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Impact of antiretroviral pressure on selection of primary human immunodeficiency virus type 1 envelope sequences *in vitro*

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The initiation of drug therapy results in a reduction in the human immunodeficiency virus type 1 (HIV-1) population, which represents a potential genetic bottleneck. The effect of this drug-induced genetic bottleneck on the population dynamics of the envelope (Env) regions has been addressed in several *in vivo* studies. However, it is difficult to investigate the effect on the *env* gene of the genetic bottleneck induced not only by entry inhibitors but also by non-entry inhibitors, particularly *in vivo*. Therefore, this study used an *in vitro* selection system using unique bulk primary isolates established in the laboratory to observe the effects of the antiretroviral drug-induced bottleneck on the integrase and *env* genes. Env diversity was decreased significantly in one primary isolate [KP-1, harbouring both CXCR4 (X4)- and CCR5 (R5)-tropic variants] when passaged in the presence or absence of raltegravir (RAL) during *in vitro* selection. Furthermore, the RAL-selected KP-1 variant had a completely different Env sequence from that in the passage control (particularly evident in the gp120, V1/V2 and V4-loop regions), and a different number of potential *N*-glycosylation sites. A similar pattern was also observed in other primary isolates when using different classes of drugs. This is the first study to explore the influence of anti-HIV drugs on bottlenecks in bulk primary HIV isolates with highly diverse Env sequences using *in vitro* selection.

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INTRODUCTION

Human immunodeficiency virus type 1 (HIV-1) shows a high degree of genetic diversity owing to its high rates of replication and recombination and the high mutation rate of the HIV-1 reverse transcriptase (Nájera *et al.*, 2002). Even in a single infected individual, the virus can best be described as a population of distinct, but closely related, genetic variants or 'quasi-species' (Eigen, 1993; Nijhuis *et al.*, 1998). The quasi-species behaviour of viruses is recognized as a key element in our understanding and modelling of viral evolution and disease control (Vignuzzi *et al.*, 2006).

Combination antiretroviral (ARV) therapy results in a contraction of the viral population, which represents a potential genetic bottleneck (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). Whilst this bottleneck has a direct effect on the region that is being targeted by the drugs (e.g. protease or reverse transcriptase), it also affects other regions of the viral genome. Indeed, the effect of the drug-induced genetic bottleneck on the population dynamics of the envelope (Env) regions has been addressed in several *in vivo* studies (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).

Virus bottleneck evolution of the HIV-1 *env* gene might be important when choosing the optimal drugs to treat a particular patient. Indeed, a CCR5 antagonist (maraviroc, MVC) and a fusion inhibitor (enfuvirtide, T-20) have now

The GenBank/EMBL/DDBJ accession numbers for the *env* sequences of HIV-1 KP-1, KP-2 and KP-4, are AB640872–AB640881, AB641341–AB641351 and AB641335–AB641340, respectively.

Two supplementary figures are available with the online version of this paper.

been approved for use as HIV-1 entry inhibitors. Analysing the dynamics of drug-induced genetic bottlenecks and studying drug-resistant mutation profiles in response to HIV-1-specific ARV drugs are both important if we are to understand fully HIV-1 drug resistance and pathogenesis.

The aim of the present study was to understand better the effect of *in vivo* drug-induced genetic bottlenecks. *In vitro* selection of different primary HIV-1 isolates was performed using the recently approved HIV integrase inhibitor raltegravir (RAL) (Steigbigel *et al.*, 2008). Two R5-, one X4-, one dual- and one mixed R5/X4-tropic isolates were passaged through a RAL-induced genetic bottleneck. We also performed *in vitro* selection of the R5/X4 isolate using lamivudine (3TC), saquinavir (SQV) and MVC, and compared the results with those from the RAL-selected isolate.

RESULTS

Genotypic profiles of the HIV-1 primary isolates

Four genetically heterogeneous HIV-1 primary isolates (KP-1–4) from Japanese drug-naïve patients were used to assess the extent to which RAL affected the selection of bulk primary viruses *in vitro*. A laboratory isolate, strain 89.6, was also used in the study (rather than a molecular clone) to allow escape mutants to be selected from each quasi-species pool and to be generated *de novo*. First, the sequences of the integrase (IN) regions of the four primary isolates were determined. Table 1 shows the detailed evaluation of the R5/X4 mixture subtype B (KP-1), R5-CRF08_BC (KP-2), R5 subtype B (KP-3) and X4-CRF01_AE (KP-4) primary isolates, and the dual-tropic subtype B laboratory virus (89.6). Although some naturally occurring polymorphisms were observed within the IN regions of these isolates compared with the subtype B consensus sequence available from the Los Alamos National Laboratory HIV sequence database, we did not identify any primary resistant mutations to RAL. Three baseline viruses (KP-1, KP-4 and 89.6) were sensitive to RAL, with IC_{50} values ranging from 1.2 to 4 nM, which are comparable with those reported previously (Kobayashi *et al.*, 2008). However, KP-2 and KP-3 showed minor resistance to RAL, with IC_{50} values of 16 and 32 nM, respectively. These two isolates contained amino acid mutations at positions 72, 125 and 201 within the IN region [previously reported as L-870,810 and S-1360 resistance mutations (Hombrouck *et al.*, 2008; Rhee *et al.*, 2008), but not as RAL-resistance mutations]. KP-2 also contained a unique insertion at position 288 (NQDME) at the C-terminal end of the IN region.

In vitro selection of variants of the primary isolates and 89.6 using RAL

To induce RAL-selected HIV-1 variants *in vitro*, PM1/CCR5 cells, a T-cell line expressing high levels of CCR5, were exposed to the four primary isolates and strain 89.6. The viruses were then serially passaged in the presence of RAL. As a control, each isolate was passaged under the same conditions, but without RAL, to allow monitoring of spontaneous changes occurring in the viruses during prolonged PM1/CCR5 cell passage (the passage control). The selected viruses were initially propagated at a RAL concentration equal to each IC_{50} value. The RAL concentrations were then increased from 20 to 85 nM during the course of the selection procedure (Table 1).

Only small shifts in the IC_{50} to RAL were observed in four of the five isolates (KP-1, KP-2, KP-4 and 89.6), with fold changes in IC_{50} values of 3.4, 6.5, 16 and 9.2, respectively. KP-3 did not show resistance to RAL. IC_{50} values in all the passage controls were comparable with those of the baseline viruses (Table 1).

IN region sequences in RAL-selected variants

The full-length *IN* genes were amplified and cloned to determine the genetic basis of selection in the presence or absence of RAL. Ten to 12 clones from each sample were sequenced.

Substitutions within IN were observed at passages 30 (G189R) and 29 (T210I) in two RAL-selected isolates (KP-2 and KP-4, respectively). Neither of these has been reported as IN inhibitor-resistant mutations. No substitutions in the IN regions of KP-3 and 89.6 were found. However, A125T and V180I substitutions were observed in the KP-3 and 89.6 control variants at the last passage. No previously reported mutations were identified in the IN region of KP-1 (an R5/X4 mixture isolate) after 17 passages. However, four amino acids (K7/K111/H216/D278) were selected by RAL from the baseline quasi-species, whereas different amino acids (R7/R111/Q216/N278) were selected in the control-passage variants (Table 1).

Taken together, these findings showed that RAL-induced selection pressure causes adaptation within the IN regions of bulk primary viruses during *in vitro* passage in the target cells, and confirmed that this system can be used to analyse drug-selected variants *in vitro*.

Comparison of *env* gene sequences in RAL-selected and passage-control isolates

A highly diverse gp120 region was observed in the baseline R5/X4 mixture isolate, KP-1; however, the viral diversity of variants passaged in the presence or absence of RAL decreased significantly during *in vitro* selection (overall mean distance after RAL selection of 0.056 at baseline to 0.007 after passage 17; mean overall distance in the passage control of 0.01 after 20 passages, Table 2). Moreover, the RAL-selected and control variants utilized CCR5 to enter the target cell; neither variant used CXCR4 (Table 3).

