactosidase activity in TZM-bl cells.

[c] IC_{50} values of the multi-round assay are based on the inhibition of HIV-1-induced cytopathogenicity in PM1/CCR5 cells.

substitution on the piperidine moiety of acidic functional groups was unfavorable.

The assay results for CD4 mimics that target hydrophobic interactions are shown in Table 2. Compound 11 showed significant anti-HIV activity (IC_{50} = 0.68 μM) comparable to that of the lead compound 12, but exhibited lower cytotoxicity. Compound 11 showed approximately four-fold less cytotoxicity than 12. The SI of 11 is 176, 3 times higher than that of 12 (SI = 57). This result suggests that substitution of bulky hydrophobic groups into the piperidine moiety may be consistent with lower cytotoxicity of CD4 mimics. It is noteworthy that compound 14, which has a p-fluoroanilino group in place of the piperidine ring, exhibits potent anti-HIV activity (IC_{50} = 3.1 μM) without significant cytotoxicity (CC_{50} >500 μM). The SI of compound 14 is >160, which is comparable to that of 11. However, replacement of the piperidine moiety with a p-bromo- or p-chloroanilino group resulted in the loss of anti-HIV activity. These results suggest that the introduction of a fluorine atom to the piperidine moiety might be consistent with improvement of the anti-HIV activity. Extension of the alkyl chain by two carbons, as in 17 resulted in a 30-fold loss of anti-HIV activity, indicating that relatively rigid structures are preferable for anti-HIV activity.

The anti-HIV activities of 12 and compound 11, which has a higher SI than the parent compound 12 were evaluated in a multi-round viral infective assay and the results are shown in Table 3. In this assay, the IC_{50} value of 12 was 0.90 μM, which was slightly larger value than measured in a single-round assay (IC_{50} = 0.61 μM). Compound 11 showed higher anti-HIV activity (IC_{50} = 0.56 μM) than compound 12, indicating that the introduction of hydrophobic cyclohexyl groups into the piperdine moiety has a positive effect on not only

the cytotoxicity but also the anti-HIV activity. This is possibly due to the stability in the assay condition derived from the hydrophobicity of cyclohexyl group(s). These results are consistent with a previous study of the analog with one hydrophobic gem-dimethyl group on the piperidine moiety, a compound with potent anti-HIV activity and efficient binding affinity for gp120.[13]

To gain insight into the interactions involved in the binding, molecular modeling of compound 11 docked into gp120 (1RZJ) was carried with Sybyl 7.1 (Fig. 3). The binding mode of compound 11 in the Phe43 cavity suggested that the orientation of the piperidine moiety of 11 is different from that in compound 12, and that the cyclohexyl group can be positioned near Val430 with whose isopropyl group it can interact hydrophobically.

Fluorescence activated cell sorting (FACS) analysis was performed as previously reported,[11,12] to evaluate the CD4 mimicry effects on conformational changes of gp120 and the results are shown in Figure 4. Comparison of the binding of an anti-envelope CD4-induced monoclonal antibody (4C11) to the cell surface pretreated with the above CD4 mimics was measured in terms of the mean fluorescence intensity (MFI). Our previous studies revealed that the profile of the binding of 4C11 to the Env-expressing cell surface pretreated with compound 12 was entirely similar to that of pretreatment of soluble CD4. In this FACS analysis, the MFI of pretreatment with compound 12 is 23.13. The profiles of the binding of 4C11 to the cell surface pretreated with compounds 3, 4 and 5 were comparable to that of compound 12 [MFI (3) = 20.54, MFI (4) = 20.85, MFI (5) = 20.24, respectively], suggesting that these derivatives offer a significant enhancement of binding affinity for 4C11. On the other hand, pretreatment with 6 and 8 did not cause significant enhancement of the binding affinity for 4C11, indicating that introduction of a carbonyl group on the piperidine nitrogen is not conducive to CD4 mimicry. The profile of the binding of 4C11 to the Env-expressing cell surface pretreated with compound 11, which had significant anti-HIV activity and lower cytotoxicity than compound 12, (MFI (11) = 22.17) was similar to that of compound 12, suggesting that compound 11 offers significant enhancement of binding affinity for 4C11. This result indicates that compound 11 retains the CD4 mimicry on the conformational changes of gp120. Although compound 14 and compound 17 showed potent anti-HIV activity and no significant cytotoxicity, the profiles pretreated with (MFI (14 and 17) = 15.20 and 15.38) were similar to that of the control (MFI = 14.94), suggesting that these compounds 14 and 17 failed to produce a significant increase in binding affinity for 4C11. These
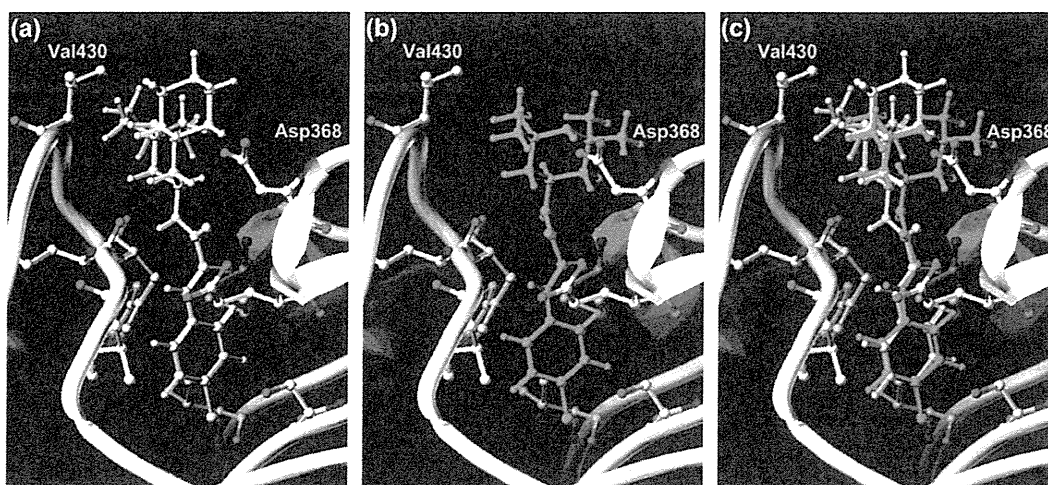
Figure 3. Docking structures of (a) compound **11** and (b) compound **12** bound in the Phe43 cavity of gp120 (1RZJ); (c) merge image of compounds **11** and **12**. Compounds **11** and **12** are represented in yellow and green sticks, respectively. Key residues in the cavity forming interactions with compounds are represented in gray sticks.
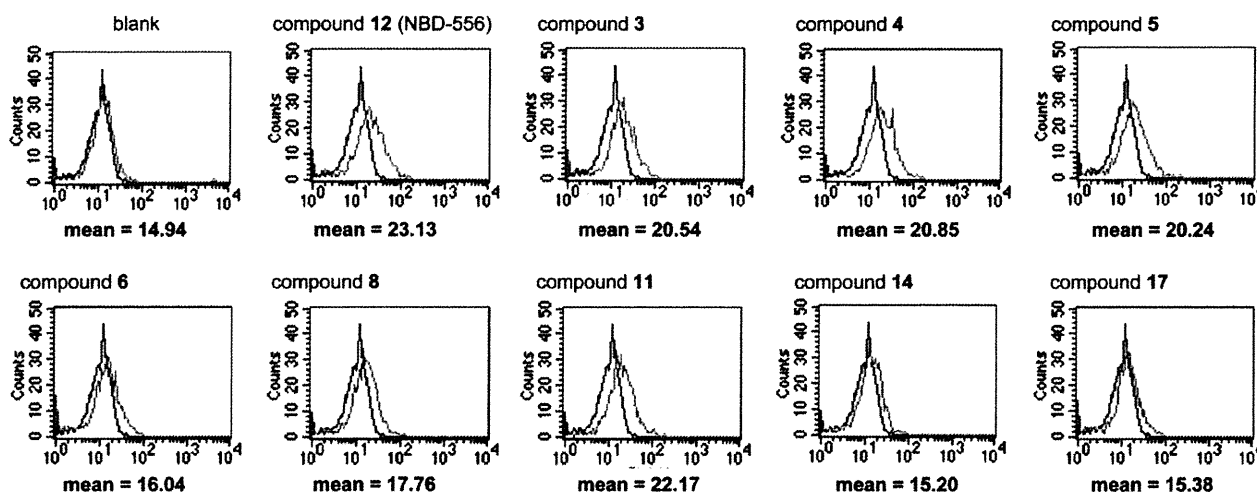

Figure 4. FACS analysis of compounds **12**, **3–6**, **8** (Table 1), **11**, **14**, and **17** (Table 2).

results are consistent with our previous finding that the piperidine ring is critical to the CD4 mimicry of the conformational changes in gp120.

3. Conclusion

A series of CD4 mimics were designed and synthesized to interact with the conserved residues in the Phe43 cavity of gp120 to investigate their anti-HIV activity, cytotoxicity, and CD4 mimicry as a function of conformational change of gp120. The biological activities of the synthetic compounds indicate that (1) the hydrogen atom of the piperidine moieties contributes significantly to cytotoxicity, and (2) installation of bulky hydrophobic groups into the piperidine moiety can increase anti-HIV activity and decrease cytotoxicity thus providing a novel compound with higher selective index than those of the original CD4 mimics. Furthermore, this modification has no great influence on the CD4 mimicry on the conformational change of gp120. Thus, compound **11** is promising for further studies. More detailed SAR investigations with respect

to the substitution on the piperidine moiety have been ongoing studies.

4. Experimentals

^{1}H NMR and ^{13}C NMR spectra were recorded using a Bruker Avance III spectrometer. Chemical shifts are reported in δ (ppm) relative to Me$_4$Si (in CDCl$_3$) as internal standard. Low- and high-resolution mass spectra were recorded on a Bruker Daltonics microTOF focus in the positive and negative detection mode. For flash chromatography, Wakogel C-200 (Wako Pure Chemical Industries, Ltd) and silica gel 60 N (Kanto Chemical Co., Inc.) were employed. For analytical HPLC, a Cosmosil 5C$_{18}$-ARII column (4.6 × 250 mm, Nacalai Tesque, Inc., Kyoto, Japan) was employed with a linear gradient of CH$_3$CN containing 0.1% (v/v) TFA at a flow rate of 1 cm^3 min^{-1} on a JASCO PU-2089 plus (JASCO Corporation, Ltd., Tokyo, Japan), and eluting products were detected by UV at 220 nm. Preparative HPLC was performed using a Cosmosil 5C$_{18}$-ARII column (20 × 250 mm, Nacalai Tesque, Inc.) on a JASCO PU-2087 plus (JASCO Corporation, Ltd, Tokyo, Japan) in a suitable

gradient mode of CH₃CN solution containing 0.1% (v/v) TFA at a flow rate of 7 cm³ min⁻¹. Microwave reactions were performed in Biotage Microwave Reaction Kit (sealed vials) in an Initiator™ (Biotage). The wattage was automatically adjusted to maintain the desired temperature for the desired period of time.

