成機構を解明し、サルエイズモデルにおける新規治療法開発の為の感染病態に基づく評価基準を確立する。具体的には、１）感染サルのウイルス増殖部位や潜伏部位等の感染動態について詳細に解析する。２）感染サルの粘膜や深部リンパ系組織における免疫細胞応答について詳細に解析する。３）感染サルの腸管をはじめとする全身の深部組織における病変の病理組織学的解析を行う。以上の解析を統合的に行うことにより、エイズウイルス感染サル個体の感染病態形成における最も重要な標的細胞群を特定し、ウイルス制御に有効に働く免疫機構を明らかにする。

（倫理面への配慮）

動物実験に当たっては、「研究機関等における動物実験等の実施に関する基本指針」に基づいた「京都大学における動物実験の実施に関する規定」を遵守した。京都大学ウイルス研究所附属動物実験施設におけるアカゲザルの飼養については、「特定外来生物による生態系等に係わる被害の防止に関する法律」の規定に基づき、環境大臣より許可を受けている。また、「感染症の予防及び感染症の患者に対する医療に関する法律」の輸入禁止地域等を定める省令に基づき輸入サル飼育施設の指定を受けている。また、「動物の愛護及び管理に関する法律」にも遵守し、実験を行った。

組換え SHIV 感染実験については第二種使用等をする間に執る拡散防止措置について大臣確認されている。

C．研究結果

近年、HIV-1 の *env* 遺伝子により決定される共受容体指向性、すなわち CCR5 指向性や CXCR4 指向性、によって感染個体における標的細胞や病態が大きく異なることが明らかになっている。そして、従来 CXCR4 指向性 SHIV を用いた研究が多くなされてきたが、HIV-1 の感染伝播と感染後の病原性に深く関与しているのは CCR5 指向性であると考えられるようになった。そこで我々は、アカゲザルに安定的に感染する CCR5 指向性 SHIV を作製することによって、より有効なエイズ霊長類モデル系を確立することを試みた。

これまでに高病原性CXCR4指向性SHIV-KS661の V3 領域に 5 箇所のアミノ酸変異を導入することによって、共受容体指向性を CCR5 指向性に変えることに成功した。この新規に作製した CCR5 指向性 SHIV-MK1 の個体内での複製能は必ずしも高くなかったのでアカゲザル個体で継代することにより、アカゲザルに安定して感染し、複製する CCR5 指向性 SHIV-MK38 株を得た。

次に、これらウイルスの中和抗体に対する抵抗性について検討した。まず、HIV-1 感染者６名分の pool 血清による中和アッセイを行ったところ、元の SHIV-KS661 と馴化前の SHIV-MK1 は、ID50 が中和抗体感受性の国際標準株(Tier1B)と同等の 500 倍以上であったのに対して SHIV-MK38 は、Tier2, 3 の国際標準株と同等の 100 倍以下であった。さらに SHIV-MK38 の *env* 遺伝子領域のシークエンス解析により、中和モノクローナル抗体 KD-247 に対する中和エピトープが保存されていることを確認した上で、KD-247 に対する中和感受性を調べたところ、SHIV-KS661 と SHIV-MK1 の IC50 は、5〜10 μg/ml 程度(Tier1B 相当)であったのに対し、SHIV-MK38 の IC50 は、50 μg/ml 以上(Tier2, 3 相当)であった。SHIV-MK1 は、CD4 mimic 低分子化合物 YYA-021 による中和増強効果がみられたが、SHIV-MK38 では、YYA-021 による中和増強効果はみられなかった。

SHIV-MK-38 は、アカゲザル継代により遺伝的多様性を獲得していたので *env* 遺伝子領域をクローニングして元の SHIV-KS661 の *env* 遺伝子領域と組み換えたクローンウイルスを１０クローン作製した。このなかで SHIV-MK38 と同等の中和抵抗性を示すクローンが２クローン得られたことから、SHIV-MK38 の中和抗体抵抗性は *env* 遺伝子の多様性に依存せず、ウイルスクローンとして成立することを明らかにした。

D．考察

今回の研究で中和抗体感受性の CCR5 指向性 SHIV-MK-1 をアカゲザルで継代して順化した

SHIV-MK38 はウイルスクローンとして中和抗体抵抗性を獲得したことを明らかにした。元のCXCR4指向性SHIV-KS661もカニクイザルで継代して順化したウイルスであるが、中和抗体抵抗性にはならなかったことから、共受容体指向性と中和抗体抵抗性獲得機構との関係が興味深い。今後、これらのウイルスが引き起こす病態の違いをアカゲザル感染実験により詳細に解析することで、共受容体指向性や中和抗体抵抗性と感染個体における病態との関係を明らかにできるものと期待される。また、低分子 CD4 mimic YYA-021 による中和増強効果がみられた SHIV-MK1 をアカゲザルに順化し、中和抗体抵抗性となった SHIV-MK38 は、YYA-021 による中和増強効果がみられなくなった。SHIV-MK38 のような中和抗体抵抗性ウイルスでも中和感受性にできる CD4 mimic を開発することが望まれる。

E．結論

高病原性 CXCR4 指向性 SHIV-KS661 の *env* 遺伝子の V3 領域の５アミノ酸を置換することにより CCR５指向性に変化させ(SHIV-MK1)、動物継代によってアカゲザルに順化させた(SHIV-MK38)。SHIV-MK1 は、SHIV-KS661 と同様に中和モノクローナル抗体 KD-247 に対しある程度中和感受性(Tier1B 相当)であり、CD4 mimic 低分子化合物 YYA-021 による中和増強効果もみられた。しかし、SHIV-MK1 をアカゲザルに順化した SHIV-MK38 は、KD-247 中和抵抗性となり、YYA-021 による中和増強効果もみられなくなった。SHIV-MK38 は、非ヒト霊長類モデルを用いた HIV-1 の中和抗体抵抗性の解析に役立つものと期待される。

F．研究発表

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G. 知的財産権の出願・登録状況

1. 特許取得

なし

2. 実用新案登録

なし

3. その他

なし

別紙４

研究成果の刊行に関する一覧表

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著者氏名	論文タイトル名	書籍全体の編集者名	書　籍　名	出版社名	出版地	出版年	ページ

雑誌

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別紙４

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なし							

雑誌

発表者氏名	論文タイトル名	発表誌名	巻号	ページ	出版年
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Adach, A. and Miura, T.	Animal model studies on viral infections.	Frontiers in Microbiology	5	Article 672	2014

Passive transfer of neutralizing mAb KD-247 reduces plasma viral load in patients chronically infected with HIV-1

Shuzo Matsushita[a], Kazuhisa Yoshimura[a,b], Kristel Paola Ramirez[a], Jaya Pisupati[c], Toshio Murakami[d], on behalf of the KD-1002 Study Group

Objective: Neutralizing antibodies against HIV-1 such as a humanized mAb KD-247 can mediate effector functions that attack infected cells *in vitro*. However, the clinical efficacy of neutralizing antibodies in infected individuals remains to be determined. We evaluated the safety, tolerability and pharmacokinetics of KD-247 infusion and its effect on plasma HIV-1 RNA load and $CD4^+$ T-cell count.

Design and methods: KD-1002 is a phase Ib, double-blind, placebo-controlled, dose-escalation study of KD-247 in asymptomatic HIV-1 seropositive individuals who did not need antiretroviral therapy. Individuals were randomized to 4, 8 or 16 mg/kg KD-247 or placebo, and received three infusions over a 2-week period.

Results: Patients were randomized to receive one of the three doses of KD-247 and the treatment was well tolerated. We observed a significant decrease in HIV RNA in the 8 and 16 mg/kg KD-247 cohorts, with two individuals who achieved more than 1 log reduction of HIV RNA. Two patients in the 16 mg/kg cohort had selections and/or mutations in the V3-tip region that suggested evasion of neutralization. Long-term suppression of viral load was observed in one patient despite a significant decrease in plasma concentration of KD-247, suggesting effects of the antibody other than neutralization or loss of fitness of the evading virus.

Conclusion: The results indicate that KD-247 reduces viral load in patients with chronic HIV-1 infection and further clinical trials are warranted.

