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Original article

HLA-A*2402-restricted HIV-1-specific cytotoxic T lymphocytes and escape mutation after ART with structured treatment interruptions

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Abstract

Although a limited duration of immune activation of structured treatment interruptions (STIs) has been reported, the immune escape mechanism during STIs remains obscure. We therefore investigated the role of three immunodominant cytotoxic T lymphocyte (epitopes) in 12 HLA-A*2402-positive patients participating longitudinally during the clinical study of early antiretroviral treatment (ART) with five series of structured treatment interruptions (STIs). The frequency of HLA-A*2402-restricted CTLs varied widely and a sustained CTL response was rarely noted. However, a Y-to-F substitution at the second position in an immunodominant CTL epitope Nef138-10 (Nef138-2F), which was previously demonstrated as escape mutation, was frequently detected in seven patients primarily and emerged in the remaining five patients thereafter, and the existence of escape mutations was correlated with high pVL levels early in the clinical course. These findings suggest that escape mutation in the immunodominant CTL epitope may be one of the mechanisms to limit HIV-1-specific immune control in STIs.

Keywords: Structured treatment interruptions; Cytotoxic T lymphocyte; HLA-A*2402; Escape variant

1. Introduction

Structured treatment interruption (STI) is considered one of the immune stimulatory interventions for HIV-1 infection, based on the hypothesis that viral rebound during treatment interruption might induce HIV-specific immune responses [1–3]. Since the 1999 case report of the early-treated patient who achieved sustained viral suppression without highly antiretroviral therapy (HAART) after two occasional treatment interruptions [1], the STI strategy has been studied in various clinical settings [4–7]. Because cytotoxic T lymphocytes (CTLs) play a critical role in the control of HIV-1 replication and HIV-specific CD4+ T-cell response is important to maintain effective HIV-1-specific CTLs [8-11], early treatment that can preserve HIV-1-specific-CD4+ T cells is considered to have the greater impact on STI in early infection than in chronic infection [11–13]. However, the majority of previous STI trials revealed the limitation of immune activation with risk of viral resistance [4,14,15] and the mechanisms of viral control failure in STI strategy have remained unclear.

Viral mutation in immunodominant epitopes is one of the obstacles to HIV-1 vaccine development [16–21]. Since HIV-1-specific T-cell responses are restricted by HLA alleles, its escape variant can be transmitted and adopted in populations sharing some dominant HLA alleles [19–21]. In Japan where HLA-A*2402 is the most frequent HLA class I allele with 70% prevalence, HLA-A*2402-restricted CTLs and its immunodominant epitopes have been extensively assessed [22]. Nef138-10, which has been proved previously as an HLA-A*2402-restricted CTL epitope provoking strong cytolytic activity [22], is one of the immunodominant CTL epitopes in HLA-A*2402-positive Japanese patients [21,22].

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Our previous study showed that a Y-to-F substitution at the second position in Nef138-10 epitope (Nef138-2F) impairs the ability of the Nef138-10-specific CTLs to suppress HIV-1 replication, indicating that Nef138-2F is an escape mutation from CTLs [23]. Since Nef138-2F is observed in both HLA-A*2402-positive and -negative patients, Nef138-2F variant may be stable and adopted at a population level [21].

In the present study of early antiretroviral treatment with five series of STIs for HLA-A *2402 positive Japanese patients, we investigated the longitudinal magnitudes of HIV-1-specific HLA-A*2402-restricted CTLs by using HLA-epitope tetramer binding assay and sequenced the most immunodominant epitopes Nef138-10 to evaluate whether escape mutation might negatively influence viral control in an STI study.

2. Methods

2.1. Study design and patient population

This trial was designed as a prospective study at the AIDS Clinical Center, International Medical Center of Japan. Between November 2000 and December 2001, patients with early HIV infection, with or without acute retroviral symptoms, were recruited. Early HIV infection was confirmed within 6 months before recruitment by a documented history of seroconversion in enzyme-linked immunosorbent assay (ELISA) or longitudinal increase of bands in Western blot test. Patients with active opportunistic infections or psychological disorders, or those treated with immunomodulatory agents were excluded. Antiretroviral therapy was initiated after obtaining a signed informed consent. The first-choice regimen for this study consisted of stavudine, lamivudine and indinavir boosted with ritonavir, but the patient was allowed to use other antiretroviral drugs when the first regimen could not be tolerated. To avoid emergence of drug resistance to indinavir, ritonavir-boosting was stopped more than 1 week before treatment interruption. The duration of treatment interruption was fixed for 3 weeks. The first treatment was interrupted after more than 3 months of HAART, when CD4+ cell count was $>500/mm^3$ and plasma viral load (pVL) had been <50 copies/ml for at least 1 month. Other interruptions were also carried out when pVL became <50 copies/ml and CD4+ cell count was $>300/mm^3$. Five series of STIs were scheduled during the treatment.

The study protocol was approved by the institutional ethical review boards (IMCJ-H13-10).