4.1. Chemistry

4.1.1. N¹-(4-Chlorophenyl)-N²-(piperidin-4-yl)oxalamide (3)

To a stirred solution of p-choroaniline (1) (14.0 g, 110 mmol) in THF (146 mL) were added ethyl chloroglyoxylate (8.13 mL, 73.2 mmol) and triethylamine (Et₃N) (15.2 mL, 110 mmol) at 0 °C. The mixture was stirred for 6 h at room temperature. After the precipitate was filtrated off, the filtrate solution was concentrated under reduced pressure. The residue was dissolve in EtOAc, and washed with 1 M HCl, saturated NaHCO₃ and brine, then dried over MgSO₄. Concentration under reduced pressure gave the crude ethyl oxalamate, which was used without further purification. To a solution of the above ethyl oxalamate (1.27 g, 5.25 mmol) in EtOH (13.0 mL) were added Et₃N (1.46 mL, 10.5 mmol) and 4-amino-1-benzylpiperidine (2.97 mL, 15.8 mmol). The reaction mixture was stirred for 3 h at 150 °C under microwave irradiation. After being cooled to room temperature, the crystal was collected and washed with cold EtOH and n-hexane, and dried under reduced pressure to provide the corresponding amide (1.58 g, 81% yield) as colorless crystals. To a stirred solution of S1 (1.46 g, 3.90 mmol) in CH₂Cl₂ (39.0 mL) was added dropwise 1-chloroethyl chloroformate (0.860 mL, 7.80 mmol) at 0 °C. After being stirred at room temperature for 30 min, the mixture was refluxed for 1 h. After concentration under reduced pressure, the residue was dissolved in MeOH and then refluxed for 1 h. After concentration under reduced pressure, the residue was diluted with EtOAc and washed with saturated NaHCO₃ and brine, then dried over MgSO₄. After concentration under reduced pressure, the residue was washed with cold EtOAc, and dried under reduced pressure to provide the title compound 3 (778 mg, 71% yield) as white powder.

¹H NMR (400 MHz, CDCl₃) δ 1.39–1.52 (m, 2H), 1.92–2.01 (m, 2H), 2.67–2.79 (m, 2H), 3.06–3.19 (m, 2H), 3.83–3.95 (m, 1H), 7.34 (d, J = 8.80 Hz, 2H), 7.44 (d, J = 7.64 Hz, 1H), 7.59 (d, J = 8.80 Hz, 2H), 9.28 (s, 1H); ¹³C NMR (125 MHz, CDCl₃) δ 33.0 (2C), 45.2 (2C), 47.9, 21.0 (2C), 129.3 (2C), 130.5, 135.0, 157.6, 158.8; HRMS (ESI), m/z calcd for C₁₃H₁₇ClN₃O₂ (MH⁺) 282.1004, found 282.1002.

4.1.2. N¹-(1-Carbamimidoylpiperidin-4-yl)-N²-(4-chlorophenyl)oxalamide (4)

To a stirred solution of 3 (50.0 mg, 0.178 mmol) in DMF (20.0 mL) was added 1-aminopyrazole hydrochlride (312 mg, 2.13 mmol) and Et₃N (0.390 mL, 28.1 mmol). The reaction mixture was stirred at room temperature for 24 h. After concentration under reduced pressure, purification by preparative HPLC gave the trifluoroacetate of the title compound 4 as white powder (36.0 mg, 61% yield).

¹H NMR (500 MHz, DMSO) δ 1.41–1.55 (m, 2H), 1.59–1.71 (m, 2H), 2.70–2.74 (m, 2H), 3.74–3.87 (m, 1H), 3.88–4.03 (m, 2H), 5.93 (s, 2H), 7.42 (d, J = 9.00 Hz, 2H), 7.85 (d, J = 9.00 Hz, 2H), 8.95 (d, J = 9.00 Hz, 1H), 10.80 (s, 1H); ¹³C NMR (125 MHz, DMSO) δ 31.3 (2C), 43.0 (2C), 47.6, 122.4 (2C), 128.6, 129.1 (2C), 137.1, 158.2, 159.3, 159.5; HRMS (ESI), m/z calcd for C₁₄H₁₉ClN₅O₂ (MH⁺) 324.1222, found 324.1213.

4.1.3. N¹-(1-Carbamothioylpiperidin-4-yl)-N²-(4-chlorophenyl)oxalamide (5)

To a stirred solution of 3 (140 mg, 0.498 mmol) in CHCl₃ (5.00 mL) was added trimethylsilyl isothiocyanate (141 mL,

1.00 mmol) and stirred at room temperature for 1 h. The precipitate was collected and washed with cold CHCl₃, and dried under reduced pressure to provide the title compound 5 as white powder. (62.0 mg, 36% yield).

¹H NMR (400 MHz, DMSO) δ 1.45–1.69 (m, 2H), 1.69–1.81 (m, 2H), 2.67–2.81 (m, 2H), 3.02–3.16 (m, 2H), 3.75–3.89 (m, 1H), 7.41 (d, J = 9.00 Hz, 2H), 7.85 (d, J = 9.00 Hz, 2H), 9.00 (d, J = 8.50 Hz, 1H), 10.80 (s, 1H); ¹³C NMR (125 MHz, DMSO) δ 27.8 (2C), 42.3 (2C), 44.4, 122.0 (2C), 128.2, 128.6 (2C), 129.5, 136.6, 158.6, 159.4; Anal. calcd for C₁₄H₁₈ClN₄O₂S: C, 49.34; H, 5.03; N, 16.44. Found: C, 49.32; H, 4.76; N, 16.11.

4.1.4. N¹-(1-Carbamoylpiperidin-4-yl)-N²-(4-chlorophenyl)oxalamide (6)

To a stirred solution of 3 (60.0 mg, 0.213 mmol) in CHCl₃ (1.10 mL) was added trimethylsilyl isocyanate (56.0 μL, 0.421 mmol), and the mixture was stirred at room temperature for 1 h. The precipitate was collected and washed with cold CHCl₃, and dried under reduced pressure to provide the title compound 6 (20.1 mg, 30% yield) as white powder.

¹H NMR (500 MHz, DMSO) δ 1.44–1.55 (m, 2H), 1.58–1.71 (m, 2H), 2.65–2.78 (m, 2H), 3.76–3.87 (m, 1H), 3.87–4.01 (m, 2H), 5.94 (s, 1H), 7.42 (d, J = 9.00 Hz, 2H), 7.86 (d, J = 9.00 Hz, 2H), 8.95 (d, J = 9.00 Hz, 1H), 10.80 (s, 1H); ¹³C NMR (125 MHz, DMSO) δ 30.8 (2C), 42.6 (2C), 47.1, 122.0 (2C), 128.1, 128.6 (2C), 136.7, 157.8, 158.8, 159.0; HRMS (ESI), m/z calcd for C₁₄H₁₈ClN₄O₃ (MH⁺) 325.1062, found 325.1060.

4.1.5. N¹-(4-Chlorophenyl)-N²-(1-(phenylcarbamoyl)piperidin-4-yl)oxalamide (7)

To a stirred solution of 3 (140 mg, 0.498 mmol) in CHCl₃ (5.00 mL) was added phenyl isocyanate (54.0 μL, 0.500 mmol) and stirred at room temperature for 1 h. The precipitate was collected and washed with cold CHCl₃, and dried under reduced pressure to provide the title compound 7 as white powder. (64.1 mg, 32% yield).

¹H NMR (500 MHz, DMSO) δ 1.52–1.66 (m, 2H), 1.68–1.80 (m, 2H), 2.81–2.95 (m, 2H), 3.84–3.96 (m, 1H), 4.08–4.20 (m, 2H), 6.91–6.94 (m, 2H), 7.21–7.24 (m, 2H), 7.36–7.52 (m, 4H), 7.86 (d, J = 9.00 Hz, 2H), 8.53 (s, 1H), 8.99 (d, J = 8.50 Hz, 2H), 10.81 (s, 1H); ¹³C NMR (125 MHz, DMSO) δ 31.3 (2C), 43.4 (2C), 47.5, 120.0 (2C), 122.0, 122.4 (2C), 128.6, 128.7 (2C), 129.1 (2C), 137.1, 141.1, 155.2, 159.2, 159.5; HRMS (ESI), m/z calcd for C₂₀H₂₂ClN₄O₃ (MH⁺) 401.1375, found 401.1372.

4.1.6. N¹-(1-Benzoylpiperidin-4-yl)-N²-(4-chlorophenyl)oxalamide (8)

To a stirred solution of 3 (500 mg, 1.78 mmol) in CHCl₃ (17.8 mL) was added benzoyl chloride (307 μL, 2.67 mmol) and the mixture was stirred at room temperature for 1 h. The precipitate was collected and washed with cold EtOAc, and dried under reduced pressure to provide the title compound 8 (232 mg, 34% yield).

¹H NMR (500 MHz, CDCl₃) δ 1.21–1.68 (br, 4H), 1.96–2.08 (br, 2H), 3.02–3.16 (br, 2H), 4.04–4.07 (m, 1H), 7.35 (d, J = 9.00 Hz, 2H), 7.41–7.43 (m, 5H), 7.52 (d, J = 8.00 Hz, 1H), 7.59 (d, J = 9.00 Hz, 2H), 9.25 (s, 1H); ¹³C NMR (125 MHz, CDCl₃) δ 31.4 (2C), 41.0 (2C), 47.6, 121.0 (2C), 126.9 (2C), 128.6 (2C), 129.3 (2C), 129.9, 130.6, 134.8, 135.6, 157.2, 159.0, 170.5; HRMS (ESI), m/z calcd for C₂₀H₂₁ClN₃O₃ (MH⁺) 386.1266, found 386.1276.

