hA3G oligomerization is associated with the inhibition of L1 retrotransposition

The inhibitory effects of the hA3G protein on *Alu* retrotransposition resembles its effects on L1 retrotransposition in two regards, first, that hA3G showed similar levels of inhibitory activity against the both retrotransposition events (Figure 1C and ref [37,40]), and second, that the hA3G restriction of retrotransposition is independent of deamination in both cases (Figure 3C and refs. 35,37). These similarities prompted us to determine whether the inhibition of L1 retrotransposition by hA3G requires hA3G oligomerization, as does the inhibition of *Alu* retrotransposition. We performed an L1 retrotransposition assay using all hA3G mutants that we created in this study. As expected, the mutants that do not form oligomers, including NΔ30, NΔ60, NΔ90, NΔ120, NΔ150, C97/100A, 5G(24–28), and 4G(124–127), did not inhibit L1 retrotransposition (Figure 7A, 7B, and 7C), whereas, as observed for *Alu* retrotransposition in Figure 3C, the E259Q deamination mutant had a wild-type level of anti-L1 activity (Figure 7B). Thus, the inhibitory effect of hA3G on *Alu* retrotransposition is associated with hA3G oligomerization but independent of its deaminase activity. We therefore postulate that the inhibitory activities of hA3G against *Alu* and L1 retrotransposition might share common mechanism(s).

Discussion

Our present study demonstrated that hA3 family proteins inhibit *Alu* retrotransposition at differential levels, which are very similar to the levels at which these host proteins block L1 retrotransposition. With respect to hA3G, the N-terminal 30 amino acids are important for the anti-*Alu* activity. The ability of hA3G to inhibit *Alu* retrotransposition was independent of its deaminase activity but associated with its oligomerization activity, as previously reported by Hulme et al. [35] and Bulliard et al. [34], respectively. In agreement with these findings, we found that the N-terminal 30 amino acids that are responsible for counteracting *Alu* retrotransposition are required for the oligomerization of this protein. We used structural modeling to identify the specific residues among the N-terminal 30 amino acids that are responsible for the oligomerization of hA3G. We finally identified amino acid residues 24–28 of hA3G as the contributors of oligomerization.

Importantly, these residues were also critical for the inhibitory activity of L1 retrotransposon, suggesting that this activity might involve the same mechanism as that of *Alu* retrotransposition. This hypothesis makes sense because *Alu* elements do not encode a functional reverse transcriptase or endonuclease, and therefore, they need to hijack the L1-encoded enzymatic machinery for retrotransposition through mechanisms that are currently unclear. It is intriguing to speculate that hA3G might be able to physically block both the *Alu* and L1 retroelements because hA3G is intrinsically an RNA-binding protein that can associate non-specifically with cellular RNAs [48,59,65,69], including those derived from *Alu* retroelements [34,70], or because this protein might directly interact with the L1 ORF2 protein. It is likely that both cases would result in the effective inhibition of *Alu* reverse transcription, and are dependent on the ability of hA3G to form oligomers. In the former case, *Alu* RNA *per se* might help stabilize hA3G oligomer formation, as suggested in Figure S2.

It was somewhat unexpected to find that the N-terminal 30 amino acids of hA3G are required for oligomerization in our study because amino acid positions 124/127 have previously been reported to be important [34,58,59]. Indeed, although only minor effects of either a single R24 or S28 mutation on oligomerization were shown by Huthoff et al. [59] and Bulliard et al. [34] (the former of which was confirmed in Figure S3A), respectively, our study revealed that the previously unappreciated amino acid positions 24–28 among these first 30 residues are responsible for the ability of hA3G to homooligomerize. The dependence of oligomerization on these residues is most likely because not only the amino acids R24 and S28 but also the residues between them are involved in the formation of the interaction interface of an hA3G dimer, as shown in our structural models (Figure 6). This study also reveals that both the amino acid residues 24–28 and 124–127 are equally important for the oligomerization of hA3G. Regarding this point, we assume that the lack or a functional defect of a single interaction interface would be able to totally abolish the protein-protein interaction by leading to the structural destabilization.

Whereas transcriptional repressors such as SRY, SOX2 and methyl-CpG-binding protein 2 have been reported to negatively regulate L1 retrotransposition at the transcriptional levels [71-73], post-transcriptional L1 regulation (apart from that by endogenously encoded small interfering RNAs [74]) like premature polyadenylation and aberrant splicing of its mRNA was also shown to result in a negative influence on L1 expression [75]. In the latter case, retrotransposition-incompetent L1 elements that encode intact ORF2 protein are still able to create DNA double-strand breaks [76] and therefore keep mobilizing *Alu* elements [5,53]. Particularly in such conditions, hA3 proteins would play pivotal roles in the inhibition of *Alu* retrotransposition, putatively through binding to either the ORF2 protein or *Alu* RNA as described above.

It should be noted that the superfamily-1 RNA helicase protein MOV10 (Moloney Leukemia Virus 10; for review, see ref[77].), which is highly conserved across a wide range of species, has recently been reported to inhibit not only infection by several retroviruses, such as HIV-1, simian immunodeficiency virus, murine leukemia virus, and equine infectious anemia virus [78,79], but also the retrotransposition of endogenous retroelements [80-82], exactly as hA3G does. Most importantly, MOV10 was identified to be a protein interacting with hA3G in an RNA-dependent manner [83], suggesting that these two proteins may play mutually supporting roles in restricting exogenous viruses and endogenous retroelements. Further analyses are required to elucidate the precise mechanisms by which hA3 family proteins negatively regulate *Alu* and L1 retrotransposition, possibly in cooperation with other cellular factor(s).

Oligomerized hA3G inhibits retrotransposition

Figure 7

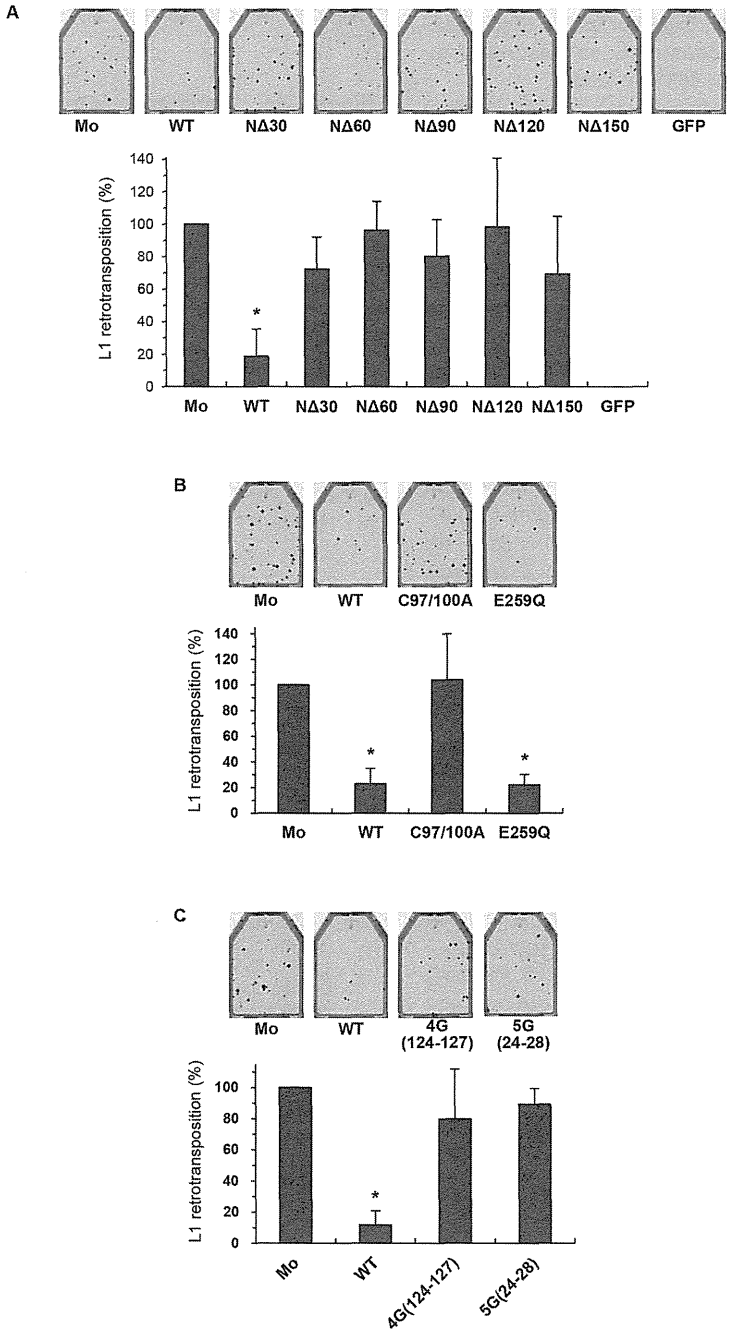

Figure 7. The oligomerization of hA3G is also associated with its anti-L1 activity. HeLa cells were cotransfected with the *neo*^{r}-based L1 expression vector pCEP4/L1mneoI/ColE1 and either a wild-type (WT) or mutant hA3G expression plasmids. Seventy-two hours later, cells were trypsinized, re-seeded into T25 or T75 flasks, and subjected to G418 (1 mg/ml) selection. At 14 days after selection, the resultant G418^R colonies fixed, stained with crystal violet, and counted to determine the level of L1 retrotransposition. (**A**) Compare the results with Figure 2D and 2E. (**B**) Compare the results with Figure 3C and 3D. (**C**) Compare the results with Figure 6H. The data shown are the mean ± SD of triplicate experiments. Mo, mock; WT, wild-type hA3G; GFP, GFP only. *$P < 0.005$, *t*-test.