2.2. Monitoring and sample collection

Patients were monitored monthly during HAART and at approximately a 4-month interval after treatment discontinuation. Unscheduled visits were permitted according to clinical needs. At each visit, clinical assessment and routine laboratory tests were performed. Blood specimens were collected in ethylenediaminetetraacetic acid (EDTA)-containing tubes, separated into peripheral blood mononuclear cells (PBMCs) and plasma, and stored at −80 °C for assessment of HIV-1-specific CTLs and sequence of the dominant epitope region. pVL was quantified by using the Amplicor HIV-1 Monitor test 1.5 (Roche Diagnostics, Indianapolis, IN) with a detection limit of 50 copies/ml. Antiretroviral drug resistance-associated mutations were examined at baseline and after HAART including STIs in all 26 participants. Each mutation was identified according to the revised August 2006 International AIDS Society Resistance-USA Panel [24].

2.3. HLA typing and epitope-HLA-A*2402 tetramer binding assays

High-resolution HLA class I typing was performed by a PCR-sequence-specific primer method. If HLA-A*2404 was positive, HIV-1 specific CTLs were investigated by using peptide-HLA-A*2402 tetrameric complex synthesized as described previously [21,22,25]. Purified complexes were enzymatically biotinylated at a BirA recognition sequence located at the C-terminus of the heavy chain, and then mixed with phycoerythrin (PE)-conjugated avidin (extravidin-PE; Sigma–Aldrich, St. Louis, MO) at a molar ratio of 4:1. Cryopreserved PBMCs ($0.5-1 \times 10^6$ cells) were stained by the tetramer at 37 °C for 30 min. After double washing with washing buffer (10% fetal calf serum in RPMI 1640), the cells were stained by fluorescein isothiocyanate (FITC)-conjugated anti-human CD8 mAb (BD Biosciences, San Jose, CA) at 4 °C for 30 min. The cells were then washed twice and analyzed using a FACS Calibur with Cell Quest software (Becton Dickinson, San Jose, CA). Based on our previous study [22], three immunodominant epitopes of HLA-A*2402 restricted CTLs; Nef138-10, Gag28-9 and Env584-9, were chosen for this assay. Since we found a high frequency of Y-to-F substitution at the second position in Nef138-10 gene (Nef138-2F) which has been suspected as an escape variant in previous studies [21], Nef138-2F-specific CTLs (Nef138-2F-CTLs) were also measured by tetramers using Nef138-2F variant alone and by competitive double staining using two types of tetramers of both wild type and Nef138-2F variant to compare the frequencies of the two types of HIV-1-specific CTLs.

2.4. Sequence analyses of Nef138-10 gene

For evaluation of escape variants from CTLs, we sequenced the region coding Nef138-10, which is the immunodominant HLA-A*2402-restricted epitope, while Nef138-2F has been suspected as escape mutation in this epitope, using the method described here. Total RNA was extracted from plasma with a High Pure viral RNA kit (Boehringer Mannheim, Mannheim, Germany), followed by RT–PCR with a One Step RNA PCR kit (TaKaRa Shuzo, Otsu, Japan) to amplify the HIV-1 Nef DNA segment (2341 bp) as described previously [21]. The PCR products were purified with SUPREC-02 (TaKaRa Shuzo) and subjected to direct sequencing with an ABI PRISM 3730 automated DNA sequencer (Applied Biosystems, Foster City, CA). Amino acid sequences were deduced with the Genetyx-Win program version 5.1 (Software Development, Tokyo).

2.5. Statistical analysis

Data from patients who completed the treatment protocol including five series of STIs were analyzed. Before analysis, pVL data were log-transformed and undetectable pVL (<50 copies/ml) was considered equivalent to 50 copies/ml. The Mann–Whitney *U*-test was used to compare the pVLs determined every 3 months after treatment cessation to the pVLs of 279 untreated chronic HIV-1 patients in order to assess the durability of viral suppression. The correlation between pVL and percentage of CTLs was assessed by simple regression analysis. Statistical analyses were performed using SPSSII software package for Windows, version 11.0J.

3. Results

3.1. Characteristics of participants

During the enrollment period, 432 new patients were referred to our clinic. Of these, 32 met the criteria of early HIV-1 infection and 6 were excluded due to psychological problems or taking systemic steroid therapy for symptoms associated with acute retroviral syndrome. All 26 recruits were Japanese infected with HIV-1 by sexual intercourse, and 24 were men (92%). The mean age of patients was 35.0 years (range, 21–56 years). The mean pVL at baseline was 5.21 $\log_{10}$ copies/ml (range, 3.28–6.91 $\log_{10}$ copies/ml) and the mean CD4+ cell count at baseline was 413/mm^3 (range, 49–1156/mm^3). Twenty-five patients presented with wide-range clinical symptoms of acute retroviral syndrome. Fifteen out of 26 participants completed the treatment protocol including five series of STI. HAART had to be continued in four patients because CD4+ cell counts had never stabilized above 300/mm^3 despite more than 6 months of treatment. The other seven patients discontinued the treatment protocol after less than five STIs due to adverse events, adherence problems, or no specific problems.