4.1.7. Amine (10)

To a stirred solution of 2,2,6,6-tetramethylpiperidin-4-one (7.75 g, 50.0 mmol) and cyclohexanone (15.5 mL, 150 mmol) in DMSO (71.0 mL) was added NH₄Cl (16.1 g, 300 mmol) and stirred at 60 °C for 5 h. The reaction mixture was diluted with H₂O

(150 mL), acidified with 7% aq HCl, and extracted with Et_2O (200 mL × 3). The water layer was adjusted to pH 9 using 10% aq K_2CO_3 and then back-extracted with EtOAc. The extract was washed with brine and dried over Na_2SO_4. After concentration under reduced pressure, the residue was dissolve in MeOH (60.0 mL) and benzylamine (10.9 mL, 100 mmol) was added. After being stirred at room temperature for 1 h, sodium cyanoborohydride was added and stirred at room temperature for 6 h. The reaction mixture was poured into saturated $NaHCO_3$ and extracted with EtOAc, then dried over $MgSO_4$. After concentration under reduced pressure, the residue was dissolve in MeOH (150 mL) and 10% Pd/C (5.32 g, 5.00 mmol) was added and stirred at room temperature for 24 h under hydrogen atmosphere. After the reaction mixture was filtered through celite, the filtrate solution was concentrated under reduced pressure followed by flash chromatography over silica gel with EtOAc–EtOH (4:1) to gave the title compound **10** (820 mg, 7 % yield) as a colorless oil.

^{1}H NMR (500 MHz, CDCl$_3$) δ 0.730 (t, J = 12.0 Hz, 2H), 1.15–1.85 (m, 23H), 2.01–3.7 (m, 2H), 2.95–3.05 (m, 1H); ^{13}C NMR (125 MHz, CDCl$_3$) δ 22.2 (2C), 22.8 (2C), 26.2 (2C), 37.3 (2C), 42.3 (2C), 43.6 (2C), 47.0, 53.2 (2C); HRMS (ESI), m/z calcd for $C_{15}H_{29}N_2$ (MH$^+$) 237.2325, found 237.2321.

4.1.8. N^1-(4-Chlorophenyl)-N^2-(2,6-dicyclohexylpiperidin-4-yl) oxalamide (11)

To a solution of **10** (722 mg, 3.05 mmol) in EtOH (15.0 mL) was added ethyl 2-((4-chlorophenyl)amino)-2-oxoacetate (363 mg, 1.50 mmol) and triethylamine (0.415 mL, 3.00 mmol) and stirred for 3 h at 150 °C under microwave irradiation. The mixture was filtered and the precipitate was collected and washed with cold EtOH, and dried under reduced pressure to provide the compound **11** (108 mg, 17% yield) as white powder.

^{1}H NMR (500 MHz, DMSO) δ 1.12–1.91 (br, 24H), 4.02–4.07 (m, 1H), 7.42 (d, J = 9.00 Hz, 2H), 7.84 (d, J = 9.00 Hz, 2H), 8.76 (br, 1H), 9.25 (s, 1H); ^{13}C NMR (125 MHz, CDCl$_3$) δ 22.1 (2C), 22.7 (2C), 26.0 (2C), 37.2 (2C), 42.5 (2C), 42.9 (2C), 43.6, 52.7 (2C), 120.9 (2C), 129.3 (2C), 130.4, 135.0, 157.6, 158.8; HRMS (ESI), m/z calcd for $C_{23}H_{33}ClN_3O_2$ (MH$^+$) 418.2256, found 418.2261.

4.1.9. N^1-(4-Chlorophenyl)-N^2-(4-fluorophenyl)oxalamide (14)

To a solution of the ethyl 2-((4-chlorophenyl)amino)-2-oxoacetate (1.21 g, 5.00 mmol) in EtOH (25.0 mL) were added Et$_3$N (1.38 mL, 10.0 mmol) and 4-fluoroaniline **12** (1.44 mL, 15.0 mmol). The reaction mixture was stirred for 3 h at 150 °C under microwave irradiation. After being cooled to room temperature, the crystal was collected and washed with cold EtOH and n-hexane, and dried under reduced pressure to provide the compound **14** (601 mg, 41% yield) as colorless crystals. Compounds **15** and **16** were similarly synthesized.

^{1}H NMR (500 MHz, CDCl$_3$) δ 7.07–7.14 (m, 2H), 7.35–7.40 (m, 2H), 7.59–7.63 (m, 4H), 9.29 (s, 1H), 9.33 (s, 1H); ^{13}C NMR (125 MHz, DMSO) δ 115.8 (d, J = 22.5 Hz, 2C), 122.5 (2C), 122.8 (d, J = 7.5 Hz, 2C), 128.8, 129.1 (2C), 134.4, 137.1, 158.3, 158.9 (d, J = 42.5 Hz), 160.2; HRMS (ESI), m/z calcd for $C_{14}H_{11}ClFN_2O_2$ (MH$^+$) 293.0488, found 293.0485.

4.1.10. N^1-(4-Chlorophenyl)-N^2-(2-(pyridin-2-yl)ethyl) oxalamide (17)

To a solution of the ethyl 2-((4-chlorophenyl)amino)-2-oxoacetate (726.3 mg, 3.00 mmol) in EtOH (10.0 mL) were added Et$_3$N (0.831 mL, 6.00 mmol) and 2-(pyridin-2-yl)ethanamine **14** (1.07 mL, 9.00 mmol). The reaction mixture was stirred for 3 h at 150 °C under microwave irradiation. After being cooled to room temperature, the crystal was collected and washed with cold EtOH and n-hexane, and dried under reduced pressure to provide the title compound **17** (336 mg, 37% yield) as colorless crystals.

^{1}H NMR (500 MHz, CDCl$_3$) δ 3.08 (t, J = 6.50 Hz, 2H), 3.82 (q, J = 6.50 Hz, 2H), 7.12–7.21 (m, 2H), 7.30–7.37 (m, 2H),7.54–7.66 (m 3H), 8.40 (s, 1H), 8.60 (d, J = 5.00 Hz, 1H), 9.26 (s, 1H); ^{13}C NMR (125 MHz, CDCl$_3$) δ 36.5, 39.0, 121.0 (2C), 121.8, 123.4, 129.2 (2C), 130.3, 135.1, 136.7, 149.5, 157.5, 158.6, 159.6; HRMS (ESI), m/z calcd for $C_{15}H_{15}ClN_3O_2$ (MH$^+$) 304.0847, found 304.0850.

4.2. Molecular modeling

The structures of compounds **11** and **12** were built in Sybyl and minimized with the MMFF94 force field and partial charges.[17] Dockings were then performed using FlexSIS through its SYBYL module, into the crystal structure of gp120 (PDB: 1RZJ).

4.3. FACS analysis

JR-FL (R5, Sub B) chronically infected PM1 cells were pre-incubated with 100 μM of a CD4 mimic for 15 min, and then incubated with an anti-HIV-1 mAb, 4C11, at 4 °C for 15 min. The cells were washed with PBS, and fluorescein isothiocyanate (FITC)-conjugated goat anti-human IgG antibody was used for antibody-staining. Flow cytometry data for the binding of 4C11 (green lines, Fig. 4) to the Env-expressing cell surface in the presence of a CD4 mimic are shown among gated PM1 cells along with a control antibody (anti-human CD19: black lines, Fig. 4). Data are representative of the results from a minimum of two independent experiments. The number at the bottom of each graph in Figure 4 shows the mean fluorescence intensity (MFI) of the antibody 4C11.

Acknowledgments

Supplementary data

Supplementary data (NMR charts of compounds) associated with this article can be found, in the online version, at doi:10.1016/j.bmc.2011.09.045.

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INTERNAL MEDICINE

Open-Label Randomized Multicenter Selection Study of Once Daily Antiretroviral Treatment Regimen Comparing Ritonavir-Boosted Atazanavir to Efavirenz with Fixed-Dose Abacavir and Lamivudine

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Abstract

Background The side-effects of anti-retroviral drugs are different between Japanese and Caucasian patients. Severe central nerve system (CNS) side-effects to efavirenz and low rate of hypersensitivity against abacavir characterize the Japanese.

Objective The objective of this study was to select a once daily regimen for further non-inferior study comparing the virological efficacy and safety of the first line once daily antiretroviral treatment regimens in the current HIV/AIDS guideline.

Methods The study design was a randomized, open label, multicenter, selection study. One arm was treated with efavirenz and the other with ritonavir-boosted atazanavir. A fixed-dose lamivudine plus abacavir were used in both arms. The primary endpoint was virologic success (viral load less than 50 copies/mL) rate at 48 weeks. Patients were followed-up to 96 weeks with safety as the secondary endpoint. Clinicaltrials.Gov (NCT 00280969) and the University hospital Medical Information Network (UMIN000000243).

Results A total of 71 participants were enrolled. Virologic success rates in both arms were similar at week 48 [efavirenz arm 28/36 (77.8%); atazanavir arm 27/35 (77.1%)], but were decreased at week 96 to 55.6% in the efavirenz arm and 68.8% in the atazanavir arm (p=0.33). At the 96-week follow-up, 52.8% of the EFV arm and 34.3% of the ATV/r arm reached total cholesterol more than 220 mg/dL and required treatment. None of the patients developed cardiovascular complications in this study by week 96.

Conclusion There was no significant difference in the efficacy of efavirenz and ritonavir-boosted atazanavir combined with lamivudine plus abacavir at 48 weeks. The evaluation of safety was extended to 96 weeks, which also showed no significant difference in both arms.

Key words: HIV, antiretroviral treatment, efavirenz, atazanavir, abacavir, lamivudine

Introduction

The use of a non-nucleoside transcriptase inhibitor (NNRTI) or ritonavir-boosted protease inhibitor as the key drug, combined with two nucleoside reverse-transcriptase inhibitors (NRTI), as the backbone drugs, is recommended as an initial therapy in human immunodeficiency virus type 1 (HIV-1) infection. For the key drug, when efavirenz (EFV) or ritonavir-boosted atazanavir (ATV/r) is selected, once daily therapy is possible. EFV is a widely used NNRTI, however, in some clinical studies conducted in Asia, a higher rate of adverse events, especially central nervous system-related symptoms, has been noted (1-3).

In terms of backbone drugs, didanosine (ddI), stavudine (d4T) and zidovudine (ZDV) were widely used NRTIs.

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However, their mitochondrial toxicity made long-term use difficult (4-7). Due to HLA-B*5701-related hypersensitivity, abacavir (ABC) is listed as the second line drug under the United States Department of Health and Human Services (DHHS) guidelines. However, HLA-B*5701 is quite rare among Japanese, and thus the incidence of hypersensitivity to ABC in Japanese patients is lower than that of Caucasians (8-10). Although tenofovir (TDF) is widely used as the first line drug, the dose-dependent nephrotoxicity is a major concern in Japanese because Japanese body weight is lighter than that of Caucasians (11, 12).

The present study was designed in 2006, when the combination of TDF, lamivudine (3TC) or entiricitabine (FTC), and EFV was the first line regimen of antiretroviral treatment (13). To explore the optimal antiretroviral combination for the best clinical outcome among Japanese HIV-1 patients (14), a selection study was designed to compare the efficacy and safety of once daily treatment with EFV or ATV/r combined with a fixed-dose ABC and 3TC (ABC/3 TC).