AIDS 2015, **29**:453–462

Keywords: antibody-dependent cell cytotoxicity, escape mutations, HIV-1, mAb, neutralizing antibody, passive immunization

Introduction

Despite the significant reduction in morbidity and mortality following combination antiretroviral therapy (cART), there is emerging evidence that people with successfully treated HIV-1 infection age prematurely, leading to progressive multiorgan diseases referred to as comorbidity. The pathogenic process has been associated with long-term use of antiviral drugs, residual viral production and subsequent chronic inflammation [1]. In contrast to the current cART that only targets viral replication, neutralizing or nonneutralizing antibodies against HIV-1 can mediate effector functions that attack infected cells *in vitro* [2,3]. However, the clinical efficacy

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of neutralizing antibodies in infected individuals remains to be determined.

Previous studies revealed that human antibodies to HIV-1 can neutralize a broad range of viral isolates *in vitro* and protect nonhuman primates against infection [4–6]. Effective control of HIV-1 by combinations of broadly neutralizing antibody (bnAb) in chronically infected humanized mice and simian–human immunodeficiency virus (SHIV)-infected macaques have been reported [7–9]. However, previous human studies concluded that treatment with neutralizing antibodies had only limited effects against established HIV-1 infection [10,11].

Here, we report the results of a phase Ib dose-escalation study of a neutralizing mAb, KD-247 (international nonproprietary name: suvizumab) in asymptomatic HIV-1 seropositive individuals who did not at the time need cART. The epitope recognized by the mAb was mapped to IGPGR at the tip of the third variable loop of HIV-1 gp120 (V3-tip) that covers about half of HIV-1 in subtype B [12,13]. KD-247 belongs to the antibodies that have limited breadth and potency in standard neutralization assays as compared with bnAbs [14]. However, passive transfer of KD-247 may have an impact on patients infected with HIV-1 that matches for KD-247 binding.

The objectives of this phase Ib study were to evaluate the safety and tolerability of three infusions of KD-247 over 2 weeks in HIV-1 seropositive individuals, to determine the pharmacokinetic parameters and to assess the effect of KD-247 infusions on plasma HIV-1 RNA load and $CD4^+$ T-cell counts.

Materials and methods

Protein-based KD-247 binding test

The binding activity of KD-247 to recombinant proteins that expressed the V3 region was examined prior to the phase Ib study. The gene containing the V3 region in viruses extracted from patients' plasma or peripheral blood mononuclear cells (PBMCs) was amplified by a nested PCR method using first primers, 5′-ACACATG GAATTAGGCCAGT-3′ (OA-4) and 5′-AAATTCCC CTCCACAATTAA-3′ (OD-4), and second primers, 5′-GCCGGATCCTCAACTCAACTGCTGTTAAAT-3′ (EB-2) and 5′-GCTCTGCAGTCAAATTTCTGGGT CCCCTCCTGAGG-3′ (EC-2). After the purification of the amplified DNA, this segment was cleaved and inserted into a vector plasmid containing β-galactosidase (β-Gal). Separately, each cloned *Escherichia coli* with its gene sequence analysed was cultured, and the recombinant fusion protein derived from the V3 region and β-Gal (V3-Gal) was obtained. An ELISA was performed to normalize the V3-Gal concentration. The expressed V3-Gal or commercially available β-Gal (CN Bioscience, La Jolla, California, USA) as a reference standard was added to a 96-well ELISA plate immobilized with the β-Gal antibody (Chemicon International, Temecula, California, USA). Peroxidase-labelled β-Gal antibody (Rockland Immunochemicals, Limerick, Pennsylvania, USA) was used as a detecting antibody. To evaluate the reactivity of KD-247 to each V3-Gal protein, 200 ng/ml of V3-Gal was captured on a plate coated with the β-Gal antibody, followed by incubation with KD-247 (1 μg/ml) and the reactivity was detected by the peroxidase-labelled anti-human IgG antibody.

KD-1002 clinical trial

KD-1002 was a phase I, double-blind, placebo-controlled, dose-escalation, cohort study of KD-247 in asymptomatic HIV-1 seropositive individuals who did not currently need ART. The study was conducted by investigators (who enrolled patients) at 15 study centres in the USA. Eligible patients were randomized to one of three doses of KD-247 (4, 8 or 16 mg/kg) or placebo (physiological saline), and received three infusions over a 2-week period (days 1, 8 and 15). A minimum of six active and three placebo patients for each dose cohort had to complete 2 weeks of infusions. Patients in all three cohorts were followed for 12–16 weeks after the final infusion of study drug. Dose escalation could proceed only after review of the safety data up to Day 18 for all patients in the lower-dose cohort.

In addition to usual entry criteria, patients were considered eligible for participation in the study if they were asymptomatic HIV-1 seropositive individuals who at the time of study did not need ART; demonstrated an HIV-1 RNA copy number of 1000–100 000 and $CD4^+$ T-cell count more than 350 cells/μl; and who by genotyping had a sequence of the portion of the HIV envelope gene encoding the principal neutralizing determinant that is consistent with neutralization by KD-247. Plasma HIV-1 RNA samples were measured using the Roche Amplicor HIV-1 RNA assay (standard) with a dynamic range of 400–750 000 copies/ml and the Roche Amplicor Ultrasensitive plasma HIV-1 RNA assay (ultrasensitive) with a dynamic range of 50–100 000 copies/ml (Roche Diagnostic Systems, Branchburg, New Jersey, USA). The $CD4^+$ and $CD8^+$ cell counts were measured using a flow cytometer (BD FACSCanto II; BD Biosciences, Franklin Lakes, New Jersey, USA). Potential switches of coreceptor use were monitored for the 8 and 16 mg/kg cohorts by the Trofile assay (Monogram Biosciences, San Francisco, California, USA), which uses the complete gp160 coding region of the HIV-1 envelope protein.

Genotypic screening for the clinical study was performed by SRL Medisearch Inc. (Tokyo, Japan). The gene containing the V3 region in viruses extracted from patients' plasma was amplified by a nested PCR method using first primers (OA-4 and OD-4) and second primers

(EB-2 and EC-2). After purification of the amplified DNA, this segment was cloned and sequenced to determine the gene containing the V3 region. Patients were screened by V3-tip amino acid sequences deduced from the results of genotypic analyses and judged as suitable for KD-247 treatment if all 10 viral clones conformed to the reference sequences. Six sequences of V3-tip that had a GPGR sequence and high binding activity to KD-247 (XIGPGRAL, XIGPGRSF, XIGPGRTF, XIGPGRAI, XIGPGRAF and XVGPGRAL; X was not K, P and R) were selected as the reference sequences for the genotyping test (Fig. 1a and b).

The study protocol and all amendments, written study patient information, informed consent form and any other appropriate study-related information were reviewed and approved by an independent ethics committee or institutional review board at each study centre. The study was conducted in accordance with Good Clinical Practice as required by the International Conference on Harmonisation guidelines and in accordance with country-specific and/or local laws and regulations governing clinical studies of investigational products. Compliance with these requirements also constituted conformity with the ethical principles of the Declaration of Helsinki. Prior to initiation of any study procedures, an informed consent agreement explaining the procedures of the study, together with the potential risk, was read by and explained to all patients.

The trial was registered at the ClinicalTrial.gov (National Library of Medicine at the National Institutes of Health) database with the registration number NCT00917813.