Interestingly, the low-diversity RAL-selected variant contained a completely different Env sequence from that of the passage-control variant (Fig. 1a). Different regions spanning

Table 1. Susceptibility of HIV-1 isolates to RAL and distinct differences in IN region sequences between RAL-selected and control-passaged viruses

Isolate	Subtype	Tropism	Passage no.	Concn (nM)	RAL-selected variant*		Passage control	
					IN sequence	RAL IC_{50} (nM)	IN sequence	RAL IC_{50} (nM)
KP-1	B	Mix	0	0	*K/R7, K/R111, Q/H216, D/N278*	4	*K/R7, K/R111, Q/H216, D/N278*	4
			8	20	**K**111, **H**216, **D**278	31 (7.8)	**R**7, **R**111, **Q**216, **N**278	4.5 (1.2)
			17†	20	**K**7, **K**111, **H**216, **D**278	26 (6.5)	**R**7, **R**111, **Q**216, **N**278	0.4 (0.1)
KP-2	CRF08_BC	R5	0	0	*I201, ins289NQDME*	16	*I201, ins289NQDME*	16
			18	40	G189G/R, *I201, ins289NQDME*	32 (2)	*I201, ins289NQDME*	16 (1)
			30	85	G189R, *I201, ins289NQDME*	55 (3.4)	*I201, ins289NQDME*	25 (1.6)
KP-3	B	R5	0	0	*V72, A125*	32	*V72, A125*	32
			11	25	*V72, A125*	25 (0.78)	*V72, A125*	33 (1)
			22	27.5	*V72, A125*	37 (1.2)	*V72*, A125T	13 (0.41)
KP-4	CRF01_AE	X4	0	0	–	2.1	–	2.1
			8	40	–	33 (16)	R166R/K, D279N	4.4 (2.1)
			29	40	T210I	22 (10)	G163E, R166R/K, D279N/S	4.1 (2)
89.6	B	R5X4	0	0	–	1.2	–	1.2
			8	15	–	34 (28)	–	4.4 (3.7)
			34	20	–	11 (9.2)	V180I	1.2 (1)

*Amino acid changes in each passage variant are shown. Italicized letters represent mutations relative to the consensus subtype BC or B present in the baseline isolates. Bold letters represent amino acids selected out of the quasi-species cloud. The fold increase in RAL IC_{50} values is shown in parentheses for *in vitro*-selected variants compared with those in the baseline isolates.
†The RAL variant selected after 17 passages was compared with the control selected after 20 passages.

Table 2. Comparison of amino acid length and number of PNGs between RAL-selected and control-passage KP-1 variants

	Passage no.	Genetic diversity*	Mean ENV $_{1-474}$ length (range)†	Mean V1/V2 length (range)	Mean V3 length (range)	Mean V4 length (range)	Mean PNGs (range)
Baseline	0	0.056	472 (461–480)	69 (60–74)	34 (33–34)	30 (29–31)	24 (22–28)
RAL-selected virus	2	0.038	479 (472–480)‡	74 (71–74)‡	34 (33–34)‡	31 (29–31)‡	27 (25–28) ‡
	8	0.0070	480	74	34	31	28 (26–29)
	17	0.0070	480	74	34	31	27 (26–27)§
Passage control	2	0.045	464 (461–466)‡	64 (60–74)‡	34 (33–34)‡	29 (29–31)‡	24 (22–27)‡
	8	0.0070	463 (462–463)	62	34	29	23 (22–23)
	10	0.0080	462 (459–463)	62	34	29	23 (22–23)
	20	0.010	463	62	34	29	23 (22–23)§
P value			<0.0001‡	<0.0001‡	0.91‡	0.0048‡	0.0019‡
							<0.0001§

*Overall mean distance.
†Sequence from gp120 SP to the V5 region (aa 1–474).
‡, § *P* values were calculated using the homoscedastic *t*-test between the RAL-selected and the passage-control variants indicated by the same symbols above.

the whole envelope sequence [from the signal peptide (SP) to V5] were compared in the RAL-selected and passage-control viruses. The results showed that, after only two passages, the gp120, V1/V2 and V4-loop regions within RAL-selected variants were longer than those in the control variants, and the number of putative *N*-linked glycosylation sites (PNGs) was significantly higher than that in the control-passage viruses (Table 2). This phenomenon was seen consistently in two independent experiments.

We also analysed the gp120 sequences in the other four isolates. Although the number of positional differences between the RAL-selected and passage-control variants for these four isolates was lower than that in KP-1 (between three and nine, compared with >40), there was a similar pattern of separation between the Env sequences (Fig. 1). In three of the four isolates (KP-2, KP-3 and KP-4), positional differences were observed in SP, C1 and all the variable regions of gp120 (Fig. 1b–d). In strain 89.6, differences were observed in the C2, C3 and V4 regions (Fig. 1e).

These results suggested that RAL treatment of target cells causes a decrease in viral diversification within quasispecies Env regions via a route different from that in untreated target cells.

In vitro induction of RAL-selected V3-loop library virus variants

To investigate further the effects of RAL on viral Env sequences, we used the V3-loop library virus (JR-FL-V3Lib) developed by Yusa *et al.* (2005), which carries a set of random combinations from zero to ten substitutions (27 648 possibilities) in the V3 loop (residues 305, 306, 307, 308, 309, 317, 319, 322, 323 and 326; V3 loop from Cys^{296} to Cys^{331}). The variants contained in the library were polymorphic mutations derived from 31 R5 clinical isolates (Yusa *et al.*, 2005). PM1/CCR5 cells were exposed to the JR-FL-V3Lib and serially passaged in the presence of RAL. After two passages, the V3 sequence within the RAL-selected variant was completely different from that in the passage control (Fig. 1f). This suggested that, under pressure from RAL, the infectious clone harbouring different V3 region sequence from the passage control had adapted to the target cells, despite containing the same IN sequences.

Phylogenetic analysis of the Env regions after passage with or without RAL

To confirm the temporal and spatial differences observed in each of the RAL-selected and passage-control viruses, phylogenetic analyses were conducted using complete SP–V5 sequences. The neighbour-joining phylogenetic tree showed a clear and distinct branching between RAL-selected and passage-control KP-1 viruses (Fig. 2a). We also identified a similar pattern in all the other isolates tested (Fig. 2b–e).

Table 3. Comparison of amino acid length, number of potential *N*-linked glycosylation sites, V3 sequences and co-receptor usage between anti-retroviral drug-selected and control-passaged KP-1 variants

	Passage no.	Genetic diversity*	Mean ENV_{1-474} length (range)†	Mean V1/V2 length (range)	Mean V3 length (range)	Mean V4 length (range)	Mean PNGs (range)	V3 region		Geno2 pheno (%)§
								Prevalence (%)	Sequence‡	
Baseline	0	0.056	472 (461–480)	69 (60–74)	34 (33–34)	30 (29–31)	24 (22–28)	41.9	CTRPNNNTRKGIHIGPGKFYATGAIIGDIRQAHC	41.2
								22.6	.....V.....	41.2
								16.1	....-..I.....T.R..T.RD...N..K...	1.7
								13.0	....-..I.....T.R..T.KT...N.KK...	2.9
								3.2	....-..I.....	7.4
								3.2	.....D.....	55.3
Passage control	8	0.0070	463 (462–463)	62	34	29	23 (22–23)	100.0	.....V.....	41.2
RAL-selected virus	8	0.0070	480	74	34	31	28 (26–29)	100.0	.....	41.2
3TC-selected virus	6	0.020	478 (475–480)	74	34	31 (29–31)	27 (25–28)	83.3	.....	41.2
SQV-selected virus	11	0.0040	474	71	34	31	26	100.0	.....	41.2
MVC-selected virus	7	0.0080	469 (468–469)	69	33	29	24 (23–24)	100.0	....-..I....R..T.R..T.KT...N.KK...	1.7

*Overall mean distance.