Objective

The objective of this study was to select a once daily regimen for further non-inferior study comparing the virological efficacy and safety of the first line once daily antiretroviral treatment regimens in the current HIV/AIDS guideline.

Subjects and Methods

Study design

The study was designed as a randomized, open label, multicenter selection study, which means the superior regimen at the end point is to be selected as alternate arm to compare with the current first line regimen in the next step. Therefore, this study was not to compare superiority or non-inferiority of both arms. As the selection study, the main objective is to select a treatment regimen for further pivotal study and the secondary objective is safety. The primary endpoint was the proportion of patients in each arm who achieved virologic success (HIV-1 RNA less than 50 copies/ mL in plasma) at week 48. The secondary endpoints were death, AIDS and serious non-AIDS events, non-AIDS defining cancer, treatment-related serious or grade 3 to 4 adverse events, and discontinuation of antiretroviral treatment before week 96.

The inclusion criteria of this study were those who were treatment-naïve, HIV-1 positive Japanese men with a CD4+ count ranging from 100 to 300 cell/mm³. The exclusion criteria included current active AIDS, acute retroviral syndrome and persistent active hepatitis B infection (HBs-Ag positive). Patients with a history of 3TC treatment for hepatitis B infection were also excluded. After obtaining informed consent, eligible participants were randomized into once daily

600 mg EFV or 100 mg RTV and 300 mg ATV (EFV arm vs ATV/r arm). All participants received a fixed dose of 600 mg of ABC and 300 mg 3TC (ABC/3TC).

At baseline, the demographic characteristics and a complete medical history were recorded, physical examination was performed, and various laboratory tests were obtained (CD4+ count, HIV-1 RNA, complete blood count, biochemistry, liver and renal function tests, and total cholesterol). Participants were examined at baseline, then every 4 weeks until week 96. Careful clinical examination was provided at each visit, including history taking of any adverse event, adherence to treatment, and physical examination. Furthermore, blood tests were obtained including complete blood count, biochemistry, liver and renal function tests, CD4+ count and HIV-1 RNA. When HIV-1 RNA became less than 50 copies/mL, participants were rescheduled to be seen every 4 to 12 weeks. All participants underwent clinical examination at week 48 as the primary endpoint, then every 12 weeks until week 96 as the secondary follow-up period for evaluation of safety.

The study recruitment period was started on September 1st of 2005 for 2 years. The study protocol was originally designed to follow patients for 48 weeks, however, during the study period, cardiovascular adverse events of ABC-containing regimen were reported (15, 16). Considering the importance of adherence to safety, the follow-up period was extended to 96 weeks.

Independent data and safety monitoring board reviewed virology and safety data by treatment allocation were obtained when all participants had completed 24 weeks of the study. A total of 18 academic medical institutions in Japan participated in this study. The study protocol was approved by the ethics committee of each site and was registered at Clinicaltrials. Gov (NCT00280969) and the University Hospital Medical Information Network (UMIN000000243).

Statistical analyses

The estimated proportion of virologic failure, representing HIV-1 RNA of more than 50 copies/mL at 48 weeks of treatment, was 30% over one year. To choose one treatment group with a probability of 0.90, if it is superior to another treatment by >10%, if any, a sample size of 40 participants per group was necessary according to the selection design (17).

To assess differences in proportions, we used Fisher's exact test and calculated exact confidence intervals (CIs). We conducted intent-to-treat analysis and used the T test to compare the efavirenz arm and the ritonavir boosted atazanavir arm, unless the data showed skewed distribution, in which case the Wilcoxon's test was used. All analyses used a two-sided alfa of 0.05. No adjustment for each test was made for multiple comparisons due to the fact that we have several tests to compare the efficacies and safeties of two groups. All analyses, unless otherwise specified, were determined a priori and were hypothesis driven. Statistical analyses were performed using SAS version 9.1.

Table 1. Baseline Characteristics of Participants

Variable	efavirenz	atazanavir/r	p
Number of patients	36	35	NS
Age (yrs) median	35	36	NS
HIV-RNA (log_{10} copies/mL)			
median	4.6	4.4	NS
range	2.8–5.4	3.0–5.3	
CD4 count (cells/mm^3)			
median	220	226	NS
range	121–323	103–324	
Total Cholesterol (mg/dL)			
median	155.5	159.5	NS
range	122–208	112–215	
Total bilirubin (mg/dL)			
median	0.6	0.5	NS
range	0.3–1.7	0.3–1.5	
ALT (IU/L)			
median	24	20	NS
range	8–71	8–78	
Creatinine (mg/dL)			
median	0.80	0.75	NS
range	0.6–1.03	0.6–1.02	

Results

Participants

In the study recruitment period, 71 participants were randomly assigned to two groups (36 in EFV arm and 35 in ATV/r arm). The baseline characteristics of the subjects are listed in Table 1. Among the 71 participants, 62 (87.3%) for the primary endpoint and 58 (80.6%) for the secondary endpoint completed the study protocol. By week 96, 9 participants had withdrawn due to clinical events, 2 declined to continue the study for personal reasons, one died by accident and 3 were transferred to other non-participating institutions.

Primary endpoint

At week 48, by intent-to-treat, missing-equals-failure analysis, 28 of 36 participants (77.8%, 95% CI: 60.9-89.9) in the EFV arm and 27 of 35 (77.1%, 95% CI: 59.9-89.9) in the ATV/r arm achieved the goal of HIV-1 RNA less than 50 copies/mL. There was no significant difference between the two arms (p=0.95).

Virologic success over time

Figure 1 shows the intent-to-treat analysis of participants who reached virologic success. At week 96, the rates of virologic success in the EFV arm were 55.6% (20 of 36) and 68.6% (24 of 35) in the ATV/r arm (p=0.33). The number of participants with a baseline HIV-1 RNA level of more than 100,000 copies/mL was 5 in the EFV arm and 2 in the ATV/r arm. One participant in each arm withdrew from the study at week 4 due to skin rash. The rest of the participants achieved virologic success in the EFV arm (4 out of 4) and in ATV/r arm (1 out of 1).

Secondary endpoints

In the EFV arm, 7 of 36 participants did not complete the study; 5 of the 7 developed psychiatric symptoms, including suicidal idealization, insomnia and irritation, 2 developed skin rashes and the remaining 2 were lost to follow-up because they were transferred to non-affiliated hospitals. In the ATV/r arm, 6 of 35 patients could not complete the study; one died by accident for unknown reason (the cause of death according to the coroner's report was not related to the cardiovascular system), 2 participants required treatment change (this was due to suicidal idealization in one and to skin rash in the other), one participant withdrew by own wish, one enrolled into another study, and one was transferred to another non-affiliated medical care facility.

Figure 2 shows the change of total cholesterol, liver function and total bilirubin from the baseline. At enrollment in the study, the median total cholesterol in the EFV arm was 155.5 mg/dL (range: 122-208) and in the ATV/r arm was 159.5 mg/dL (range: 112-215). The total cholesterol was not more than 220 mg/dL in any of the participants of both arms at baseline, and there was no significant difference between the two arms. During the study period, the total cholesterol increased to more than 220 mg/dL and required treatment with hypolipidemic agents in 52.8% of the EFV arm and 34.3% of the ATV/r arm. There was a significant increase in total cholesterol from the baseline in both arms (p < 0.05). There was no significant change in liver function tests during the study. New onset grade 3 hyperbilirubinemia was noted in 27 of 35 (77.1%) of the ATV/r arm but in none of the EFV arm. None of the hyperbilirubinemia in the ATV/r arm was associated with altered liver function, altered renal function, nephrolithiasis, or cholelithiasis.

Discussion

This study was designed as selection study, which means the superior regimen at the endpoint is to be selected as an alternate arm to compare with the current first line treatment in the next step. By definition of the selection study, the superior arm does not require statistical significance (17). At week 48, 77.8% of ATV/r arm and 77.1% of EFV arm reached HIV-VL of less than 50 copies/mL. Based on the definition of the selection study, the combination ABC/3TC/ EFV was selected to compare the current first line treatment while the efficacy of each arm was almost even in this study.

In this clinical trial of 71 participants over a period of 96 weeks, no cardiovascular events or severe hypersensitivity reaction against ABC was observed. In this study, the efficacy of EFV combined with ABC/3TC and ATV/r combined with ABC/3TC was similar. Therefore, ABC based regimen can be selected as a safe combination to compare the efficacy of the first line combinations, such as EFV plus TDF/ FTC or ATV/r plus TDF/FTC (18-20), in the next step for the best clinical benefits in Japanese patients.
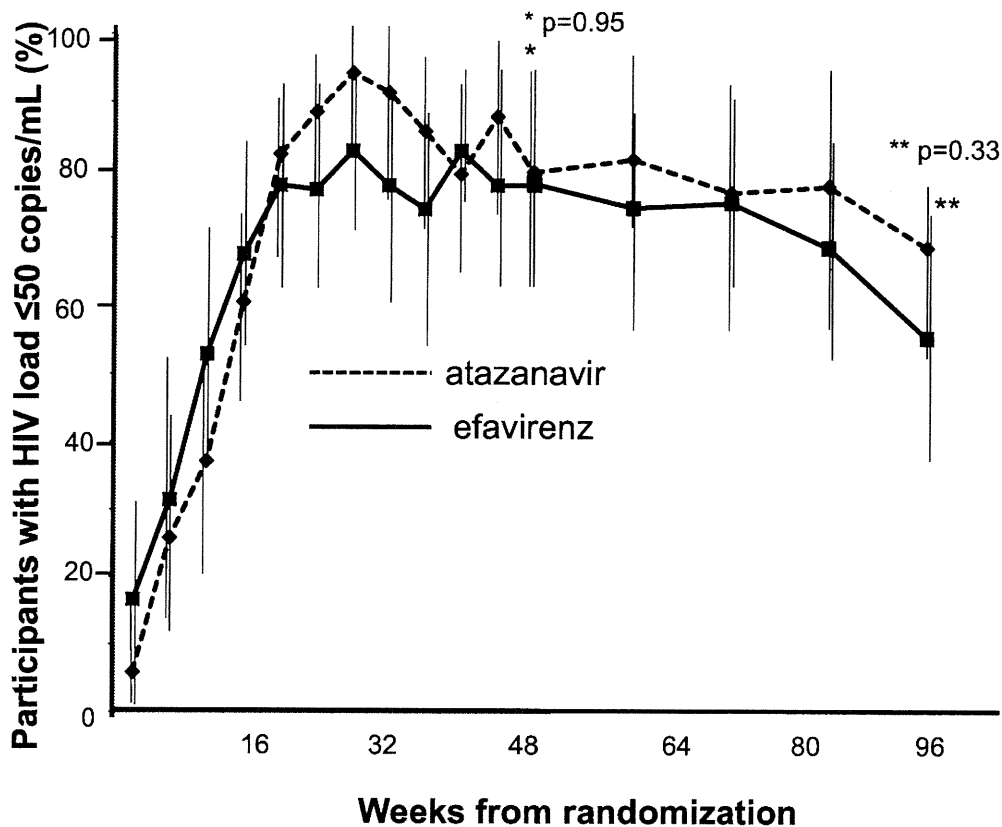
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Figure 1. **Proportions of participants with HIV-RNA less than 50 copies/mL.**
The efficacies of the efavirenz arm and ritonavir-boosted atazanavir arm were compared with intent-to-treat analysis. There were no significant difference between arms at both week 48 (p=0.95) and week 96 (p=0.33).