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Supporting Information

Figure S1. Inhibitory effect of hA3G deletion mutants on HIV-1 infection was evaluated by cotransfecting 293T cells with hA3G and VSV-G plasmids, together with a luciferase-based Vif (-) Env (-) HIV-1 construct, as described by Iwabu et al. (J. Biol. Chem., 285: 35350-8, 2010).
After 48 h, each viral supernatant was harvested. Normalized supernatants were incubated with 293T cells for additional 48 h. Cells were then lysed and subjected to luciferase assay. The data shown are the mean ± SD of triplicate experiments. RLU: relative light units.
(TIF)

Figure S2. Cellular RNA contributes to the stabilization of hA3G's oligomer. HA-tagged hA3G-WT in the immunoprecipitate as described in Figure 4, with or without RNase A treatment.
(TIF)

Figure S3. hA3G mutants with individual amino acid substitutions. (A) Oligomerization assay was performed by IP-Western blot analysis, as described in Figure 4; upper, IP; lower, cell lysates. (B) An *Alu* retrotransposition assay was performed as described in Figure 1. Crystal violet-stained $G418^R$ colonies were counted to determine the level of *Alu* retrotransposition. The data shown are the mean ±SD of triplicate experiments. Mo, mock; WT, wild-type hA3G; GFP, GFP only. $^*P < 0.05$, $^{**}P < 0.005$, *t*-test.
(TIF)

Figure S4. Inhibitory effect of hA3G oligomerization mutant proteins on HIV-1 infection. The assay was performed as described in Figure S1. The data shown are the mean ± SD of triplicate experiments. RLU: relative light units.
(TIF)

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Author Contributions

Conceived and designed the experiments: KT. Performed the experiments: TK JFA YI MY HF. Analyzed the data: TK JFA YI MY HS HF KT. Wrote the manuscript: KT.

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Significant Reductions in Gag-Protease-Mediated HIV-1 Replication Capacity during the Course of the Epidemic in Japan

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Human immunodeficiency virus type 1 (HIV-1) evolves rapidly in response to host immune selection pressures. As a result, the functional properties of HIV-1 isolates from earlier in the epidemic may differ from those of isolates from later stages. However, few studies have investigated alterations in viral replication capacity (RC) over the epidemic. In the present study, we compare Gag-Protease-associated RC between early and late isolates in Japan (1994 to 2009). HIV-1 subtype B sequences from 156 antiretroviral-naïve Japanese with chronic asymptomatic infection were used to construct a chimeric NL4-3 strain encoding plasma-derived *gag-protease*. Viral replication capacity was examined by infecting a long terminal repeat-driven green fluorescent protein-reporter T cell line. We observed a reduction in the RC of chimeric NL4-3 over the epidemic, which remained significant after adjusting for the $CD4^+$ T cell count and plasma virus load. The same outcome was seen when limiting the analysis to a single large cluster of related sequences, indicating that our results are not due to shifts in the molecular epidemiology of the epidemic in Japan. Moreover, the change in RC was independent of genetic distance between patient-derived sequences and wild-type NL4-3, thus ruling out potential temporal bias due to genetic similarity between patient and historic viral backbone sequences. Collectively, these data indicate that Gag-Protease-associated HIV-1 replication capacity has decreased over the epidemic in Japan. Larger studies from multiple geographical regions will be required to confirm this phenomenon.

It has been almost 30 years since the discovery of human immunodeficiency virus type 1 (HIV-1) (1), a pathogen that first infected human populations approximately 100 years ago (2, 3). Over the course of the pandemic, substantial and various selection pressures have been exerted on HIV-1 by its human host, possibly resulting in alterations in viral replication capacity (RC), virulence, and/or other properties (4). However, few studies to date have examined population-level alterations in HIV-1 replication capacity over the epidemic's course (5, 6), and none have investigated the potential role of immune escape mutations selected by cellular immune responses in modulating this phenomenon.

Cytotoxic T lymphocytes (CTLs) play a major role in controlling viremia and disease progression in HIV-1 infection (7–11). However, the selection of escape mutations within or near CTL epitopes facilitates viral immune evasion (12–16) and represents a major challenge for HIV vaccine design. Since CTL responses are restricted by human leukocyte antigen (HLA) class I alleles, CTL escape mutations emerge in an HLA-specific manner. Many CTL escape mutations have been identified experimentally (15, 17–20); moreover, statistical analyses of large population-level data sets have yielded HLA-associated mutation maps of HIV-1 protein sequences, thereby identifying putative CTL escape sites (21–27). Importantly, these escape variants may be transmitted both vertically and horizontally (12, 28, 29). Furthermore, CTL escape variants selected by common HLA class I alleles may have been accumulating at the population level over the course of the epidemic in some regions, most notably, Japan (30, 31). If this is the case, active CTL epitopes restricted by common HLA class I alleles may be lost through mutational escape as the epidemic matures, possibly leading to increased viral virulence through enhanced immune evasion in these populations.

Although CTL escape mutations allow HIV to evade immune detection, they can also reduce viral replication capacity (28, 32–38). Furthermore, while certain virus-attenuating escape mutations revert upon transmission to recipients lacking the relevant HLA class I allele (20, 28, 36), this is not always the case (39, 40). Indeed, a recent study suggested that fixation of viruses carrying such attenuating escape mutations is increasing in an allele frequency-dependent manner in certain populations (30). These observations have led to the hypothesis that the *in vitro* replication capacity of HIV-1 may have been decreasing over the epidemic's course in certain populations, at the expense of the loss of active CTL epitopes at the population level through mutational escape.

In the present study, we generated chimeric HIV-1 isolates by inserting plasma HIV RNA-derived *gag-protease* sequences from 156 asymptomatic, chronically infected treatment-naïve Japanese patients dating from 1994 to 2009 into a laboratory strain backbone (HIV-1 NL4-3) and examined their replication capacity using published methods (33, 41–44). We specifically focused on the

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TABLE 1 Demographic characteristics of the participants[a]

Characteristic	Value
Median (range) age (yr)	31 (18–73)
No. (%) of participants by gender	
Male	167 (94)
Female	10 (5.6)
Median (IQR) $CD4^+$ T cell count (no. of cells μl^{-1})	339 (269–452)
Median (IQR) pVL (no. of RNA copies/ml)	23,000 (5,700–46,000)
No. (%) of participants by route of transmission[b]	
Men who have sex with men	147 (83)
Heterosexual	25 (14)
Unknown	5 (2.8)

[a] Data are for 177 participants.
[b] Hemophilia patients were excluded from this study.

Gag protein, as it is likely to be the most important target of HLA-restricted CTLs (45) and because numerous fitness-reducing HLA-associated escape mutations have been described therein (28, 32–38). As such, Gag is ideal for investigating the potential effects of immune-mediated HIV attenuation over time. Overall, we have observed a significant reduction in Gag-Protease-mediated HIV-1 replication capacity as the epidemic has matured in Japan.

MATERIALS AND METHODS

Study participants. A total of 177 antiretroviral-naïve Japanese individuals with asymptomatic chronic HIV-1 infection who visited the Research Hospital of the University of Tokyo from April 1992 through March 2009 were enrolled. Individuals with acute HIV infection, chronically infected individuals with a history of AIDS-defining illnesses, and hemophilia patients were excluded (hemophilia patients were excluded because Japanese hemophiliacs acquired HIV-1 from imported blood products in the mid-1980s [46, 47], a fact which could confound our analyses). The sociodemographic characteristics of the participants are shown in Table 1. Blood collected at the earliest available time point during the asymptomatic chronic phase of infection (median, 173 days after diagnosis; interquartile range [IQR], 56 to 525 days after diagnosis; range, 0 to 4,313 days after diagnosis) was studied. Plasma and peripheral blood mononuclear cells (PBMCs) were separated by standard procedures and stored at −80°C and in liquid nitrogen, respectively, until use. The study was approved by the Institutional Review Board of the Institute of Medical Science, University of Tokyo. Written informed consent was obtained from all participants.

HLA class I typing. Genomic DNA was extracted from PBMCs using a QIAamp DNA blood minikit (Qiagen Inc., Valencia, CA) following the manufacturer's instructions. High-resolution HLA class I typing was performed using a WAKFlow HLA typing kit (Wakunaga, Hiroshima, Japan) and a Luminex multianalyte profiling system (Luminex Corporation, Austin, TX).

Viral RNA isolation. Plasma (500 μl) was quickly spun down to remove cell debris. The resulting clarified plasma was then centrifuged at 14,000 rpm (20,000 × *g*) for 120 min to pellet the virions. After centrifugation, 360 μl of the supernatant was discarded, leaving 140 μl plasma for which viral RNA was extracted using a QIAamp viral RNA minikit (Qiagen Inc., Valencia, CA). Extracted viral RNA was eluted in 80 μl of elution buffer and stored at −80°C until use.

