the first time that the downstream region (aa 76–79) is important for suppression of A3F activity through binding (Fig. 4). Furthermore, an aa critical for suppression of both proteins was newly identified (Figs. 3 and 4).

It has been reported that negatively charged residues Asp128 and Asp130 in A3G are critical for interaction with HIV-1 Vif [19]. Our new result that aa residues 21–43 in HIV-1 Vif play a functional role for interaction with A3G is quite reasonable, considering that the region is rich in positively charged aa residues and that Vif–A3G interaction is dependent on electrostatic interaction. While Glu76 and Trp79 residues were not essential for A3G suppression (Fig. 3), they were critical for A3F suppression (Fig. 4). Of note, whereas E76A and W79A almost normally exclude A3G from virions, they degraded A3G more poorly than WT in producer cells and efficiently interacted with it (Fig. 3B and C). Inhibition of A3G incorporation into virions by HIV-1 Vif may not be a direct outcome of the Vif-mediated degradation of A3G in producer cells. It can be also claimed here that the virion-associated A3 protein is a final and fatal factor for modulation of viral infectivity in target cells. We previously reported that the region containing Tyr69 is important for formation of β-strand structure and for stable expression of Vif [13]. Similarly, a mutation of Ile9 required for β-strand structure abolished the ability of Vif to interact with A3G [20,21]. Thus, it is likely that Tyr69 is important for a proper folding of Vif molecule, and accordingly, the mutant Y69A is inactive against both of A3G and A3F.

It has been reported that some mutants of HIV-1 Vif still retain selective neutralizing activity against A3F but not A3G in a single-cycle infection [7,22]. Moreover, Asp128 of A3G is critical for recognition by HIV-1 Vif but a mutation of Glu128 in A3F does not affect the recognition [1,23]. Our data also showed that HIV-1 Vif recognizes A3G and A3F by different regions. A3G generates GG-to-AA mutations, whereas A3F causes GA-to-AA mutations [1]. GA-to-AA mutations are frequently observed in viral sequences recovered from HIV-1-infected individuals [24]. Therefore, A3F may be important for restriction of HIV-1 infection *in vivo*. In fact, our data showed that mutations of Glu76 and Trp79, which are essential for suppression of A3F activity by Vif, abolished viral multi-cycle replication in H9 cells (Fig. 1).

In this study, we demonstrated that new regions in HIV-1 Vif are critical for interaction with A3G/F. It is well anticipated that the Vif–A3G/F interaction represents a novel and important target of chemical therapy for suppression of HIV-1 replication. Understanding more fully the region in Vif required for A3G/F-binding would provide useful information on the design of antiviral drugs.

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Short communication

Replication potentials of *vif* variant viruses generated from monkey cell-tropic HIV-1 derivative clones NL-DT5/NL-DT5R

Kazuki Hatcho, Kazuya Kamada, Tomoki Yamashita, Akio Adachi, Masako Nomaguchi*

Department of Virology, Institute of Health Biosciences, The University of Tokushima Graduate School, Tokushima 770-8503, Japan

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Abstract

To obtain monkey-tropic viruses that are more closely related to HIV-1 than the original NL-DT5/NL-DT5R clones, we constructed six *vif*-chimeric and two site-specific *vif*-mutant viruses, and examined their growth ability. Different from NL-DT5/NL-DT5R, these viruses did not grow in monkey cells. We monitored the capability of the mutants to antagonize monkey APOBEC3G/F by single-cycle infectivity assays. They counteracted poorly or not at all the action of the APOBEC3G/F. Our results have indicated that the native SIVmac Vif is required to overcome the species barrier against HIV-1.

Keywords: HIV-1; SIV; Vif; APOBEC3G; APOBEC3F; Species tropism

1. Introduction

Human immunodeficiency virus type 1 (HIV-1) displays a very narrow host range, infecting only humans and chimpanzees at both cellular and individual levels. In contrast, simian immunodeficiency virus isolated from rhesus monkeys (SIVmac) can grow in Asian macaques in addition to humans and chimpanzees, although it has a genomic organization similar to that of HIV-1. The distinct host range and similar genome organization of HIV-1 and SIVmac prompted us to generate HIV-1 derivative clones that efficiently grow in macaque cells and are pathogenic for macaques. By these viruses, we would be able to have an ideal animal model for basic and clinical studies on HIV-1/AIDS. Recent attempts by us and others have demonstrated that the genomic regions responsible for the species tropism of HIV-1 are located at *gag* and *vif* genes [1,2]. We have also shown that the substitution of cyclophilin A-binding loop within Gag-CA of HIV-1 with the corresponding region of SIVmac is critical for viral growth in monkey cells [1]. Whether the entire *vif* of SIVmac is essential to overcome the monkey barrier against HIV-1 remained to be determined.

In this study, we have asked whether some specific amino acids and/or domains of SIVmac Vif confer the ability on the virus to productively infect monkey cells. Towards this end, we adopted the strategy to construct *vif* chimeras and site-specific *vif*-mutants, and evaluate their potentials to grow in monkey cells. In addition, we determined the activity of variant Vif proteins against the target proteins APOBEC3G (A3G) and APOBEC3F (A3F) present in monkey cells. We demonstrate here that the whole *vif* gene of SIVmac is required for the productive infection of HIV-1 variants in monkey cells.

2. Materials and methods

2.1. Proviral molecular clones

Full-length infectious molecular clones designated pNL4-3 (HIV-1) [3], pMA239 (SIVmac) [4], pNL-DT5 (monkey cell-tropic HIV-1 derivative defective for *vpr* expression) [1], and pNL-DT5R (monkey cell-tropic HIV-1 derivative) [1] have been previously described. Various *vif*-chimeric variants (Fig. 1A) were constructed by connecting two PCR products

* Corresponding author. Tel.: +81 88 633 9232; fax: +81 88 633 7080.
E-mail address: nomaguchi@basic.med.tokushima-u.ac.jp (M. Nomaguchi).

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amplified from pNL-Sca [1] and pNL-ScaV [1] using the primers in Table 1, and by their insertion into pNL-DT5. To generate site-specific *vif*-mutants (Fig. 1A), Sca-pUC which carries the *vif* gene of pNL-Sca were first constructed. Mutant sequences were then amplified from Sca-pUC by the QuikChange® Site-Directed Mutagenesis Kit (Stratagene, LA Jolla, CA) using the primers in Table 1 as previously described [5,6], and the altered *vif* genes were inserted into pNL-DT5R. The *vif*-deficient clone of pNL-DT5R designated pNL-DT5R-ΔV was constructed by introducing a frame-shift mutation at *Bgl*II site.

2.2. Expression vectors of species-specific APOBEC proteins

Expression vectors of species-specific A3G have been previously described [1]. Species-specific A3F genes were cloned from cDNAs amplified from human H9 and cynomolgus monkey HSC-F cells by RT-PCR. The A3F gene was amplified with forward (GCTCTAGAATGAAGCCTCACTTCAGAAA CACAG) and reverse (ACGCGTCGACCTCGAGAATCTCC TGCAGCTTGC) primers containing embedded *Xba*I and *Sal*I sites (underlined), respectively. The reaction mixtures were heated at 95 °C for 3 min for 1 cycle; 95 °C for 1 min, 63 °C for 1 min, 72 °C for 2.5 min for 10 cycles; 95 °C for 1 min, 65 °C for 1 min, 72 °C for 2.5 min for 25 cycles; and 72 °C for 5 min for 1 cycle. The PCR products were inserted into pcDNA3.1-FLAG vector at the *Nhe*I and *Xho*I sites. Expression level of A3F proteins in transfected 293T cells were determined by Western blotting analysis using anti-FLAG antibody as previously described [1]. Because the expression level in cells of the original clone for cynomolgus monkey A3F was found to be quite low, three point mutations (as judged by the GenBank data on A3F) were corrected for high level expression.

2.3. Cell culture, transfection, and infection

A human kidney cell line 293T [7] was cultured in Eagle's minimal essential medium supplemented with 10% heat-inactivated fetal bovine serum. M8166 (human T-cell line) [4] and HSC-F (simian T-cell line) [8] cells were cultured in RPMI-1640 medium supplemented with 10% heat-inactivated fetal bovine serum. Virus stocks were prepared from 293T cells transfected with various variant clones by the calcium-phosphate coprecipitation method [3]. On day 2 post-transfection, culture supernatants were collected and stored at −80 °C until use. Infection of M8166 and HSC-F cells with viruses was performed essentially as previously described [9].

2.4. RT assay

Virion-associated RT activity was measured as previously described [10].

2.5. Single-cycle infectivity assay

To determine single-cycle infectivity of *vif* variant viruses in the presence of APOBEC proteins, we used luciferase reporter assay as previously described [11]. For this assay, we utilized VSV-G-pseudotyped viruses prepared from 293T cells co-transfected with a luciferase reporter clone and an expression vector of the species-specific APOBEC protein at a ratio of 15:1 (total 10 μg plasmids), and 0.8 μg of the VSV-G expression vector [12]. As reporters, proviral clones structurally similar to that described previously [13] were used. The culture supernatants were harvested on day 2 post-transfection, and were measured for RT activity. 293T cells (4.0×10^4) were infected with 8.0×10^3 RT units of VSV-G-pseudotyped viruses, and on day 2 post-infection, cell lysates were prepared for luciferase assay. Luciferase activity was determined by the Luciferase Assay System (Promega, Madison, WI) using Lumat LB9507 luminometer (BERTHOLD TECHNOLOGIES GmbH & Co. KG, Bad Wildbad, Germany), and normalized by protein amount.