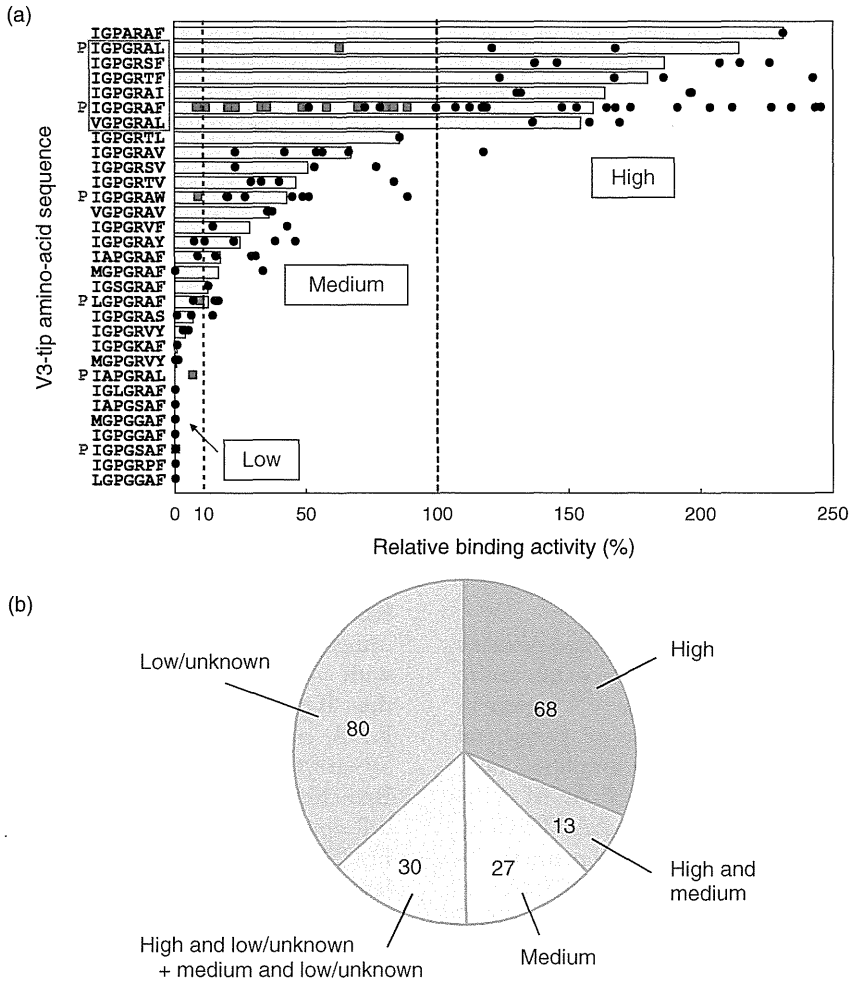

Fig. 1. Determination of reference sequences by a protein-based KD-247 binding test. (a) The binding of KD-247 to the recombinant fusion protein derived from the V3 region of HIV-1 gp120 and β galactosidase (V3-Gal) was indicated as relative activity of 100% in the case of the V3 sequence from the MN strain. The amino acid sequences of the V3-tip region in the viral clones whose mean relative KD-247 binding activity exceeded 100% were IGPARAF, IGPGRSF, IGPGRAL, IGPGRTF, IGPGRAI, VGPGRAL, and IGPGRAF. Above 100%, 10–100%, and <10% of binding activity was categorized as high, medium, and low, respectively. (b) Frequency of estimated KD-247 binding abilities using the 218 data from screened patients is shown. All 10 viral clones derived from 68 patients were estimated as high binding activity.

Pharmacokinetic analysis

Serum concentrations of KD-247 in pharmacokinetic samples were determined by ELISA using an antigen peptide [15]. The lower limit of quantitation for KD-247 was 0.2 μg/ml. Similarly, the two samples that were collected from the infusion bag were analysed for KD-247 concentration and reported as two individual concentrations. The average of the two concentrations was used for the calculation of actual total dose infused. Pharmacokinetic parameters for KD-247 were calculated from serum concentrations of the antibody by compartmental and noncompartmental methods. Actual sampling times were used for the computation of pharmacokinetic parameters. All pharmacokinetic calculations were performed using WinNonlin Professional version 5.2 (Pharsight Corp., Mountain View, California, USA) or SAS version 9.2 (SAS Institute, Cary, North Carolina, USA) or NONMEM version 6.0 (Certara USA, Inc., Princeton, New Jersey, USA).

Statistical analyses

Analyses of independent virological and immunological data were performed by two-tailed Mann–Whitney *U* tests. Statistical differences among groups were determined by performing one-way analysis of variance or the Kruskal–Wallis test with Dunn multiple comparison posthoc test. *P* value less than 0.05 was considered significant. Statistical analysis was performed using GraphPad Prism (GraphPad Software, Inc., La Jolla, California, USA).

Results

Determination of reference sequences

Prior to the phase Ib study, the binding activity of KD-247 to a protein that expressed the V3 region was evaluated, and patient selection criteria by genotyping were established (Fig. 1a). The binding of KD-247 to V3-Gal was indicated as relative activity of 100% in the case of the V3 sequence derived from a subtype B strain MN, which had the subtype B consensus sequence at the V3-tip. Relative binding activities of KD-247 and the amino acid sequence of the V3-tip of the recombinant V3-region expressing proteins were analysed using 122 HIV-1 clones derived from plasma or PBMCs. The amino acid sequences of the V3-tip region in the viral clones whose mean relative KD-247 binding activity exceeded 100% were IGPARAF, IGPGRSF, IGPGRAL, IGPGRTF, IGPGRAI, VGPGRAL and IGPGRAF, although the number of IGPARAF was only one. Most of the results using the recombinant V3 protein were in accord with the results using the short peptides by Pepscan [12]. However, a proline residue at the amino terminal of the V3-tip sequence markedly decreased the binding activity of KD-247 (Fig. 1a, red squares). The value bar of this graph indicates the mean binding activity, except for V3-Gal wherein there was a proline residue at the amino terminus. Considering the results of the examinations using V3-Gal and short peptides, and the consensus sequence of the subtype B virus, six sequences that had GPGR sequences and high binding activity to KD-247 (XIGPGRAL, XIGPGRSF, XIGPGRTF, XIGPGRAI, XIGPGRAF and XVGPGRAL; X was not K, P and R) were selected as the reference sequences of genotyping on the phase Ib clinical study.

Individual disposition

For the genotyping test for suitability, all 10 clones amplified from plasma RNA from 68 patients out of 218 matched the reference sequences corresponding to the high binding activity to KD-247 (Fig. 1b). A total of 295 patients were screened and 30 from the population with high binding activity were randomized and received study treatment, with seven receiving 4 mg/kg KD-247, six receiving 8 mg/kg KD-247, seven receiving 16 mg/kg KD-247 and 10 receiving placebo. Twenty-eight patients (93.3%) completed the study. There were no imbalances in the patient demographics that were expected to affect the data or interpretation of the results. Patient disposition and demographic and baseline information are summarized in Table 1 and Supplementary Table 1, http://links.lww.com/QAD/A629.

Safety and pharmacokinetic analysis

In general, KD-247 was well tolerated. There was no evidence of allergic or hypersensitivity reactions. Although the number of patients in each cohort was small, there was no evidence to support any hepatic, renal or cardiac toxicity. Supplementary Fig. 1, http://links.lww.com/QAD/A629 shows the phramacokinetic profiles of KD-247 for Day 1 following Infusion 1 and up to Day 99 following Infusion 3 on Day 15. All patients had concentrations above the lower limit of quantification (0.2 μg/ml) on Day 99. Dose proportionality across the dose range of 4–16 mg/kg for both Day 1 and Day 15 was observed. The systemic clearance varied from 18.3 to 22.9 ml/h, indicating that KD-247 was cleared slowly from the central compartment. Accumulation ratio as measured by Day 15/Day 1 exposure varied from 1.41 to 1.61 for C_{max} and from 1.67 to 1.78 for $AUC_{(0-\tau)}$, indicating that there was some accumulation of KD-247 following three infusions.

Effect of KD-247 infusions on plasma HIV-1 RNA load and $CD4^+$ T-cell counts

There was a trend towards moderate increase in $CD4^+$ and $CD8^+$ counts across dose cohorts (Supplementary Fig. 2a and b, http://links.lww.com/QAD/A629). The counts were not significantly higher than those for placebo. The changes in log-transformed plasma HIV-1 RNA from baseline in each cohort after Infusion 1 (a, Day 1), 2 (b, Day 8) and 3 (c, Day 15) are shown in Fig. 2. The impact of Infusion 1 was not evident for the viral load

Table 1. Patient demographics and baseline information.