Plasma virus sequencing. The HIV-1 *gag-protease* region was amplified from extracted plasma HIV RNA as described previously, with some modifications (48). We included *protease* since disruption of the autologous combination of Gag and Protease may negatively affect Protease-mediated cleavage of Gag protein products, thus compromising the RC of the recombinant viruses. Briefly, reverse transcriptase PCR (RT-PCR) was performed using a Superscript III one-step RT-PCR system with Platinum *Taq* DNA polymerase with high fidelity (Invitrogen, Carlsbad, CA). Each 50-μl reaction mixture was composed of 4 μl of viral RNA, 25 μl of 2× reaction mix, 200 nM forward and reverse outer primers, 1 μl of enzyme mix, and water. RT-PCR primer sequences were AAATCTCTAGCAGTG GCGCCCGAACAG (strain HXB2 nucleotide numbering, positions 623 to 649) for the forward primer and TAACCCTGCGGGATGTGGTA TTCC (positions 2849 to 2826) for the reverse primer. Thermal cycling conditions for the RT-PCR were 50°C for 30 min and 94°C for 2 min, followed by 35 cycles of 94°C for 15 s, 56°C for 30 s, and 68°C for 2 min. Second-round DNA PCR was performed using TaKaRa Ex *Taq* DNA polymerase Hot Start enzyme (TaKaRa Bio Inc., Shiga, Japan). Each reaction mixture contained 2 μl of the PCR product from the RT-PCR. PCR primer sequences were GCGGCGACTGGTGAGTACGCC (positions 734 to 754) for the forward primer and TCCTTTAGTTGCCCCCCTATC for the reverse primer (positions 2314 to 2294). Thermal cycling conditions were 94°C for 2 min, followed by 35 cycles of 94°C for 30 s, 60°C for 30 s, and 72°C for 2 min and, finally, 10 min at 68°C. To examine *protease* sequences, the *gag-protease* region was reamplified from existing 1st-round RT-PCR products using forward primer GCTAGAAGGAGAGAG ATGGG (positions 775 to 794 on HXB2) and reverse primer CAGTCTC AATAGGACTAATGGG (positions 2550 to 2571) with the same thermal cycler conditions described above. PCR amplifications were confirmed by agarose gel electrophoresis, and successful amplicons were purified using a QIAquick PCR purification kit (Qiagen Inc., Valencia, CA) according to the manufacturer's instructions. Population sequences were obtained by bidirectional reading using an ABI Prism BigDye Terminator (version 3.1) cycle sequencing kit (Applied Biosystems, Foster City, CA) on an Applied Biosystems 3130xl genetic analyzer. Chromatograms were edited using Sequencher software (Gene Codes Corporation, Ann Arbor, MI); nucleotide mixtures were called if the height of the secondary peak exceeded 25% of the dominant peak height. Multiple alignments were constructed using the ClustalW program. Maximum-likelihood phylogenetic trees were drawn from nucleotide alignments using DNAml of the PHYLIP program integrated into the BioEdit software package. HIV-1 subtypes were determined by the REGA HIV subtyping tool (http://hivdb.stanford.edu/). Recombinant viruses were detected using the recombination identification program (RIP; available at http://www.hiv.lanl.gov/content/sequence/RIP/RIP.html) and the jpHMM program (GOBICS; University of Göttingen). Pairwise genetic distances between individual *gag* sequences and the HIV-1 reference strain NL4-3 were calculated using DNAdist of the PHYLIP program integrated into BioEdit software.

Generation of chimeric viruses. Chimeric NL4-3 viruses were generated as previously described (33, 49). Briefly, the *gag-protease* region was reamplified from the 1st-round RT-PCR products using 100-bp-long primers homologous to the NL4-3 reference strain (forward primer, GAC TCG GCT TGC TGA AGC GCG CAC GGC AAG AGG CGA GGG GCG GCG ACT GGT GAG TAC GCC AAA AAT TTT GAC TAG CGG AGG CTA GAA GGA GAG AGA TGG G [positions 695 to 794 on HXB2]; reverse primer, ATG CTT TTA TTT TTT CTT CTG TCA ATG GCC ATT GTT TAA CTT TTG GGC CAT CCA TTC CTG GCT TTA ATT TTA CTG GTA CAG TCT CAA TAG GAC TAA TGG G [positions 2649 to 2550]). Note that the forward primer overlapped the *gag*-coding sequence by five bases (underlined), and the reverse primer ended one base downstream of the protease gene. The PCR was undertaken in a final volume of 100 μl, consisting of 4 μl of 10 μM forward and reverse primers, 90 μl of Invitrogen Platinum PCR SuperMix high fidelity (Invitrogen, Carlsbad, CA), and 2 μl of the RT-PCR product. Thermal cycling conditions were 95°C for 2 min, followed by 35 cycles of 94°C for 30 s, 65°C for 30 s, and 72°C for 2 min and a 7-min extension of 72°C. PCR products were purified with the QIAquick PCR purification kit (Qiagen Inc., Valencia, CA) and eluted in 50 μl of elution buffer. pNL4-3 with a *gag-protease* deletion (33) and 5 to 10 μg of purified PCR product were cotransfected into 2.5×10^6 cells of a long terminal repeat (LTR)-driven green fluorescent protein (GFP)-reporter T cell

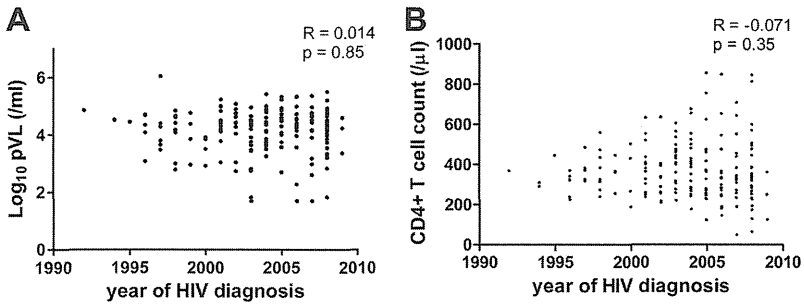

FIG 1 Correlation between plasma virus load, $CD4^+$ T cell count, and year of HIV-1 diagnosis. No significant correlation between plasma HIV-1 load and the year of diagnosis (A) or the $CD4^+$ T cell count and the year of diagnosis (B) was observed. Plasma virus loads and $CD4^+$ T cell counts are based upon a single time point (date of blood sampling). Each dot represents a single individual (n = 177).

line (GXR cells, CEM origin [50]) in 800 μl of R10+ medium (RPMI medium with 10% fetal calf serum containing penicillin and streptomycin) by electroporation (exponential protocol, 300 V, 500 μF). Cells were incubated for 45 min at room temperature, subsequently transferred to T25 flasks in 10 ml of R10+ medium, and incubated at 37°C with 5% CO_2. GFP expression was monitored by flow cytometry (FACSCalibur; BD Biosciences, San Jose, CA) every 1 to 2 days after day 5. Supernatants containing recombinant virus stocks were harvested after GFP expression reached 15% among viable cells, and 1-ml aliquots were stored at −80°C until use. To verify the patient origin of each recombinant virus stock and rule out contamination or sample mix-up, viral RNA was extracted from 30 μl of virus stock using a ChargeSwitch EasyPlex viral kit (Invitrogen, Carlsbad, CA). *gag* sequences were obtained using the same method used for plasma virus sequencing described earlier, and maximum-likelihood phylogenetic trees incorporating the original bulk and recombinant virus sequences were constructed using DNAml.

Determination of recombinant virus titers and RC assay. Determination of the titers of recombinant virus stocks and viral RC assays were performed as described previously (32, 35, 48, 50, 51). For determination of viral titer, 400-μl viral stocks were mixed with 1.0×10^6 GXR cells in 100 μl of R10+ medium in a 24-well plate and incubated at 37°C with 5% CO_2. After 24 h, 1 ml R10+ medium was added to each culture. After 48 h, the titers of virus stocks were determined by measuring the percentage of GFP-positive (GFP^+) cells using flow cytometry. In the subsequent replication capacity assay, virus stocks were used to infect 1.0×10^6 GXR cells at a multiplicity of infection of 0.002 in 500 μl of R10+ medium in a 24-well plate. All assays included a positive (wild-type NL4-3) and a negative (cells-only) control. Assay mixtures were incubated overnight at 37°C with 5% CO_2, and 1 ml of R10+ medium was added on the following day (day 1). The percentage of GFP^+ cells was then measured by flow cytometry every other day for the following week (days 2 to 8). For each virus, the natural log slope of the percentage of GFP^+ cells was calculated during the exponential phase of viral spread (days 2 to 6). This value was divided by the mean rate of spread of the wild-type NL4-3 control to generate a normalized, quantitative measure of RC. An RC value of 1.0 indicates a rate of viral growth that was equal to that of NL4-3, while RC values of <1.0 and >1.0 indicate rates of spread that were lower and higher than the rate for wild-type NL4-3, respectively. All viruses were tested in a single experiment by a single operator; this experiment was performed in triplicate using fresh viral stocks for each one. Final RC values therefore represent the averages of wild-type NL4-3-normalized triplicate measurements.

Statistical analysis. Statistical comparisons between independent groups were performed using the Mann-Whitney U test. Univariate correlation analysis was performed using Spearman's correlation. Multiple-regression analyses were performed using standard least-squares methods. For these analyses, a P value of <0.05 was considered significant. Analyses were performed in GraphPad Prism (version 5.03) software (GraphPad Software, La Jolla, CA).

Published phylogenetically informed methods were used to identify amino acids in Gag and Protease significantly associated with HLA class I alleles expressed in our data set (52, 53). Associations between viral RC and specific amino acid residues within Gag and Protease observed with a minimum frequency of 3 were identified using the Mann-Whitney U test. In these analyses, multiple comparisons were addressed using q values, the P value analogue of the false discovery rate (FDR) (54). The FDR is the expected proportion of false positives among results deemed significant at a given P-value threshold; for example, at a q value of ≤ 0.2, we expect 20% of identified associations to be false positives.

Nucleotide sequence accession numbers. *gag* and *protease* sequences have been submitted to GenBank (accession numbers JX264247 to JX264562).

RESULTS

No significant temporal changes in $CD4^+$ T cell count or pVLs by year of HIV-1 diagnosis. A total of 177 asymptomatic, chronically HIV-1-infected Japanese individuals were enrolled. Since the replicative capacity of viruses within an individual's quasispecies tends to increase over the infection course (55–58) and immune-driven selection in Gag by protective HLA alleles predominantly affects viral RC in acute/early infection (44), individuals with acute infection and those with a history of AIDS-defining illnesses were excluded. Clinical markers of HIV infection ($CD4^+$ T cell count and plasma virus loads [pVLs] at the time of sampling) were comparable among subjects, despite differences in year of HIV diagnosis (Fig. 1). Furthermore, although the timing of blood sampling varied substantially between subjects, no correlation between diagnosis year and the duration from diagnosis to blood sampling was observed (data not shown; $R = 0.0084$, $P = 0.92$).