3. Results

3.1. Construction and characterization of vif variants in the genomic background of NL-DT5 and NL-DT5R

To generate monkey-tropic HIV-1 derivatives which are more closely related to HIV-1 than NL-DT5/NL-DT5R [1], we first constructed six NL-DT5-based *vif*-chimeric clones as shown in Fig. 1A. Viral samples were prepared from 293T cells transfected with these clones, and inoculated into HSC-F cells. No virus production was noted for any chimeras during observation period (30 days) as summarized in Fig. 1A. We, therefore, constructed new mutants from NL-DT5R (Fig. 1A) based on a recently published report [14] to obtain virus clones infections for HSC-F cells. The variants designated NL-DT5R-VSa and NL-DT5R-VSm contained the SIVagm SERQ and SIVmac PER sequences, respectively (Fig. 1A). The HIV-1 Vif containing the SERQ at 14–17 residues was shown to counteract the anti-viral effect of human and rhesus monkey A3Gs [14]. Although the SIVmac PER is the corresponding sequence of SIVagm SERQ, its functional importance was not tested yet [14]. To determine the growth ability of these NL-DT5R-based *vif* variant viruses in human and monkey cells, virus samples prepared from transfected 293T cells were inoculated into M8166 and HSC-F cells. As shown in Fig. 1B (upper), all the viruses grew to a various degree in permissive human M8166 cells as expected. In contrast, only MA239 (SIVmac) and NL-DT5R grew considerably in HSC-F cells (Fig. 1B, lower), indicating that variant Vif proteins are not functional in HSC-F cells.

3.2. Single-cycle infectivity of site-specific HIV-1 vif-mutants in the presence of APOBEC3G/F

To know whether mutant Vif proteins (Fig. 1A) can suppress the negative effect of human and monkey A3Gs, viral infectivity in the presence of A3Gs was determined by single-round replication assays. VSV-G-pseudotyped luciferase reporter viruses were prepared from transfected 293T cells

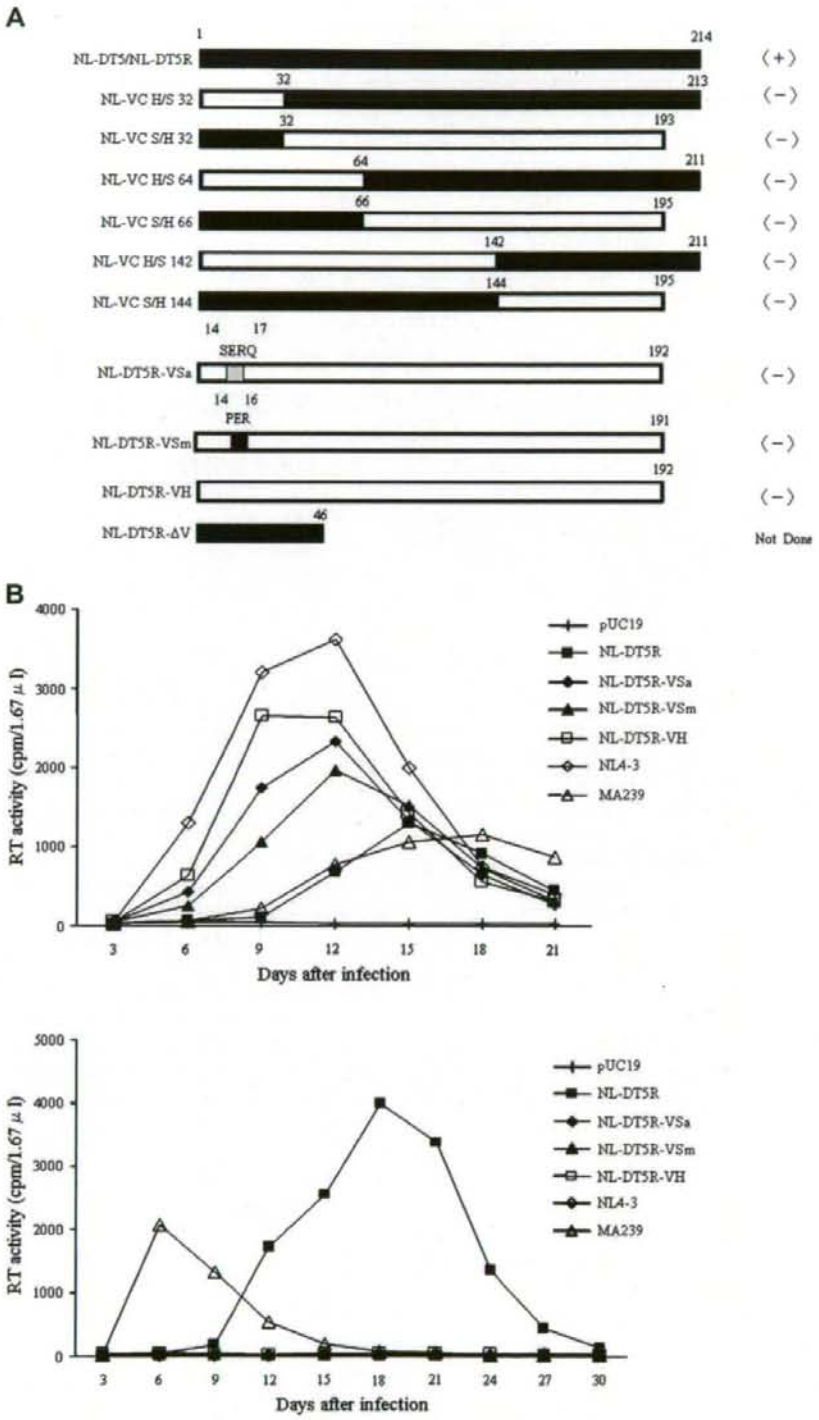

Fig. 1. Structure of variant Vif proteins and growth kinetics of variant viruses. (A) Chimeric and mutant Vif proteins derived from NL-DT and NL-DT5R. White, black and gray areas indicate the Vif sequence of HIV-1, SIVmac and SIVagm, respectively. The figures above the bars indicate nos. of amino acids. (+) and (−) on the right show positive and no viral growth in HSC-F cells, respectively. (B) Growth kinetics of various viruses in human and simian cells. Virus samples were prepared from 293T cells transfected with the indicated plasmid clones, and were inoculated into human M8166 (upper) and cynomolgus monkey HSC-F (lower) cells. M8166 (1×10^6) and HSC-F (1×10^7) cells were infected with an equal amount of viruses (1×10^6 and 1×10^7 RT units for each cell line, respectively). Viral growth was monitored at intervals by RT activity in the culture supernatants. Clones pNL4-3 (HIV-1), pMA239 (SIVmac) and pUC19 served as controls.

Table 1
Oligonucleotides used to construct *vif* variants in this study

Clone	Primer	Template
H/S 32	5′-GGGGCAGTAGTAATACAAGATAATAGTGAC	NL-Sca
	5′-GCTCTAGAAATATACATATGGTGTTTTA CTAATC	
	5′-GCTCTAGAGATCTACAAAAGGTTTGCTA TGTGCCC	NL-ScaV
	5′-ATTTCTTGCTCTCCTCTGTCGAGTAACGCC	
S/H 32	5′-GGGGCAGTAGTAATACAAGATAATAGTGAC	NL-ScaV
	5′-GCTCTAGATTTATATTTCAGATATTTTA TGAGGC	
	5′-GCTCTAGAAAAGCTAAGGACTGGTTTT ATAGAC	NL-Sca
	5′-ATTTCTTGCTCTCCTCTGTCGAGTAACGCC	
H/S 64	5′-GGGGCAGTAGTAATACAAGATAATAGTGAC	NL-Sca
	5′-TACCGCTCGAGTTTAGCATCCCCTAG TGGGATGTG	
	5′-ATCCGCTCGAGGTACAAGGGTATTGGCA TTTGAC	NL-ScaV
	5′-ATTTCTTGCTCTCCTCTGTCGAGTAACGCC	
S/H 66	5′-GGGGCAGTAGTAATACAAGATAATAGTGAC	NL-ScaV
	5′-TACCGCTCGAGATGGCTTCCTTCCTGTA GTGGG	
	5′-ATCCGCTCGAGATAACAACATATTGGG GTCTGC	NL-Sca
	5′-ATTTCTTGCTCTCCTCTGTCGAGTAACGCC	
H/S 142	5′-GGGGCAGTAGTAATACAAGATAATAGTGAC	NL-Sca
	5′-CATGGTACCTTGTTATGTCCTGCTTGAT ATTCAC	
	5′-ATGGGTACCAAGCCTACAGTACTTAGCACTG AAAG	NL-ScaV
	5′-ATTTCTTGCTCTCCTCTGTCGAGTAACGCC	
S/H144	5′-GGGGCAGTAGTAATACAAGATAATAGTGAC	NL-ScaV
	5′-CATGGTACCTGGTACTTATGAGCTCTCGGG AACC	
	5′-ATGGGTACCATCTCTACAGTACTTGGCAC TAGCAG	NL-Sca
	5′-ATTTCTTGCTCTCCTCTGTCGAGTAACGCC	
VSa	5′-GATTGTGTGGCAAGTAAGCGAGAGGCAGA TTAACACATGGAAAAG	Sca-pUC
	5′-CTTTTCCATGTGTTAATCTGCCTCTCGCTT ACTTGCCACACAATC	
VSm	5′-GATTGTGTGGCAAGTACCGGAGAGGAT TAACACATG	Sca-pUC
	5′-CATGTGTTAATCCTCTCCGGTACTTGCC ACACAATC	

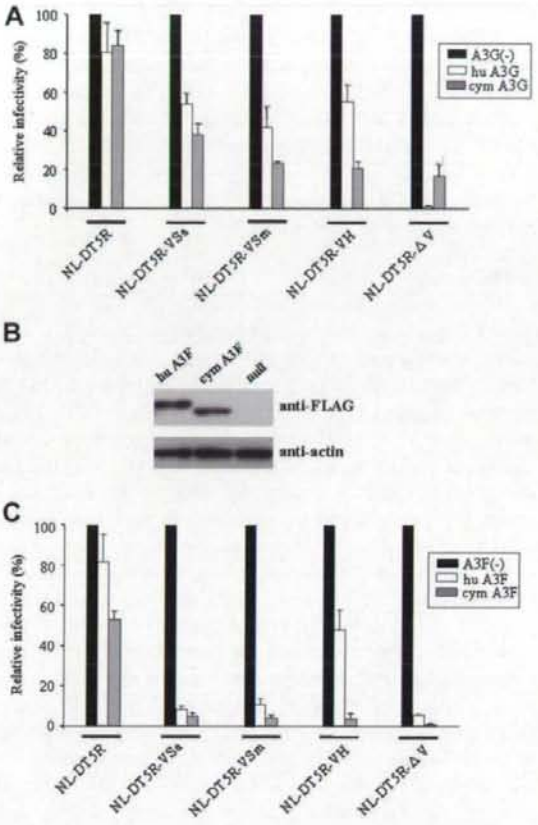

Fig. 2. Single-cycle infectivity of *vif* variants in the presence of human and monkey A3G/Fs. (A) Single-cycle infectivity of various viruses produced in the presence of human and cynomolgus monkey A3Gs (hu A3G and cym A3G, respectively). The infectivity was determined as described in Section 2. Infectivity relative to that of the virus sample prepared in the absence of A3G [A3G(−)] is shown. Viral clones used are indicated at the bottom. (B) Expression of A3Fs by newly constructed vectors as monitored by Western immunoblotting analysis. Antibodies used are indicated on the right. (C) Single-cycle infectivity of *vif* variants produced in the presence of human and monkey A3Fs. The infectivity was determined as described in Section 2. Infectivity relative to that of the virus sample prepared in the absence of A3F [A3F(−)] is shown. Viral clones used are indicated at the bottom.