†Sequence from gp120 SP to the V5 region (aa 1–474).

‡V3 sequences of each variant are shown. Dots denote sequence identity and dashes indicate a deletion mutation.

§Prediction of viral co-receptor tropism using Geno2pheno based on a selectable 'false positive rate'.

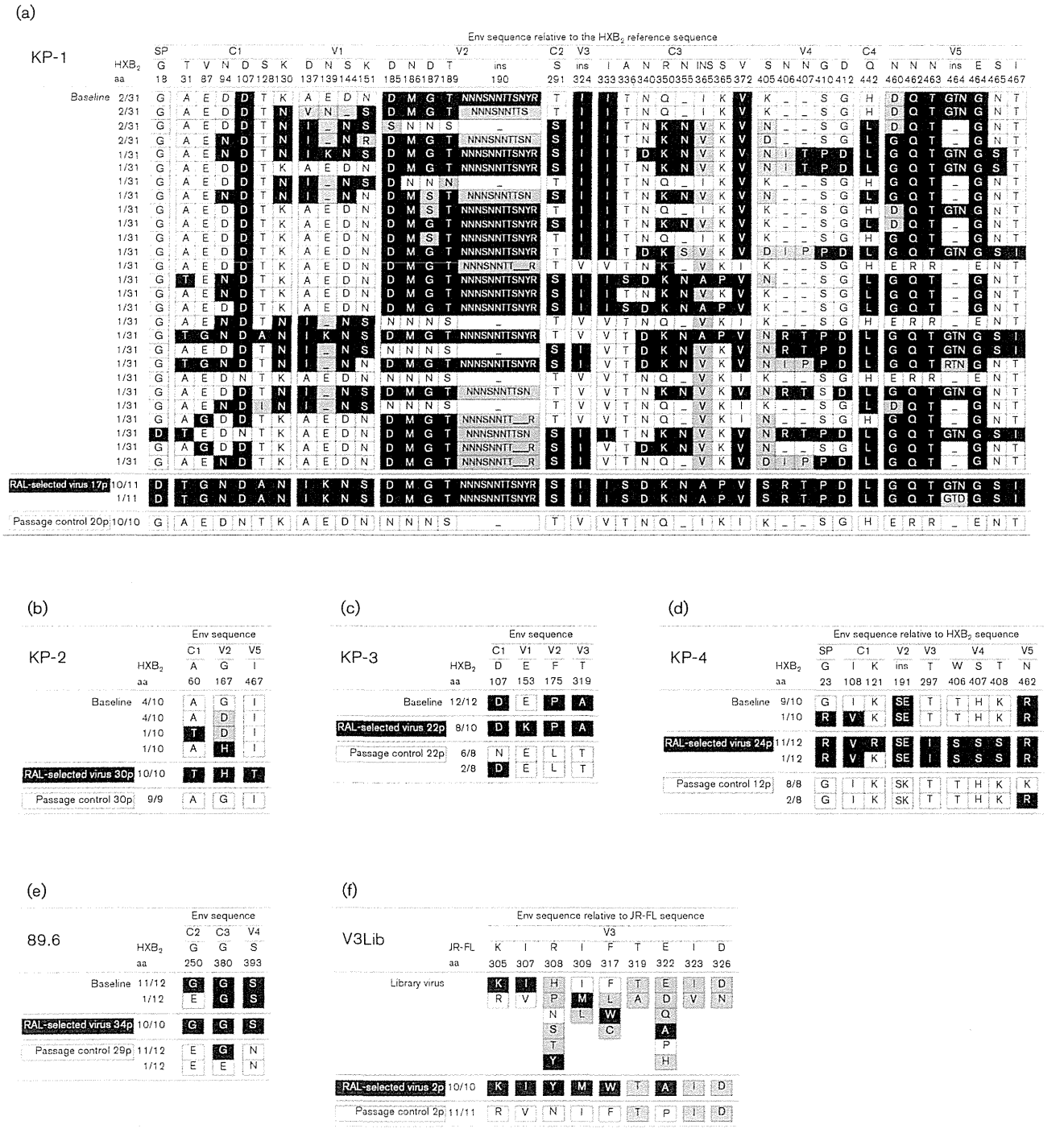


Fig. 1. Comparison of the gp120 sequences between RAL-selected and control-passaged viruses. The gp120 sequences of baseline, RAL-selected and the passage-control viruses were aligned for KP-1 (a), KP-2 (b), KP-3 (c), KP-4 (d) and strain 89.6 (e). Each amino acid in (a)–(e) is numbered relative to the 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,