In February 2008, the United States National Institution of Allergy and Infectious Disease announced that the data and safety monitoring board of ACTG 5202 recommended a modification of the study design because they found that among participants with high viral loads (100,000 or more copies/mL) at the time of screening, treatment combinations that included ABC/3TC were not as effective in controlling the virus as those of regimens containing TDF/FTC (19, 21). At that point, all of the present 71 participants were already enrolled in the study and the baseline HIV-1 RNA of 7 participants was more than 100,000 copies/mL. Of these 7 participants, 2 had already withdrawn from the study by week 4, and the rest of participants had reached HIV-1 RNA of less than 50 copies/mL. The safety monitor board made no recommendation to amend the protocol.

As a primary endpoint, 77.8% of the EFV arm and 77.1% of the ATV/r had reached virological success, however, total cholesterol in 58.1% of the EFV arm and 46.9% of the ATV/r arm increased to more than 220 mg/dL, which required treatment. Thus, the overall proportion of participants with good viral suppression and without severe adverse events or treatment modification was 39.6% for the EFV arm and 62.3% for the ATV/r arm. Considering the reasons

for treatment modification, the neuro-psychiatric side effects required a regimen change in the EFV arm. Although several studies concluded that the neuro-psychiatric side effects are transient in nature, one study reported that treatment had to be changed in 16% of patients on EFV due to neuro-psychiatric side effects (22-24). Although there was no significant difference even with the small sample size, 5 out of 36 (13.9%) participants on EFV in our study required treatment change, compared with only 1 out of 35 (2.9%) of the ATV/r arm. This aspect of our study was similar to that reported in the Euro SIDA study (24). In the Swiss Cohort study, the treatment-limiting CNS adverse events was 3.8 (95% CI 2.7-5.2) per 100 person-years and it was clearly related to EFV (25). Considered together, these results emphasize the need for close observation of patients treated with EFV.

The incidence of hyperbilirubinemia in the present study was 77.1% in the ATV/r arm but none of these patients was above grade 4. Furthermore, none of the patients in this study developed liver function abnormality, altered renal function, renal stones, or cholelithiasis. As reported by Torti et al and Josephson et al, such clinical outcome can be used as a marker of adherence to ATV therapy (26, 27).

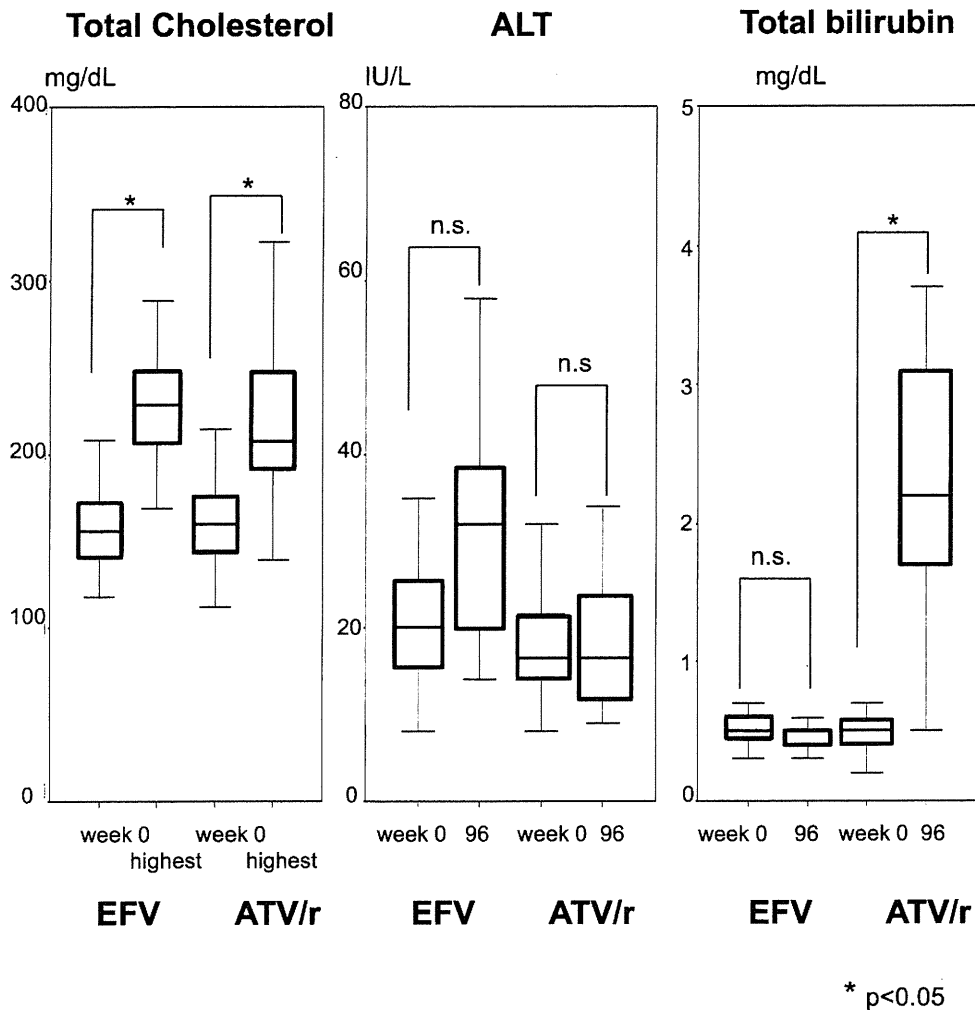Limitations of this study include a small sample size.

Figure 2.　Changes from baseline in total cholesterol, ALT and total bilirubin.
ALT and total cholesterol at week 96 were compared with the baseline values. Since participants who developed hyperlipidemia were treated with lipid-lowering agents during the study period, the highest levels registered in each participant during the follow-up were collected for analysis. There were no significant differences in total cholesterol and ALT between the two arms, while hyperbilirubinemia was significantly higher in the ATV/r arm. Modification of treatment due to hyperbilirubinemia was not required in any of the patients of the ATV/r arm. In these box-and-whisker plots, the lines within the boxes represent median values; the upper and lower lines of the boxes represent the 25th and 75th percentiles, respectively; and the upper and lower bars outside the boxes represent the 90th and 10th percentiles, respectively.

Considering many studies on HIV treatment held in western countries that enrolled few Asian HIV-1 patients, it is important to collect data from Asian population. The current United States Department of Health and Human Services guidelines recommend TDF/FTC as the first line regimen, while the European AIDS Clinical Society recommends 3TC and ABC addition to TDF and FTC alone (28, 29). TDF/FTC is a known potent antiretroviral agent, however, its long-term efficacy and safety remain unclear (11, 12). Considering that the combinations of NRTI are limited, the efficacy and safety of ABC in the low HLA-B*5701 population need to be evaluated for wider treatment options for HIV-1 patients (9, 10).

Conclusion

This study was designed as a selection study to compare the virologic efficacy and treatment safety of EFV and ATV/r, both with ABC/3TC, in Japanese patients. The results showed no significant differences in efficacy between the two regimens at week 48. The evaluation of safety was extended to 96 weeks, which also showed no significant difference in both arms. The results of the present study have already been applied as the basis of a follow-up study that is

currently being conducted in Japan to compare NRTI combinations of ABC/3TC and TDF/FTC with ATV/r as key drugs.

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Review Article   **Open Access**

In vitro and In vivo Resistance to Human Immunodeficiency Virus Type 1 Entry Inhibitors

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Abstract

Viral entry is one of the most important targets for the efficient treatment of Human immunodeficiency virus type 1 (HIV-1)-infected patients. The entry process consists of multiple molecular steps: attachment of viral gp120 to CD4, interaction of gp120 with CCR5 or CXCR4 co-receptors, and gp41-mediated fusion of the viral and cellular membranes. Understanding the sequential steps of the entry process has enabled the production of various antiviral drugs to block each of these steps. Currently, the CCR5 inhibitor, maraviroc, and the fusion inhibitor, enfuvirtide, are clinically available. However, the emergence of HIV-1 strains resistant to entry inhibitors, as commonly observed for other classes of antiviral agents, is a serious problem. In this review, we describe a variety of entry inhibitors targeting different steps of viral entry and escape variants that are generated in vitro and in vivo.

Keywords: CD4-gp120 binding inhibitor; CCR5 antagonist; CXCR4 antagonist; Fusion inhibitor; Resistance; HIV-1

Introduction

The development of chemotherapy with antiretroviral agents has reduced the morbidity and mortality of Human immunodeficiency virus type 1 (HIV-1)-infected individuals. Successful treatment of HIV-1-infected patients using chemotherapy is partly due to a combination of different classes of antiviral agents against the viral protease or reverse transcriptase. However, successful eradication of the virus from infected individuals has not been achieved by antiviral treatment, and is often limited by the emergence of drug-resistant HIV-1 strains [1-3]. These problems highlight the need to develop novel anti-HIV-1 drugs that target different steps of the viral replication process. Viral entry is currently one of the most attractive targets for the development of new drugs to control HIV-1 infection. Viral entry proceeds through Env

(gp120, gp41)-mediated membrane fusion, and consists of sequential steps: (i) attachment of viral gp120 to the CD4 receptor; (ii) binding of gp120 to CCR5 or CXCR4 co-receptors; and (iii) fusion of the viral and cellular membranes (Figure 1). A large number of inhibitors targeting different steps of the viral entry process have been developed, including peptides/peptide mimics, small molecules, and monoclonal antibodies (MAb).