Characteristic	Statistics	Patient group: Placebo ($n=10$)	KD-247 4 mg/kg ($n=7$)	KD-247 8 mg/kg ($n=6$)	KD-247 16 mg/kg ($n=7$)	Total ($n=30$)
Sex						
Percentage male	*n* (%)	90.0%	100%	100%	85.7%	93.3%
Age (years)	Mean	36.7	38.6	35.8	43.4	38.5
	SD	11.9	8.8	8.1	13.0	10.7
Weight (kg)	Mean	81.45	86.29	88.40	74.33	82.31
	SD	12.72	19.19	14.44	11.79	14.77
BMI (kg/m^2)	Mean	26.156	28.097	28.932	24.837	26.856
	SD	2.330	6.725	3.668	1.762	4.052
HIV-1 RNA (copies/ml)	Mean	15093	20226	20797	49729	25513
	SD	14404	17020	25059	28603	24335
CD4$^+$ cell count (cells/μl)	Mean	690	405	426	424	509
	SD	293	155	51	151	232
CD8$^+$ cell count (cells/μl)	Mean	823	1113	932	848	918
	SD	277	436	290	338	339
Coreceptor use[a]	R5 cases/total	6/6	NT[b]	3/5	4/5	13/16

CCR5, chemokine CC receptor 5; SD, standard deviation.
[a]Coreceptor use of plasma viruses was monitored for the 8 and 16 mg/kg cohorts by Trofile assay and expressed numbers of CCR5 use (R5) in total cases.
[b]Not tested.

reduction, and changes in plasma RNA were comparable to those in the placebo cohort in many cases (Fig. 2a). However, a moderate decrease in HIV-1 RNA was observed in the 8 and 16 mg/kg cohorts after Infusion 2, and three of six cases in the 8 mg/kg cohort and four of seven cases in the 16 mg/kg cohort showed a reduction greater than the average ± standard deviation (SD) of the placebo cohort (Fig. 2b). There was a significant reduction in HIV-1 RNA in the 8 and 16 mg/kg cohorts after Infusion 3, and five of six cases in the 8 mg/kg cohort and five of six cases in the 16 mg/kg cohort showed a reduction greater than the average ± SD of the placebo cohort (Fig. 2c). Longitudinal follow-up of HIV-1 RNA loads and log-transformed changes from baseline for each patient in all cohorts are summarized in Supplementary Table 2, http://links.lww.com/QAD/A629. The time points at which we detected a significant reduction of HIV-1 RNA load over the placebo cohort are shown in Fig. 2d and summarized in Supplementary Table 3, http://links.lww.com/QAD/A629. The changes in log-transformed plasma HIV-1 RNA from baseline in each cohort throughout the trial are shown in Fig. 2e, with additional time points that had a significant reduction in viral load. The dose proportional reduction of viral load continued for nearly 29 days, and thereafter, the level of suppression decreased with the plasma concentration of KD-247 (Fig. 2e). Although the mean profiles showed moderate decreases in viral RNA, the impact of KD-247 on individual cases was noteworthy. Among these, Case #03017 on Day 8 and Case #12044 on Day 16 achieved more than 1 $\log_{10}$ copies/ml reduction in HIV-1 RNA. The emergence of neutralization escape mutation (R315K) was observed on Day 22 for both cases (Table 2).

To clarify the impact of KD-247 on the reduction of plasma viral load, we analysed longitudinal changes in plasma concentration of KD-247 with HIV-1 RNA for the 16 mg/kg cohort (Fig. 3). We observed a reduction of HIV-1 RNA and viral-load set points in four of six cases. Case #10012 (Fig. 3a) was a typical case in which the reduction of plasma viral load was not seen on Day 1. However, reduction of HIV-1 RNA was observed at the predose of Infusion 2 on Day 8, and a further decrease was observed at Day 15. The plasma viral load remained at a lower level than baseline. Escape mutants for KD-247 were not found in this case. In contrast, Case #03017 (Fig. 3b) followed a different clinical course. Plasma viral load suppression was observed immediately after Infusion 1 and the effect persisted on Days 8 and 15. However, viral rebound was detected owing to the emergence of the neutralization escape mutants with R315K on Day 22. Case #12044 was remarkable in that the suppression of plasma viral load was observed at the predose of Infusion 2 on Day 8, and continued on Day 99 when the plasma concentration of KD-247 decreased to the lower level (Fig. 3c). We detected emergence of R315K mutation at a low frequency (1 in 10 clones) on Day 22, but the mutant was not found on Day 99 (Table 2). These results suggest that a sustained level of KD-247 blood concentration may not be necessary to control the viral load in blood.

We observed moderate suppression of plasma viral load in Case #01037 (Fig. 3d), especially after Infusion 3 on Day 15. Although the effect was marginal, the suppression persisted long after the final infusion. Viral load reduction by KD-247 was not evident for Cases #15017 and #01034 (Fig. 3e and f, respectively), although temporal suppression was observed after Infusion 3 on Day 15. The