Relationship between viral replication capacity and clinical markers of HIV infection. Of the 177 enrolled patients, full-length amplification of *gag-protease* was successful for 168 of these (94.9%). Eight individuals infected with non-clade B viruses (6 infected with CRF01_AE, 1 with CRF02_AG, and 1 with A1) and two individuals with intersubtype clade B *gag* recombinants were excluded from study. After construction of chimeric viral stocks and confirmation of their patient origin (Fig. 2), a further two samples were excluded due to suspected contamination. Viral RC was thus assessed for the remaining 156 recombinant viruses. Each recombinant virus was used to infect a GFP reporter T cell line, and its *in vitro* RC was examined over a 7-day period. Since

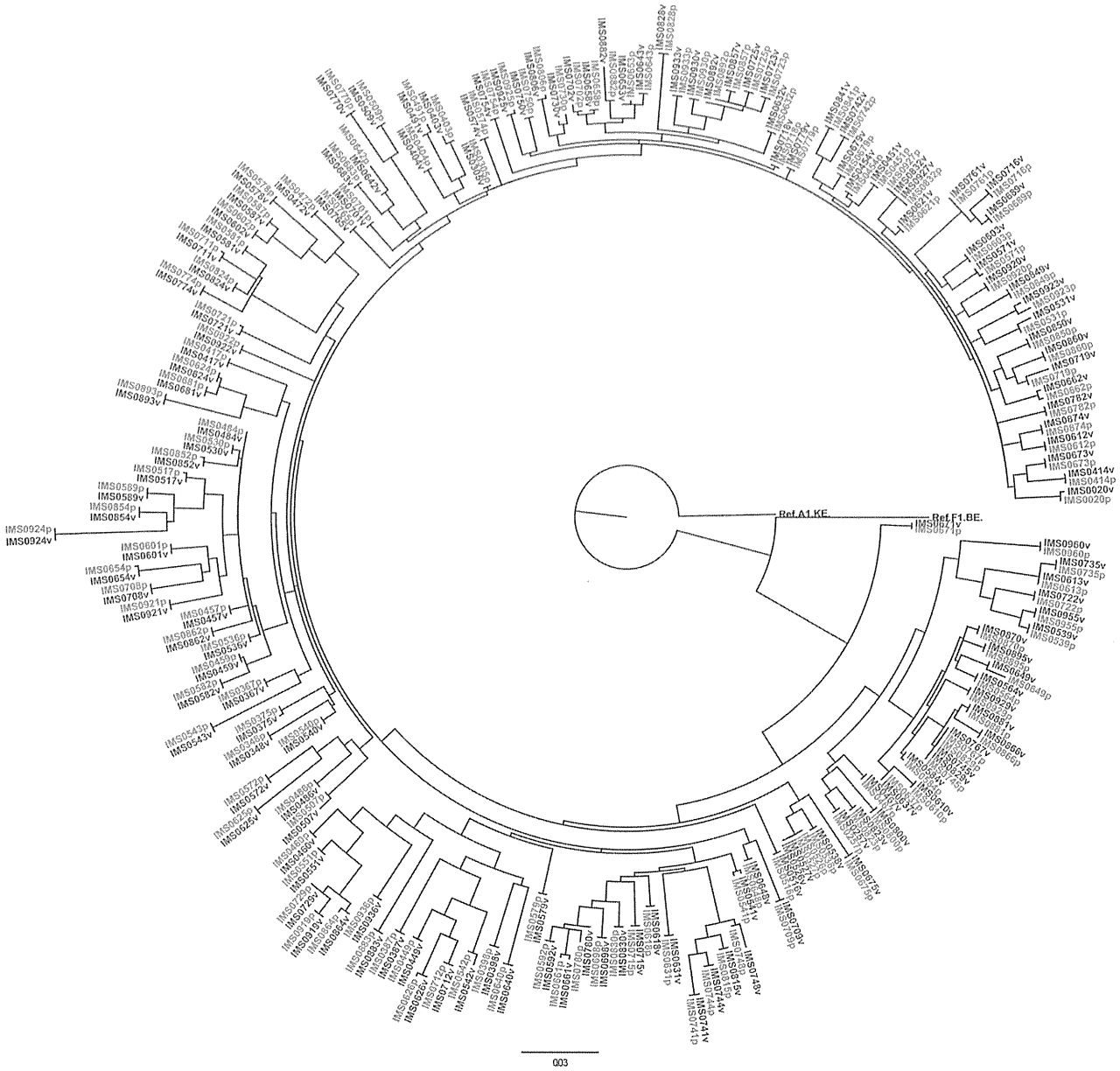

FIG 2 Validation of the origin of the *gag-protease* region in chimeric NL4-3 viruses. To verify the patient origin of each chimeric virus, a maximum-likelihood phylogenetic tree was constructed using plasma (red) and chimeric (blue) *gag* sequences. This tree includes 156 validated chimeric viruses that clustered with their original bulk sequences (two viruses were removed due to suspected contamination). The tree is rooted using the HIV-1 subtype A1 reference strain with GenBank accession number AF004885.

the set-point viral load has been associated with the *in vitro* replication of chimeric viruses (33, 42, 43, 55–59), we first examined the potential correlation between plasma viral load, $CD4^+$ T cell count, and RC of chimeric NL4-3 strains. A significant positive correlation between RC and plasma virus load was observed ($R = 0.21$, $P = 0.0072$; Fig. 3A), consistent with previous reports of the reduced RC of chimeric NL4-3 derived from HIV-1 controllers (33, 41, 42). No significant correlation between $CD4^+$ T cell count and RC was observed ($R = -0.042$, $P = 0.60$; Fig. 3B), possibly due to exclusion of individuals with advanced disease from the present study.

Change in Gag-Protease-associated viral replication capacity over the epidemic in Japan. In order to investigate temporal changes in viral RC over the epidemic in Japan, the correlation between RC and year of HIV diagnosis was analyzed, revealing a significant inverse correlation ($R = -0.27$, $P = 0.0006$; Fig. 4A). This observation remained statistically significant in a multivariate linear regression model adjusting for $CD4^+$ T cell count and plasma virus load ($P = 0.0008$; partial regression coefficients, -0.0064; 95% confidence interval [CI], -0.0101 to -0.0027). Consistent results were obtained when the original analysis was stratified by $CD4^+$ T cell count at blood sampling (for CD4 T cell

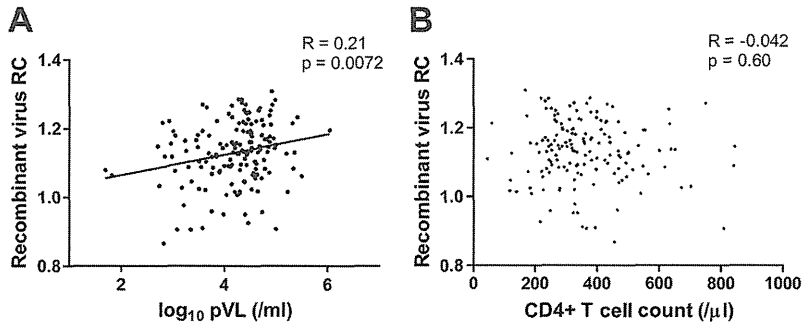

FIG 3 Correlation between replication capacity of chimeric NL4-3 and clinical markers of HIV infection. The correlation of replication capacity of chimeric NL4-3 with pVL (A) and CD4 T cell count (B) at the time of blood sampling ($n = 156$) is shown. A statistically significant positive correlation between RC and pVL was observed ($R = 0.21$, $P = 0.0072$).

counts of >200, $R = -0.28$ and $P = 0.0009$; for CD4 T cell counts of >300, $R = -0.25$ and $P = 0.013$; for CD4 T cell counts of >500, $R = -0.39$ and $P = 0.080$; Fig. 4B to D). Taken together, these results support a decline in Gag-Protease-mediated RC in HIV-1 over the course of the Japanese epidemic which is independent of differences in pVLs and CD4 T cell counts in the studied population. Since the duration from HIV diagnosis to blood sampling varied among the subjects, the analysis was repeated and was lim-