In the protocol-completed 15 patients, 14 were men (92%). The mean age was 34.0 years (range, 21–56 years). At baseline, the median pVL was 5.14 $\log_{10}$ copies/ml (range, 3.28–6.91 $\log_{10}$ copies/ml) and the median CD4+ cell count was 475/mm^3 (range, 245–990/mm^3). The demographic, immunological, and virological factors before initiation of HAART of the protocol-completed group were not statistically different from those of the uncompleted group (Mann–Whitney *U*-test) (data not shown), although baseline CD4+ cell counts of four ART-continued patients: 49, 185, 210, and 351/mm^3 respectively seemed lower than those who completed the treatment protocol. Twelve (80%) patients were positive for HLA-A*2402 and its incidence was similar to those reported previously in Japanese population [21,22]. No specific HLA genotypes that are known to influence the clinical course of HIV infection such as HLA-B*27, HLA-B*57 and HLA-B*35 (except B*3501) [26] were detected in participants. The median length of follow-up after treatment cessation was 961 days (range, 462–1255 days).

No resistance-associated mutations were identified among all the 26 participants at study enrollment except one who had M184V, D30N and L90M mutations despite good virologic responses throughout HAART. There was no increase in resistance-associated mutations during and after five STIs in all participants (data not shown).

3.2. Plasma viral load and CD4+ cell count in protocol-completed 15 patients

Fig. 1 shows serial changes in median pVLs and CD4+ cell counts in protocol-completed 15 patients. Peaks of viral

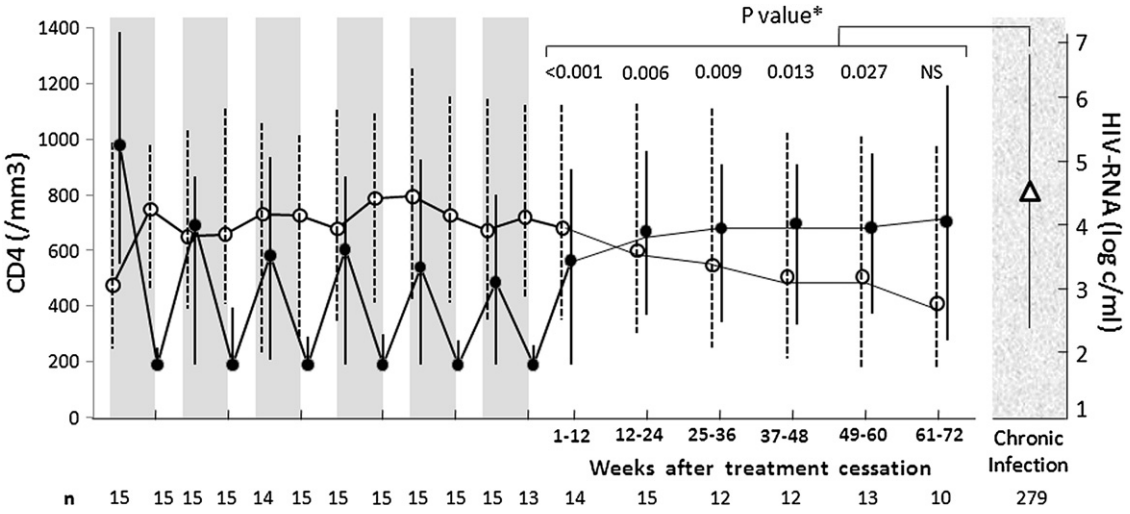

Fig. 1. Serial changes in plasma viral loads and CD4+ cell counts of 15 protocol-completed patients. Plasma viral loads (pVLs) and CD4+ cell counts are expressed as median of 15 protocol-completed patients; at baseline, at the times of treatment interruption, at the peaks of pVL rebound during structured treatment interruption and at every 12 weeks after treatment cessation. Open circles: CD4+ cell counts; solid circles: pVLs; triangle: the median pVL of 279 untreated chronic HIV-1 patients who were referred to our clinic during the study and whose CD4 count was >200/mm^3. Vertical lines provide the ranges with dotted lines in CD4+ cell counts and with light lines in pVLs. Shaded area: time on antiretroviral therapy; unshaded area: time off therapy. Numbers of patients whose data were evaluated at each time point appear at the bottom of the graph. *pVLs of every 12 weeks after treatment cessation were compared to the pVLs of 279 untreated chronic HIV-1 patients by Mann–Whitney *U*-test.

rebounds during treatment interruptions decreased gradually. The pVLs of every 12 weeks after treatment cessation were under 4 $\log_{10}$ copies/ml in most of the patients and they were significantly lower for 60 weeks than the pVLs of 279 untreated chronic HIV-1 patients in our clinic. However, pVLs gradually increased and there was no difference at week 61–72 from pVLs of chronically infected patients. The proportion of patients with a favorable viral control whose median pVL at every 12 weeks after treatment cessation were less than 4.0 $\log_{10}$ copies/ml was 66% in the first 12 weeks but the proportion decreased to 33% in the 61–72 weeks. Along with the increase in pVL, CD4+ cell counts declined after treatment cessation and one patient (KI-134) required restart of HAART because CD4+ cell count decreased below 200/mm^3 at week 52. None of the patients developed episode of opportunistic infections or HIV-related diseases throughout this study.