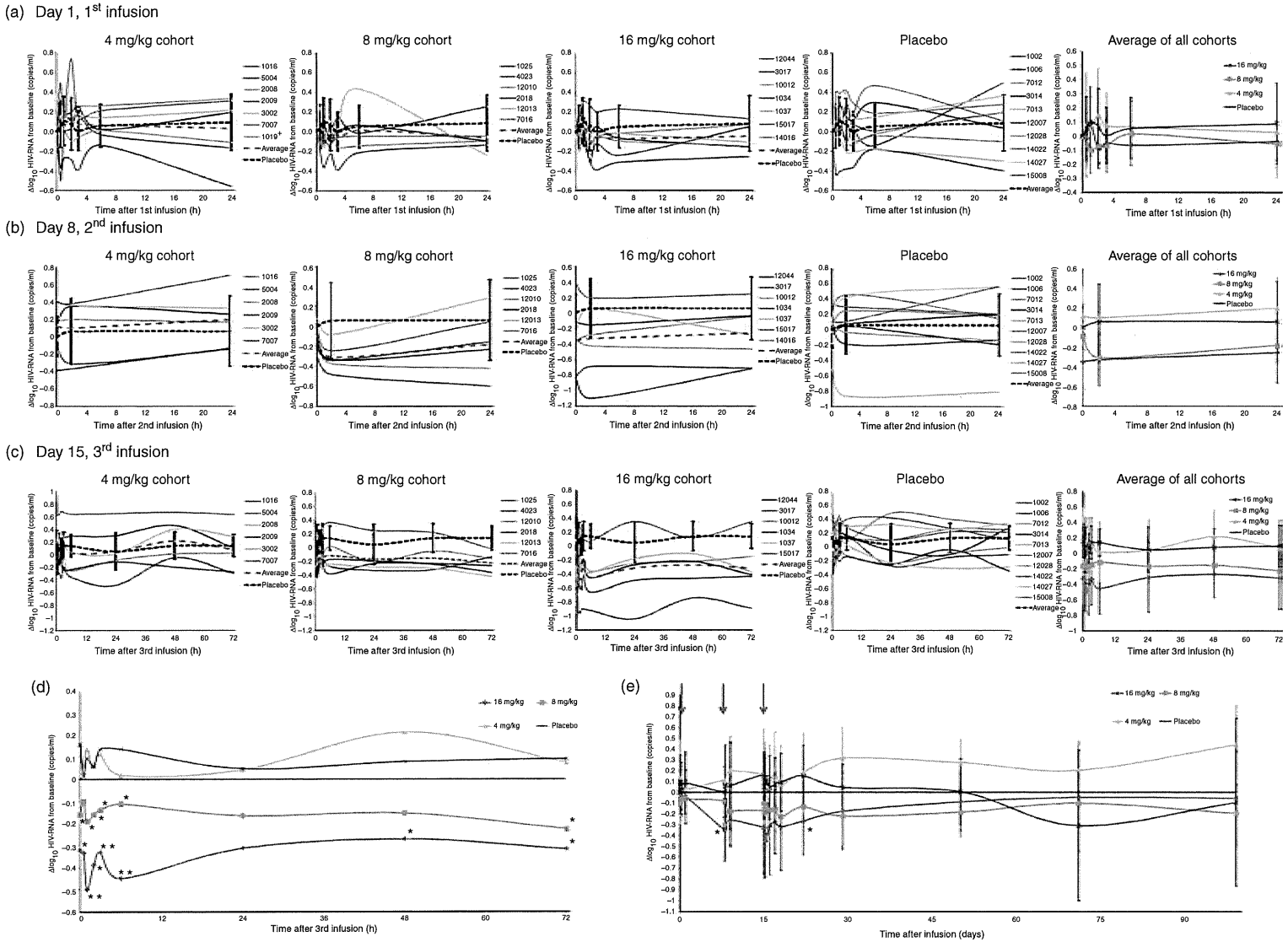

Fig. 2. Impact of three infusions of KD-247 on plasma HIV-RNA in each cohort. Changes in log-transformed plasma HIV-1 RNA from baseline in each cohort after Infusion 1 (a, Day 1), 2 (b, Day 8), and 3 (c, Day 15) of KD-247 are shown with average ± standard deviation (SD) of all cohorts. Each line represents a single patient. Black dotted line shows average ± SD of that observed for the placebo cohort, and red broken line shows the geometric mean changes for each treatment cohort. The average ± SD of the changes in plasma viral load in each cohort are shown with colors: red for 16 mg/kg, blue for 8 mg/kg, green for 4 mg/kg, and purple for placebo. The time points of significant reduction of HIV-1 RNA load are indicated in (d), which corresponds to the time points after Infusion 3, when most of the difference was observed. Changes in plasma HIV-1 RNA from baseline in each cohort throughout the trial are shown in (e). Black dotted line shows the zero level for changes in (e) and (d). Red arrows represent days of infusions. Significance was determined by two-tailed Mann–Whitney U tests. $^{*}P < 0.05$, $^{**}P < 0.01$.

Table 2. Emergence of KD-247 neutralization escape and mismatched variants.

Patient group	Cohort	Patient	Variations of the V3-tip sequence (number of clones)[a]		
			Screening	FU1 (Day 22)	FU5 (Day 99)
Placebo	3	12028	HIGPGRAF (10)	HIGPGRAF (10)	HIGPGRAF (9) HISPGRAF (1)
	3	15008	SIGPGRAF (10)	SIGPGRAF (10)	PIGPGRAF (10)
4mg/kg	1	02009	SIGPGRAF (10)	PIGPGRAF (6) TMGPGRVF (3) PIGPGIMQ (1)	TMGPGRVF (4) PIGPGRAF (3) SIGPGRAF (3)
	1	07007	HIGPGRAF (10)	HIGPGRAF (10)	HIGPGRAF (5) HIGPGRAV(5)
8mg/kg	2	07016	SIGPGRAF (10)	SIGPGRAF (3) TIGPGRAF (3) NIGPGRAF (2) PIGPGRAF (2)	TIGPGRAF (8) SIGPGRAF (1) PIGPGRAF (1)
16mg/kg	3	03017	TIGPGRAF (10)	NMGPGRAF (5) TIGPGKAF (5)	NMGPGRAF (8) TIGPGKAF (2)
	3	12044	HIGPGRAF (10)	HIGPGRAF (9) HIGPGKAF (1)	HIGPGRAF (8) PIGPGRAF (2)

[a]Red letters indicate mismatched variants including escape mutation of R315K.

data suggested that the selection process of the patients appropriate for KD-247 infusion only by V3 genotyping was a limitation. Some primary isolates with reference V3 sequences have a resistance phenotype to KD-247; therefore, involvement of outside V3 for resistance to KD-247 may have accounted for the lack of response [16,17].

Emergence of resistant mutants or mismatched variants

The genotyping test performed for the follow-up samples revealed the emergence of resistant mutants or mismatched variants in seven patients, including two in the placebo cohort (Table 2). Potential switches of coreceptor use were monitored for the 8 and 16 mg/kg cohorts by the Trofile assay. Dual/mixed virus populations of HIV-1 isolates were found in three patients on Day 1. No tropism shifts were observed in the placebo group. Only two patients in the 8 mg/kg cohort had tropism shifts during the study. None of the patients with a tropism shift had significant antiviral response (Supplementary Table 4, http://links.lww.com/QAD/A629).

Discussion

In this phase Ib study, KD-247 was well tolerated and we observed significant decreases in HIV RNA in the 8 and 16 mg/kg KD-247 cohorts. We observed reduction of HIV-1 RNA and viral load set-point in four of six cases in the 16 mg/kg cohort, and long-term suppression of viral load in one patient, despite a significant decrease in plasma concentration of KD-247. It may be necessary to raise the blood concentration of KD-247 to a high level to achieve the initial suppressive effect on viral load. However, maintenance of blood concentration of the antibody may not be essential for a prolonged effect on viral load. In a previous animal model study, KD-247 was administered weekly eight or nine times to monkeys after challenge with pathogenic SHIV. The effects of KD-247 were observed in the lymph node compartment rather than the peripheral blood. The effects of KD-247 on $CD4^+$ T cells in the lymph nodes were observed in a monkey who was unable to maintain the blood concentration of KD-247 because of the emergence of antiidiotype antibody to KD-247 [15]. The observation may partly relate to the prolonged effect of KD-247.

Long-term suppression of viral load observed in one patient (Case #12044) despite a significant decrease in plasma concentration of KD-247 may have interesting implications. Recently, Barouch *et al.* [8] demonstrated the profound therapeutic efficacy of PGT121 and PGT121-containing mAb cocktails in rhesus monkeys chronically infected with SHIV-SF162P3. Virus rebounded in most animals when serum mAb titres declined to undetectable levels, although a subset of animals maintained long-term virological control in the absence of further mAb infusions. Direct antibody-mediated cytotoxic effects on cells chronically infected with HIV-1 were suggested in a humanized mouse model [18]. The phenomenon may be relevant to that observed for Patient #12044 in the present study. The prolonged impact of the neutralizing mAb may partly be owing to the effects other than neutralization, such as antibody-dependent cellular cytotoxicity (ADCC) and antibody-dependent cell-mediated virus inhibition (ADCVI) that can attack virus-producing cells. The importance of nonneutralizing effector activities of bnAbs *in vivo* has been reported in mouse models [19]. Although it is difficult to evaluate ADCC and ADCVI *in vivo*, these