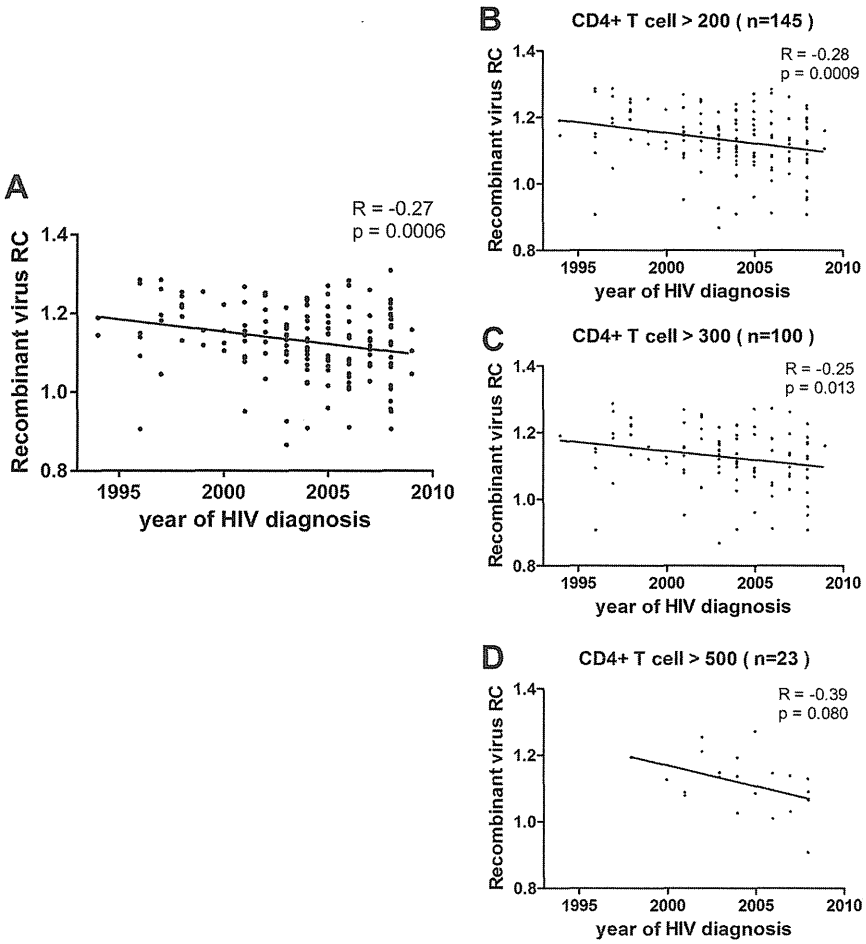

FIG 4 Change in Gag-Protease-associated viral replication capacity over the epidemic in Japan. A statistically significant inverse correlation between year of diagnosis and replication capacity was observed in all subjects regardless of CD4 T cell count ($n = 156$) (A), only in subjects with a $CD4^+$ T cell count of >200/μl ($n = 145$) (B), and only in subjects with a $CD4^+$ T cell count of >300/μl ($n = 100$) (C). A similar tendency was observed when the analysis was limited to subjects with a $CD4^+$ T cell count of >500/μl ($n = 23$) (D).

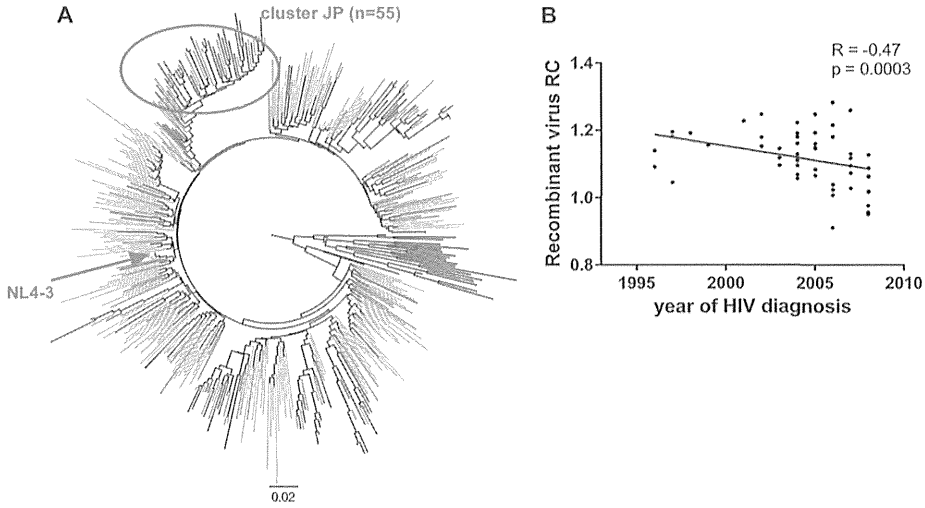

FIG 5 Temporal change in Gag-Protease-associated viral replication capacity of 55 sequences from a phylogenetic cluster. (A) Maximum-likelihood phylogenetic tree constructed using *gag* sequences from 156 Japanese individuals obtained in the present study and 263 individuals from other countries (randomly selected from the Los Alamos National Laboratory HIV sequence database). Purple, light blue, and blue branches, Japanese sequences with HIV diagnoses of 1999 or earlier, 2000 to 2004, and 2005 or later, respectively; green branches, sequences from the United States and Canada; yellow branches, sequences from other countries (Argentina, Australia, Brazil, China, Cuba, Cyprus, Denmark, France, Germany, Hong Kong, India, Italy, Jamaica, Myanmar, Netherlands, Russia, South Africa, South Korea, Spain, Taiwan, Thailand, and the United Kingdom). Reference strains (which include two reference sequences for each of the HIV-1 group M subtypes, as well as inferred ancestral sequences of the A, B, and C subtypes [obtained from the Los Alamos National Laboratory database]) are shown in black. NL4-3 is shown as red. The tree is rooted using the HIV-1 subtype A1 reference strain with GenBank accession number AF004885. A large cluster of Japanese sequences ($n = 55$) is indicated by the large red circle. (B) A significant inverse correlation between the replication capacity of chimeric viruses and year of HIV diagnosis for the viruses within this large Japanese cluster ($n = 55$).

ited to the subjects whose blood collection had been performed within a year of diagnosis of HIV infection; however, the inverse correlation remained significant ($n = 105$, $R = -0.25$, $P = 0.0080$; data not shown).

A potential confounder in such analyses is the molecular epidemiology of the epidemic itself. Theoretically, if distinct subtype B lineages with differential replication capacities were introduced into Japan at different times during the study period, this could influence our results. In order to exclude this possibility, we constructed a phylogenetic tree featuring global HIV-1 subtype B sequences (retrieved from the HIV sequence database at Los Alamos National Laboratory). Multiple clusters of Japanese clade B sequences were interspersed throughout the tree; however, all clusters contained sequences spanning the entire study period, indicating that there have been no major intraclade shifts within Japan in the past 2 decades (Fig. 5A). To further address this issue, we restricted our analysis to one particularly large cluster containing 55 sequences sampled over the study period (Fig. 5A) and found that the significant inverse correlation between RC and the year of diagnosis remained highly statistically significant in this cluster ($R = -0.47$, $P = 0.0003$; Fig. 5B). Taken together, these results support a decline in Gag-Protease-mediated RC in HIV-1 over the course of the Japanese epidemic which is not likely explained by shifts in the molecular epidemiology of HIV-1 over the period studied.

No correlation between replication capacity of chimeric viruses and their genetic distance from wild-type strain NL4-3. Chimeric NL4-3 virus carrying *gag-protease* derived from subtype C isolates (42, 43) displayed reduced RC compared to viruses derived from subtype B, likely due in part to the substantial genetic distance between insert and backbone. It is therefore conceivable that subtype B sequences sampled from the early part of the epidemic may be more similar to the NL4-3 backbone sequence (first characterized in 1986 [60]) than those sampled later and that this may influence RC. To investigate this potential confounder, we calculated the genetic distance between each patient isolate and the wild-type NL4-3 *gag* sequence, and we examined the correlation between genetic distance and viral RC. No such relationship was observed ($R = 0.0015$, $P = 0.98$; Fig. 6). Moreover, RC of chimeric viruses remained inversely correlated with the year of HIV diagnosis in multivariate analyses controlling for genetic distance from NL4-3 ($P = 0.0001$; partial regression coefficients, -0.0086; 95% CI, -0.0129 to -0.0044). It is therefore reasonable

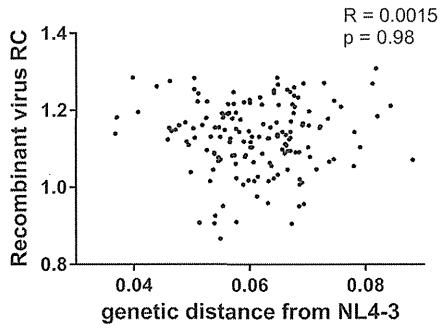

FIG 6 Chimeric virus replication capacity is not related to genetic distance between the insert and backbone. Pairwise genetic distances between the *gag* nucleotide sequence of each insert (clinical isolate sequence) and backbone (wild-type NL4-3) were calculated as described in Materials and Methods. No statistically significant correlation between the genetic distance and replication capacity of chimeric NL4-3 was observed.

to conclude that the decline in Gag-Protease-associated viral RC observed over the epidemic in Japan is unlikely to be explained by gross genetic incompatibility between NL4-3 and later clinical sequences circulating in the Japanese population.

Accumulation of PI resistance-associated mutations over time? Twelve major protease inhibitor (PI) resistance-associated mutations have been reported in the HIV Drug Resistance Database at Stanford University (http://hivdb.stanford.edu/), and some of these reduce viral replication capacity (61–67). To address the temporal accumulation of PI resistance mutations as a potential confounder, HIV-1 *protease* sequences were examined for 140 subjects for whom chimeric viruses were generated (for the remaining 15 patients, PCR or sequencing was unsuccessful). PI resistance-associated mutations were observed in 6 subjects, none of whom carried more than one PI resistance-associated mutation (4 were M46L and 2 were N88S), and all but 1 were enrolled after 2005. The median RC of chimeric NL4-3 derived from subjects with these PI resistance-associated mutations ($n = 6$) was higher than that of the others ($n = 134$) (1.21 versus 1.13; $P = 0.013$). Moreover, after excluding viruses derived from these 6 subjects from the original analysis, the temporal decline in chimeric virus RC remained significant ($R = -0.33$, $P < 0.0001$). Collectively, these data indicate that accumulation of PI resistance-associated variants in the population does not explain the change in viral RC over time in Japan.