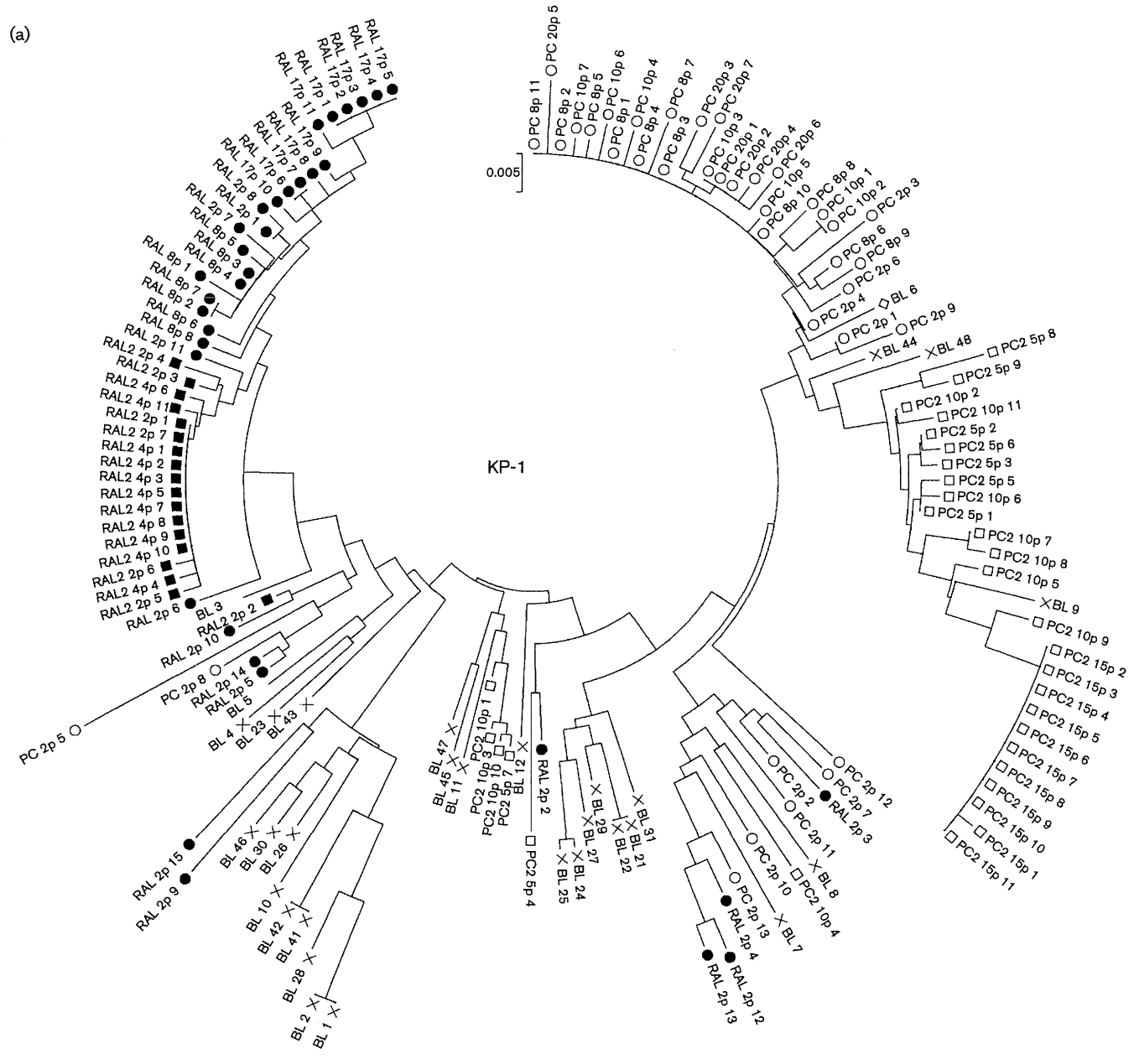
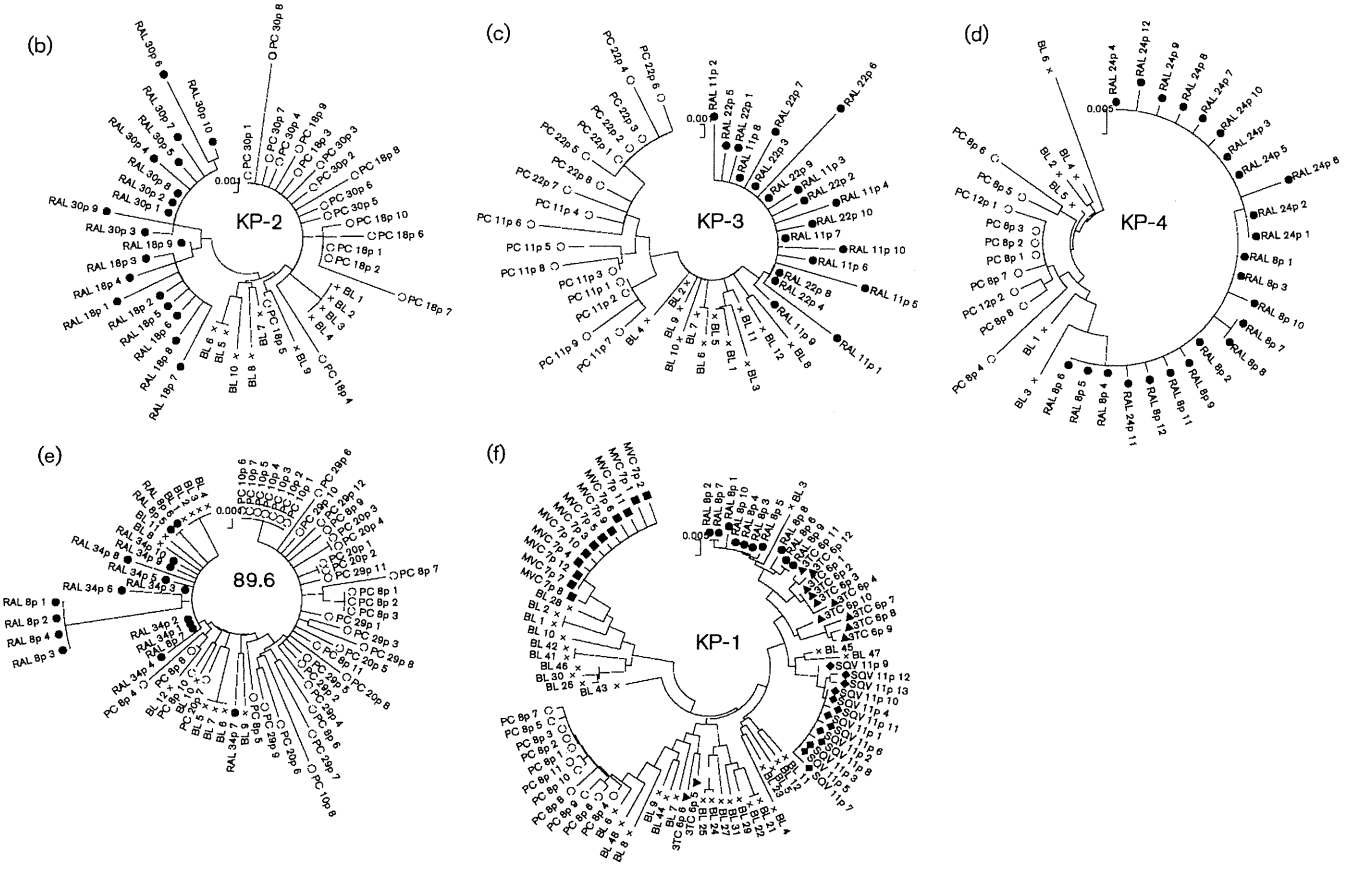


Fig. 2. Phylogenetic analyses of the Env regions from *in vitro*-passaged viruses selected with or without ARV drugs. (a–e) Phylogenetic trees were constructed using gp120 SP–V5 sequences from RAL-selected and passage-control variants of KP-1 (a), KP-2 (b), KP-3 (c), KP-4 (d) and strain 89.6 (e). An '×' 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.

ACKNOWLEDGEMENTS

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INTERNAL MEDICINE

□ ORIGINAL ARTICLE □

Abacavir/Lamivudine versus Tenofovir/Emtricitabine with Atazanavir/Ritonavir for Treatment-naive Japanese Patients with HIV-1 Infection: A Randomized Multicenter Trial

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Abstract

Objective To compare the efficacy and safety of fixed-dose abacavir/lamivudine (ABC/3TC) and tenofovir/emtricitabine (TDF/FTC) with ritonavir-boosted atazanavir (ATV/r) in treatment-naïve Japanese patients with HIV-1 infection.

Methods A 96-week multicenter, randomized, open-label, parallel group pilot study was conducted. The endpoints were times to virologic failure, safety event and regimen modification.

Results 109 patients were enrolled and randomly allocated (54 patients received ABC/3TC and 55 patients received TDF/FTC). All randomized subjects were analyzed. The time to virologic failure was not significantly different between the two arms by 96 weeks (HR, 2.09; 95% CI, 0.72-6.13; p=0.178). Both regimens showed favorable viral efficacy, as in the intention-to-treat population, 72.2% (ABC/3TC) and 78.2% (TDF/FTC) of the patients had an HIV-1 viral load <50 copies/mL at 96 weeks. The time to the first grade 3 or 4 adverse event and the time to the first regimen modification were not significantly different between the two arms (adverse event: HR 0.66; 95% CI, 0.25-1.75, p=0.407) (regimen modification: HR 1.03; 95% CI, 0.33-3.19, p=0.964). Both regimens were also well-tolerated, as only 11.1% (ABC/3TC) and 10.9% (TDF/FTC) of the patients discontinued the allocated regimen by 96 weeks. Clinically suspected abacavir-associated hypersensitivity reactions occurred in only one (1.9%) patient in the ABC/3TC arm.

Conclusion Although insufficiently powered to show non-inferiority of viral efficacy of ABC/3TC relative to TDF/FTC, this pilot trial suggested that ABC/3TC with ATV/r is a safe and efficacious initial regimen for HLA-B*5701-negative patients, such as the Japanese population.