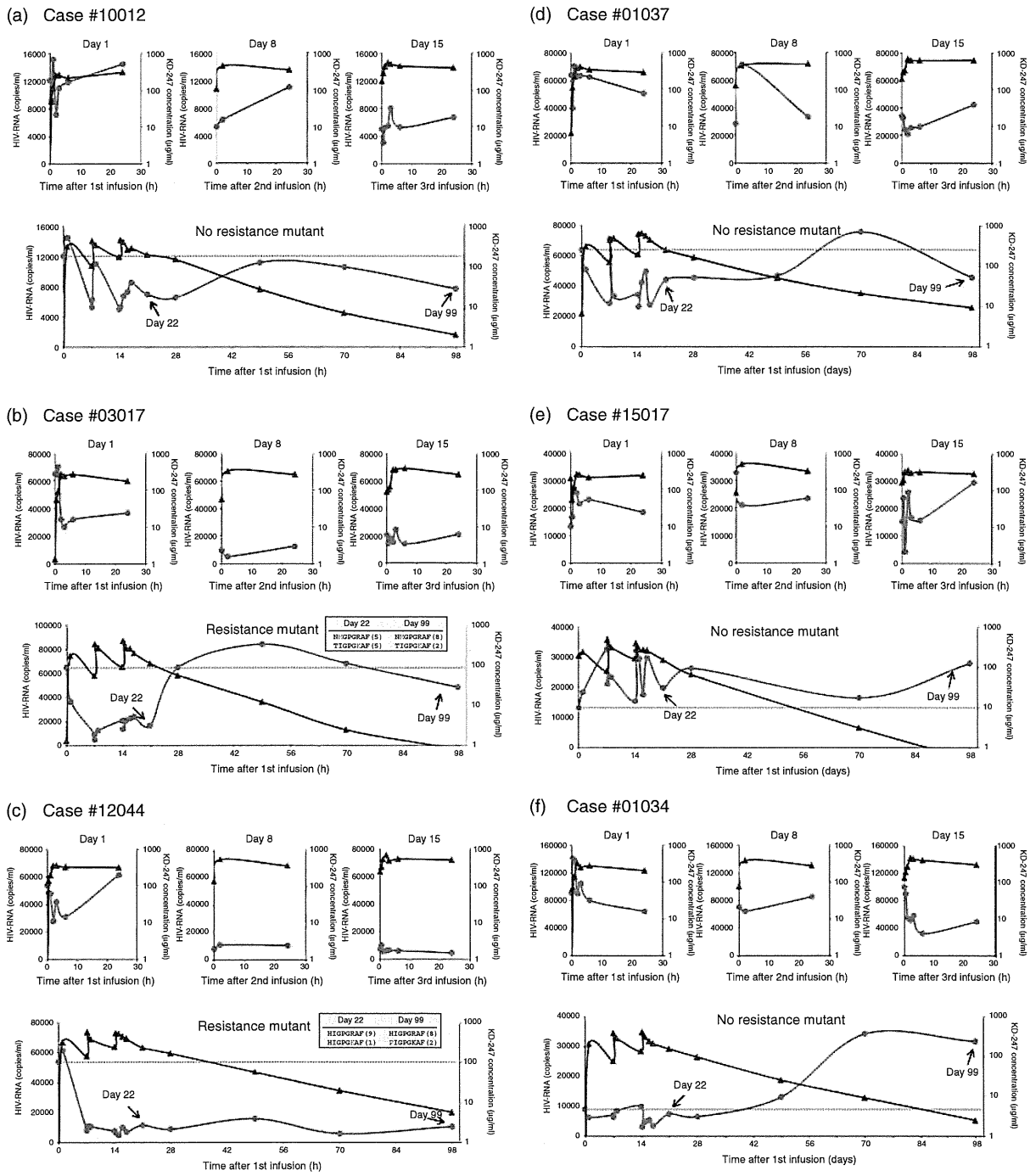

Fig. 3. Longitudinal analysis of HIV-1 RNA reduction and plasma concentration of KD-247 for 16 mg/kg cohort. Plasma concentration of KD-247 is shown as blue triangles with three peaks in an earlier period corresponding to the three infusions of antibody. Plasma HIV RNA is shown as red circles. Emergence of KD-247 resistance mutants with R315K was indicated on Days 22 and 99.

FC-receptor mediated functions were detected for KD-247 *in vitro* (Supplementary Fig. 3, http://links.lww.com/QAD/A629). In addition, secondary immunological responses following viral degradation in antigen-presenting cells by antibody-dependent phagocytosis may have an impact on host antiviral immune responses, including HIV-specific $CD8^+$ T cells, as suggested by the animal model [8]. The enhancement of cell-mediated immunity may in part account for the apparent reduction of viral load set-points after viral rebound from the baseline. We previously reported a KD-247 escape mutant with R315K that showed a less-fit phenotype as compared with the wild-type virus [20]. Although subsequent recovery of the fitness was observed with additional

mutations, fitness cost of the escape mutants may have contributed in part to the reduction of HIV-1 RNA in patients with R315K mutation.

The data in the present clinical trial together with recent studies in animal models [7–9,18] may have an implication for future combination therapy because passive transfer of KD-247 had a significant effect on HIV-1 replication in chronically infected patients. We reported that the neutralization escape mutants to KD-247 became sensitive to chemokine CC receptor (CCR)5 inhibitors [21]. Conversely, resistance mutants to a CCR5 inhibitor, maraviroc, became sensitive to several neutralizing mAbs including KD-247 [22]. Furthermore, a series of in-vitro experiments suggested synergistic effects of the combination of KD-247 and CCR5 antagonists including maraviroc ([21], unpublished observation by S.M. and K.Y.). In view of such a complementary nature of resistance, combination therapy using KD-247 and CCR5 inhibitors warrants future clinical trials. The current results may also imply limitations of monotherapy with conventional antibodies such as KD-247. New-generation bnAbs, especially used in combination, are better candidates for antibody-based treatment in terms of potency and breadth of action. KD-247 may have a role in patients infected with certain viruses that match for neutralization. Combination of KD-247 with certain $CD4^+$-mimetic compounds that markedly enhances the neutralization/binding activity of the antibody may also deserve further investigation [23,24].

Results of this clinical trial should be interpreted with caution because of the small sample size. However, current data and the results from recent primate models taken together warrant further clinical trials of neutralizing mAbs in several different settings with or without ART [25,26].

Acknowledgements

S.M., K.Y. and T.M. designed the study. K.P.R. conducted some of the in-vitro assays for KD-247, including ADCC and ADCVI. J.P. and S.M. led the statistical analysis of the clinical trial. S.M. led the studies and wrote the article with all coauthors. In addition to the authors, the KD-1002 study group includes the following investigators and contributors to the design, conduct or analysis of the study: Principal investigators: E. DeJesus, M. Markowitz, G. Richmond, M. Thompson, R. Liporace, P. Ruane, C. Brinson, K. Staszkow, J. Gathe, Jr., A. Scribner, S. Shoham, H. Marcelin, R. Redfield, T. Sligh and A. Scarsella; and the KD-1002 Protocol Team of Quintiles: E. Vigdorth, J. Bush, C. Gibson G. Breed, D. Despard, P. Ajiboye, B. Tedrow, P. Udeshi, J. Hoglind, R. Rao, R. Kalmadi and A. Armitage.

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Conflicts of interest

S.M., K.Y. and K.P.R. declare no competing financial interests. J.P. is an employee of Quintiles Inc. T.M. is an employee of the Chemo-Sero-Therapeutic Research Institute (Kaketsuken). Kaketsuken paid Quintiles to conduct the clinical trial and analyse the results of the study. The authors have no competing interests or other interests that might be perceived to influence the results and/or discussion reported in this article.

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Complementary and synergistic activities of anti-V3, CD4bs and CD4i antibodies derived from a single individual can cover a wide range of HIV-1 strains

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ABSTRACT

Antibodies with modest neutralizing activity and narrow breadth are commonly elicited in HIV-1. Here, we evaluated the complementary and synergistic activities of a set of monoclonal antibodies (MAb) isolated from a single patient, directed to V3, CD4 binding site (CD4bs), and CD4 induced (CD4i) epitopes. Despite low somatic hypermutation percentages in the variable regions, these MAbs covered viral strains from subtypes B, C, A and CRF01_AE and transmitted/founder viruses in terms of binding, neutralizing and antibody-dependent cell-mediated cytotoxicity (ADCC) activities. In addition, a combination of the anti-V3 and CD4bs MAbs showed a synergistic effect over the neutralization of HIV-1_{JR-FL}. A humoral response from a single patient covered a wide range of viruses by complementary and synergistic activities of antibodies with different specificities. Inducing a set of narrow neutralizing antibodies, easier to induce than the broadly neutralizing antibodies, could be a strategy for developing an effective vaccine against HIV-1.

Introduction

Despite the great advances in the treatment of HIV-1 infection, there are still major obstacles to effective control of HIV-1 infection. Active replication persistence and immune activation under suppressive highly active antiretroviral therapy (HAART) (Buzon et al., 2010; Palmer et al., 2008; Richman et al., 2009), secondary effects of the drugs (Montessori et al., 2004; Reust, 2011), and the socio-economic burden of long-term treatment (Boyer, 2009; Naik et al., 2009) are still present; making the development of a protective vaccine desirable. Neutralizing antibodies are an important component of a protective vaccine-induced immune responses and much effort has been focused on the development of broadly neutralizing antibodies against conserved epitopes on the functional Env trimer of HIV-1 (Bonsignori et al., 2011; Corti et al., 2010; Walker et al., 2009).