Relationship between HLA class I alleles and temporal change in replication capacities of chimeric viruses. Chimeric NL4-3 virus derived from recent patient sequences displayed reduced *in vitro* RC compared to earlier isolates. To investigate whether immune selection pressure by specific HLA class I alleles could have contributed to this relative attenuation, the RCs of chimeric viruses were compared with respect to the presence versus absence of particular HLA-A, -B, and -C alleles in their host (note that analyses were limited to HLA alleles expressed in >20 individuals). In a cross-sectional analysis undertaken on the whole cohort regardless of sampling date, no significant associations between HLA class I expression and viral RC were observed (data not shown). However, when recombinant viruses were stratified on the basis of the year of HIV diagnosis (2002 or earlier versus 2003 or later), significantly lower median RC values were observed among A*24-expressing persons in early stages (for A*24-positive [$A*24^+$] versus A*24-negative [$A*24^-$] persons, 1.14 versus 1.21; $P = 0.024$) but not later stages (for $A*24^+$ versus $A*24^-$ persons, 1.12 versus 1.11; $P = 0.20$) of the epidemic (Fig. 7A), suggesting that the viral RC in $A*24^-$ persons in the early stage might have declined to levels comparable to those of $A*24^+$ persons in the late stage. Such a phenomenon was not observed for other HLA class I alleles (the results for A*02, B*40, and C*03 are shown in Fig. 7B to D, respectively). Nearly 70% of Japanese express HLA-A*24, making it the most common class I allele in this population. Our finding raises the intriguing hypothesis that A*24-associated escape mutations, alone or in combination, reduce viral RC to a modest extent and that these A*24-attenuated viruses have increased in prevalence at the population level over the course of the Japanese epidemic via transmission to and persistence in non-A*24-expressing persons.

Due to the relative rarity of this allele in Caucasians and Africans, HLA-A*24-restricted CTL epitopes have not been studied extensively; nevertheless, two optimal A*24 CTL epitopes within Gag and Protease have been reported: KW9 in p17 (Gag positions 28 to 36) (68) and RL11 in p24 (Gag positions 294 to 304) (69). However, we observed no accumulation of particular mutations within either of these known epitopes (data not shown). A published *in silico* analysis undertaken on >1,500 subtype B-infected individuals from Canada, the United States, and Australia reported a putative escape association between HLA-A*24 and the K30R substitution in $p17^{Gag}$ (21). However, the accumulation of K30R was not observed in the present study (data not shown), and the RCs of chimeric viruses with this substitution were not statistically different from the RCs of those without it. In addition, a phylogenetically corrected analysis of HLA-associated polymorphisms in 156 Japanese viral sequences from the present study identified Gag V362I to be significantly associated with HLA-A*24 (present in 17% of $A*24^+$ patients versus 4.1% of $A*24^-$ patients; $P < 0.001$, $q < 0.1$). However, as this substitution was observed in only 3 of 74 A*24-negative individuals in the present study, it was not possible to demonstrate its accumulation over the study period.

Accumulation of mutations associated with reduced replication capacity. Lastly, we conducted an exploratory analysis to identify specific amino acids in Gag and Protease associated with viral RC in our data set. Although no associations were observed at a q value of <0.2, 34 amino acids within Gag and 5 within Protease were identified as being associated with a lower RC at a P value of <0.05 (all q values were <0.4; not shown). We then investigated whether the frequencies of viruses carrying these Gag or Protease mutations increased over the course of the epidemic. Of the 34 polymorphisms identified in Gag, 6 significantly increased over the study period (V46L, L64I, D121G, A224P, T470A, I479L), while of the 5 mutations identified in Protease, 1 (R41K) significantly increased over the study period. However, with the exception of Gag L64I (reported to be associated with A*68) (21), none of these polymorphisms are known to be HLA associated.

DISCUSSION

In the present study, we observed a significant reduction in Gag-Protease-associated HIV-1 replication capacity over the past 15 years of the HIV-1 epidemic in Japan.

Our analyses addressed a number of potential confounders. First, viral RC is known to change over the course of HIV infection (70, 71). Examining the RCs of viruses isolated from acutely infected subjects is therefore ideal; however, the availability of such historic panels of specimens from a particular geographical area is extremely limited. Therefore, to rule out infection stage as a potential confounder, we undertook multivariate analyses adjusting for CD4 count and pVL as surrogate markers of disease stage. Second, to exclude the possibility that the molecular epidemiology of HIV in Japan differed in the early and late phases of the epidemic, we performed a subanalysis limited to a particularly large cluster composed of only Japanese clade B sequences sampled over the study period. Lastly, to address a concern about incompatibility between backbone NL4-3 and *gag-protease* from recent clinical isolates, we demonstrated that the year of HIV diagnosis correlated with RC independently of the genetic distance between patient-derived sequences and the wild-type NL4-3 sequence. In all cases, our original findings still held after controlling for these potential confounders. Furthermore, temporal trends in RC did not appear to be driven by protease inhibitor resistance mutations (which were infrequent in the studied population). Nevertheless, we cannot rule out the possibility that the introduction of increas-

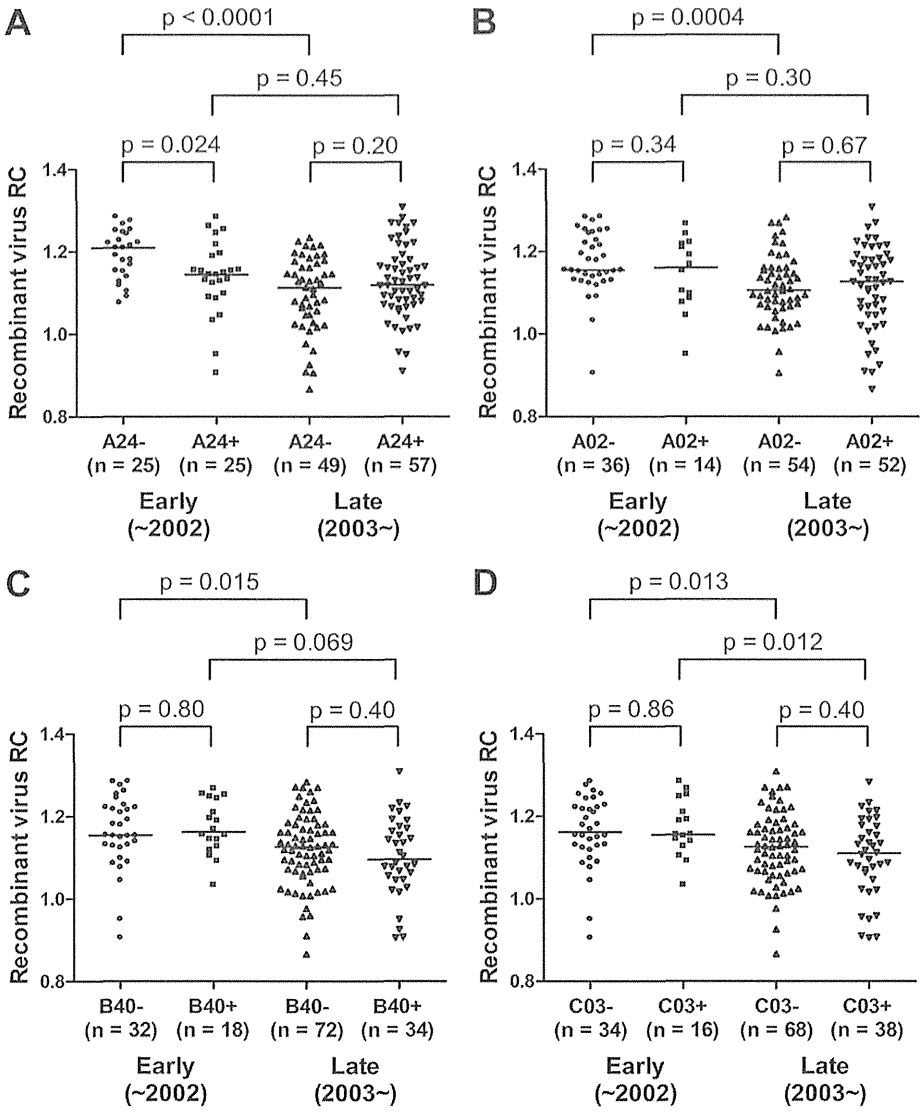

FIG 7 Relationship between common HLA alleles and chimeric virus replication capacity during early and late epidemic periods. To examine the potential impact of selection pressures by common HLA alleles in the Japanese population on the change in viral replication capacity, chimeric viruses were grouped according to year of HIV diagnosis (early [2002 or earlier] and late [2003 or later]), and associations between replication capacity and expression of particular HLA class I alleles were examined. Recombinant viruses from HLA-A*24-expressing hosts exhibited reduced RC before 2002 but not thereafter (A). However, such a phenomenon was not observed for other alleles investigated: A*02, B*40, and C*03 (B to D). Horizontal bars indicate the median values.

ingly more potent protease inhibitors over time is driving the selection of novel secondary drug resistance-associated polymorphisms that compromise RC and that such polymorphisms may be increasing in frequency in the general population.

Attempts have been made to study population-level changes in plasma HIV loads, CD4 T cell counts, and rates of disease progression over time as indirect evidence for altered HIV virulence over the epidemic's course. However, the lack of historic data, inherent limitations in conducting observational studies, and changes in the technologies used to measure clinical parameters have made this an extremely difficult issue to address. Despite this, a pattern appears to be emerging. While studies undertaken prior to the mid-1990s yielded conflicting results (72–76), more recent reports support the observation that HIV may be increasing in virulence as the epidemic progresses (77–85).