in the presence or absence of A3G, and were inoculated into 293T cells. On day 2 after inoculation, intracellular luciferase activity was determined. The expression levels in cells of the A3Gs were similar on this condition [1]. As shown in Fig. 2A, all the viruses, except for a negative control NL-DT5R-ΔV, counteracted the effect of huA3G (human). While NL-DT5R-VSa containing a small portion of SIVagm Vif counteracted cymA3G (cynomolgus monkey) approximately 2-fold more effectively than NL-DT5R-VH containing HIV-1 Vif, its activity was approximately 2-fold less than that of NL-DT5R containing the entire Vif of SIVmac. These results showed that the mutant HIV-1 Vif carrying the SERQ sequence was partially active against cymA3G and that the SIVmac Vif more effectively and powerfully suppressed cymA3G activity than the mutant. On the other hand, NL-DT5R-VSm containing a small portion of SIVmac Vif suppressed huA3G activity but not considerably cymA3G activity.

To examine whether NL-DT5R and NL-DT5R-based *vif* variants counteract the effect of A3Fs, we performed single-cycle infectivity assays as above in the presence of species-specific A3Fs. A3F has been reported to be one of the APOBEC3 families and a Vif-dependent antiretroviral restriction factor like A3G [15,16]. In the first, species-specific A3F expression vectors were constructed as described in Section 2. Expression level of A3F proteins in transfected 293T cells were analyzed by immunoblotting using anti-FLAG and anti-actin antibodies as shown in Fig. 2B. Both hu and cymA3F were equally expressed in transfected 293T cells as expected. Single-cycle infectivity of various virus clones produced in 293T cells in the

presence or absence of hu and cymA3Fs was then determined. As shown in Fig. 2C, control clones NL-DT5R, NL-DT5R-VH and NL-DT5R-ΔV behaved exactly as expected. However, test samples NL-DT5R-VSa and NL-DT5R-VSm did not suppress the effect of hu and cymA3Fs at all. These results indicated that the HIV-1 Vif containing alterations at amino acid positions 14–17 was unable to counteract cymA3F activity. Furthermore, we noticed that the alteration in HIV-1 Vif also inactivated the inhibition potential against huA3F.

4. Discussion

In this study, we constructed eight HIV-1 derivatives which contain the mutated *vif* gene and examined their growth potentials to narrow down the necessary *vif* sequence of SIVmac from the genome of the prototype monkey-tropic HIV-1 designated NL-DT5/NL-DT5R (Fig. 1). However, none of them were able to grow in monkey HSC-F cells (Fig. 1). To clarify the underlying molecular mechanism for this, we evaluated the ability of mutant viruses to invalidate the activity of anti-viral APOBEC3G/F (Fig. 2). As a result, inhibitory activity against cymA3G of *vif* variant viruses was less than that of NL-DT5R. Of note, NL-DT5R-VSa containing the SERQ sequence at residues 14–17 of HIV-1 Vif counteracted cymA3G activity approximately 2-fold less effectively than NL-DT5R carrying the whole SIVmac Vif. Furthermore, none of the *vif* variant viruses counteracted cymA3F (and also huA3F) at all, strongly suggesting the possibility that A3F inhibited the replication of NL-DT5R-based *vif* variant viruses in monkey cells as well as A3G. We also noticed that NL-DT5R having the SIVmac Vif was only partially active against cymA3F as previously reported [17]. Given that SIVmac grows well in monkey cells and in monkeys, our result here suggested that the expression level of A3F in these cells might be low. In this regard, it would be interesting to quantitatively analyze various APOBEC3 proteins in natural target cells. It has been recently reported that several monkey APOBEC3 proteins such as A3B, A3F, A3G and A3H inhibit the growth of HIV-1 [17]. Taken all together, it would be critical to inhibit the activity of many of monkey APOBEC3 proteins for construction of monkey-tropic HIV-1 that grows similarly efficiently with SIVmac in monkey cells.

In sum, it is difficult or impossible to suppress the negative effect of all monkey APOBEC3 proteins active against the virus through the partial alteration of HIV-1 Vif. Therefore, chimeric virus clones containing the entire SIVmac *vif* gene, such as NL-DT5R, would be more useful monkey-tropic HIV-1 derivatives to obtain replication-competent HIV-1 that is highly pathogenic for monkeys.

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Short communication

Functional region mapping of HIV-2 Vpx protein

Mikako Fujita [a], Masami Otsuka [a], Masako Nomaguchi [b], Akio Adachi [b,*]

[a] *Department of Bioorganic Medicinal Chemistry, Faculty of Medical and Pharmaceutical Sciences, Kumamoto University, Kumamoto 862-0973, Japan*
[b] *Department of Virology, Institute of Health Biosciences, The University of Tokushima Graduate School, 3-18-15 Kuramoto-cho, Tokushima 770-8503, Japan*

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Abstract

To determine functional regions of HIV-2 Vpx, we analyzed a series of site-specific *vpx*-mutants for their growth potentials in lymphocytic cells and compared the results with those in macrophages. We found that amino acid residues important for virus growth in lymphocytic cells, in macrophages, and in both are clustered separately in Vpx. Through generation and characterization of new *vpx*-mutants, we further demonstrated that a remarkable proline-stretch present at the C-terminus of Vpx is critical for its stable expression, thereby contributing to its functional activity. Taken together, there can be functionally distinct regions in HIV-2 Vpx.

Keywords: HIV-2; Vpx; Macrophage; Lymphocyte; Proline-stretch

1. Introduction

Viruses of human immunodeficiency virus type 2 (HIV-2) group carry a *vpx* gene that encodes virion-associated accessory protein Vpx. While Vpx is essential for virus replication in primary monocyte-derived macrophages (MDMs) [1–4], it is dispensable in primary and immortalized lymphocyte cells [3,5,6]. In these lymphocyte cultures, *vpx*-minus or -defective viruses grow to a lesser extent than wild-type (WT) virus. The mechanism underlying this cell type specificity is largely unknown. We have recently shown by extensive mutational analyses that HIV-2 Vpx is important for processes of the reverse transcription of viral RNA genome and the nuclear import of viral DNA in MDMs and lymphocytic HSC-F cells, respectively [3,4]. These findings have suggested the presence of some unidentified cellular factor(s) which interact with Vpx in a cell type dependent manner. In this study, to better understand molecular basis for cell-dependent activity of Vpx, we have performed a systemic genetic analysis by using a series of site-specific mutants of HIV-2 Vpx [4]. We show here that there are distinct and common functional regions in HIV-2 Vpx important for virus growth in two different cell types, and demonstrate that the C-terminal proline-stretch of Vpx is critical for its stable expression.

2. Materials and methods

2.1. Molecular clones

Proviral molecular clones of HIV-2 designated pGL-AN and pGL-St have been previously described [6]. Construction and characterization of proviral site-specific *vpx*-mutants (Fig. 1) also have been described previously [4]. In this study, a number of proviral mutant clones and expression vectors of the mutated Vpx proteins (Fig. 2) were newly constructed by the QuikChange site-directed mutagenesis kit (Stratagene, La Jolla, CA) as previously reported [4].

2.2. Cell culture, transfection, and infection

A human kidney cell line 293T [7] was cultured in Eagle's minimal essential medium supplemented with 10% heat-inactivated fetal bovine serum. A simian lymphocyte cell line HSC-F [8,9] was cultured in RPMI-1640 medium

* Corresponding author. Tel.: +81 88 633 7078; fax: +81 88 633 7080.
E-mail address: adachi@basic.med.tokushima-u.ac.jp (A. Adachi).

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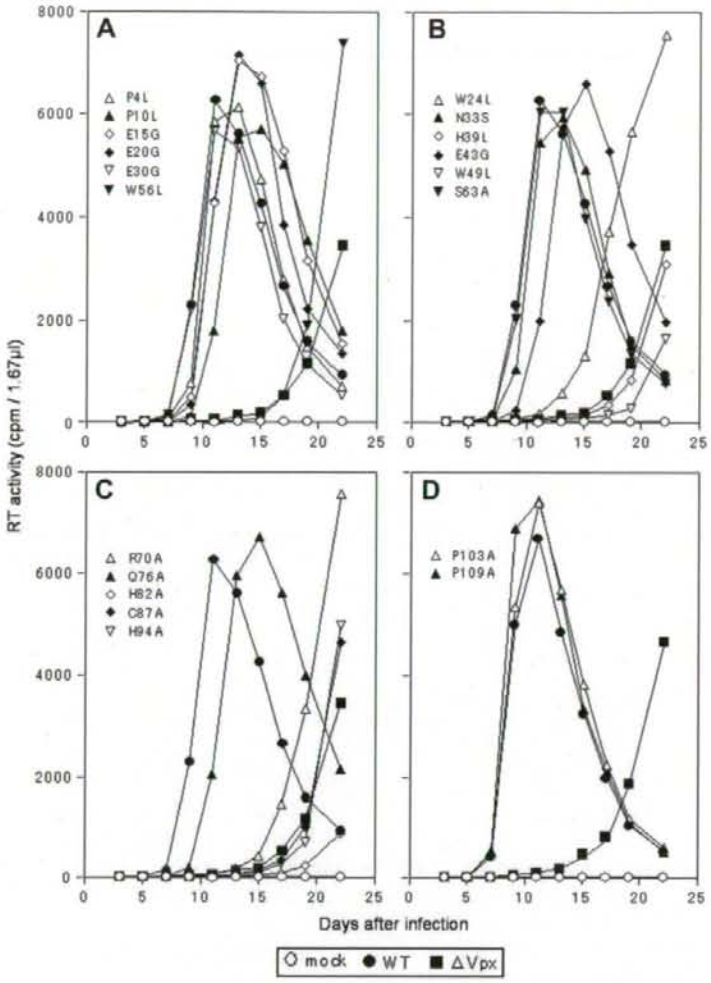

Fig. 1. Growth kinetics in HSC-F cells of various *vpx*-mutants. HSC-F cells (1×10^7) were infected with equivalent RT units of cell-free viruses (3×10^3), and viral replication was monitored at intervals by RT activity in the culture supernatants [13]. Input cell-free viruses were prepared from 293T cells transfected with 20 μg of WT pGL-AN [6] or its *vpx*-mutants. Designations of the *vpx*-mutants are indicated. Mock, pUC19; ΔVpx, pGL-St [6].

supplemented with 10% heat-inactivated fetal bovine serum. Human MDMs were prepared and cultured as previously described [3,4,10], and were 95–97% CD68-positive and completely negative for CD3. Virus stocks were prepared from 293T cells transfected with various mutant clones by the calcium-phosphate coprecipitation method [11,12]. On day 2 post-transfection, culture supernatants were collected and stored at −80 °C until use. Infection of HSC-F cells and MDMs with viruses was performed essentially as previously described [3].