Enfuvirtide (also known as T-20) was the first of a new class of drugs known as fusion inhibitors, which was approved by the U.S. Food and Drug Administration (FDA) in 2003. Approval was given for the use of this drug in combination with other anti-HIV-1 medications to treat advanced HIV-1 infection in adults and children aged six years and older. The drug is an antiviral peptide that prevents HIV-1 entry by blocking gp41-mediated fusion [4-6]. Small compounds that can bind to the pockets of the extracellular loops of a coreceptor are expected to be potent antiviral agents. Several small-molecule CCR5 inhibitors have progressed through clinical development [7]. Maraviroc [8,9], a CCR5 antagonist, is the second entry inhibitor approved by the FDA in 2007 for treatment-experienced patients infected with a CCR5-tropic (R5-tropic) virus. Extensive research is currently underway to develop the next generation of entry inhibitors, however, the emergence of viral strains resistant to entry inhibitors, as well as other classes of antiviral
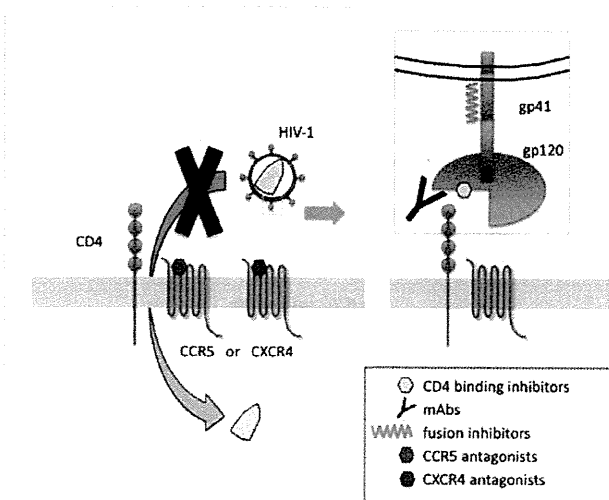

Figure 1: Molecular targets of inhibitors of HIV-1 entry into the target cell.

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agents, has been reported *in vitro* and *in vivo* [7,10]. In this review, we describe the current status of *in vitro* and *in vivo* resistance to HIV-1 entry inhibitors.

Resistance to CD4-gp120 binding inhibitors

Inhibition of CD4-gp120 binding: Entry of HIV-1 into target cells is mediated by the trimeric envelope glycoprotein complex, each monomer consisting of a gp120 exterior envelope glycoprotein and a gp41 transmembrane envelope glycoprotein [11]. Attachment of HIV-1 to the cell is initiated by the binding of gp120 to its primary CD4 receptor, which is expressed on the surface of the target cell. The gp120-CD4 interaction induces conformational changes in gp120 that facilitate binding to additional coreceptors (for example, CCR5 or CXCR4). Attachment inhibitors are a novel class of compounds that bind to gp120 and interfere with its interaction with CD4 [12]. Thus, these agents can prevent HIV-1 from attaching to the CD4+ T cell and block infection at the initial stage of the viral replication cycle (Figure 1). There are two primary types of HIV-1 attachment inhibitors: nonspecific attachment inhibitors and CD4-gp120 binding inhibitor [13].

In this section, we focus on the CD4-gp120 binding inhibitors, the soluble form of CD4 (sCD4), a fusion protein of CD4 with Ig (PRO542), a monoclonal anti-CD4 antibody (Ibalizumab, formerly TNX-355), CD4 binding site (CD4bs) monoclonal antibodies (b12 and VRC01), small-molecule HIV-1 attachment inhibitors (BMS-378806 and BMS-488043), and a new class of small-molecule CD4 mimics (NBD-556 and NBD-557) and a natural small bioactive molecule (Palmitic acid) (Figure 2). We also describe the resistance profiles against these CD4-gp120 binding inhibitors *in vivo* and/or in vitro.

Soluble CD4 (sCD4) and PRO542: In the late 1980s, various recombinant, soluble proteins derived from the N-terminal domains of CD4 were shown to be potent inhibitors of laboratory strains of HIV-1 [14]. Based on the potential of sCD4 to inhibit HIV-1 infection in vitro, this protein was tested for clinical efficacy in HIV-1-infected individuals; however, no effect on plasma viral load was observed [14]. Further examination revealed that doses of sCD4 significantly higher than those achieved in the clinical trial were required to neutralize primary clinical isolates of HIV-1, in contrast to the relatively sensitive, laboratory-adapted strains [15].

The first report of sCD4-resistant variants induced by *in vitro* selection showed that the resistant variant had a single mutation (M434T) in the C4 region [16]. During selection with sCD4, it was also reported that, seven mutations (E211G, P212L, V255E, N280K, S375N, G380R, and G431E) appeared during *in vitro* passage [17]. Further, a recombinant clone containing a V255E mutation was found to be highly resistant to sCD4 compared with the wild-type virus (114-fold higher 50% inhibitory concentration [IC_{50}] value). To determine the mutation profiles obtained during *in vitro* selection with sCD4, the atomic coordinates of the crystal structure of gp120 bound to sCD4 was retrieved from public protein structure database (PDB entry: 1RZJ). From these analyses, it was determined that almost all the described resistance mutations were located the inside the CD4-binding cavity of gp120 [17].

Recently, a novel recombinant antibody-like fusion protein (CD4-IgG2; PRO542) was developed in which the Fv portions of both the heavy and light chains of human IgG2 were replaced with the D1D2 domains of human CD4 [18]. PRO542 was shown to broadly and po-
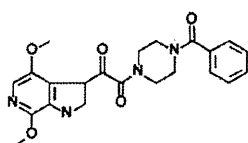
Profile of CD4-gp120 binding inhibitors

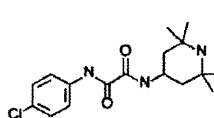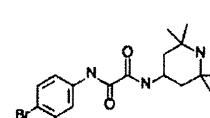|	Structure	Feature	Target	Resistant related mutations (region of gp160) [ref]
sCD4	Soluble form of CD4 domain1-4	First CD4-gp120 binding inhibitor	CD4 binding site of gp120	M434T (C4) [16], V255E(C2) [17]
PRO542	Tetravalent CD4 (domain1-2)-IgG	Developing for microbicide	CD4 binding site of gp120	* N/A
Ibalizumab	Anti-CD4 monoclonal antibody (MAb)	First-in-class, MAb inhibitor of CD4-mediated HIV entry	Domain 2 of CD4	N/A
b12	Anti-CD4 binding site Mab	Neutralizing around 40% of HIV-1 primary isolates	CD4 binding site of gp120	P369L (C3) [27]
VRC01	Anti-CD4 binding site Mab	Neutralizing over 90% of diverse HIV-1 primary isolates	CD4 binding site of gp120	K121A(C1), L179A(V2), T202A(C2), D279A(C2), R304A(V3), I420A(C4), I423A(C4), Y435A(C4), G471A (C5), D474A(C5) [31]
BMS-378806	see below Figure	First small molecule HIV-1 CD4 attachemnt inhibitor	CD4 binding site of gp120	V68A(C1), M426L(C4), M475I(V5), I595F(gp41) [33]
BMS-488043	see below Figure	improved in vitro antiviral activity and PK properties compared to BMS-378806	CD4 binding site of gp120	V68A(C1), L116I(C1), S375I/N(C3), M426L(C4) [34]
NBD-556	see below Figure	Inhibition of HIV-1 entry and enhancing neutralizing potency of Abs	CD4 binding site of gp120	S377N(C3), A433T(C4) [17], S375W(C3), I424A(C4), W427A(C4), V475A(C5) [38]
NBD-557	see below Figure	Inhibition of HIV-1 entry and enhancing neutralizing potency of Abs	CD4 binding site of gp120	N/A
Palmitic acid	CH₃(CH₂)₁₄COOH	A natural small bioactive molecule from *Sargassum fusiforme*	Domain 1 of CD4	N/A

* N/A : not available
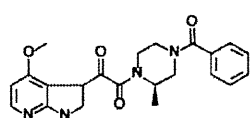
BMS-378806   BMS-488043   NBD-556   NBD-557

Figure 2: Profile of CD4-gp120 binding inhibitors including molecular structures of selected small molecular inhibitors.

tently neutralize HIV-1 subtype B isolates, and was also able to neutralize strains from non-B isolates with the same breadth and potency as for subtype B strains. PRO542 blocks attachment and entry of the virus into CD4+ target cells and were mainly developed for the prevention and transmission of HIV-1 through external application agents, such as microbicides.

Ibalizumab (TNX-355): Monoclonal anti-CD4 antibodies block the interaction between gp120 and CD4 and, therefore, inhibit viral entry [19]. Ibalizumab (formerly TNX-355) was a first-in-class, monoclonal antibody inhibitor of CD4-mediated HIV-1 entry [20]. By blocking CD4-dependent HIV-1 entry, ibalizumab was shown to be active against a broad spectrum of HIV-1 isolates, including recombinant subtypes, as well as both CCR5-tropic and CXCR4-tropic HIV-1 isolates. Many clinical trials with HIV-1-infected patients have demonstrated the antiviral activity, safety, and tolerability of ibalizumab. A nine-week phase Ib study investigating the addition of ibalizumab monotherapy to failing drug regimens showed transient reductions in HIV-1 viral loads and the evolution of HIV-1 variants with reduced susceptibility to ibalizumab. Further, clones with reduced susceptibility to ibalizumab contained fewer potential N-linked glycosylation sites (PNGSs) within the V5 region of gp120. Reduction in ibalizumab susceptibility due to the loss of V5 PNGSs was confirmed by site-directed mutagenesis [21].

Monoclonal antibodies, b12 and VRC01: Several broadly neutralizing MAbs isolated from HIV-1-infected individuals define conserved epitopes on the HIV-1 Env. These include the membrane proximal external region of gp41 targeted by MAbs 4E10 and 2F5 [22]; the carbohydrate-specific outer domain epitope targeted by 2G12 [23]; a V2-V3-associated epitope targeted by PG9/PG16 [24]; and the CD4bs [25] targeted by b12 and VRC01. The CD4bs overlaps with the conserved region on gp120 that is involved in the engagement of CD4. The prototypical CD4bs-directed MAb, b12, neutralizes around 40% of primary isolates, and its structure (in complex with the core of gp120) has been defined [26]. However, Mo et al. [27] reported the first resistant variant induced by *in vitro* selection with b12 that showed a P369L mutation in the C3 region of HIV-1$_{JRCSF}$. Further, several b12-resistant viruses commonly display an intact b12 epitope on the gp120 subunits [28], suggesting that quaternary packing of Env also confers resistance to b12.