At first, published reports of increased virulence over time may appear to be inconsistent with our findings of reduced *in vitro* viral RC over the course of the Japanese epidemic. However, it is important to note that *in vitro* RC does not necessarily equate with viral virulence, as the former assesses the ability of a recombinant virus to replicate in a controlled *in vitro* environment devoid of host or other selection pressures, while the latter reflects the far more complex capacity of the virus to cause disease in its host. Indeed, while certain immune escape mutations reduce *in vitro* viral RC (28, 32–38), we must also consider that mutants with such escape mutations are highly adapted to their *in vivo* environ-

ment within a host expressing the relevant HLA class I allele. Indeed, while RC may be somewhat compromised compared to that of wild type, escape mutant viruses able to fully or partially evade CTL detection *in vivo* are almost certainly more virulent in the HLA-matched host environment, leading to increased virion production and thereby enhanced pathogenesis. The context dependency of viral fitness is similarly illustrated by antiretroviral resistance mutations such as M184V within reverse transcriptase (86–91): viruses harboring this mutation display relative *in vitro* replicative defects but are certainly more fit than their wild-type counterparts in the presence of lamivudine both *in vivo* and *in vitro*.

It is notable that viremia remained relatively unchanged over the study period. One potential explanation for this observation is the existence of two conflicting processes that offset each other: on the one hand, an increase in virus production (manifested as pVL) as a result of viral adaptation to its host and, on the other, a concomitant decrease in RC as a result of the fitness costs of this adaptation. To investigate this hypothesis, we conducted a multivariate analysis to examine the relationship between pVL and the year of diagnosis when conditioned on RC; however, no apparent trend was observed (data not shown); larger-scale studies will therefore be necessary to further investigate the interplay between these factors.

It was surprising to see such a clear decline in viral RC over the relatively short study period, especially in a country where HIV incidence and prevalence are low (HIV prevalence in Japan is <0.1%; [HIV and AIDS Data Hub for Asia-Pacific, http://www.aidsdatahub.org/]). However, Japan is relatively ethnically homogeneous and its population exhibits a far narrower HLA frequency spectrum than the populations of Western countries (92). This more limited HLA diversity may facilitate the rapid accumulation of CTL escape mutations in circulating HIV-1 sequences (93), most notably, those restricted by common Japanese HLA class I alleles (30, 31).

Intriguingly, lower viral RC was observed in HLA-A*24$^+$ patients than HLA-A*24$^-$ patients in earlier but not later periods of the Japanese epidemic. We propose the following interpretation for this observation: regardless of epidemic stage, viruses from HLA-A*24-positive patients carry A*24 escape mutations; therefore, no differences in RC are observed between early and late isolates from A*24-positive individuals. However, if single (or combinations of) A*24 escape mutants, some of which carry modest replicative costs, are transmitted to A*24-negative individuals and if some of these escape mutants persist in A*24-negative individuals, despite these modest replicative costs, it is possible that such mutations will increase in frequency in the general population over the course of the epidemic. If so, it is conceivable that the RC in A*24-negative individuals will concomitantly decline to levels similar to those in A*24-positive individuals over time. Although we did not observe any differences in the prevalence of particular amino acids within known A*24-restricted CTL epitopes in Gag and Protease in early versus later sequences, accumulation of A*24 CTL escape mutations within Nef in circulating viruses in Japan has been reported (31), suggesting that a similar phenomenon could be occurring in Gag. The link between A*24-associated immune pressure and temporal reductions in RC therefore remains speculative; future studies will be required to define CTL escape mutations for HLA alleles frequently observed in Japanese populations and demonstrate the accumulation of such mutations during the HIV epidemic.

Despite the limited statistical power of the present study to detect such associations, we performed an exploratory analysis to identify specific amino acid residues that could explain observed reductions in viral RC. Although we identified a number of putative amino acids that were associated with lower RCs at a P value of <0.05 and whose frequency appeared to increase over the study period, these associations did not remain significant after correction for multiple comparisons, and thus, our results should be interpreted with caution. Larger studies aimed at identifying amino acids associated with temporal alterations in RC are therefore warranted.

Another caveat is that only Gag-Protease-associated viral RC was evaluated in the present study; as such, our results may not be representative of RC of whole virus isolates. The reasons for specifically investigating Gag-Protease-associated RC are 2-fold. First, our primary purpose was to investigate temporal changes in viral RC potentially attributable to HLA-associated immune pressures in Gag, a critical target of CTL responses. Whole-virus assays would have been confounded by the autologous envelope sequence, which is a major determinant of viral fitness (57) but is highly sensitive to infection stage due to shifts in coreceptor usage (94–96). Second, the generation and evaluation of large numbers of viruses require higher-throughput methods. Whole-virus isolates are traditionally replicated in primary CD4$^+$ T cells, but the laborious and costly nature of these assays precludes their application to large sample panels such as that used in the present study.

Despite these limitations, the present study sheds light on the replicative costs of HIV-1 adaptation to its human host. Additional, larger studies spanning greater durations of the HIV epidemic undertaken in different geographic areas and host populations, as well as studies elucidating the clinical implications of alterations in viral RC, are warranted, to determine whether this is a local or global phenomenon.

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Natural OX40L expressed on human T cell leukemia virus type-I-immortalized T cell lines interferes with infection of activated peripheral blood mononuclear cells by CCR5-utilizing human immunodeficiency virus

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Abstract

Background: OX40 ligand (OX40L) co-stimulates and differentiates T cells via ligation of OX40 that is transiently induced on T cells upon activation, resulting in prolonged T cell survival and enhanced cytokine production by T cells. This view has led to the targeting of OX40 as a strategy to boost antigen specific T cells in the context of vaccination. In addition, the ligation of OX40 has also been shown to inhibit infection by CCR5-utilizing (R5) but not CXCR4-utilizing (X4) human immunodeficiency virus type-1 (HIV-1) via enhancement of production of CCR5-binding β-chemokines. It was reasoned that human T cell leukemia virus type-I (HTLV-1) immortalized T cell lines that express high levels of OX40L could serve as an unique source of physiologically functional OX40L. The fact that HTLV-1$^+$ T cell lines simultaneously also express high levels of OX40 suggested a potential limitation.

Results: Results of our studies showed that HTLV-1$^+$ T cell lines bound exogenous OX40 but not OX40L, indicating that HTLV-1$^+$ T cell lines express an active form of OX40L but an inactive form of OX40. Anti-OX40 non-blocking monoclonal antibody (mAb), but not blocking mAb, stained HTLV-1$^+$ T cell lines, suggesting that the OX40 might be saturated with endogenous OX40L. Functionality of the OX40L was confirmed by the fact that a paraformaldehyde (PFA)-fixed HTLV-1$^+$ T cell lines inhibited the infection of autologous activated peripheral blood mononuclear cells (PBMCs) with R5 HIV-1 which was reversed by either anti-OX40L blocking mAb or a mixture of neutralizing mAbs against CCR5-binding β-chemokines.

Conclusions: Altogether, these results demonstrated that autologous T cell lines immortalized by HTLV-1 can be utilized as a conventional source of physiologically functional OX40L.

Background

OX40 ligand (OX40L, CD252) belonging to the tumor necrosis factor (TNF) superfamily is a co-stimulatory molecule [1,2] that was first described by our laboratory as gp34 that is constitutively expressed at high levels on the surface of human T cell leukemia virus type-I (HTLV-1)-immortalized T cell lines [3,4]. It is now clear that OX40L can be induced on a wide variety of human hematopoietic cell lineages including antigen presenting cells (APCs) such as dendritic cells (DCs) [5] and B cells [6], natural killer (NK) cells [7], mast cells [8], endothelial cells [9] and T cells [10,11]. OX40 (CD134), a member of the TNF receptor (TNFR) superfamily that is rapidly induced predominantly on T cells upon cell activation is the cognate receptor for OX40L [12-14]. Interaction of OX40 on T cells with OX40L on APCs generates a variety of biological changes that include enhanced production of cytokines by T cells, Th2 cell differentiation, prolonged T cell survival, activation of B cells and DCs, to name a few

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[1,12,15]. OX40L is naturally expressed on the cell surface as a trimeric protein that binds to three copies of monomeric OX40 within close proximity [16]. Such close interactions between OX40/OX40L promotes tight cell to cell adhesion facilitating T cell-DC communication and skin infiltration of $OX40^+$ leukemic T cells in adult T cell leukemia (ATL) [17].

It has been proposed that the targeting of OX40 on activated T cells by OX40L or with the use of anti-OX40 agonistic antibodies may provide a strategy for the selective expansion of the limited frequencies of antigen specific T cells that are normally induced during vaccination and thereby achieve more effective immune responses [18-20]. Another immunological role of OX40L-OX40 interaction that we have previously documented includes the ability of OX40L in either soluble or membrane-bound form to effectively inhibit the infection of activated PBMCs with R5 HIV-1 *in vitro* [21]. This inhibition was shown to be mediated via the enhanced production of the CCR5-binding β-chemokines that include RANTES, MIP-1α and MIP-1β, followed by the down-modulation of cell surface CCR5 expression. These findings brought into focus the potential use of OX40L as a therapeutic tool and prompted us to investigate methodologies that would provide a convenient source for biologically active OX40L. One such source of OX40L was reasoned to be $HTLV\text{-}1^+$ T cell lines that unlike normal activated T cells or non-T cells have been shown to express both OX40L and OX40 on the cell surface at a single cell level due to the action of the HTLV-1-encoded oncogenic protein Tax [4,22]. Tax, in addition, also induces the expression of 4-1BB and its cognate ligand both of which belong to the TNF/TNFR family [23]. Selective induction of these ligand/receptor pairs has been implicated in the survival of HTLV-1-infected cells.

Studies were therefore carried out in efforts to examine whether OX40L and OX40 were expressed in a biologically active form by $HTLV\text{-}1^+$ T cell lines. We report herein for the first time that $HTLV\text{-}1^+$ T cell lines express a biologically active form of OX40L while the OX40 molecule appears biologically inactive or masked. The OX40L expressed by $HTLV\text{-}1^+$ T cell lines was capable of inhibiting R5 HIV-1 infection of activated PBMCs via production of CCR5-binding β-chemokines. These findings suggest that autologous HTLV-1-immortalized T cell lines can be utilized as a readily available convenient source of natural OX40L in large quantities for various immunological studies.