2.3. Reverse transcriptase (RT) assay

Virion-associated RT activity was measured as previously described [13].

2.4. Immunoblot analysis

293T cells were transfected with various molecular clones as above, and on day 2 or 3 post-transfection, virion and cell lysates were prepared for Western immunoblot analysis with appropriate antibodies (Fig. 2) as previously described [4].

3. Results and discussion

We firstly monitored the growth property in lymphocytic cells of the site-specific *vpx*-mutants carrying a single amino acid (aa) change previously reported [4]. As described above, although Vpx is essential for virus growth in MDMs, it is not strictly required in lymphocytic cells and even the *vpx*-minus (ΔVpx) viruses can grow to a considerable level. In our

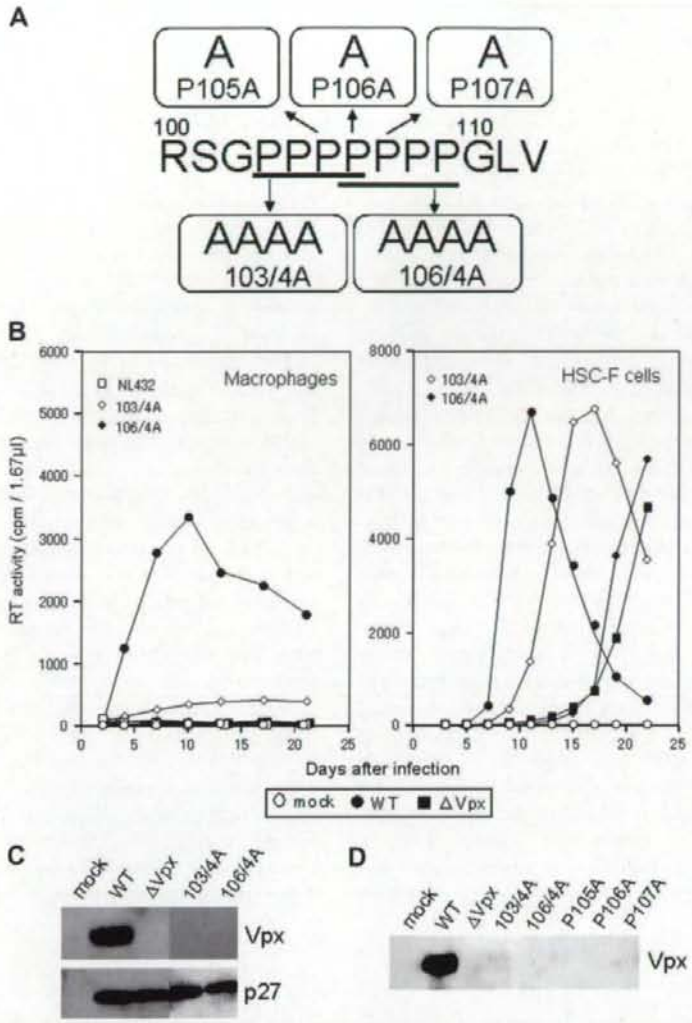

Fig. 2. Effect of proline-mutations in Vpx on viral infectivity and expression of Vpx. (A) Structure of five proline-mutants. Proviral clones were not constructed for P105A, P106A and P107A (see text). (B) Growth kinetics in MDMs and HSC-F cells of mutants 103/4A and 106/4A. Confluent MDMs in a well of 24-well tissue culture plates were infected with equivalent RT units of cell-free viruses (6×10^5) in the presence of DEAE-dextran (5 μg/ml), and viral replication was monitored at intervals by RT activity in the culture supernatants. HSC-F cells were infected with viruses and monitored for virus growth as described in the legend to Fig. 1. Input viruses were prepared from 293T cells transfected with 20 μg of WT proviral clone pGL-AN [6], its *vpx*-mutants or an HIV-1 infectious clone pNL432 [11] as a negative control. Mock, pUC19; ΔVpx, pGL-St [6]. (C) Immunoblot analysis of mutant Vpx proteins in virions. 293T cells were transfected with 20 μg of WT proviral clone pGL-AN [6] or its mutants, and on day 3 post-transfection, virion lysates were prepared as previously described [15]. The lysates were then analyzed by Western immunoblotting [10,15,21] with an HIV-2 ROD Vpx polyclonal antibody and an antiserum to SIV p27. Mock, pUC19; ΔVpx, pGL-St [6]. (D) Immunoblot analysis of mutant Vpx proteins in transfected cells. 293T cells were co-transfected with 7.5 μg of an expression vector of WT Vpx designated pME18Neo-Fvpx [21]/its *vpx*-mutants and 2.5 μg of an expression vector of luciferase (pGL3-Control Vector, Promega, Madison, WI), and on day 2 post-transfection, cell lysates were prepared as previously described [10,15,21]. The lysates normalized by luciferase activity were then analyzed by Western immunoblotting [10,15,21] with an anti-FLAG antibody (ANTI-FLAG M2 Monoclonal Antibody, Sigma-Aldrich, St. Louis, MO).

preliminary experiments, the *vpx*-minus and -mutated viruses were leaky in peripheral blood mononuclear cells (PBMCs) from different individuals, and their susceptibility to viruses was quite different depending on the donors. We, therefore, selected the HSC-F cell line [8,9] as target for virus infection to obtain consistent results. HSC-F cells were frequently and successfully used in place of PBMCs [3,14–17]. Various mutant DNA clones were transfected into 293T cells, and cell-free viruses prepared on day 2 post-transfection were inoculated into HSC-F cells. As shown in Fig. 1, all the clones including ΔVpx did grow in the cells, but to various degrees. Out of 19 mutants tested, five clones (H39L, W49L, H82A, C87A and H94A) grew similarly or even more poorly than ΔVpx, and three (W24L, W56L and R70A) showed medium

growth property between ΔVpx and WT. The infection experiments were extensively repeated and similar results were obtained.

There is a long stretch of proline residues at the C-terminal region of Vpx (Fig. 2A). It is quite conceivable that this unique sequence is important for Vpx function, and in fact, it has been reported that deletion of the C-terminal proline-rich tail in Vpx results in the complete loss of WT phenotype [2]. However, our mutants carrying mutations in this region (P103A and P109A) showed a normal or slightly affected growth phenotype [4]. We, therefore, studied the region more extensively. Two new mutant clones (103/4A and 106/4A) were constructed from WT pGL-AN by the QuikChange site-directed mutagenesis kit (Stratagene) (Fig. 2A), and examined for their properties. The mutations were confirmed by sequence analysis. Fig. 2B shows the growth kinetics of the new mutant viruses in human MDMs and HSC-F cells. As is clear in the figure, mutant 106/4A displayed the ΔVpx phenotype both in MDMs and HSC-F cells, but mutant 103/4A was less growth-defective in both cell types and grew somewhat in MDMs. These results indicated that the latter half of the proline-stretch is more important for virus growth in MDMs and HSC-F cells than the first. The infection experiments were repeated with similar results. We then examined the level of Vpx in the mutant virions. We previously reported that virions of all the site-specific mutants (19 mutants in Fig. 1) contain a comparable level of Vpx [4]. Virions were prepared from transfected 293T cells and analyzed by Western immunoblotting with a polyclonal anti-HIV-2 ROD Vpx antiserum as previously described [4,15]. As shown in Fig. 2C, mutant virions 103/4A and 106/4A clearly lacked Vpx. Thus, we then examined the intracellular expression of mutant Vpx proteins. Because detection of Vpx in cells transfected with proviral clones was quite difficult, we constructed expression vectors of mutant Vpx proteins from a FLAG-tag expression vector of WT Vpx designated pME18Neo-Fvpx as previously described [4]. In addition to expression vectors of 103/4A and 106/4A, those of P105A, P106A and P107A (Fig. 2A) were constructed for more detailed analysis. All mutations were confirmed by sequence analysis. 293T cells were transfected with these clones, and on day 2 post-transfection, cell lysates were prepared and monitored for Vpx expression by immunoblotting with an anti-FLAG antibody. An expression vector of luciferase was also transfected into the cells for normalization. As shown in Fig. 2D, no Vpx was detected for any of the mutants examined, indicating the proline residues are critical for stable expression of Vpx.

Fig. 3 summarizes the results in this study (Figs. 1 and 2) and a previous report by us [4]. As shown in panel B, many point mutations significantly affected viral infectivity in MDMs and/or HSC-F cells. The amino acids in Vpx important for virus replication in two different cell types (macrophage and lymphocyte) and in both were readily identified, and were separately clustered (regions a–d). It is also clear that most mutations did not affect significantly the expression of Vpx. The only mutations that abolish Vpx expression to an undetectable level resided in the C-terminal proline region. Based on these data, we have demonstrated here for the first time that there are several distinct regions in HIV-2 Vpx for its functionality.