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Introduction

The fixed-dose combinations of tenofovir disoproxil fumarate 300 mg/emtricitabine 200 mg and abacavir sulfate 600 mg/lamivudine 300 mg are components of antiretroviral therapy for treatment-naïve patients with HIV-1 infection in developed countries (1, 2). The efficacy and safety of tenofovir/emtricitabine (TDF/FTC) and abacavir/lamivudine (ABC/3TC) remain the focus of ongoing debate. The ACTG 5202 trial demonstrated that the viral efficacy of ABC/3TC is inferior to that of TDF/FTC among treatment-naïve patients with a baseline HIV viral load of >100,000 copies/mL receiving efavirenz or ritonavir-boosted atazanavir as a key drug (3). On the other hand, the HEAT study showed that the viral efficacy of ABC/3TC is not inferior to that of TDF/FTC, regardless of the baseline viral load when used in combination with lopinavir/ritonavir (4).

With regard to safety, the occurrence of ABC-associated serious hypersensitivity reactions, the most important adverse effect of ABC affecting 5-8% of patients, has limited its use (5). However, screening for HLA-B*5701 or prescribing ABC in HLA-B*5701-negative populations, such as the Japanese, can reduce the incidence of immunologically-confirmed hypersensitivity to 0% (6, 7). Another negative aspect of ABC use is its association with myocardial infarction, as reported by the D:A:D study (8). However, the possible association of myocardial infarction with ABC was not confirmed by a recent meta-analysis report of the US Food and Drug Administration (9). On the other hand, renal proximal tubular damage leading to renal dysfunction and a loss of phosphate, which can result in decreased bone mineral density, is a well-known adverse effect of TDF (10-14).

Taking this background into account, the American Department of Health and Human Services (DHHS) Guidelines place TDF/FTC as the preferred drug and ABC/3TC as an alternative choice, whereas other international guidelines, including the European AIDS Clinical Society (EACS) Guidelines and the Japanese Guidelines, recommend both TDF/FTC and ABC/3TC as preferred choices (1, 2, 15).

Randomized control trials comparing TDF/FTC and ABC/3TC have been conducted in the US and Europe, but not in other parts of the world (4, 16, 17). The efficacy and safety of these two fixed-dose regimens in patients with different genetic backgrounds and body statures might not be similar to the results of previous trials, especially considering that the prevalence of HLA-B*5701 is zero in the Japanese population (7). Moreover, the degree of decrement in the renal function with TDF is larger in patients with a low body weight, such as the Japanese, which might limit the use of TDF in patients with a high risk for renal dysfunction (18-20).

Based on the above described background, the present randomized trial was originally designed in 2007 to elucidate whether the viral efficacy of ABC/3TC is not inferior to that of TDF/FTC with ritonavir-(100 mg) boosted atazanavir (300 mg) in treatment-naïve Japanese patients, whose body weight is much lower than Whites or Blacks (21). However, the independent data and safety monitoring board (DSMB) recommended that the protocol be modified to examine the efficacy, safety and tolerability among Japanese patients with HIV-1 infection for 96 weeks as a pilot trial because only 109 patients were enrolled and randomized at the end of the enrollment period despite a planned sample size of 240 patients, primarily due to the above mentioned negative reports of ABC use in the D:A:D study and ACTG 5202 (3, 8).

Materials and Methods

This clinical trial was designed and reported according to the recommendations of the Consolidated Standard of Reporting Trials (CONSORT) statement (22). The protocol and supporting CONSORT checklist are available as supplementary files (see Supplementary files 1 and 2).

Ethics statement

The Research Ethics Committee of each participating center approved the study protocol. All patients enrolled in this study provided a written informed consent. This study was conducted according to the principles expressed in the Declaration of Helsinki.

Study design

The Epzicom-Truvada study is a phase 4, multicenter, randomized, open-label, parallel group pilot study conducted in Japan that compared the efficacy and safety of a fixed dose of ABC/3TC and TDF/FTC, both combined with ritonavir-boosted atazanavir (ATV/r) for the initial treatment of HIV-1 infection for 96 weeks. Enrollment of patients began in November 2007 and ended in March 2010, and the follow-up period ended in February 2012. With a one to one ratio, the patients were randomly assigned to receive either a fixed dose of ABC/3TC or TDF/FTC, both administered with ATV/r. The randomization was stratified according to each participating site and conducted at the data center with

independent clinical research coordinators using a computer-generated randomization list prepared by a statistician with no clinical involvement in the trial.

Study patients

This study population included treatment-naïve Japanese patients aged 20 or over with HIV-1 infection who met the eligibility criteria for the commencement of antiretroviral therapy according to the DHHS Guidelines in place in the U.S. at the time of the writing of the study protocol (a CD4 count <350/μL or a history of AIDS-defining illness regardless of the CD4 count) (23). Patients were screened and excluded if they had previously taken lamivudine, tested positive for hepatitis B surface antigens, had comorbidities such as hemophilia or diabetes mellitus that required medical treatment, congestive heart failure or cardiac myopathy or if they were considered not suitable for enrollment by the attending physicians. Candidates were also excluded if their alanine aminotransferase level was 2.5 times greater than the upper limit of normal, they had an estimated glomerular filtration rate (eGFR) calculated using the Cockcroft-Gault equation of <60 mL/min, {creatinine clearance = [(140- age) × weight (kg)]/(serum creatinine ×72)(×0.85 for females)} or a serum phosphate level <2 mg/dL or had active opportunistic diseases that required treatment (24). Each patient's actual body weight was used for the calculation of eGFR. At screening, a genotypic drug resistant test and screening for the HLA-B*5701 allele were permitted but not required because the prevalence of both the drug resistant virus and the HLA-B*5701 allele are low in Japanese patients (7, 25). Medical history, including a history of AIDS-defining illnesses and other comorbidities, was also collected. Enrollment stopped on March 3, 2008 due to the recommendation from the DSMB of the trial based on the interim analysis of the ACTG5202 that ABC/3TC is less effective than TDF/FTC in patients with a baseline viral load >100,000 copies/mL (3). Accordingly, the DSMB recommended that the trial should be restarted with modified inclusion criteria: to enroll patients with an HIV-1 viral load of <100,000 copies/mL at screening, and the enrollment restarted from April 1, 2008.

Study procedures

Required visits for participants for clinical and laboratory assessments were at screening, enrollment and every 4 weeks until the viral load diminished to <50 copies/mL. For patients with a viral load <50 copies/mL, the required visit interval was every 12 weeks for the duration of the study. The evaluation performed at each visit included a physical examination, CD4 cell count, HIV-1 RNA viral load, a complete blood cell count and blood chemistries (total bilirubin, alanine aminotransferase, lactate dehydrogenase, serum creatinine, potassium, phosphate, triglycerides and low-density lipoprotein (LDL) cholesterol) and a urine examination of the levels of phosphate, creatinine and β2 microglobulin. The values of urinary β2 microglobulin were expressed relative to a urinary creatinine level of 1 g/L (/g Cr). The percent tubular resorption of phosphate was calculated using the following formula: {1-[(urine phosphate × serum creatinine)/(urine creatinine × serum phosphate)]} ×100 (26). All data, including the HIV-1 RNA viral load, were collected at each participating site and sent to the data center. Grade 3 or 4 serious adverse events were reported to the DSMB, which made a judgment whether they were caused by the study drugs. Independent research coordinators at the data center visited at least 10 facilities every year to monitor the accuracy of the submitted data and compliance to the study protocol. All authors vouch for the completeness and accuracy of the reported data.

Statistical analysis

The sample size calculation was originally conducted as follows: Assuming a 90% success rate in the TDF/FTC arm at week 48, a sample size of 224 patients (112 patients per arm) provided 80% power (one sided, α=0.05) to establish non-inferiority of ABC/3TC to TDF/FTC each in combination with ATV/r. Non-inferiority was defined as the lower bound of the two-sided 95% confidence interval (CI) with the treatment difference being above -10%. Based on this assumption, the targeted sample size was set to 240 patients (120 in each arm). However, as previously described, due to the shortage of accrued subjects, this study was underpowered and conducted as a pilot trial.