Advances in antibody technology have uncovered broadly neutralizing Abs (bNAbs) (Marasco and Sui, 2007; Zhu et al., 2013; Zuo et al., 2011) and their efficacy has been proved in non-human animal models. Protection from infection by Simian immunodeficiency virus (SIV) was correlated with the humoral response produced after vaccination with Env and/or Gag and Pol of rhesus macaques (Barouch et al., 2013; Roederer et al., 2014). Protection was also observed in rhesus macaques vaccinated with Env derived peptides and challenged with chimeric simian-human immunodeficiency viruses (SHIV) $SHIV_{162P3}$ and $SHIV_{C2/1}$ (DeVico et al., 2007; Eda et al., 2006a). Passive administration of antibodies was also proved useful in protecting for and controlling SHIV and HIV-1 infection. In rhesus macaques chronically infected with $SHIV_{162P3}$, passive administration of bNAbs (PGT121, 3BNC117 and b12 combined or alone) reduced viral load and resulted in control of the infection (Barouch et al., 2013; Ng et al., 2010). Similar results were observed in humanized mice chronically infected with HIV-1_{YU2} after the passive administration of bNAbs 45–46^{G54W}, PG16, PGT128, 10-1074 and 3BC176 (Klein et al., 2012). Passive administration of MAbs PGT121, b12, 2G12, 2F5 and 4E10 also offered protection from infection with SHIV (Hessell et al., 2010, 2009a, 2009b; Mascola et al., 2000, 1999; Moldt et al., 2012; Parren et al., 2001) even when the antibody (b12) was administered topically (Veazey et al., 2003); or when the administered antibodies were purified IgG from infected chimpanzees (Shibata et al., 1999).

It has been proposed that an immunization strategy that could elicit such antibodies would be protective in humans (Stamatatos

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et al., 2009); however, to date there is no vaccine that induces their production.

In naturally infected HIV-1 patients, bNAbs are not commonly produced; instead, antibodies are often directed against strain-specific or non-neutralizing sites in Env (Burton et al., 1991; Corti et al., 2010). Only 10 to 25% of HIV-1-infected individuals generate neutralizing antibodies, and a minority of these individuals, approximately around 1%, is considered elite neutralizers, besides, bNAbs appear late (1 to 3 years) after infection (Binley et al., 2008; Deeks et al., 2006; Dhillon et al., 2007; Doria-Rose et al., 2010, 2009; Gray et al., 2011; Sather et al., 2009; Simek et al., 2009) and frequently harbor uncommon characteristics which probably pose obstacles to their generation, including high levels of somatic mutations, long heavy-chain complementarity-determining regions 3 (CDRH3s), frequent insertions or deletions, and high levels of polyreactivity (Haynes et al., 2012b; Huber et al., 2010; Klein et al., 2013; Scheid et al., 2011; Sok et al., 2013; Xiao et al., 2009). Moreover, when the immunoglobulin sequences of bNAbs are experimentally reverted to their germline precursors, as they are found on naive B cells, binding to HIV-1 Env is often significantly diminished or even completely abrogated (Bonsignori et al., 2011; Haynes et al., 2012b; McGuire et al., 2014; Scheid et al., 2011; Wu et al., 2011; Xiao et al., 2009). This suggests difficulties in inducing bNAbs in HIV-1-infected patients and also by vaccination, because many rounds of affinity maturation are required which means that immunizations should be repeated many times as well.

Antibodies to the V3 loop, CD4bs and CD4i have been produced by HIV infection or vaccination, but neutralization by these antibodies is generally not broadly effective for preventing HIV-1 infection because of steric constraints blocking the access of these antibodies to the epitopes, and mutations in their epitopes that allow to escape from these antibodies. However, these modest neutralizing antibodies appear faster after infection (even as early as 2 weeks after sero-conversion) and are also capable of exert pressure over the virus (Bar et al., 2012; Haynes et al., 2012b; McGuire et al., 2014; Overbaugh and Morris, 2012; Pollara et al., 2014).

Besides neutralization, non-neutralizing responses, specifically the ADCC activity has been associated with protection from HIV. The most remarkable case is the RV144 trial result, which showed a 31.2% of vaccine efficacy (Rerks-Ngarm et al., 2009) and it has been proposed that the ADCC activity of V1/V2 antibodies induced by the vaccine may be the most important correlation for protection (Haynes et al., 2012a; Rerks-Ngarm et al., 2009; Wren et al., 2012). Vaccination in animal models has shown similar results (Hessell et al., 2007; Xiao et al., 2010) and it has also been reported that broader ADCC responses correlate with long-term control of HIV, slow progression of disease and lower viremia (Nag et al., 2004; Wren et al., 2013; Xiao et al., 2010).

It is certainly desirable for HIV-vaccines to induce antibodies that neutralize global isolates of diverse subtypes. However, in view of the difficulty in inducing bNabs in uninfected subjects, the induction of a complementary set of antibodies with limited neutralizing activity may be an attainable alternative approach. We have been following a single patient infected with HIV that has a cross-neutralizing activity to a variety of HIV-1 isolates including a panel of clinical isolates belonging to subtypes B, C, CRF01_AE and A. The patient is a hemophiliac who has been infected with HIV-1 for more than 25 years without any antiretroviral treatment. To elucidate the mechanism to control viruses in this patient we established a series of MAbs and demonstrated that a combination of antibodies to the V3 loop, CD4bs and CD4i covered effectively a wide range of viruses by their complementary and synergistic activities.

Results

Isolation and classification of monoclonal antibodies from an HIV-1 infected patient with long-term non-progressive disease

A total of 1718 B-cell clones were established by Epstein-Barr virus (EBV) transformation from the patient KTS376 who has had controlled HIV-1 infection for more than 25 years without any

Table 1
Subclass, target and genetic characteristics of human monoclonal antibodies against HIV-1 obtained from a patient with non-progressive disease.

No	Clone	Subclass	Target	Gene usage		Somatic mutation (%)		CDRH3 length
				VH	VL	VH	VL	
1	0.5γ (1C10)	IgG1κ	V3	VH3-30	VK2-28	10.8	4.1	18
2	1D9	IgG1κ	V3	VH3-30	VK2-28	12.8	3.5	16
3	5G2	IgG1κ	V3	VH3-30	VK2-28	12.8	6.5	16
4	16G6	IgG1λ	V3	VH5-51	VL3-19	4.9	6.4	7
5	717G2	IgG2κ	V3	VH3-30	VK2D-29	10.8	7.1	21
6	2F8	IgG1λ	V3	–	–	–	–	–
7	3E4	IgG1κ	V3	–	–	–	–	–
8	3G8	IgG1κ	V3	–	–	–	–	–
9	42F9	IgG1κ	CD4bs	VH3-20	VK1-39	2	2.5	19
10	49G2	IgG1λ	CD4bs	VH1-18	VL1-44	5.9	1.8	22
11	82D5	IgG1λ	CD4bs	VH1-18	VL1-44	6.2	1.7	22
12	0.5δ(3D6)	IgG1λ	CD4bs	–	–	–	–	–
13	4E3	IgG1κ	CD4bs	–	–	–	–	–
14	7B5	IgG2λ	CD4bs	–	–	–	–	–
15	4E9C	IgG1κ	CD4i	VH1-69	VK3-15	6.6	1.8	22
16	916B2	IgG1λ	CD4i	VH1-69	VL7-46	8.7	5.9	16
17	917B11	IgG1λ	CD4i	VH1-69	VL1-51	5.9	2.8	28
18	4C11	IgG1λ	CD4i	–	–	–	–	–
19	5D6S	IgG1κ	CD4i	VH1-69	VK3-20	9.3	9.6	26
20	7F11	IgG2κ	CD4i	–	–	–	–	–
21	5E8	IgG2κ	–	–	–	–	–	–
22	7B9N	IgG3κ	–	–	–	–	–	–
23	9F7	IgG1κ	–	–	–	–	–	–
24	39D5	IgG3κ	–	–	–	–	–	–
25	43D7	IgG2κ	–	–	–	–	–	–

VH: Variable heavy chain. VL: Variable light chain. CDRH3: Third complementary determinant region of the heavy chain. Not determine.

antiretroviral treatment. Out of these B cell clones, we identified 25 clones continuously producing MAbs reactive to gp120 (Table 1). First, MAbs were examined for their reactivity to the V3-peptide corresponding to the V3-region of the $gp120_{JR\text{-}FL}$ (NNT20) and the reactive MAbs, 0.5γ, 1D9, 2F8, 3E4, 3G8, 5G2, 717G2 and 16G6, were classified as anti-V3 antibodies. Later, using a set of peptides that have different V3 sequences and overlapping short peptides, we identified the minimum epitope and the cross-reactivity of these antibodies (Supplementary Table 1). The reactivity of these MAbs to short peptides was decreased, and only 1D9 and 5G2 bound to 10 mer peptides. Although 2F8 did not recognize any overlapping short peptides, this MAb was capable to bind to the V3 peptide from NSI, correspondent to the CRF01_AE subtype.