We have recently reported that HIV-2 Vpx is critical for the reverse transcription of viral RNA genome and nuclear import of viral DNA in MDMs and HSC-F cells, respectively [3,4]. Also, it has been shown that the Vpx of simian immunodeficiency virus from the rhesus monkey (SIVmac) of the HIV-2 lineage is crucial for the reverse transcription process in human dendritic cells [18] and MDMs [19]. This cell type dependent or specific requirement of Vpx for early events in

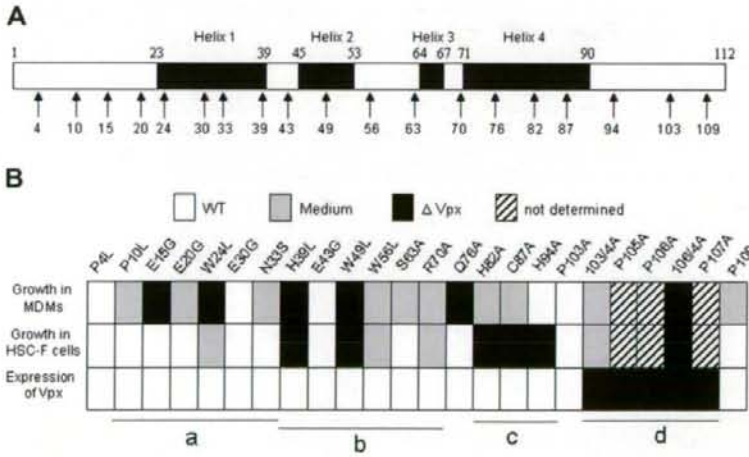

Fig. 3. Phenotype of various *vpx*-mutants. (A) Structure of HIV-2 Vpx [GL-AN clone, 112 aa (GenBank accession no. M30895)]. Black areas represent the four predicted helices [21]. Positions of point mutations (aa nos.) previously reported [4] are indicated by arrows. (B) Summary of the properties of various *vpx*-mutants. Based on our genetic studies, there can be four functional regions (a, b, c and d) in HIV-2 Vpx as shown. Region a is more important for virus growth in MDMs than that in HSC-F cells, and region c is the reverse. Region b is critical for virus growth in both cell types. Region d is essential for the expression of Vpx.

HIV-2 replication may account for the observation reported in this study, and represents a virologically very important question. Extensive molecular biological analyses of our mutants to determine precisely their defective sites in MDMs and HSC-F cells are required. Finally, to elucidate this subject, we need to identify cellular factors which are negatively or positively involved in the early process of HIV-2 replication.

Pancio et al. claimed that the C-terminal proline-rich tail of HIV-2 is necessary for nuclear localization of the viral preintegration complex in non-dividing cells [2]. Their conclusion was based on the results obtained by using a GFP-Vpx (the proline-rich tail is deleted) fusion protein and a proviral clone carrying the same deletion. They did not examine at all the expression of native mutant Vpx protein in cells and virions. Our data (Fig. 2) clearly showed that the site-specific mutations do abolish Vpx expression in cells and virions. Therefore, it is reasonable to conclude that the proline cluster at the C-terminal region of HIV-2 Vpx is essential for its expression at a normal level to maintain viral infectivity in target cells such as MDMs and HSC-F cells. As shown in Fig. 2, the mutant 106/4A displayed more attenuated growth phenotype than the mutant 103/4A. This is probably due to a difference of Vpx expression level between the two mutants, albeit undetectable. This assumption needs to be experimentally confirmed by a system more sensitive than that used here. In addition, an extensive mutational analysis of the proline region by making and characterizing proviral clones for P105A, P106A and P107A to substantiate our stability hypothesis is in progress in our laboratory.

Needless to say, it is interesting to know the mechanism by which the proline region confer stability on the entire Vpx. It has been reported that the Vpx protein associates with a complex of Cullin 4 E3 ubiquitin ligase [19,20], and this binding, in turn, may cause proteasome degradation of Vpx. The proline-rich region of Vpx may be critical for resistance to the degradation. We and others have found that the Q76A mutation abolishes viral growth ability in MDMs [4,19], and the mutant is unable to bind to the E3 ligase complex [19]. The mutant, however, grew well in HSC-F cells (Fig. 1), suggesting that the binding of Vpx to the Cullin 4 E3 ubiquitin ligase complex is important for the reverse transcription of viral RNA genome [4,19] but not for the nuclear import of viral DNA [3]. Biochemical approaches would be necessary to clarify this issue.

Acknowledgments

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Trans-species activation of human T cells by rhesus macaque CD1b molecules

Daisuke Morita [a,b], Kumiko Katoh [a,b], Toshiyuki Harada [c], Yoshiaki Nakagawa [c], Isamu Matsunaga [a,b], Tomoyuki Miura [d], Akio Adachi [e], Tatsuhiko Igarashi [d,*], Masahiko Sugita [a,b,*]

[a] Laboratory of Cell Regulation, Institute for Virus Research, Kyoto University, 53 Kawahara-cho, Shogoin, Sakyo-ku, Kyoto 606-8507, Japan
[b] Laboratory of Cell Regulation and Molecular Network, Graduate School of Biostudies, Kyoto University, Kyoto 606-8501, Japan
[c] Division of Applied Life Sciences, Graduate School of Agriculture, Kyoto University, Kyoto 606-8502, Japan
[d] Laboratory of Primate Model, Institute for Virus Research, Kyoto University, Kyoto 606-8507, Japan
[e] Department of Virology, Institute of Health Biosciences, The University of Tokushima Graduate School, Tokushima 770-8503, Japan

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ABSTRACT

Despite crucial importance of non-human primates as a model of human infectious diseases, group 1 CD1 genes and proteins have been poorly characterized in these species. Here, we isolated *CD1A*, *CD1B*, and *CD1C* cDNAs from rhesus macaque lymph nodes that encoded full-length CD1 proteins recognized specifically by monoclonal antibodies to human CD1a, CD1b, and CD1c molecules, respectively. The monkey group 1 CD1 isoforms contained amino acid residues and motifs known to be critical for intramolecular disulfide bond formation, N-linked glycosylation, and endosomal trafficking as in human group 1 CD1 molecules. Notably, monkey CD1b molecules were capable of presenting a mycobacterial glycolipid to human CD1b-restricted T cells, providing direct evidence for their antigen presentation function. This also detects for the first time a trans-species crossreaction mediated by group 1 CD1 molecules. Taken together, these results underscore substantial conservation of the group 1 CD1 system between humans and rhesus macaque monkeys.

Besides MHC class I- and II-restricted αβ T cells that recognize protein antigens (Ags), discrete subsets of T cells exist in humans that specifically recognize non-protein Ags in a T-cell receptor (TCR)-dependent manner. These include αβ T cells that recognize lipid, glycolipid, and lipopeptide Ags in the context of group 1 CD1 molecules (CD1a, CD1b, and CD1c) as well as $V\gamma2^+V\delta2^+$ γδ T cells that recognize pyrophosphorylated isoprenoid intermediates [1,2]. Both T cell subsets have been implicated in host defense against mycobacterial infection [3], and therefore, animal species that have evolved these T cells in addition to MHC-restricted T cells would serve as an ideal animal model of human tuberculosis. The murine model has long been studied extensively, and by taking advantage of versatile genetic manipulation and a fine array of reagents, many important aspects of host defense against tuberculosis have been demonstrated explicitly, that include a critical role for MHC-restricted T cells [4]. However, a significant difference in pathology has been noted between the two species [3], and the lack of T cells in mice that correspond to human group 1 CD1-resricted T cells and $V\gamma2^+V\delta2^+$ γδ T cells makes the animals less useful particularly in an attempt to develop a new chemical class of non-protein vaccines against tuberculosis. In contrast to mice and rats, guinea pigs exhibit pathology that is comparable, if not identical, to that in human tuberculosis, and recent studies have shown that they contain four *CD1B* genes and three *CD1C* genes [5,6]. Nevertheless, CD1a-restricted T cells as well as CD1d-restricted NKT cells may not exist in guinea pigs. These and other significant differences in the organization and function of the immune system between humans and rodents often make it difficult to translate the results obtained from rodent models to humans. Further, certain human pathogens, such as HIV-1, exhibit highly limited host selectivity, and are unable to infect into rodents and other commonly used laboratory animals.

Recently, the value of non-human primates as a model of human infectious diseases has been appreciated greatly for elucidating pathogenesis and for developing vaccines and therapies against microbial infections, such as AIDS and tuberculosis [7,8]. Nevertheless, little has been defined about the genes, proteins, and function of the group 1 CD1 molecules in non-human primates, and therefore, the present study was aimed at identifying the rhesus macaque group 1 CD1 system. We found it highly comparable to that in humans, and rhesus macaque CD1b molecules were indeed able to present a human CD1b-presented mycobacterial glycolipid Ag to specific human T cells.

* Corresponding authors. Fax: +81 75 752 3232 (M. Sugita), +81 75 761 9335 (T. Igarashi).
E-mail addresses: tigarash@virus.kyoto-u.ac.jp (T. Igarashi), msugita@virus.kyoto-u.ac.jp (M. Sugita).

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Materials and methods

Isolation of rhesus macaque group 1 CD1 cDNAs. Rhesus monkeys (*Macaca mulatta*) were used in accordance with the institutional regulations approved by the Committee for Experimental Use of Nonhuman Primates of the Institute for Virus Research, Kyoto University, Kyoto, Japan. Total RNA was extracted from rhesus macaque lymph nodes using the RNeasy mini kit (Qiagen, Hilden, Germany), and the first-strand cDNA was synthesized from 0.5 mg of the total RNA using oligo(dT) and PrimeScript reverse transcriptase (Takara Bio, Inc., Otsu, Japan). To amplify specific transcripts, the samples were subjected to PCR amplification with *Pfu* DNA polymerase (Stratagene, La Jolla, CA) for 35 cycles of 30 s at 94 °C, 1 min at 55 °C (for *CD1A*) or 60 °C (for *CD1B* and *CD1C*), 2 min at 72 °C, and a final cycle of 10 min at 72 °C. The primers used were: 5′-GCG GTA CCA AAT AAC ATC TGC AAA TGA C-3′ (sense) and 5′-GCC TCG AGA AGG AGG ATC ATG GTG TAT C-3′ (anti-sense) for *CD1A*; 5′-GCG GTA CCA GTA AGA AGT TGC ATC TCC C -3′ (sense) and 5′-GCC TCG AGG GAG CAG ACA TGG TGA GGG C-3′ (anti-sense) for *CD1B*; 5′-GCG GGT ACC ACC ATG CTG TTT CTG CAG TTT-3′ (sense) and 5′-GCG GCG GCC GCA TTG TAC TAG GCT CCT GG-3′ (anti-sense) for *CD1C*. The PCR products were purified and cloned into pcDNA3.1(+) (Invitrogen, Carlsbad, CA), and DNA sequencing was done in both directions. This procedure was repeated twice to confirm that no PCR-associated errors were introduced.

