



Original Article

A model-based comparative meta-analysis of the efficacy of dolutegravir-based and efavirenz-based regimens in HIV-infected patients[☆]



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ABSTRACT

Currently, combinations of typical types of antiretroviral agents have been adopted as chemotherapy for human immunodeficiency virus (HIV) infection, comprising two nucleoside analogue reverse transcriptase inhibitors plus one of a non-nucleoside reverse transcriptase inhibitor, an integrase strand-transfer inhibitor, and a protease inhibitor. Although several meta-analyses have been conducted to determine first-line combination antiretroviral therapy, this has yet to be confirmed due to the technical limitation associated. In the present study, we applied a model-based meta-analysis (MBMA) approach, because it allows integration of information from clinical trials with varying dosing, duration, and sampling time points, resulting in enlargement of available data sources. We performed a bibliographic search to identify clinical trials involving dolutegravir (DTG)-based and efavirenz (EFV)-based regimens in HIV-infected, antiretroviral therapy-naïve adults, and then identified 30 independent trial data. The time course of drug effect was described by a consecutive first-order kinetic model and analyzed using the nonlinear mixed effect modeling approach. The developed model suggests that the DTG-based regimen provides a faster-acting and more sustainable drug effect than the EFV-based regimen. Moreover, the drug effect tends to appear more slowly and decay faster in severe patients having higher viral load or smaller baseline CD4 count.

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1. Introduction

Since the first discovery of acquired immunodeficiency syndrome (AIDS) in 1981, the number of human immunodeficiency virus (HIV)-infected patients has been unceasingly increasing, as accounting for approximately 36.9 million people in 2017 [1]. Although no fundamental solutions have been established to date, recent progress in anti-HIV therapy has changed the prognosis of the disease from lethal to chronic illness. Currently, combinations of typical types of antiretroviral agents have been adopted as

chemotherapy for HIV infection, which consist of two nucleoside analogue reverse transcriptase inhibitors (NRTI) plus one of a non-nucleoside reverse transcriptase inhibitor (NNRTI), an integrase strand-transfer inhibitor (INSTI), and a protease inhibitor (PI).

It is known that selection of initial antiretroviral therapy is critical in determining successful long-term virologic suppression [2]. Efavirenz (EFV), a non-nucleoside reverse transcriptase inhibitor, had been used as a key drug of the first-line combination regimen for many years until the advent of integrase strand transfer inhibitors [3]. Particularly, epoch-making change occurred with the approval of dolutegravir (DTG), which overcame the issue of rapid drug resistance development [4,5]. Within two years after the approval in 2013, the Department of Health and Human Services (DHHS) and the European AIDS Clinical Society (EACS) started to recommend DTG-based regimens as the first-line combination

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antiretroviral therapy [6,7]. Nowadays, EFV is hardly used in developed countries, but a considerable amount of EFV is still being used worldwide [8]. In fact, it was only very recently that the World Health Organization (WHO) gave DTG a higher priority than EFV [9].

Superiority of DTG-based regimens to other key drugs has been demonstrated by systematic reviews and their analyses. Rutherford et al. [10] conducted a meta-analysis to compare efficacy of DTG-based and EFV-based regimens in HIV-infected, combination antiretroviral therapies-naïve adults. They demonstrated that DTG-based regimens appear to be superior to EFV-based regimens in terms of durable viral suppression, absence of resistance, and immunologic recovery. However, the number of trials that allow a direct comparison of efficacy of DTG-based and EFV-based regimens is limited and the meta-analysis of Rutherford et al. [10] covers only two clinical trials. Network meta-analysis, which allows to estimate relative efficacy indirectly from head-to-head study results, has also been adopted to antiretroviral therapies [11,12]. The results have supported superiority of the use of DTG in HIV-1-infected treatment-naïve patients. However, these analyses are subject to the limitation of only being applicable to static data at fixed time points (e.g., 48-week or 96-week efficacy).

In recent years, increasing attention has been paid to model-based meta-analysis (MBMA) [13,14]. MBMA differs from conventional meta-analysis in terms of dealing with time-series data. By defining a therapeutic response as a function of time, MBMA facilitates the integration of information from clinical trials varying the dosing, duration, and sampling time points [14]. These attractive features prompted us to apply MBMA to compare therapeutic efficacy in HIV-infected patients between DTG-based and EFV-based regimens. In the present study, we refined information of 30 clinical trials through a systematic review and analyzed the compiled data by MBMA. The analysis would quantitatively delineate clinical and programmatic advantages of DTG-based regimens in combination antiretroviral therapies settings.

2. Materials and methods

2.1. Data sources and searches

The present analysis was performed in accordance with the preferred reporting items for systematic reviews and meta-analyses (PRISMA) guidelines [15] and methods described in the Cochrane Handbook [16]. PubMed, Cochrane Central Register of Controlled Trials (CENTRAL), and clinicaltrials.gov were systematically searched to identify randomized controlled trials (RCTs) that evaluated efficacy of DTG-based and EFV-based regimens in treatment-naïve HIV-1 patients. Search terms for DTG were chosen with reference to the report of Rutherford et al. [10], while those for EFV were taken from the report of Kryst et al. [17].

2.2. Inclusion and exclusion criteria

RCTs were retrieved that targeted to either or both of DTG + two NRTIs and EFV + two NRTIs in HIV-infected, combination antiretroviral therapies-naïve adults aged ≥ 16 years and defined proportion of participants with viral load of < 50 copies/mL in plasma as drug effect. Studies were excluded in which; participants were pregnant or tuberculosis co-infected; the number of participants in the arm was lower than 10; and arms were not separated with individual dosage regimens. Concomitant NRTIs were restricted to any two of abacavir (ABC) + lamivudine (3TC), tenofovir disoproxil fumarate (TDF) + emtricitabine (FTC), or TDF + 3TC, which have been widely used as a part of first-line combination antiretroviral therapies.