3.3. Plasma viral loads and frequency of HLA-A*2402-restricted CTLs

We investigated induction of 3 HLA-A*2402-restricted immunodominant epitope-specific CTLs in 12 patients with HLA-A*2402 by using the corresponding tetramers. Fig. 2 shows the serial changes in HLA-A*2402-restricted HIV-1-specific CTLs. Overall, the frequency of HLA-A*2402-restricted CTLs varied widely among the patients and a sustained CTL response was rarely noted. We investigated the correlation between pVLs at every 12 weeks after treatment cessation and frequency of HLA-A*2402-restricted CTLs according to the epitope. None of Nef138-10-, Gag28-9- or Env584-9-specific CTLs was statistically correlated to pVLs (Fig. 3A).

3.4. Effect of Nef138-10 escape mutation on suppression of HIV replication

A Y-to-F substitution at the second position of Nef138-10 (Nef138-2F) has been suspected as an escape mutation from HLA-A*2402-restricted Nef138-10-specific CTLs in a previous study [21]. In fact, we recently demonstrated that Nef138-10-specific CTLs fail to suppress replication of Nef138-2F mutant [23]. We therefore performed serial sequence analyses of Nef138-10 epitope and investigated whether this 2F mutation is responsible for the limited duration of viral suppression. As shown in Table 1, we found high frequency of this mutation. Seven out of 12 patients had Nef138-2F variant in viral RNA or proviral DNA in the earliest samples (KI-091, KI-126, KI-134, KI-144, KI-150, KI-154 and KI-163). The Nef138-2F variant was not detected in the earliest samples of the other five patients (KI-092, KI-099, KI-102, KI-158 and KI-161) and these patients were considered to have Nef138-10 wild-type infection except a T-to-C substitution at the fifth position (Nef138-5C) in KI-099 which has also been suspected as one of the escape variants from Nef138-10-specific CTLs in a previous study [21], and an L-to-I substitution at the forth position (Nef138-4I) in KI-161. However, Nef138-2F mutation was detected at the latter stage in all the other five patients.

We speculated that Nef138-10-specific CTLs can control replication of HIV-1 in patients who had been infected with Nef138-WT virus. Therefore we compared pVLs according to the existence of escape mutants Nef138-2F or 138-5C at the earliest sample drawn during early phase of infection before treatment initiation. As shown in Fig. 3B, the pVLs between 13 and 36 weeks were significantly lower in the other four patients who were confirmed as Nef138-WT or Nef138-4I infection than in the remaining eight patients who had Nef138-2F or Nef138-5C variant in the earliest samples, which has been suspected as an escape variant from Nef138-10-specific CTLs in a previous study. These indicate that Nef138-10-specific CTLs control replication of wild-type virus but the presence of either Nef138-2F or Nef138-5C negatively influences viral control.

3.5. Nef138-2F variant specific CTLs

We found Nef138-WT-tetramer and Nef138-2F-tetramer bound to both Nef138-WT-specific CTL clones and Nef138-2F-specific CTL clones. In addition, Nef138-WT-tetramer had stronger affinity to Nef138-WT-specific CTL clones than Nef138-2F-specific CTL clones (Fig. 4A) and vice versa (our unpublished work). Therefore, the double-staining assay using both tetramers simultaneously was performed to differentiate the two types of CTLs.

The frequencies of the two types of CTLs are shown in Table 1. In patients negative for Nef138-2F or Nef138-5C initially, Nef138-WT-CTLs were detected early after the treatment cessation (KI-092, KI-102, KI-158 and KI-161) but declined after evolution of Nef138-2F (KI-092, KI-102, and KI-161). Although only a slight elevation of Nef138-2F-CTLs was noted after emergence of Nef138-2F (KI-092 and KI-161), the magnitude was smaller than that of Nef138-WT-specific CTLs before emergence of Nef138-2F.

In patients having Nef138-2F variant initially and suspected as Nef138-2F variant infection, the frequencies of Nef138-2F-CTLs were relatively smaller than those of Nef138-WT-specific CTLs in Nef138-10 wild-type infection, except KI-144 who had marked increase of Nef138-2F-CTLs in week 37.

Fig. 4B and C illustrate the clinical courses of two representative cases; KI-161 was non-Nef138-2F variant infection and KI-144 was suspected as Nef138-2F variant infection. In KI-161 (Fig. 4B), Nef138-WT-CTL response diminished after the emergence of Nef138-2F mutation. Interestingly, the pVL of this patient seemed to increase along with the fall in Nef138-WT-CTLs (Fig. 2). In KI-144 (Fig. 4C), Nef138-2F-CTLs were induced but there was no suppression of pVLs. These results indicate that either infection or emergence of Nef138-2F variant might limit the CTL induction.