Transfection. A rhesus macaque kidney epithelial cell line, LLC-MK2 [9], was obtained from ATCC (Manassas, VA). The cells were transfected with pcDNA3.1(+) containing either rhesus macaque *CD1A*, *CD1B*, or *CD1C* by a calcium phosphate precipitation method, using the mammalian transfection kit (Stratagene). The transfected cells were then cultured in DMEM media (Invitrogen) supplemented with 10% fetal calf serum (Hyclone, Logan, UT) and G418 (0.5 mg/ml) (Invitrogen), and the CD1-expressing cells were then enriched by labeling with specific antibodies (Abs), followed by positive selection with magnetic beads coated with goat anti-mouse IgG Abs (Invitrogen). A human lymphoblastoid cell line, T2 [10], was transfected with pCEP4 (Invitrogen) containing *CD1A* or *CD1B* of either human or rhesus macaque origin by electroporation as described [11], followed by selection in RPMI1640 media (Invitrogen) containing 0.2 mg/ml hygromycin B (Invitrogen). A human cervical epithelial cell line, HeLa [12], was transfected with rhesus macaque *CD1C* in pcDNA3.1(+) by a calcium phosphate precipitation method, and selection was performed as described above. These stably transfected cells were used as Ag-presenting cells (APCs) in T cell transfectants stimulation assays.

Flow cytometry. The expression of CD1 proteins on the surface of the LLC-MK2 cell transfectants as well as rhesus macaque thymocytes were analyzed by flow cytometry as described [13,14], using the BD FACSCanto II flow cytometer. The mouse monoclonal Abs (mAbs) used were 10H3 (anti-human CD1a) [15], SN13 (anti-human CD1b) (Ancell, Bayport, MN), M241 (anti-human CD1c) (Ancell), and SP34 (anti-monkey CD3) (BD Biosciences, Franklin Lakes, NJ). MAbs MOPC-31C (BD Biosciences) and RPC5.4 (ATCC) were used as negative controls.

T cell transfectants stimulation assays. TCR-deficient Jurkat cells, J.RT3, reconstituted with either the dideoxymycobactin-specific, CD1a-restricted TCR (J.RT3/CD8-2), the glucose monomycolate (GMM)-specific, CD1b-restricted TCR (J.RT3/LDN5) or the mannosyl phosphomycoketide-specific, CD1c-restricted TCR (J.RT3/CD8-1) have been described previously [16]. The TCR-reconstituted cells (5×10^4/well) were cultured with irradiated APCs expressing a relevant CD1 isoform (1×10^5/well) in wells of 96-well, flat-bottomed microtiter plates (200 μl media/well) in the presence of 10 ng/ml phorbol myristate acetate (PMA) (Sigma, St. Louis, MO) and either the organic extract of *Mycobacterium tuberculosis* H37Ra (for J.RT3/CD8-2 and J.RT3/CD8-1) or *Rhodococcus equi* GMM (for J.RT3/LDN5) at indicated concentrations. After 20 h, aliquots of the culture supernatants were collected, and the amount of interleukin-2 (IL-2) released into the supernatants was measured by the IL-2 ELISA kit (BD Biosciences).

Molecular modeling of rhesus macaque CD1b proteins. Molecular modeling of the rhesus macaque CD1b molecule was performed, using the homology modeling software PDFAMS (Protein Discovery Full Automatic Modeling System; In-Silico Sciences, Inc., Tokyo, Japan) as described [17]. Briefly, the primary sequence of the rhesus macaque CD1b molecule was aligned with the sequence of the human CD1b molecule available from the Protein Data Bank (1UQS), using RPS-BLAST. Amino acid residues differing between the two molecules were mutated, and the obtained 3-dimensional structure was optimized by the simulated annealing method. Subsequently, the molecular model was subjected to energy minimization, using the SYBYL software. The overall structure and the cavity surface of the modeled rhesus macaque CD1b molecule were depicted in association with GMM from *Nocardia farcinica* by utilizing the MOLCAD module of SYBYL.

Results and discussion

Identification of rhesus macaque group 1 CD1 cDNAs

To isolate full-length cDNAs encoding rhesus macaque CD1a and CD1b, the first strand cDNA was synthesized from lymph node total RNA by reverse transcription, and then, PCR was carried out with specific pairs of 5′-end and 3′-end primers that were designed based on the rhesus macaque genomic *CD1A* and *CD1B* sequences. The rhesus macaque genomic *CD1C* sequence was only partially available, and the 3′-end sequence was undermined. Therefore, rhesus macaque *CD1C* cDNA was amplified by PCR using a specific 5′-end primer and a 3′-end primer that was designed based on the sequence of 3′-untranslated region of the human *CD1C* genome. The PCR products thus obtained were of expected size (approximately 1 kb) and the identity of the products was determined by DNA sequences. Identical nucleotide sequences were obtained after two independent PCR amplifications, ruling out the possibility for PCR-associated errors.

Alignment of the deduced amino acid sequences of the putative rhesus macaque *CD1A*, *CD1B*, and *CD1C* genes with the corresponding human CD1 proteins revealed a high-degree homology between the two species (85.6% for CD1a, 94.6% for CD1b, 90.4% for CD1c) (Fig. 1). The cysteine residues (indicated with triangles) involved in the intrachain disulfide bond formation in the α2 and the α3 domains as well as the putative N-linked glycosylation sites (indicated with asterisks) in the α1 and the α2 domains were totally conserved [2]. Further, the cytoplasmic tyrosine-based motif (YXXZ where Y is tyrosine, X is any amino acid, and Z is a hydrophobic amino acid) and its flanking sequences that are known to regulate differential early endosomal and lysosomal trafficking of CD1b and CD1c proteins [12,18,19] were identical between the two species (Fig. 1).

To monitor protein expression of these rhesus macaque *CD1* genes, we first screened mAbs against human CD1 proteins for their cross-reactivity to rhesus macaque thymocytes, a cell type that is presumed to express all forms of group 1 CD1 molecules. As shown in Fig. 2A, mAb clones 10H3 (anti-human CD1a), SN13 (anti-human CD1b), and M241 (anti-human CD1c) labeled a significant fraction of $CD3^{dim}$ thymocytes in a pattern comparable to that for human thymocytes [20]. We then stably transfected each

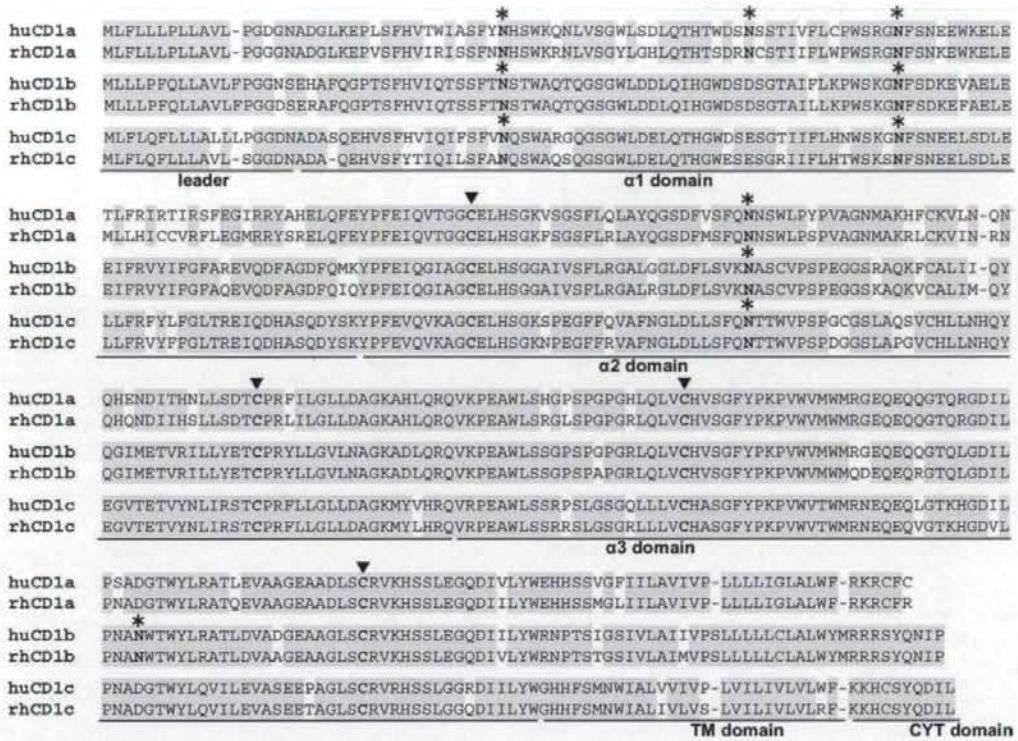

Fig. 1. Alignment of deduced amino acid sequences of human (hu) and rhesus macaque (rh) group 1 CD1 proteins. Residues conserved between the two species are shaded in light gray. Solid triangles denote cysteines conserved in all the group 1 CD1 proteins of both species that are presumed to be involved in intradomain disulfide bond formation. Asterisks indicate potential N-linked glycosylation sites. Dashes represent gaps that have been introduced to maximize alignment. TM domain, transmembrane domain; CYT domain, cytoplasmic domain.

of the putative rhesus macaque *CD1A*, *CD1B*, and *CD1C* genes into a rhesus macaque kidney epithelial cell line, LLC-MK2, and their protein expression was monitored by flow cytometry using the cross-reactive mAbs (Fig. 2B). The 10H3 anti-human CD1a mAb recognized only *CD1A* transfected cells, but not those transfected with the other genes. Similarly, the SN13 anti-human CD1b mAb and the M241 anti-human CD1c mAb showed specific reactivity to cells transfected with the *CD1B* and the *CD1C* genes, respectively. These results provided both evidence for protein expression of the isolated genes and further support for their identity, and therefore, the nucleotide sequences of the putative *CD1A*, *CD1B*, and *CD1C* cDNAs were deposited to the DDBJ/GenBank/EMBL databases as those of rhesus macaque *CD1A* (Accession Nos: AB458511), *CD1B* (AB458512), and *CD1C* (AB458513), respectively.