A recently described CD4bs-directed MAb, VRC01, had been shown to be able to neutralize over 90% of diverse HIV-1 primary isolates [29]. The structure of VRC01 in complex with the gp120 core reveals that the VRC01 heavy chain binds to the gp120 CD4bs in a manner similar to that of CD4 [30]. The gp120 loop D and V5 regions contain substitutions uniquely affecting VRC01 binding, but not b12 or CD4-Ig binding. In contrast to the interaction of CD4 or b12 with the HIV-1 Env, occlusion of the VRC01 epitope by quaternary constraints was not a major factor limiting neutralization. Interestingly, many Ala substitutions at non-contact residues increased the potency of CD4- or b12-mediated neutralization; however, few of these substitutions enhanced VRC01-mediated neutralization [31]. This study suggests that VRC01 approaches its cognate epitope on the functional spike with less steric hindrance than b12 and, surprisingly, with less hindrance than the soluble form of CD4 itself. These differences might be related to the distinctly different angle of approach to the CD4bs employed by VRC01, in contrast to the more loop-proximal approach employed by CD4 and b12.

BMS-378806 and BMS-488043: BMS-378806 (Figure 2) is a recently identified small-molecule HIV-1 attachment inhibitor with good anti-viral activity and pharmacokinetic properties [32]. BMS-378806 binds directly to gp120 with a stoichiometry of approximately 1:1 and with a binding affinity similar to that of soluble CD4. The potential BMS-378806 target site was localized to a specific region within the CD4 binding pocket of gp120 using HIV-1 gp120 variants carrying either compound-selected resistant substitutions or gp120-CD4 contact site mutations [32]. M426L (C4) and M475I (V5) substitutions located at or near gp120/CD4 contact sites were shown to confer high levels of resistance to the *in vitro* mutated HIV-1 variants, suggesting that the CD4 binding pocket of gp120 was the antiviral target. M434I and other secondary changes (V68A and I595F) also affect the drug susceptibility of recombinant viruses, presumably by influencing the gp120 conformation [33]. BMS-378806 (Figure 2) exhibited decreased, but still significant activity against subtype C viruses, low activity against viruses from subtypes A and D, and poor or no activity against subtypes E, F, G, and Group O viruses [33].

BMS-488043 (Figure 2) is a novel and unique small-molecule that inhibits the attachment of HIV-1 to CD4+ lymphocytes. BMS-488043 exhibits potent antiviral activity against macrophage-, T-cell-, and dual-tropic HIV-1 laboratory strains (subtype B) and potent antiviral activity against a majority of subtype B and C clinical isolates [34]. Data from a limited number of clinical isolates showed that BMS-488043 exhibited a wide range of activity against the A, D, F, and G subtypes, with no activity observed against three subtype AE isolates [34]. The antiviral activity, pharmacokinetics, viral susceptibility, and safety of BMS-488043 were evaluated in an eight-day monotherapy trial that demonstrated significant reductions in viral load. To examine the effects of BMS-488043 monotherapy on HIV-1 sensitivity, phenotypic sensitivity assessment of baseline and post-dosing (day 8) samples were performed. The analyses revealed that four subjects showed emergent phenotypic resistance. Population sequencing and sequence determination of the cloned envelope genes revealed five gp120 mutations at four loci (V68A, L116I, S375I/N, and M426L) associated with BMS-488043 resistance; the most common (substitution at the 375 locus) located near the CD4 binding pocket [35].

NBD-556 and NBD-557: Targeting the functionally important and conserved CD4bs on HIV-1 gp120 represents an attractive potential approach to HIV-1 therapy or prophylaxis. Recently, a new class of small-molecule CD4 mimics was identified [36-38]. These compounds, which include the prototypic compound, NBD-556, and its derivatives, mimic the effects of CD4 by inducing the exposure of the co-receptor-binding site on gp120 [17,39]. NBD-556 and -557 (Figure 2) show potent cell fusion and virus-cell fusion inhibitory activity at low (micromolar) concentrations. A mechanistic study showed that both compounds target viral entry by inhibiting the binding of gp120 to its cellular receptor, CD4. A surface plasmon resonance study showed that these compounds bind to unliganded HIV-1 gp120, but not to CD4 [37]. Another recent study identified NBD-analogs as CD4 mimetics that were used for the prophylaxis and treatment of HIV-1 infection [39]. These compounds inhibited HIV-1 transmission by inhibiting the binding of the natural ligand, CD4, and prematurely triggering the envelope glycoprotein to undergo irreversible conformational changes. NBD-556 binds to the F43 cavity, which is formed by binding of gp120 to the CD4 receptor in a highly conserved manner [17,39].

Recently, our group reported that NBD-556 has potent neutralizing antibody-enhancing activity toward plasma antibodies that cannot access neutralizing epitopes hidden within the trimeric Env, such as gp120-CD4 induced epitope (CD4i) and anti-V3 antibodies [17]. Therefore, to investigate the binding site of NBD-556 on gp120, we in-

duced HIV-1 variants that were resistant to NBD-556 in vitro. Two amino acid substitutions (S375N in C3 and A433T in C4) were identified at passage 21 in the presence of 50 μM NBD-556. The profiles of the resistance mutations after selection with NBD-556 and sCD4 were very similar with regard to their three-dimensional positions.

Elucidation of the detailed molecular mechanisms governing the interaction between gp120 and NBD compounds will enable the optimization and evaluation of this strategy in more complex biological models of HIV-1 infection. Consequently, we will continue to synthesize NBD analogs and search for drugs with greater potency to change the tertiary structure of the envelope glycoproteins and reduce host cytotoxicity [40,41].

Palmitic acid : Previous studies with whole *Sargassum fusiforme* (*S. fusiforme*) extract and with the bioactive SP4-2 fraction demonstrated inhibition of HIV-1 infection in several primary and transformed cell lines [42]. Palmitic acid (PA), which was isolated from the SP4-2 bioactive fraction, specifically block productive X4 and R5-tropic HIV-1 infection [43]. PA occupies a novel hydrophobic cavity on the CD4 receptor that is constrained by amino acids F52-to-L70 [44], which encompass residues that have been previously identified as a region critical for gp120 binding. PA is mainly developed as microbicides [45].

Resistance to CCR5 antagonists

CCR5 antagonists: The binding of HIV-1 to CD4 molecules induces conformational change in gp120, resulting in the recognition of either CCR5 or CXCR4 as a coreceptor for HIV-1 (Figure 1). It has been shown that CCR5-utilizing HIV-1 (R5 virus) is associated with human-to-human transmission that predominate throughout the infection, while CXCR4-utilizing HIV-1 (X4 virus) emerges during the late stage of infection in approximately half of HIV-1-infected individuals and is associated with disease progression [46]. Most strikingly, it had been shown that homozygous individuals having a 32-bp deletion in the CCR5 coding region (CCR5Δ32) were found to be resistant to R5 HIV-1 and remained apparently healthy [47,48]. These findings suggested that CCR5 would be an attractive therapeutic target for treating HIV-1 infection, although it is a host factor. Several small molecule compounds have been developed and were found to bind CCR5 and inhibit R5 virus replication [49-53]. Molecular studies using CCR5 mutants indicated that these compounds bind to a cavity formed by transmembrane helices of CCR5, and thereby inducing the conformational change in an allosteric manner that is not recognized by gp120 of HIV-1 [54-58]. Among these, TAK-779 (Figure 3) was the first compound developed [49] that could inhibit not only HIV-1 infection, but also binding of RANTES (CCR5 ligand) to CCR5-expressing cells at nanomolar concentrations, but was terminated due to poor oral bioavailability. Maraviroc (MVC, UK427, 857) (Figure 3), however, has been approved and used in the clinic for the treatment of HIV-1 infection [8]. Another promising drug, vicriviroc (VCV, SCH-D, SCH-417690) (Figure 3), recently completed phase III trials but has not yet been approved [53].

Resistance to CCR5 antagonists: Although CCR5 antagonists target

Profile of CCR5 antagonist-resistant mutants

| drug | virus used | | resistant-related mutations | | references |
	virus name or *in vivo*	subtype	V3	Non-V3	
AD101	CC1/85	B	H305R, H308P, A316V, G321E	none	[60, 78]
TAK-779	JR-FL_{V3lib}	B	I304V, H305N, I306M, F312L, E317D	none	[63]
TAK-652	KK	unknown	ND*	ND	[59]
VVC	CC1/85	B	none	G516V, M518V, F519I (gp41)	[69, 84, 85]
VVC	RU570	G	K305R, R315Q, K319T	P437S (C4)	[64, 81]
VVC	S91	D	Q315E, R321G	E328K, G429R (C4)	[65]
VVC	*in vivo*	C	K305R, T307I, F316I, T318R, G319E	none	[67]
MVC	CC1/85	B	A316T, I323V	ND	[61]
MVC	JR-FL_{V3lib}	B	I304V, F312W, T314A, E317D, I318V	T199K, T275M (C2)	[62]
MVC	*in vivo*	B	P/T308H, T320H, I322V	D407G, Δ^bN386 (V4)	[66]

*ND, not determined; ^bΔ, deletion

TAK-779   Vicriviroc   Maraviroc

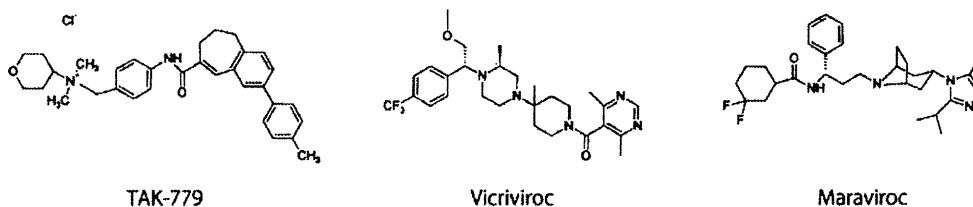**Figure 3:** Profile of CCR5 antagonist-resistant mutants. The CCR5 antagonist-resistant mutants were isolated in vitro and in vivo across different subtypes of HIV-1. Resistance-related mutations were found in the V3 and non-V3 regions including the C2, V4, C4, and gp41. Chemical structures of representative CCR5 antagonists are shown.

a host cell receptor, the *in vitro* [59-64] and *in vivo* [65-67] emergence of viruses resistant to CCR5 antagonists in different subtypes has been reported, as shown in Figure 3. The most intuitive mechanism of resistance to CCR5 antagonists is likely to be the acquisition of CXCR4 use or selection of minority variants of CXCR4- or dual/mixed-tropic viruses [61,68-70]. Numerous studies showed that coreceptor selectivity of HIV-1 is primarily dependent on the third hypervariable region (V3 loop) of gp120 [71-74]. Furthermore, there is a simple rule to predict HIV-1 coreceptor usage called the 11/25 rule: if either the 11th or 25th amino acid position of V3 is positively charged, the virus will use CXCR4 as the coreceptor, otherwise it will use CCR5 [75]. Thus, a single amino acid substitution in the V3 loop is sufficient to acquire usage of CXCR4. However, these are rare cases when the viruses exclusively use CCR5.