4. Discussion

In this study, we could not demonstrate the lowered set-point pVLs in patients who received HAART with five series of STIs in early HIV-1 infection. Previous studies revealed that a vigorous HIV-1-specific CD4 response is associated

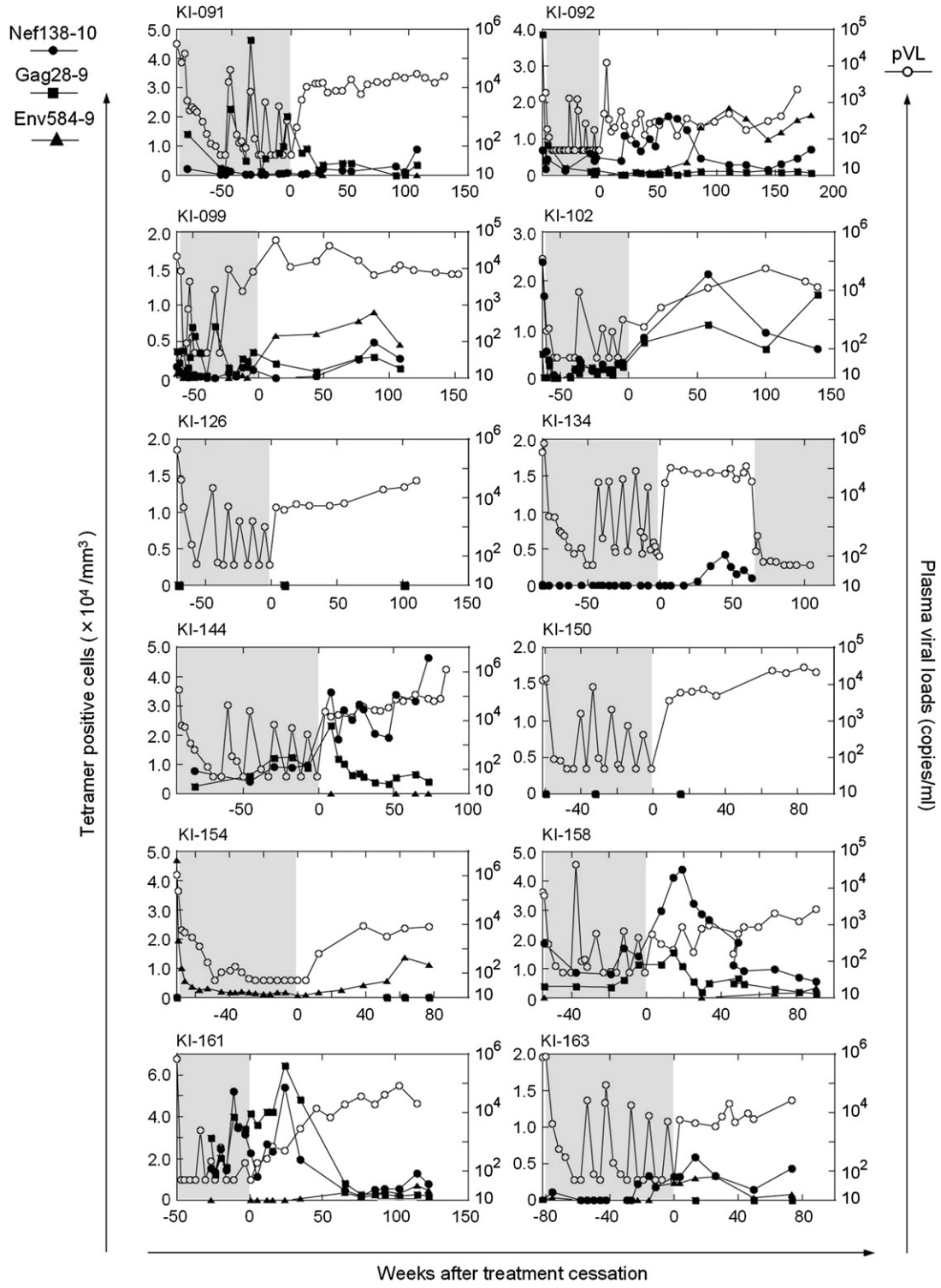

Fig. 2. Frequencies of HLA-A*2402 restricted HIV-1-specific CTLs determined by tetramer binding assay. HLA-A*2402 restricted HIV-1-specific CTLs in PBMCs were determined by using tetrameric complexes of HLA-A*2404 and each of the three types of epitopes. Solid circle: Nef138-10-specific CTL; solid squares: Gag28-9-specific CTL; solid triangles: Env584-9-specific CTL; open circles: plasma viral load. Shaded area: time on antiretroviral therapy; unshaded area: time off therapy.

with a slower disease progression [8–11]; however, despite some reports of boosted immunological responses in acutely treated patients, the evidence of clinical benefits of early treatment has not been established [12,13]. In line with these trials of early initiation of HAART with or without STI, the CTL responses in our study were mostly transient and did not correlate with pVL levels.