The primary efficacy endpoint was the time from randomization to virologic failure (defined as a confirmed HIV-1 RNA >1,000 copies/mL at or after 16 weeks and before 24 weeks or >200 copies/mL at or after 24 weeks) (3). The secondary efficacy endpoints included the time from randomization to either virologic failure or ART modification and a comparison of the proportions of patients with HIV-1 RNA <50 copies/mL at weeks 48 and 96 regardless of previous virologic failure. The intent-to-treat (ITT) population comprising all randomized subjects was used to assess the efficacy data; however, a comparison of the proportion of virologically-suppressed patients was conducted with both the ITT and a per protocol population while on the initial randomized regimen.

The safety endpoint was the time from randomization to the first occurrence of grade 3 or 4 laboratory data or abnormal symptoms that were at least one grade higher than the baseline. Isolated hyperbilirubinemia was excluded from the safety endpoints. The grade of adverse events was classified according to the Division of AIDS Table for grading the severity of adult and pediatric events, version 2004 (27). The tolerability endpoint was the time from randomization to any regimen modification. The safety and tolerability endpoints were calculated in the ITT population. Changes per protocol in the CD4 cell count, lipid markers and renal tubular markers at weeks 48 and 96 were compared using the Mann-Whitney test. A repeated measures mixed model was used to estimate and compare changes in the renal function between the two arms (17). The renal function was calculated using the Modification of Diet in Renal Disease study

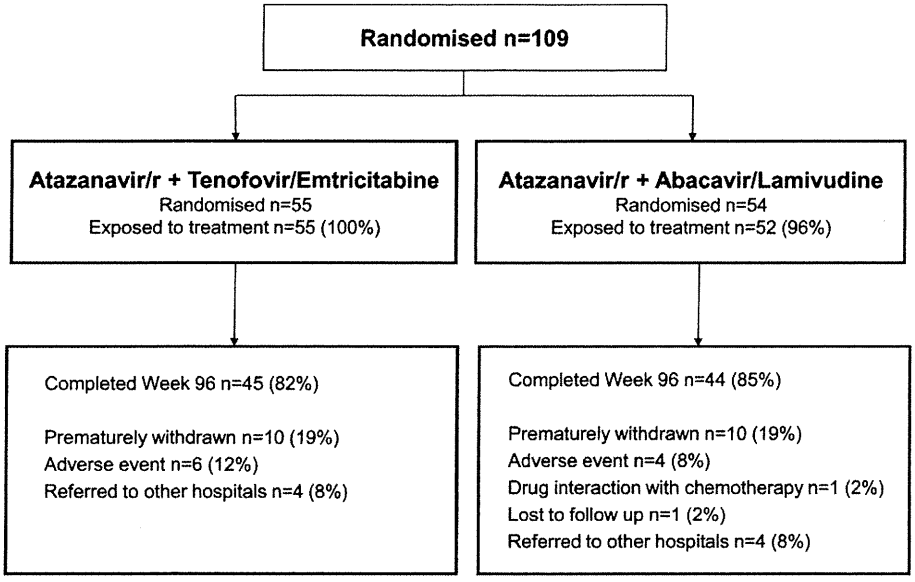

Figure 1. Enrollment, randomization and disposition of patients.

Table 1. Demographic and Baseline Characteristics

	ABC/3TC (n=54)	TDF/FTC (n=55)	Total (n=109)
Sex (male), n (%)	53 (98.1)	54 (98.2)	107 (98.2)
Age (years)†	39 (28.8-44)	35 (29-42)	36 (29-42.5)
CD4 count (/μL)†	236.5 (194-301.3)	269 (177-306)	257 (194-305)
HIV RNA viral load (log_{10}/mL)†	4.29 (3.92-4.67)	4.28 (3.86-4.60)	4.28 (3.89-4.67)
HIV RNA viral load >100,000 log_{10}/mL, n (%)	1 (1.9)	0 (0)	1 (0.9%)
Route of transmission (homosexual contact), n (%)	47 (87)	49 (89.1)	96 (88.1)
History of AIDS n (%)	1 (1.9)	5 (9.1)	6 (5.5)
Body weight (kg)†	64 (59-72.1)	63.1 (58-69)	64 (58.3-70.7)
Body mass index (kg/m^2)†	22.6 (20.4-24.2)	21.9 (20.3-23.6)	22.4 (20.3-23.7)
eGFR (mL/min/1.73 m^2)†	96.9 (82.7-107.3)	94.4 (83.6-105.7)	96.7 (83.0-106.7)
Creatinine clearance (mL/min)†	119.3 (105.4-136.6)	124.6 (103-139.3)	120.3 (104.7-138.3)
Serum creatinine (mg/dL)†	0.76 (0.67-0.83)	0.75 (0.68-0.84)	0.76 (0.68-0.83)
Urinary β2 microglobulin (μg/g Cre)†	195.8 (98.3-505.3)	138.4 (86.8-426.4)	172.9 (88.3-458.7)
Tubular resorption of phosphate (%)†	92.9 (90-95.1)	92.3 (87.7-95.2)	92.7 (89.3-95.1)
LDL-cholesterol (mg/dL)†	91.5 (75-125.5)	94 (72.5-111.5)	94 (74.5-114)
Triglycerides (mg/dL)†	132 (98-170.5)	114 (73-184)	127 (85.5-175)
Hypertension, n (%)	3 (5.6)	1 (1.8)	4 (3.7)
Diabetes mellitus, n (%)	0 (0)	0 (0)	0 (0)
Concurrent use of nephrotoxic drugs, n (%)	10 (18.5)	10 (18.2)	20 (18.3)
Hepatitis C, n (%)	0 (0)	0 (0)	0 (0)

†median (interquartile range)

IQR: interquartile range, AIDS: acquired immunodeficiency syndrome, eGFR: estimated glomerular filtration rate, LDL: low-density lipoprotein

equation adjusted for the Japanese population (28), and a sensitivity analysis was conducted using the above mentioned Cockcroft-Gault equation.

Time-to-event distributions were estimated using the Kaplan-Meier method and compared using the two-sided log-rank test. Hazard ratios (HRs) and 95% confidence intervals (95% CIs) were estimated using the Cox proportional hazards model. For grade 3 or 4 serious adverse events caused by the study drugs, the description and severities were recorded. Statistical significance was defined at two-sided p values <0.05. All statistical analyses were performed with The Statistical Package for Social Sciences ver. 17.0 (SPSS, Chicago, IL).

Results

Patient disposition and baseline characteristics

109 patients from 18 centers were enrolled and randomized between November 2007 and March 2010. Of these patients, 54 and 55 were allocated to the ABC/3TC and TDF/FTC arms, respectively (Fig. 1). The baseline demographics and characteristics are shown in Table 1. Most patients were men, with a median body weight of 64 kg. The median CD4 cell count was 257/μL (IQR: 194-305). One patient in the ABC/3TC arm had a baseline HIV-1 RNA level of >100,000