MAbs other than anti-V3 were classified in three groups according to the effect of soluble CD4 (sCD4) on the reactivity to gp120: CD4bs, CD4i and other epitopes (Figs. 1 and 2). MAbs, 0.5δ, 4E3, 7B5, 42F9, 49G2 and 82D5, were classified as CD4bs antibodies according to the reduction of reactivity in the presence of sCD4. MAbs, 4C11, 4E9C, 5D6S, 7F11, 916B2 and 917B11, were classified as CD4i antibodies according to the enhancement effect by sCD4. The rest of MAbs, which did not react to the V3 peptide and did not show enhancement or inhibition by sCD4, were classified as MAbs to other epitopes. Anti-V3 MAb, KD-247 (Eda et al., 2006a), CD4bs MAb, b12 (Burton et al., 1991) and CD4i MAbs, 17b (Thali et al., 1993) were also analyzed as controls.

For the anti-V3 antibodies, no influence in their binding to monomeric gp120 was noted in the presence of sCD4 when analyzed by ELISA (Fig. 1). However, the enhanced reactivity by sCD4 was observed against Env on the cell surface in most of anti-V3 MAbs (Fig. 2). This is consistent with the previous reports (Huang et al., 2005; Thali et al., 1993), which showed that the binding of CD4 to gp120 caused the V3 to protrude and became more available, particularly in the strains that use the CCR5 co-receptor. Although a reduction of reactivity was observed for the CD4bs MAbs in ELISA, this reduction of reactivity against trimeric Env was not obvious in the MAbs, such as 4E3 and 49G2 (Fig. 2). The enhanced reactivity by sCD4 was observed in all the CD4i MAbs, both in ELISA and flow cytometry analysis (Figs. 1 and 2) as previously reported for the CD4i MAbs (Lusso et al., 2005; Mbah et al., 2001; Wu et al., 2008). The MAbs to other epitopes did not show reactivity to trimeric Env, suggesting that these MAbs recognized the unexposed region of the Env trimer (Fig. 2).

Genetic characterization of MAbs

Generally, gp120 epitope reactivity is mediated by IgG1, although IgG2 can also be found (Banerjee et al., 2010). MAbs predominantly consisted of IgG1. IgG3 was observed only in the "other epitope" group, and none of the antibodies isolated was IgG4 (Table 1). Representative MAbs were genetically cloned, and gene usage, somatic mutation percentage and CDRH3 length was determined (Table 1). Anti-V3 antibodies showed a marked preference of the usage of the VH3-30 gene for the variable region of the heavy chain (VH) and VK2-28 for the variable region of the light chain (VL); and only the MAb 16G6 used the VH5-51 gene and λ light chain, which were previously reported as preferential gene usage by anti-V3 antibodies (Gorny et al., 2009). All the anti-V3 antibodies analyzed had the V to I substitution in position 55 (IMGT unique numbering) of FR2 (Supplementary Fig. 1). MAbs, 1D9 and 5G2, used the same genes and the length of CDRH3 was also the same among them. These characteristics, as well as the close similarity in their sequences (Supplementary Fig. 1), suggested that these two MAbs originated from a common ancestor. In contrast, 0.5γ, which used the same genes as 1D9 and 5G2, was considered as from another lineage, because 0.5γ had the CDRH3 different from 1D9 and 5G2 in terms of length and sequences (Table 1 and Supplementary Fig. 1). Two of the three CD4bs MAbs used the same genes, VH1-18 and VL1-44, suggesting that these MAbs had the same origin. All four of the CD4i MAbs analyzed used the VH1-69 gene, which is consistent with previous reports (Gorny et al., 2009; Huang et al., 2004), but did not use the same light chain gene. This indicates that CD4i antibodies with the VH1-69 gene were

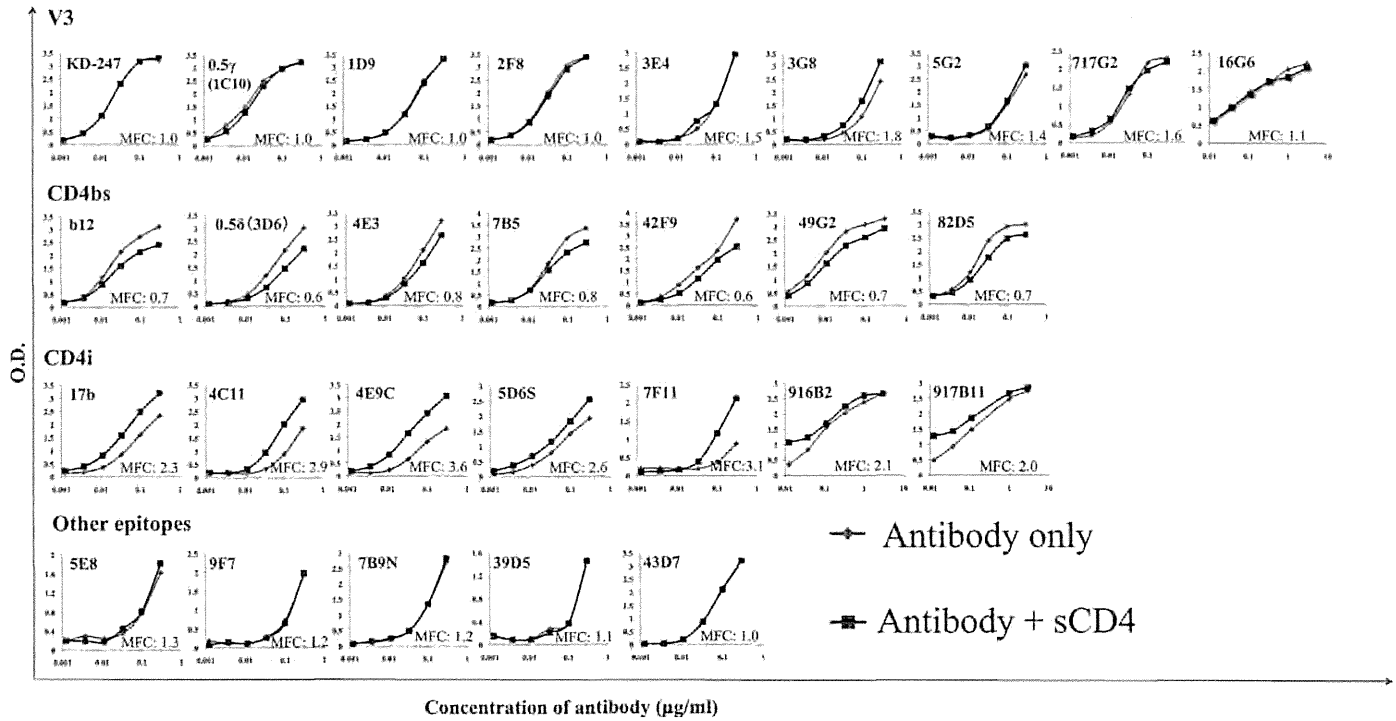

Fig. 1. Effect of sCD4 over binding of MAbs isolated from patient KTS376 to monomeric $SF2_{gp120}$. Reactivity to gp120 was examined for each MAb alone (gray diamond) or in the presence of sCD4 (black square) by capture ELISA assay. No effect was observed for MAbs to V3 and "other epitopes". Meanwhile, inhibition of binding was observed for MAbs to CD4bs and enhancement of binding was observed for MAbs to CD4i epitope. Maximum fold change (MFC) was calculated as follows: O.D. sCD4 positive/ O.D. sCD4 negative.