We adopted HLA-epitope tetramer analysis for evaluating CTL responses, which provides specific information on HLA class I allele and HLA-restricted epitopes, because CTL

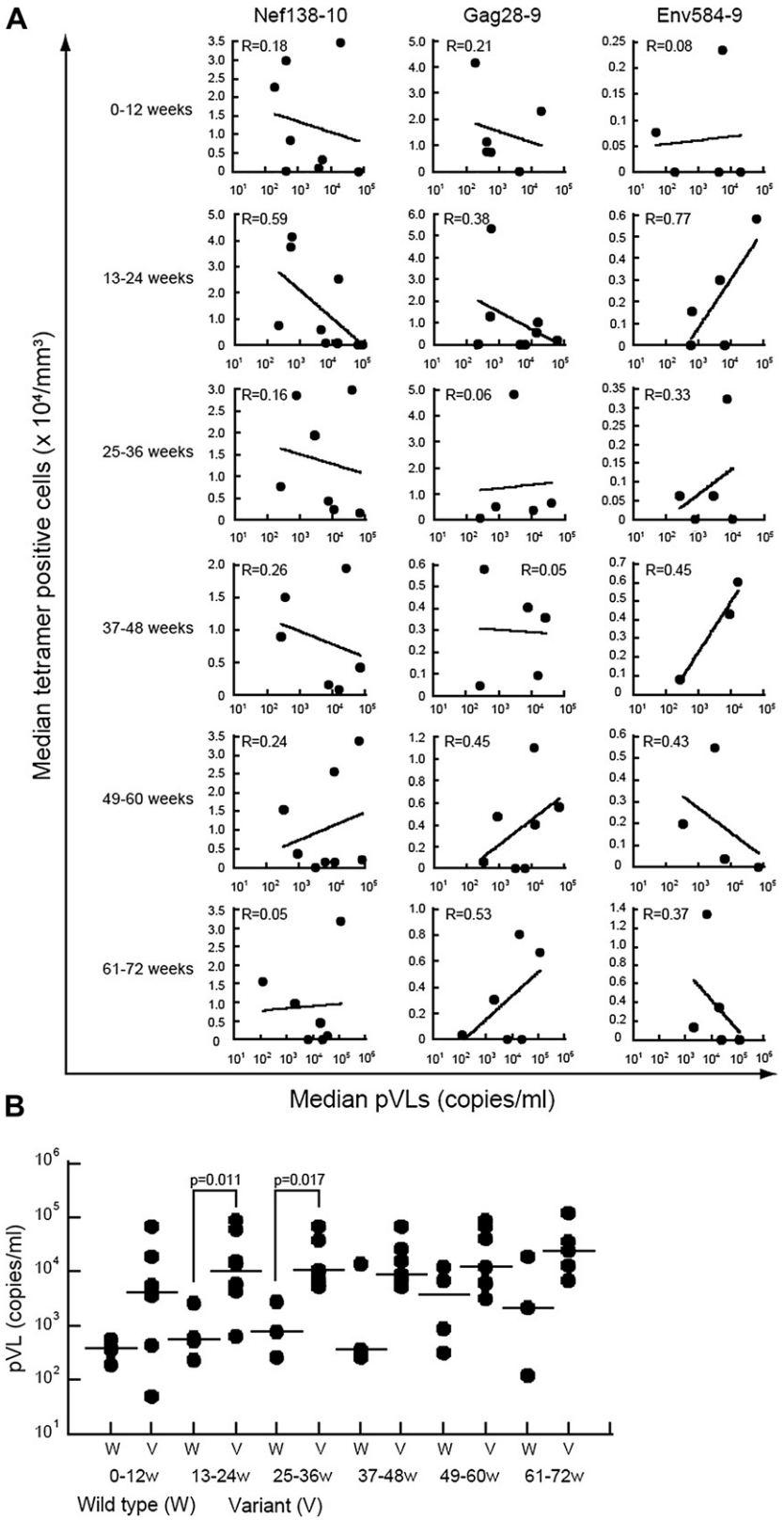

Fig. 3. (A) Plasma viral loads and frequency of HLA-A*2402-restricted HIV-1-specific CTLs. The correlation between the pVL values of every 12 weeks after treatment cessation and frequency of HLA-A*2402-restricted CTLs was assessed by simple regression analysis according to the epitope in 12 HLA*A2402-positive patients. None of Nef138-10-, Gag28-9- or Env584-9-specific CTLs was statistically correlated to pVLs at any time point. R: correlation coefficient. (B) Plasma viral loads and initial type of virus. pVL was compared according to the existence of escape variant in the earliest sample drawn during early phase of infection. Wild type group (W) includes four patients: KI-092, KI-102, KI-158 and KI-161. Variant type group (V) includes eight patients: KI-091, KI-099, KI-126, KI-134, KI-144, KI-150, KI-154 and KI-163, having Nef138-2F or Nef138-5C, which were previously reported as escape variants, in viral RNA or proviral DNA in the earliest samples. The pVLs between 12 and 36 weeks were significantly higher in Variant type group than in Wild-type group. Horizontal lines: median values.