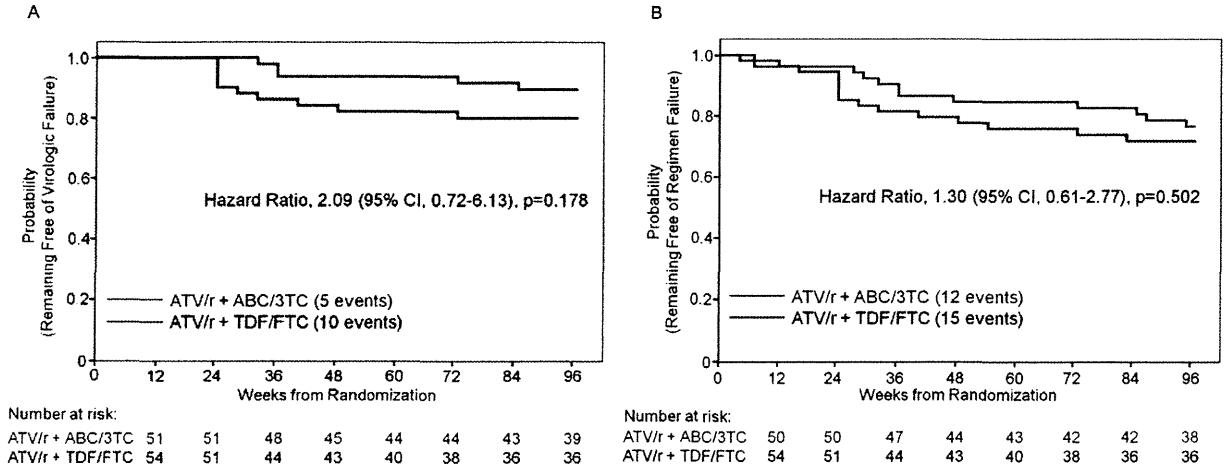

Figure 2. Efficacy results over 96 weeks. (A) Time to protocol-defined virologic failure. (B) Time to the first occurrence of either virologic failure or discontinuation of the initially randomized regimen. ATV/r: ritonavir-boosted atazanavir, ABC/3TC: abacavir/lamivudine, TDF/FTC: tenofovir/emtricitabine

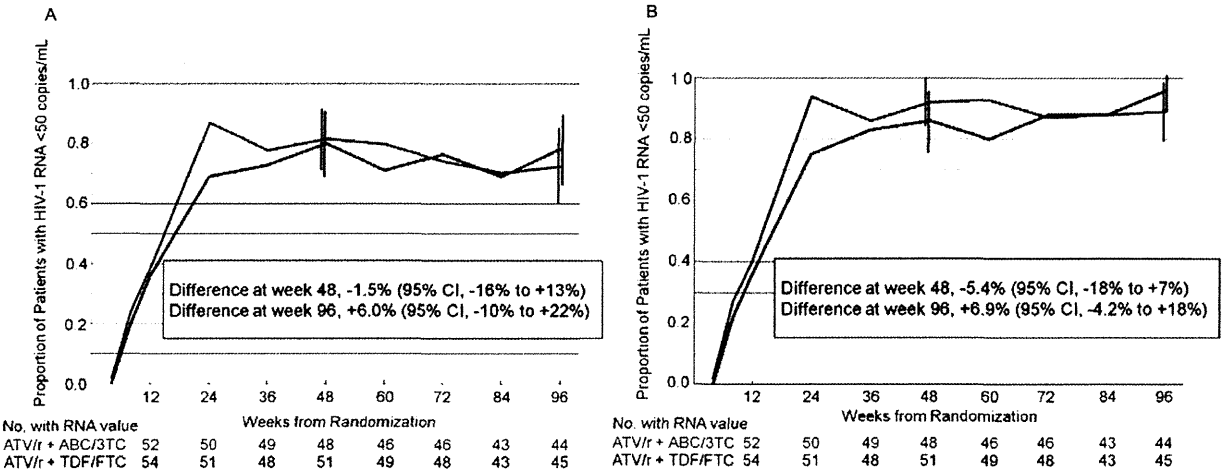

Figure 3. Efficacy results at 48 and 96 weeks. Proportion of patients with an HIV RNA level <50 copies/mL regardless of previous virologic failure with 95% binomial confidence intervals at 48 and 96 weeks. (A) Intention-to-treat analysis. (B) Per protocol analysis. ATV/r: ritonavir-boosted atazanavir, ABC/3TC: abacavir/lamivudine, TDF/FTC: tenofovir/emtricitabine

copies/mL. This patient was enrolled before the announcement of the interim analysis of ACTG5202 in March 2008 and achieved an HIV-1 RNA level of <50 copies/mL by the end of that month. One patient in the TDF/FTC arm had a history of lamivudine use. That patient was included in the analysis because this aspect of the medical history was identified after randomization and initiation of the allocated treatment.

Efficacy results

In the primary efficacy analysis, the time to virologic failure was not significantly different in the ABC/3TC arm from that observed in the TDF/FTC arm by 96 weeks (HR, 2.09; 95% CI, 0.72-6.13; p=0.178). Virologic failure occurred in 5 and 10 patients in the ABC/3TC and TDF/FTC arms, respectively (Fig. 2A). In the secondary efficacy analysis, the times to the first occurrence of confirmed virologic failure or discontinuation of the initially allocated regimen were not different between the two arms (HR, 1.30; 95% CI, 0.61-2.77; p=0.502) (Fig. 2B). Among the ITT population, the proportion of patients with an HIV RNA level <50 copies/mL at week 48 regardless of previous virologic failure was 81.5% in the ABC/3TC group and 80% in the TDF/FTC group, for a difference of -1.5% (95% CI, -16% to 13%), and at week 96, 72.2% and 78.2% for the ABC/3TC and TDF/FTC groups, respectively, for a difference of 6% (95% CI, -10% to 22%) (Fig. 3A). The per protocol analysis showed that the proportions at week 48 were 91.7% and 86.3% for the ABC/3TC and TDF/FTC groups, respectively, for a difference of -5.4% (95% CI, -18% to 7%). At week 96, the proportions were 88.6% and 95.6% for the ABC/3TC and TDF/FTC groups, respectively, for a

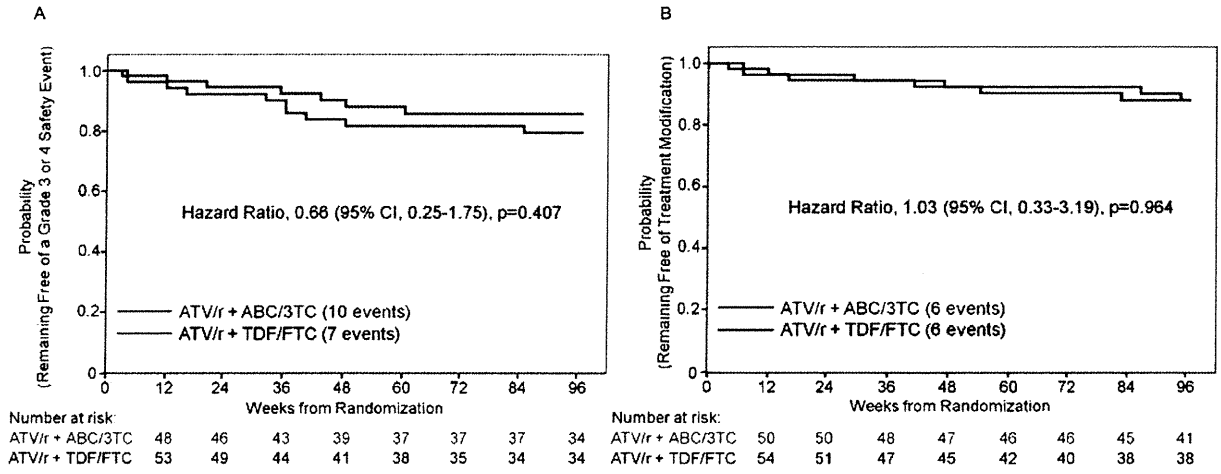

Figure 4. Safety and tolerability results over 96 weeks. (A) Time to first primary safety endpoint, defined as the first grade 3 or 4 event on the initial randomized regimen, which was at least one grade higher than baseline. (B) Time to tolerability endpoint, defined as the first change in regimen. ATV/r: ritonavir-boosted atazanavir, ABC/3TC: abacavir/lamivudine, TDF/FTC: tenofovir/emtricitabine

Table 2. Selected Grade 3 or 4 Events While Receiving Randomized Antiretroviral Drugs

	ABC/3TC (n=54)	TDF/FTC (n=55)	Total (n=109)
Overall, n (%)	13 (24)	10 (18)	23 (21)
Laboratory, n (%)	12 (22)	7 (13)	19 (17)
Alanine aminotransferase, n	0	1	1
LDL-cholesterol, n	6	2	8
Triglycerides, n	0	3	3
Uric acid, n	1	0	1
Serum phosphate, n	2	0	2
Serum calcium, n	1	0	1
Serum creatinine, n	1	0	1
Platelets count, n	1	1	2
Symptoms, n (%)	1 (2)	3 (5)	4 (4)
Depression, n	0	2	2
Fever, n	1	1	2

More than one event occurred in 2 patients.
LDL: low-density lipoprotein

difference of 6.9% (95% CI, -4.2% to 18%) (Fig. 3B). The primary and secondary efficacy analyses did not show a significant difference in viral efficacy between the two arms.