Results

HTLV-1-immortalized T cell lines express active OX40L together with inactive OX40

In order to determine whether OX40L and OX40 co-expressed on the cell surface of $HTLV\text{-}1^+$ T cell lines were biologically active, we examined their capacities to bind biotinylated rec-OX40 and rec-OX40L, respectively. The finding that rec-OX40 and rec-OX40L bound specifically to the OX40L-transfected CEM cells (CEM/OX40L) and the OX40-transfected CEM/OX40 cells, respectively, demonstrated the specificity of the assay being utilized (Figure 1). Interestingly, although the standard $HTLV\text{-}1^+$ T cell line (MT-2) was stained double positive with anti-OX40L (clone 5A8) and anti-OX40 (clone B-7B5) mAbs, they bound only rec-OX40 but not rec-OX40L. This finding indicated that while OX40L was expressed in an active form on MT-2 cells, the OX40 was likely to be expressed in an inactive form. Similar results were obtained by the testing of a number of additional $HTLV\text{-}1^+$ T cell lines, including T cell lines spontaneously established from a HTLV-1-infected patient with adult T cell leukemia (ILT-H2) and a HTLV-1-associated myelopathy (HAM/TSP) patient (ILT-M1), and various *in vitro*-HTLV-1-immortalized $CD4^+$ or $CD8^+$ T cell lines from different healthy donors (such as YT/cM1, RT/cH2 cells) (Figure 1). Thus, these results suggest that on the cell surface of the $HTLV\text{-}1^+$ T cell lines only OX40L, but not OX40, is capable of binding its respective ligand.

Characterization of OX40 on $HTLV\text{-}1^+$ T cells

A series of studies were subsequently conducted in efforts to identify the potential reason(s) for the failure of $HTLV\text{-}1^+$ T cell lines to bind rec-OX40L. Western Blot analysis of OX40 expressed by $HTLV\text{-}1^+$ T cell line was first carried out to determine whether the OX40 expressed by these cells was truncated. Cell lysates prepared from surface biotinylated *in vitro* activated PBMCs and the OX40 transfected CEM cell line (CEM/OX40) were analyzed in parallel with the $HTLV\text{-}1^+$ T cell line MT-2 using standard Western Blot techniques. Results of these studies displayed in Figure 2 showed that there were no detectable differences in the molecular weight of the glycosylated authentic OX40 (50 kDa) among these three samples. The 35 kDa band corresponding to the non-glycosylated form of OX40 was apparent in CEM/OX40 cells and activated PBMCs, but it was faint in MT-2 cells. These data indicated that there was no detectable deletion or modification in the glycosylated OX40 molecules expressed by the $HTLV\text{-}1^+$ T cell lines.

To further probe for the molecular basis for the inability of the OX40 expressed by the $HTLV\text{-}1^+$ T cell lines to bind rec-OX40L, we utilized an additional anti-OX40 specific mAb (W4-54 mAb) along with B-7B5 mAb. While the clone W4-54 anti-OX40 mAb inhibited the binding of OX40 and OX40L, the clone B-7B5 failed to show any detectable inhibition (Additional file 1: Figure S1). These two mAbs are reasoned to react against conformational epitopes since they failed to bind any overlapping 15-mer peptides spanning the entire OX40 protein (data not shown). As shown in Figure 3(A), control mock treated CEM/

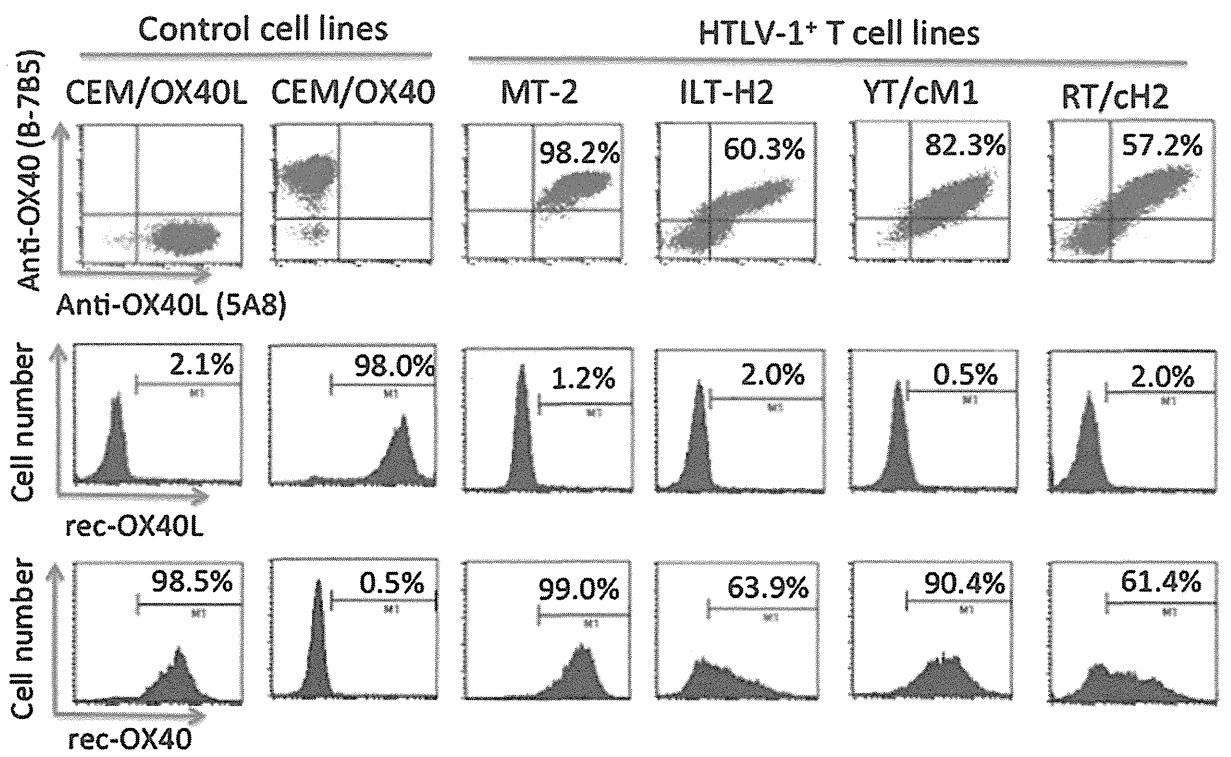

Figure 1 HTLV-1$^+$ T cells co-express both OX40L and OX40 but only OX40L is expressed in an active form. The OX40 and OX40L co-expressing control CEM cells and the HTLV-1$^+$ cells were dually stained with FITC-labeled anti-OX40 (B-7B5) and Cy-5 labeled anti-OX40L (5A8) (upper row), or singly stained either with biotinylated recombinant OX40L (rec-OX40L) or rec-OX40 followed by PE-streptavidin (middle and lower rows, respectively). Data shown are representative profiles of 3 independent experiments.

OX40 and activated PBMCs, as expected, both stained dual-positive with the B-7B5 mAb and W4-54 mAbs. These data show that the comparative staining with B-7B5 and W4-54 mAbs can be potentially utilized to distinguish between non-ligated versus OX40L ligated forms of OX40. Figure 3(B) shows that although B-7B5 mAb stained HTLV-1$^+$ T cell lines at high levels, little or no staining was noted with the use of the W4-54 mAb. In contrast, results of a WB analysis showed that the W4-54 mAb readily reacts to the p50 of the OX40 molecule in lysates of the HTLV-1$^+$ T cell line, YT/cM1 (Additional file 2: Figure S2). These results suggest that the OX40L binding site of OX40 expressed by the HTLV-1$^+$ T cell lines was altered, most probably due to pre-occupation with endogenous OX40L. To confirm this possibility, we explored the presence of OX40-OX40L complexes expressed by HTLV-1$^+$ T cell lines using our in-house ELISA. Cell lysates of the ATL-derived HTLV-1$^+$ T cell line (ILT-H2) were first captured with the use of immobilized anti-OX40L (clone HD-1) or anti-OX40 (clone B-7B5) mAb, respectively. The levels of captured antigens were assayed with the use of HRP-labeled anti-OX40 mAb or anti-OX40L mAb. Although it is reasonable to assume that the natural interaction between OX40 and OX40L on the living cell surface may be dissociated by the detergent treatment, as shown in Figure 4, low but significant levels of OX40-OX40L complex were still detectable in the cell lysates.

Functional OX40L expressed by HTLV-1$^+$ T cell lines

To confirm that the OX40L expressed on the HTLV-1$^+$ T cell lines is biologically functional, we performed co-culture experiments using the experimental *in vitro* infection of autologous activated PBMCs with HIV-1 as a read out. PBMCs activated with anti-CD3/anti-CD28 mAbs for 24 hours were washed and infected with either R5 HIV-$1_{JR\text{-}FL}$ or X4 HIV-$1_{NL4\text{-}3}$ at a low m.o.i., and then co-cultured with paraformaldehyde (PFA)-fixed autologous HTLV-1$^+$ T cell line in the presence or absence of anti-OX40L mAb or a mixture of the three CCR5-binding chemokine-blocking mAbs (anti-RANTES, anti-MIP-1α and anti-MIP-1β). The reasons why we utilized autologous PFA-fixed HTLV-1$^+$ T cell lines were to avoid any allogeneic stimuli and minimize the secretion of any anti-HIV-1 factors by the HTLV-1$^+$ T cell lines. As shown in Figure 5, the frequencies of HIV-1 p24$^+$ T cells in the cultures were reduced by co-culture with not only autologous HTLV-1$^+$ T cell line but also with the