Indeed, escape variants from selective pressure by natural ligand for CCR5, such as MIP-1α (CCL3) [76], or CCR5 antagonists [60], still use CCR5 and do not involve acquisition of CXCR4 usage. These studies indicate that acquisition of CXCR4 usage conferred by mutations in the V3 loop of gp120 results in the loss of replication fitness, as previously described [77]. However, the escape variants from CCR5 antagonists usually retain CCR5 usage [60,61,69,78], and recognize the antagonist-bound form of CCR5 as well as the free CCR5 form for entry by the accumulation of multiple amino acid mutations, called non-competitive resistance [61,79]. In non-competitive resistance, once saturating concentrations of antagonists were achieved, further inhibition was not observed, resulting in the plateau of inhibition, while competitive resistance can achieve inhibition of viral replication by a sufficient inhibitor concentration, resulting in a shift in the IC_{50} value (Figure 4). A principal determinant for the reduced sensitivity to CCR5 antagonists has been shown to be the V3 loop of gp120 although the mutations appear to be isolate-specific and antagonist-dependent [33].

In general, primary R5 viruses or laboratory-adapted R5 infectious clones cultured in stimulated peripheral mononuclear cells (PBMCs) have been used for the selection of CCR5 antagonist-resistant variants. However, the use of PBMCs for virus passage is donor-dependent and labor-intensive. Additionally, the use of a single clone for selection would need long-term passage to induce resistant viruses. To overcome these problems, we constructed R5-tropic infectious clones containing a V3 loop library, HIV-1$_{V3Lib}$. To construct replication competent HIV-1$_{V3Lib}$, we chose 10 amino acid positions in the V3 loop and incorporated random combinations of the amino acid substitutions derived from 31 subtype B R5 viruses into the V3 loop library (Figure 5). This novel

in vitro system enabled the selection of escape variants from CCR5 antagonists over a relatively short time period.

In addition to the V3 library, we are currently using PM1/CCR5 cells for virus passages. The PM1/CCR5 cell line was generated by standard retrovirus-mediated transduction of parental PM cell line with the CCR5 gene, as previously described [63,76], and is highly sensitive to the R5 viruses compared to the parental PM1 cell line. Remarkably, the infection of PM1/CCR5 cells with R5 viruses induces prominent cell fusion, which is clear sign of virus proliferation. Thus, the use of PM1/CCR5 cells with the HIV-1$_{V3Lib}$ allows us to focus on the contribution of the V3 loop in gp120 in CCR5 antagonist-resistance with a shortened selection period compared to the use of PBMCs with wild-type virus. As expected, we were able to isolate TAK-779- [63] and MVC-resistant [62] variants using replication competent HIV-1$_{V3Lib}$. Indeed, TAK-779- and MVC-resistant variants were determined to contain several amino acid substitutions within the V3 loop sequence. However, MVC-resistant variants also contained several amino acid substitutions in non-V3 regions (T199K and T275M), such as elsewhere in the gp120 to retain infectivity [80,81]. However, these mutations could not confer non-competitive resistance, indicating the importance of the V3 loop for non-competitive resistance.

Mechanisms of resistance: It is thought that docking of gp120 to CCR5 without CCR5 antagonists involves interactions of both the V3 tip with the second extracellular loop of CCR5 (ECL2) and the V3 stem-C4 region (bridging sheet) with the CCR5 N-terminus (NT) [82]. Since small molecule inhibitors interact with the pocket formed by transmembrane helices, thereby inducing allosteric conformational change in the ECL2, the wild-type virus can no longer interact with the ECL2. It is assumed that binding of small molecule inhibitors alters orientation between the ECL2 and NT regions, disrupting multi-point binding sites for gp120, thereby impeding gp120-CCR5 interaction [83]. Indeed, studies using CCR5 mutants showed that the escape variants were more dependent on tyrosine-sulfated CCR5 NT than wild-type viruses [65,66,84]. Furthermore, these escape variants were more sensitive to monoclonal antibodies recognizing the NT portion of CCR5 [65]. These studies indicated that the escape variants from CCR5 antagonists showed enhanced interactions with the NT that may be a consequence of a weakened interaction with the ECL2 (Figure 6).

Another genetic pathway is independent of V3 mutations. Vicriviroc-resistant mutants have been developed with multiple amino acid substitutions throughout the gp120 spanning the C2-V5 region without any changes in the V3 loop [69]. Recently, three amino acid changes in the fusion peptide domain of gp41 have been shown to be responsible for resistance although the effect of these mutations was
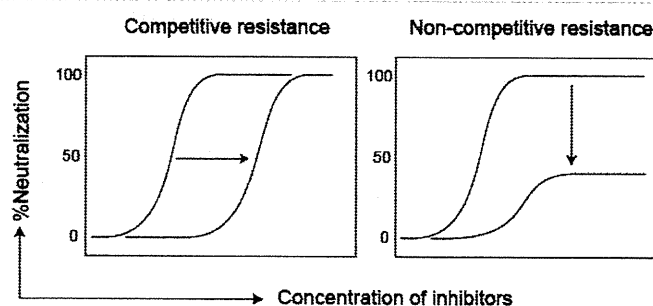

Figure 4: Typical competitive and non-competitive resistance profiles. Competitive resistance can achieve inhibition of viral replication by a sufficient inhibitor concentration, resulting in a shift in the IC50 value (left panel). In non-competitive inhibition, increasing concentrations of inhibitors have no effect, resulting in no increase in the inhibitory effect (right panel).
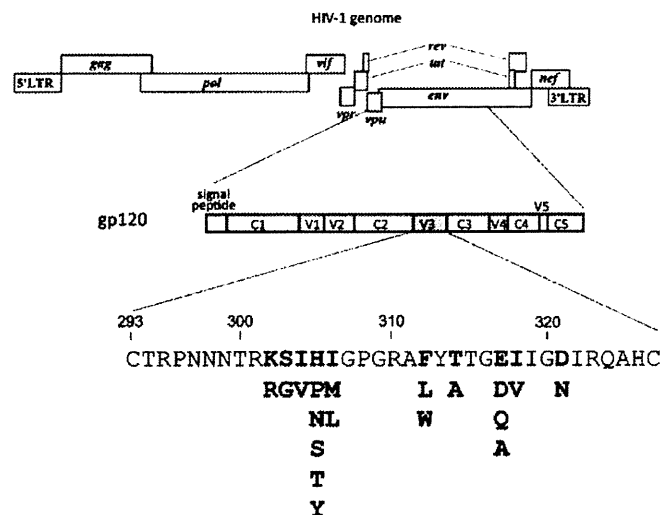
Figure 5: Schematic structure of HIV-1 V3 loop library showing introduced mutations in V3 for the analysis of escape mutants. Residues in boldface indicate the substitutions that were randomly incorporated in the V3 loop, possible >2 x 104 combinations. The amino acid substitutions were detected in 31 R5 clinical isolates.
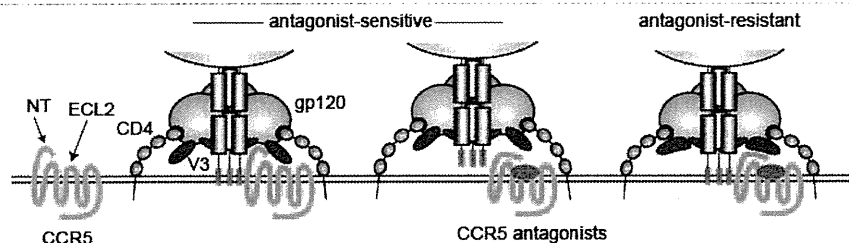

Figure 6: Resistant HIV-1 viruses can enter host cells in the presence of the CCR5 antagonist. The successful viral fusion requires the interaction of the V3 loop in gp120 with the ECL2 and NT of CCR5. CCR5 antagonists bind to the pocket formed by TM helices and induce allosteric conformational changes in the ECL2, thereby disrupting the interaction of gp120 with CCR5. The CCR5 antagonists-resistant viruses containing multiple amino acid substitutions in the V3 loop can recognize antagonist-bound forms of CCR5 by enhanced interaction with the NT.

context-dependent [84,85]. Thus, the mechanisms by which changes in the fusion peptide alter the gp120-CCR5 interaction still remain to be determined.

As previously mentioned, the patterns of mutations in escape variants against CCR5 antagonists were hypervariable and context-dependent, due in part to extensive sequence heterogeneity of HIV-1 *env*. Resistance to CCR5 antagonists was also found to be dependent upon cellular conditions such as cell tropism and the availability of CCR5. The differential staining of CCR5-expressing cells by various CCR5 monoclonal antibodies suggested that CCR5 exists in heterogeneous forms [86] and compositions of these multiple forms differed in cell type [87]. These findings suggested that different conformations of CCR5 with CCR5 antagonists might induce different substitutions in gp120. Moreover, the development of cross-resistance to other CCR5 antagonists is inconsistent, where some studies suggest that it may occur [69,78,79] and some suggest that it may not occur [61]. Additional data from *in vitro* and *in vivo* studies will be needed to elucidate the meaning of these studies.

Resistance to CXCR4 antagonists

CXCR4 as a target: CXCR4 is a coreceptor that is used for entry by X4-tropic viruses [88]; however, it is not always regarded as a suitable

therapeutic target molecule for HIV-1 infection (Figure 1). R5 and X4 HIV-1 variants are both present in transmissible body fluids; however, R5-tropic HIV-1 transmits infection and dominates the early stages of HIV-1 pathogenesis [89], whereas X4-tropic HIV-1 evolves during the later stages and leads to acceleration of disease progression due to faster decline in $CD4^+$ T lymphocytes [90,91]. Coreceptor switching from CCR5 to CXCR4 occurs in approximately 40–50% of infected individuals [92]; in addition, the R5 virus is still present as a minor viral population even after emergence of the X4 virus. Furthermore, CXCR4 deletion in mice was shown to induce a variety of severe disorders and resulted in embryonic lethality [93], suggesting that CXCR4-targeting drugs may be less well tolerated than CCR5 inhibitors. These studies indicate that administration of CXCR4 inhibitors is relatively restricted to the later stage of infection after coreceptor switching. Therefore, the development of CXCR4 antagonists has proceeded at a deliberate pace when compared with that of other types of entry inhibitors.

Escape from CXCR4 antagonists: Based on the manner of escape of R5-tropic HIV-1 from CCR5 antagonists, four main resistance pathways may be intuitively possible for X4 HIV-1 escape from CXCR4 antagonists: (i) coreceptor switching from CXCR4 to CCR5; (ii) outgrowth of the pre-existing R5 virus; (iii) decrease in CXCR4 susceptibility by mutation(s) in Env; and (iv) utilization of the drug-bound