Table 1
Nef138-10 sequence and Nef138-specific CTLs in HLA-A*2402 positive patients

Patient ID	Time (weeks)[a]	Sample	Nef138-10 sequence (RYPLTFGWCF)	Tetramer positive cell (% in CD8+ cells)	
				Wild type	2F
KI-091	−55	Proviral DNA	-F————	NA	NA
	21	RNA	-F————	0	0.46
	89	RNA	-F————	0	0.83
KI-092	39	RNA	————	1.48	0.05
	86	RNA	-F————	0.41	0.13
KI-099	−44	Proviral DNA	——C———	NA	NA
	−4	RNA	-F–C————	0.04	0.06
	44	RNA	-F————	0.02	0.12
KI-102	58	RNA	————	2.11	0.45
	137	RNA	-F————	0.45	0.10
KI-126	−68	Proviral DNA	-F————	NA	NA
	19	RNA	-F————	0.01	0.06
	101	NA	NA	0	0.11
KI-134	9	Proviral DNA	-F————	NA	NA
	49	RNA	-F————	0	0.22
KI-144	−46	Proviral DNA	-F————	NA	NA
	37	RNA	-F————	0.02	2.45
	71	RNA	-F————	NA	NA
KI-150	−43	RNA	-F————	NA	NA
	21	RNA	-F————	0	0.03
	63	NA	NA	0	0.02
KI-154	−70	Proviral DNA	-F————	0.06	0.13
	77	RNA	-F————	0.01	0.35
KI-158	14	Proviral DNA	————	2.91	0.41
KI-161	−26	Proviral DNA	—I————	NA	NA
		RNA	-F-I————		
	24	Proviral DNA	-F-I————	3.94	0.05
		RNA	-F-I————		
	86	Proviral DNA	-F-I————	0.29	0.79
		RNA	-F-I————		
	52	RNA	-F————	0.71	0.66
KI-163	−81	Proviral DNA	-F————	NA	NA
		RNA	-F————		
	26	RNA	-F————	0.09	0.57
	73	NA	NA	0.02	0.59

[a] Time: Time in weeks after treatment cessation. Negative time numbers: before treatment cessation. NA, not available.

responses are different between HLA class I alleles and influenced by viral mutations in epitope regions as described elsewhere [16–22]. HLA-A*2402 is the most frequent HLA class I allele with 70% prevalence in the Japanese population [21,22]. Therefore, the majority of the study participants could be assessed by using HLA-A*2402-epitope tetramer and thus it is most beneficial to evaluate HLA-A*2402 restricted CTL responses for Japanese patients. Moreover, HLA-A*2402-restricted epitopes have been studied extensively [22] and we were able to focus on three immunodominant epitopes. This approach allowed us to find a high frequency of the escape variant Nef138-2F efficiently.

Viral mutation is one of the important mechanisms of immune escape of HIV-1 [16–23,27–29], which occurs at amino acids responsible for HLA binding, T-cell receptor recognition, or in flanking regions that affect antigen presentation. In our study Nef138-2F, which is a mutation in the immunodominant CTL epitope Nef138-10, had emerged in 5 of 12 HLA-A*2402-positive patients. Although the magnitude of Nef138-10-specific CTLs was not significantly correlated with pVLs as previous trials [15], Nef138-2F variant infection was correlated with high pVL levels in early clinical course and seemed to contribute to lower CTL response. Furthermore, we previously demonstrated the strong and weak ability of Nef138-10-specific CTL clones to suppress replication of the wild-type and 2F mutant viruses respectively [23]. In addition, although Nef138-2F-specific CTL clones suppressed the replication of both wild-type and Nef138-2F variant, their ability to suppress the replication of Nef138-2F virus was much weaker than that of Nef138-10-specific CTLs or Nef138-2F-specific CTLs against the wild-type virus replication. Furthermore, the present study demonstrated that 2F mutant appeared at the late phase in patients who had wild-type virus at the early phase. Together with these findings, frequent detection of Nef138-2F in this study strongly supports the idea that Nef138-2F is one of the escape mutations from HLA-A*2402-restricted CTLs and that Nef138-2F virus was selected by CTL pressure.

Nef138-2F mutation could occur not only by positive selection by CTLs but also by Nef138-2F-variant transmission [19–21]. Furutsuki et al. [21] reported frequent detection of