Trans-species activation of human T cells by rhesus macaque CD1b molecules

With the exception of mice and rats, group 1 CD1 genes have been identified in virtually all mammalian animals so far analyzed, but the Ag presentation function of their products has not been demonstrated so explicitly as in humans [21]. This is partly due to difficulties in obtaining specific T cell lines and clones that recognize lipid Ags in the context of CD1 molecules of a given animal species. Because of the highly conserved amino acid sequences of human and rhesus macaque group 1 CD1 proteins, we considered the possibility that rhesus macaque CD1 molecules might bind lipid Ags that were known to be presented by human CD1 molecules, and interact with specific human TCRs. To address this, human TCRs derived either from a dideoxymycobactin-specific, CD1a-restricted T cell line (CD8-2), from a GMM-specific, CD1b-restricted T cell line (LDN5) or from a mannosyl phosphomycoketide-specific, CD1c-restricted T cell line (CD8-1) were reconstituted in TCR-deficient Jurkat cells (J.RT3) by gene transfer, and the T cell reactivity to specific Ag in the presence of cell transfectants expressing a relevant CD1 isoform of either human or rhesus macaque origin was assessed by measuring IL-2 released from the T cells. J.RT3/CD8-2 cells responded to dideoxymycobactin in the presence of APCs expressing human CD1a molecules, but not those expressing rhesus macaque CD1a molecules (Fig. 3, top panel). Similarly, J.RT3/CD8-1 cells responded to mannosyl phosphomycoketide in the presence of APCs expressing human CD1c molecules, but not those expressing rhesus macaque CD1c molecules (bottom panel). Strikingly, however, APCs expressing rhesus macaque CD1b molecules were capable of presenting GMM efficiently to J.RT3/LDN5 cells (middle panel), providing evidence for their Ag presentation function. The apparently more efficient Ag presentation function for rhesus macaque CD1b molecules as compared with human CD1b molecules could be accounted for by the slightly higher expression on rhesus macaque CD1b transfectants than on human CD1b transfectants (data not shown).

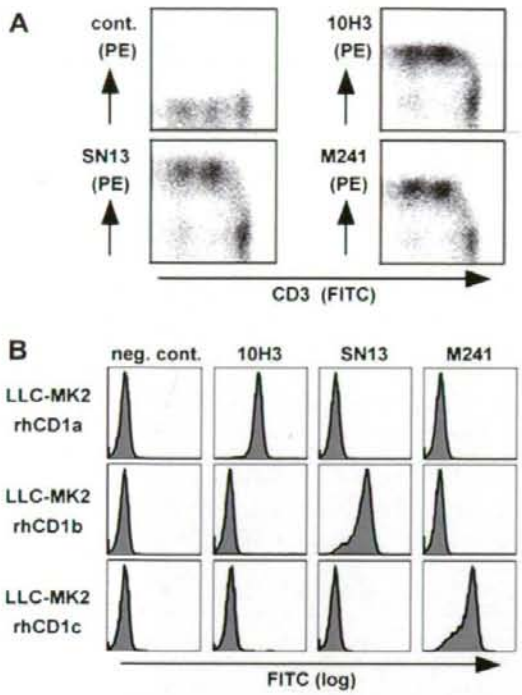

Fig. 2. Cross-reactivity of anti-human CD1 mAbs to rhesus macaque group 1 CD1 proteins. (A) Rhesus macaque thymocytes were double-labeled with the SP34 anti-CD3 mAb and either the 10H3 anti-human CD1a mAb, the SN13 anti-human CD1b mAb, the M241 anti-human CD1c mAb, or negative control Abs, followed by analysis by flow cytometry. (B) A rhesus macaque kidney cell line, LLC-MK2, that stably transfected with either rhesus macaque *CD1A* (LLC-MK2 rhCD1a), *CD1B* (LLC-MK2 rhCD1b), or *CD1C* (LLC-MK2 rhCD1c) were labeled with indicated mAbs and analyzed by flow cytometry.

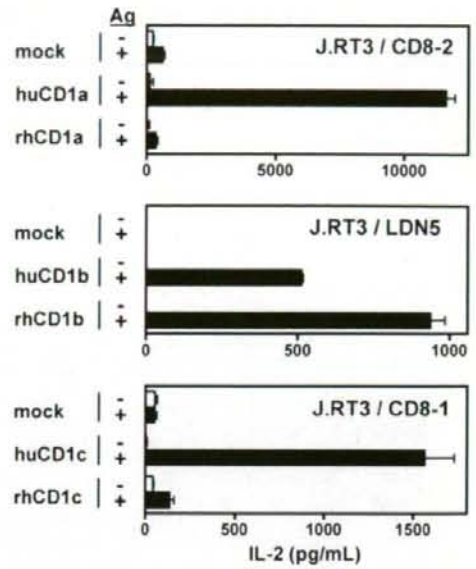

Fig. 3. Ag presentation function of rhesus macaque CD1b molecules. The J.RT3/CD8-2 cells were cultured in the presence or absence of the organic extract of *M. tuberculosis* (50 mg/ml) with T2 cells expressing either human CD1a (huCD1a) or rhesus macaque CD1a (rhCD1a) or those that were mock-transfected (top panel). The J.RT3/LDN5 cells were cultured in the presence or absence of purified GMM (5 mg/ml) with T2 cells expressing either human CD1b (huCD1b) or rhesus macaque CD1b (rhCD1b) or those that were mock transfected (middle panel). The J.RT3/CD8-1 cells were cultured in the presence or absence of the organic extract of *M. tuberculosis* (1.56 mg/ml) with HeLa cells expressing either human CD1c (huCD1c) or rhesus macaque CD1c (rhCD1c) or those that were mock transfected (bottom panel). After 20 h, the culture supernatants were harvested and the amount of IL-2 secreted into the supernatants were measured.

Trans-species crossreaction has never been observed previously for any of the group 1 CD1 molecules. Nevertheless, a molecular model of the rhesus macaque CD1b molecule has detected the α1 and α2 helix structure as well as intramolecular pockets (A′, C′, and F′) and a tunnel (T′) virtually identical to those for human CD1b molecules [22,23], allowing stable interaction with a human CD1b-presented mycobacterial Ag, GMM (Fig. 4). Further, amino acid residues, such as E80 and D83 in the α1 domain and T157 and T165 in the α2 domain, that are proposed to be critical for interaction with specific TCRs [24] are shared between rhesus macaque and human CD1b molecules, suggesting a conserved function for CD1b in these two species. The extent of amino acid sequence conservation is higher in CD1b than in CD1a and CD1c (Fig. 1), which may imply that immune responses to mycolic acid-containing glycolipds are critical for host defense against tuberculosis. So far, no experimental animals have proved extremely useful as a model for studying the group 1 CD1-mediated immunity in human infectious diseases. The present study underscores that monkeys are indispensable for a variety of challenges, including development of a new type of lipid-based vaccines against tuberculosis.

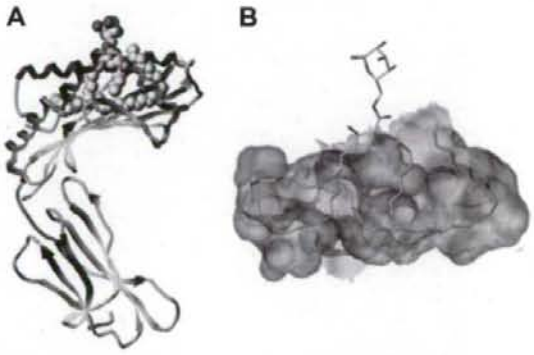

Fig. 4. A molecular model of rhesus macaque CD1b proteins. The rhesus macaque CD1b structure was constructed, based on the crystal structure of the human CD1b-GMM complex. (A) The overall structure of the rhesus macaque CD1b-GMM complex is shown, in which the CD1b heavy chain is depicted in ribbon diagram and the non-hydrogen atoms of GMM are drawn as van der Waals spheres (carbon in gray; oxygen in red). The associated β2-microglobulin is not depicted for simplicity purposes. (B) The binding surface of the Ag-binding groove is drawn in green with the bound GMM in stick (carbon in gray; oxygen in red). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this paper).

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Transmission of Simian Immunodeficiency Virus Carrying Multiple Cytotoxic T-Lymphocyte Escape Mutations with Diminished Replicative Ability Can Result in AIDS Progression in Rhesus Macaques[▽]

Sayuri Seki,[1] Miki Kawada,[1,2,3] Akiko Takeda,[1] Hiroko Igarashi,[2] Tetsutaro Sata,[4] and Tetsuro Matano[1,2,5,6]*

International Research Center for Infectious Diseases, The Institute of Medical Science, The University of Tokyo, 4-6-1 Shirokanedai, Minato-Ku, Tokyo 108-8639, Japan[1]; Graduate School of Medicine, The University of Tokyo, 7-3-1 Hongo, Bunkyo-Ku, Tokyo 113-0033, Japan[2]; Japanese Foundation for AIDS Prevention, 1-3-12 Misaki-cho, Chiyoda-Ku, Tokyo 101-0061, Japan[3]; Department of Pathology, National Institute of Infectious Diseases, 1-23-1 Toyama, Shinjuku-ku, Tokyo 162-8640, Japan[4]; AIDS Research Center, National Institute of Infectious Diseases, 1-23-1 Toyama, Shinjuku-ku, Tokyo 162-8640, Japan[5]; and Tsukuba Primate Research Center, National Institute of Biomedical Innovation, 1 Hachimandai, Tsukuba, Ibaraki 305-0843, Japan[6]

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Cytotoxic T-lymphocyte (CTL) responses frequently select for immunodeficiency virus mutations that result in escape from CTL recognition with viral fitness costs. The replication in vivo of such viruses carrying not single but multiple escape mutations in the absence of the CTL pressure has remained undetermined. Here, we have examined the replication of simian immunodeficiency virus (SIV) with five *gag* mutations selected in a macaque possessing the major histocompatibility complex haplotype *90-120-Ia* after its transmission into *90-120-Ia*-negative macaques. Our results showed that even such a "crippled" SIV infection can result in persistent viral replication, multiple reversions, and AIDS progression.