Safety and tolerability results

10 (18.5%) and 7 (12.7%) patients in the ABC/3TC and TDF/FTC groups, respectively, experienced 23 grade 3 or 4 adverse events related to the study drugs while on the initial regimen. The time to the first adverse event was not significantly different between the two arms (HR 0.66; 95% CI, 0.25-1.75, p=0.407) (Fig. 4A). Table 2 shows a list of selected grade 3 or 4 safety events. Among the adverse events, 48% included elevation of lipid markers. The tolerability endpoint, the time to first ART modification, was not significantly different between the two arms (HR 1.03; 95% CI, 0.33-3.19, p=0.964), and only 6 (11.1%) and 6 (10.9%) patients in the ABC/3TC and TDF/FTC arms, respectively, discontinued the initially allocated regimen by 96 weeks (Fig. 4B). The most common reason for regimen modification was drug toxicity (n=10; 4 in ABC/3TC and 6 in TDF/FTC arm; suspected ABC hypersensitivity reactions based on the appearance of rash and fever in HLA-B*5701-negative patient; n=1, depression; n=3, jaundice; n=3, nausea; n=2, and lipodystrophy; n=1). One patient in the ABC/3TC group developed a cerebral infarction during week 39 but was able to continue the study drugs. No deaths were registered during the study period.

Changes in the CD4 cell count and other parameters of interest

The increase in the median CD4 count from baseline to 48 weeks was marginally larger in the ABC/3TC arm than in the TDF/FTC arm (median: ABC/3TC: 216, TDF/FTC: 192, p=0.107). This difference was significantly larger at 96

Table 3. Median Values of Changes in Parameters of Interest from Baseline to 96 Weeks

	ABC/3TC (n=54)				TDF/FTC (n=55)				
	Number tested (baseline, week 96)	Baseline	Week 96	Median Δ	Number tested (baseline, week 96)	Baseline	Week 96	Median Δ	p value
CD4 cell count (/μL)	54, 43	236.5	545	328	55, 45	269	493	216	0.031
Lipids									
LDL-cholesterol (mg/dL)	54, 16	91.5	149	31.5	53, 16	94	97	2	0.026
Triglyceride (mg/dL)	54, 29	132	257	111	55, 26	114	202	40.5	0.037
Renal tubular markers									
Urinary β2 microglobulin (μg/g Cre)	49, 32	195.8	99.2	-94.9	52, 38	138.4	303.9	86.6	<0.001
Tubular resorption of phosphate (%)	49, 32	93	92	-1.4	50, 36	92	91	-2.6	0.930

LDL: low-density lipoprotein

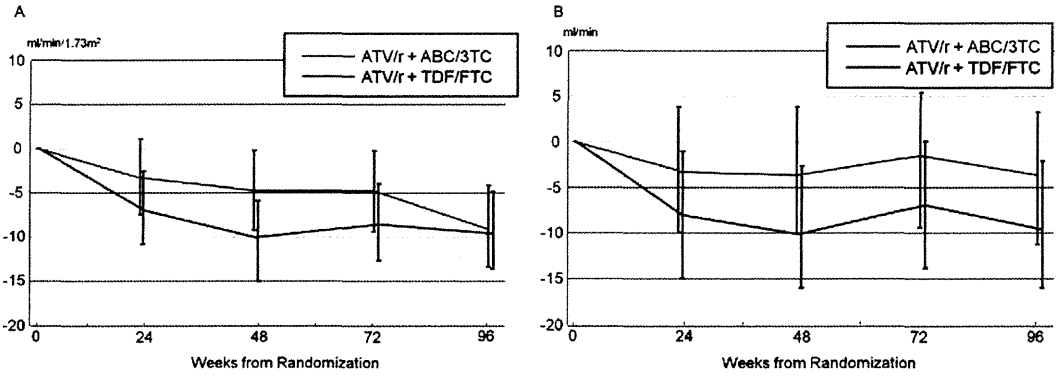

Figure 5. Changes in the renal function between baseline and 96 weeks. (A) Changes in the estimated glomerular filtration rate calculated with the Modification of Diet in Renal Disease study equation adjusted for the Japanese population. (B) Changes in creatinine clearance calculated with the Cockcroft-Gault equation. The data are presented as the mean±95% confidence interval. ATV/r: ritonavir-boosted atazanavir, ABC/3TC: abacavir/lamivudine, TDF/FTC: tenofovir/emtricitabine

weeks (ABC/3TC: 328, TDF/FTC: 236, p=0.031, Table 3). The increases in both LDL-cholesterol and triglycerides from baseline to 96 weeks were more significant in the ABC/3TC arm than in the TDF/FTC arm. One patient in the TDF/FTC arm had been treated with lipid-lowering medications prior to study enrollment. Furthermore, 7 patients and 1 patient in the ABC/3TC and TDF/FTC arms, respectively, started lipid-lowering agents during the study period. With regard to renal tubular markers, the levels of urinary β2 microglobulin increased in the TDF/FTC arm (median: 86.6 μg/g Cre), whereas it decreased in the ABC/3TC arm (median: -94.9 μg/g Cre). These changes were significantly different between the two arms (p<0.001). On the other hand, tubular resorption of phosphate did not show changes from baseline to 96 weeks in the two groups, and the levels were not different between the two arms (Table 3).

Changes in the renal function

A data analysis using repeated measures mixed models showed a significant decrease in the mean eGFR from baseline to 96 weeks in both groups (ABC/3TC: -8.7 mL/min/1.73 m^2, 95%CI -13.3 to -4.2, p<0.001; TDF/FTC: -9.2 mL/min/1.73 m^2, 95%CI -13.7 to -4.7, p<0.001) (Fig. 5A). There was no significant interaction between the trend of the two arms over time (p=0.202), thus indicating that the change in eGFR from baseline to 96 weeks was not significantly different between the two arms. A sensitivity analysis of creatinine clearance calculated using the Cockcroft-Gault equation showed that creatinine clearance decreased significantly from the baseline in the TDF/FTC arm (-9.6 mL/min, 95%CI -16.6 to -2.5, p<0.001) but not in the ABC/3TC arm (-4.1 mL/min, 95%CI -11.2 to 3.0, p=0.466)(Fig. 5B). No significant interaction between the trend of the two arms was observed with respect to creatinine clearance (p=0.403). Two patients in the ABC/3TC arm progressed to more advanced chronic kidney disease (CKD) stage by the last per protocol visit: one patient progressed to stage 4 CKD (eGFR <30 mL/min/1.73 m^2) and the other to stage 3 CKD (eGFR <60 mL/min/1.73 m^2). However, ABC/3TC did not appear to be the causative drug for renal dysfunction in these two cases because the deterioration in the renal function was associated with the development of malignant lymphoma in the former patient and with the commencement of fenofibrate treatment in the latter; renal function recovered rapidly in the latter patient after the discontinuation of fenofibrate.

Discussion

Although insufficiently powered to show the non-inferiority of the viral efficacy of ABC/3TC relative to TDF/