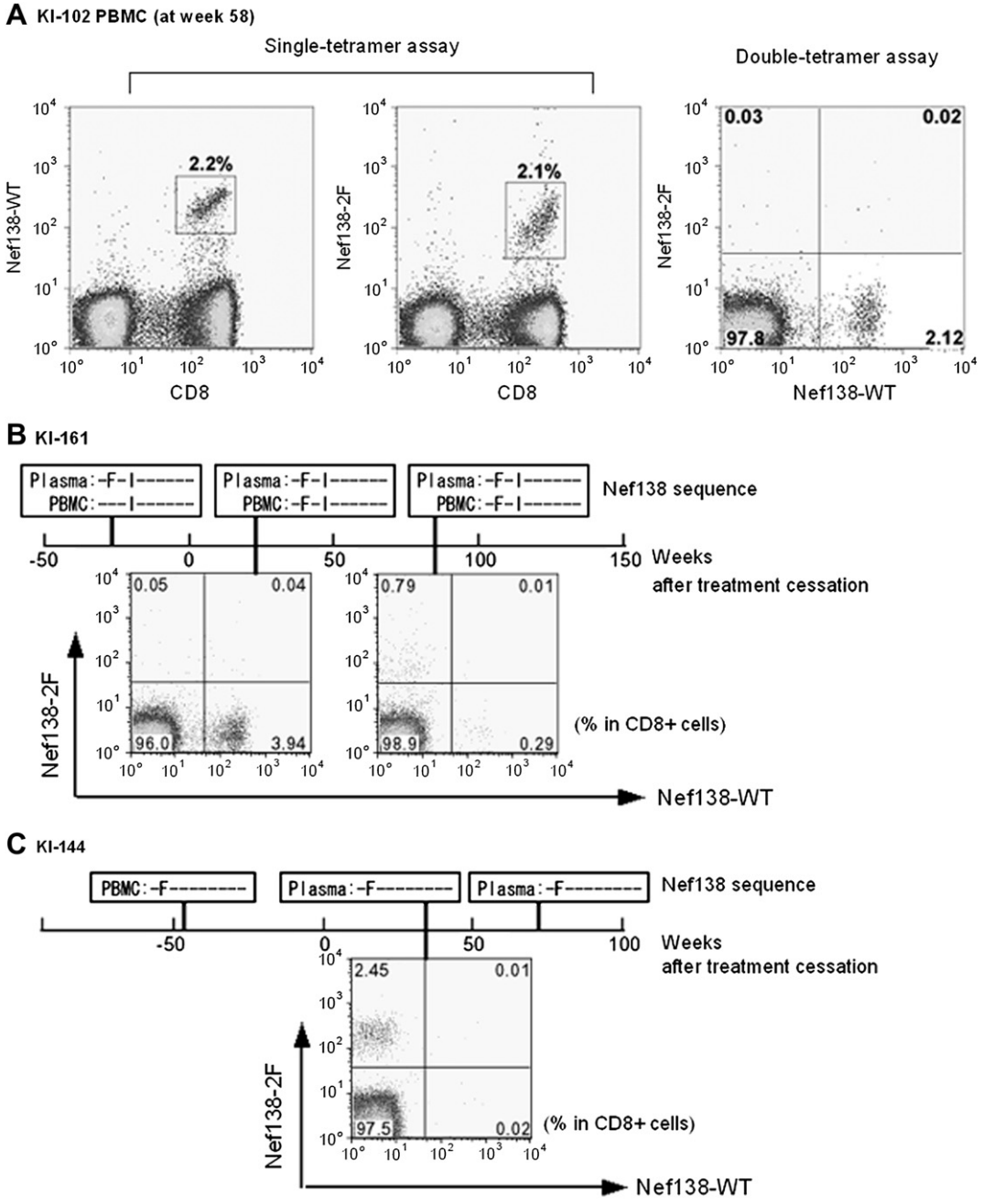

Fig. 4. Nef138-2F variant and CTL specificity. (A) PBMC of KI-102 at week 58, known to coincide with Nef138-10 wild-type infection, were assayed for wild-type Nef138-10-specific CTL (Nef138-WT-CTL) by tetramer-staining with Nef138-WT-tetramer and Nef138-2F-tetramer. The left two charts depict the results of single-tetramer-staining, showing the two tetramers stained for Nef138-WT-CTL equally (2.2% by Nef138-WT-tetramer versus 2.1% by Nef138-2F-tetramer). The right chart depicts the result of double-tetramer-staining with Nef138-WT-tetramer and Nef138-2F-tetramer, showing Nef138-WT-CTL was stained by Nef138-WT-tetramer and was differentiated from Nef138-2F-CTL. (B) Serial changes in Nef138-10 sequence and Nef138-specific-CTLs of KI-161 infected by non-Nef138-2F strain. Top: the Nef138-10 sequence; bottom charts: results of double-staining assay with Nef138-WT-tetramer and Nef138-2F-tetramer. Numbers in each quadrant represent the frequency of tetramer-positive cells among total CD8+ cells. Right lower quadrant: frequency of Nef138-WT-tetramer-positive cells; left upper quadrant: frequency of Nef138-2F-tetramer-positive cells. Note the induction of Nef138-WT-CTL and reduction in their proportion after emergence of Nef138-2F mutation. Nef138-2F-CTLs were induced after emergence of Nef138-2F mutation but their proportion was relatively lower. (C) Serial changes in Nef138-10 sequence and Nef138-specific-CTLs of KI-144 infected by Nef138-2F variant. Note the induction of Nef138-2F-CTL. Nef138-WT-CTLs were never detected throughout the study.

Nef138-2F variant in HLA-A*2402 negative Japanese patients who were infected by sexual intercourse and reversion from Nef138-2F to wild type occurred very slowly over years. These might allow horizontal spread of Nef138-2F variant. Even if the transmission of this variant in Japanese patients is very frequent, our study included the five patients who did not have this variant initially and were considered as wild-type infection, and we provided longitudinal evidence of positive selection of Nef138-2F variant under the pressure of Nef138-WT-CTLs in those.

In conclusion, our study demonstrated that early antiretroviral treatment with five series of STI did not induce a sustained immune response. A high frequency of escape mutation in the immunodominant HLA-A*2402-restricted CTLs was found, which could be one of the causes of limited immune responses by STIs.

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