Virus-specific $CD8^+$ cytotoxic T-lymphocyte (CTL) responses exert a suppressive effect on human immunodeficiency virus (HIV) and simian immunodeficiency virus (SIV) replication (1, 10, 15, 21, 27). Under the CTL pressure, viral mutations resulting in viral escape from CTL recognition are frequently selected for, with viral fitness costs (2, 5, 8, 9, 12, 16, 19, 20, 24, 25, 26, 28). The transmission of the virus carrying a CTL escape mutation with lower viral fitness between major histocompatibility complex class I (MHC-I)-mismatched individuals can result in reversion of the mutation due to the absence of the CTL pressure (7, 14, 16, 17, 18). Such CTL escape mutations and their reversions have been suggested to be involved in viral evolution (3, 11, 13, 23).

We have developed a prophylactic vaccine using a Sendai virus vector expressing SIVmac239 Gag and shown its protective efficacy against SIVmac239 challenge in a group of Burmese rhesus macaques (*Macaca mulatta*) possessing MHC-I haplotype *90-120-Ia* (20). In these vaccinated macaques that are controlling SIVmac239 replication, $Gag_{206–216}$ epitope-specific CTL responses exerted strong selective pressure on the virus, and rapid selection of a mutant escaping from this CTL was observed at week 5 postchallenge. The virus, SIVmac 239Gag216S, with this CTL escape mutation, GagL216S, leading to a substitution from leucine (L) to serine (S) at amino acid (aa) 216 in Gag showed lower replicative ability than the wild type (14, 20). Two of these vaccinees (macaques V3 and V5) showed an accumulation of additional viral CTL escape mutations in *gag* during the period of viral control and then the reappearance of plasma viremia around week 60 after SIVmac239 challenge (12). The SIV carrying these multiple CTL escape mutations showed lower replicative ability in vitro than the SIV carrying the single GagL216S mutation.

How such viruses with multiple CTL escape mutations replicate and evolve in the absence of the CTL pressure has not yet been well determined, while the reversion of CTL escape mutations has previously been shown by the transmission of viruses with single escape mutations (7, 14, 18). In the present study, we have examined the replication, in the absence of the CTL pressure in *90-120-Ia*-negative macaques, of the SIV with multiple *gag* CTL escape mutations that were accumulated in a *90-120-Ia*-positive macaque.

The induction of $Gag_{206–216}$-specific CTL, $Gag_{241–249}$-specific CTL, and $Gag_{373–380}$-specific CTL responses has previously been observed after SIVmac239 challenge in *90-120-Ia*-positive macaques (12). The *90-120-Ia*-positive vaccinees V5 and V3 showed rapid selection of the GagL216S mutation ($Gag_{206–216}$ CTL escape mutation) and then of an additional two mutations resulting in escape from $Gag_{241–249}$-specific CTL and $Gag_{373–380}$-specific CTL recognition, respectively, during the period of viral control. These were a $Gag_{241–249}$ CTL escape mutation leading to a GagD244E (aspartic acid [D] to glutamic acid [E] at aa 244 in Gag) substitution and a $Gag_{373–380}$ CTL escape mutation leading to GagA373T (alanine [A] to threonine [T] at aa 373) in vaccinee V5 or GagV375A (valine [V] to A at aa 375) or GagP376S (proline [P] to S at aa 376) in vaccinee V3. Viruses at the reappearance of viremia had one or two additional mutations in *gag*, GagI247 L (isoleucine [I] to L at aa 247) and GagA312V (A to V at aa

* Corresponding author. Mailing address: International Research Center for Infectious Diseases, The Institute of Medical Science, The University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan. Phone: 81-3-6409-2078. Fax: 81-3-6409-2076. E-mail: matano@m.u-tokyo.ac.jp.

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312) in vaccinee V5 or GagP172S (P to S at aa 172) or GagV145A (V to A at aa 145) in vaccinee V3. All of these mutations except for the $Gag_{373-380}$ CTL escape mutations resulted in amino acid changes in the Gag CA. We constructed molecular clones of SIVs with these *gag* mutations (12). The SIVs with three CTL escape mutations ($Gag_{206-216}$, $Gag_{241-249}$, and $Gag_{373-380}$ CTL escape mutations) were referred to as group Q SIV mutants, and the SIVs with four or five *gag* mutations selected at the reappearance of viremia as group R SIV mutants. These group Q and R SIV mutants both showed lower replicative ability in vitro than SIVmac239Gag216S, while in the competition assay between groups Q and R, the viral replicative ability was not significantly affected by the GagP172S or GagV145A mutation but was reduced by the addition of the GagI247L and GagA312V mutations (12). These results do not support the possibility of compensation for loss of viral fitness from these mutations (4, 6). In the present study, we have examined the in vivo replication of the SIV carrying five *gag* mutations, GagL216S, GagD244E, GagI247L, GagA312V, and GagA373T, selected in macaque V5 at the reappearance of viremia, which was assumed to show the lowest replicative ability among group Q and R SIV mutants. The macaques were maintained in accordance with the guidelines for animal experiments performed at the National Institute of Infectious Diseases (22).

We first compared the in vivo replication abilities of the SIV with a single GagL216S mutation and the SIVs with multiple CTL escape mutations in *90-120-Ia*-negative macaques (Fig. 1). In the competition between SIVmac239Gag216S and group Q SIV mutants, macaque R02-017 was coinoculated intramuscularly with molecular-clone DNAs of SIVmac239Gag216S and SIVmac239Gag216S244E373T and macaque R05-002 with molecular-clone DNAs of SIVmac239Gag216S and all three group Q SIV mutants. The results of the analysis of plasma viral *gag* genome sequences (Fig. 2) showed selection of SIV mac239Gag216S; i.e., all the mutations other than GagL216S became undetectable in 3 weeks postinoculation, indicating lower replicative abilities in vivo of group Q SIV mutants than of SIVmac239Gag216S, as indicated previously by in vitro competition (12). Further analysis revealed reversion of the selected GagL216S mutation to the wild-type sequence in a few months.

In the competition between SIVmac239Gag216S and group R SIV mutants, macaque R02-023, coinoculated with molecular clone DNAs of SIVmac239Gag216S and SIVmac239Gag 216S244E247L312V373T, showed selection of the former (Fig. 2). This macaque was euthanized at week 6 before exhibiting reversion of the GagL216S mutation. In macaque R02-022, coinoculated with molecular clone DNAs of SIVmac239Gag 216S and all three group R SIV mutants, almost all mutations other than GagL216S became undetectable rapidly but the GagV145A mutation was detected even at week 14. The GagL216S mutation was still dominant without reversion at week 14, and plasma viremia became undetectable after week 14 in this macaque. Both cases indicated a lower replicative ability in vivo of SIVmac239Gag216S244E247L312V373T than of SIVmac239Gag216S.

Additionally, macaque R03-022, coinoculated with the molecular-clone DNAs of SIVmac239Gag216S244E373T and SIV mac239Gag216S244E247L312V373T, showed selection of the

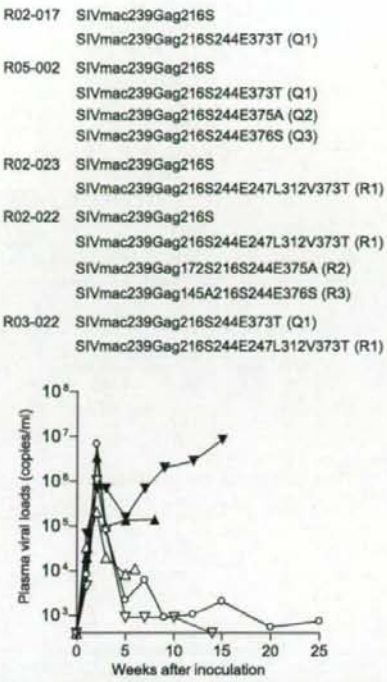

FIG. 1. Plasma viral loads of macaques used for in vivo competition assay (SIV *gag* RNA copies/ml plasma) after inoculation with SIV molecular-clone DNAs. Animals received 10 mg in total of DNAs consisting of an equal amount of each DNA; i.e., macaques R02-017, R02-023, and R03-022 were inoculated with 5 mg of each DNA, and macaques R05-002 and R02-022 with 2.5 mg of each DNA. Plasma viral loads were determined as described previously (20).

former (Fig. 2), indicating a lower replicative ability in vivo of SIVmac239Gag216S244E247L312V373T than of SIVmac239 Gag216S244E373T. In this macaque, reversion of the GagL216S mutation was observed in 6 months, while the GagD244E and GagA373T mutations were still dominant without reversion.

Next, we inoculated *90-120-Ia*-negative macaques with the SIV carrying multiple *gag* CTL escape mutations that was selected in *90-120-Ia*-positive macaque V5 (Fig. 3). The SIV carrying five gag mutations, GagL216S, GagD244E, GagI247L, GagA312V, and GagA373T, that was dominant at the reappearance of viremia in macaque V5, was propagated on rhesus macaque peripheral blood mononuclear cells to prepare the SIVmac239Gag216S244E247L312V373T challenge stock for macaques R05-001 and R06-016. Sequencing analysis confirmed no *gag* mutation except for the five mutations in the challenge virus. These two macaques were challenged intravenously with 1,000 50% tissue culture infective dose of SIVmac 239Gag216S244E247L312V373T. Both of them showed persistent viremia, although the levels of set-point plasma viral loads were low in macaque R06-016. Macaque R05-001, maintaining high viral loads, showed typical signs of AIDS, such as a reduction in peripheral $CD4^+$ T-cell counts, diarrhea, and general weakness, and was euthanized approximately 2 years postchallenge. Autopsy revealed postpersistent generalized