2.3. Data extraction

We imported search results into a bibliographic citation management software (Refworks 2.0, ProQuest LLC, Ann Arbor, MI) and excluded duplicated references. We initially screened the articles based on their title and abstract, and subsequently reviewed the full-text of each selected paper to extract all the necessary information and to verify if the inclusion criteria were met.

2.4. Model analysis

The time course of drug effect (E) was mathematically described by assuming its onset and decay to obey a consecutive first-order kinetics;

$$E = \hat{E} + \sqrt{\hat{E}(1 - \hat{E})/N} \cdot \varepsilon$$

$$\hat{E} = E_{max} \cdot \left(1 - e^{-k_o \cdot (t - t_{lag})}\right) \times e^{-k_d \cdot (t - t_{lag})}$$

$$k_o = \hat{k}_o \cdot e^{\eta_{ko}}$$

$$k_d = \hat{k}_d \cdot e^{\eta_{kd}}$$

where E_{max} is the maximum drug effect; k_o is the onset rate constant; k_d is the decay rate constant; t_{lag} is the time lag prior to the onset; N is the number of patients in the study; η_{ko} and η_{kd} are inter-study variabilities, having a normal probability distribution with mean 0 and variance $\omega_{k_o}^2$, $\omega_{k_d}^2$, respectively. ε is a random residual error, having a normal probability distribution with mean 0 and variance σ^2 . Considering that E is restricted to the range between 0 and 1, ε was weighted with the standard deviation around fitted values. The model-based analysis was conducted using nonlinear mixed effects modeling with NONMEM software, version 7.3, ICON Development Solutions, Hanover, MD. The models were run with the first-order conditional estimation with interaction (FOCE-I).

Visual predictive checks were performed using 10,000 datasets from original data, and 90% confidence interval (CI) and mean of each regimen were calculated. Bootstrap was performed 1000 times to determine the median and the 95% CI of the parameter estimates.

3. Results

3.1. Data collection

Fig. 1 depicts the PRISMA flow diagram. The literature search in Pubmed, CENTRAL, and clinicaltrials.gov yielded 2622 records. Following duplication removal, abstract screening, and full-text screening, 104 publications remained. The remaining studies contained 30 trials in total, of which 5, 9, 16, and 3 trials dealt with DTG + ABC+3TC, EFV + ABC+3TC, EFV + TDF + FTC, and EFV + TDF+3TC regimens, respectively [18–48].

3.2. Model construction and validation

Assuming that the onset and decay of drug effect obeys sequential first-order kinetics with inter-study variability, nonlinear mixed effect modeling was performed. Table 1 summarizes parameter estimates for the base model. The model equations fitted reasonably to observed data (Fig. 2), where drug effect increased in a time-dependent manner before it gradually decayed.

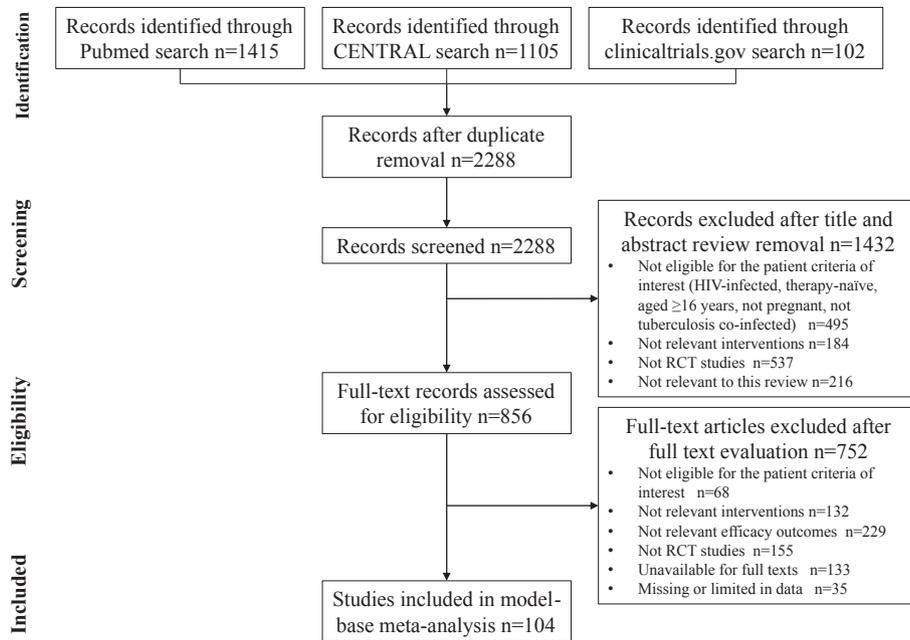


Fig. 1. PRISMA statement 2009 flow diagram. The diagram depicts the selection process of studies undertaken in the present meta-analysis. Reasons for exclusion are provided along with their relevant counts.

Table 1

Parameter estimates for each regimen based on the base population model.

Parameters	Parameter estimates			
	DTG + ABC+3TC	EFV + ABC+3TC	EFV + TDF + FTC	EFV + TDF+3TC
E_{max}	0.833 ± 0.014	0.905 ± 0.052	0.963 ± 0.015	0.910 ± 0.076
k_o	0.474 ± 0.052	0.0779 ± 0.0087	0.0862 ± 0.0076	0.118 ± 0.021
η_{ko}^a	0.0720 ± 0.0274			
$k_d (\times 10^{-3})$	0.864 ± 0.356	3.83 ± 1.41	2.81 ± 0.47	1.72 ± 0.26
η_{kd}^a	0.149 ± 0.018			
t_{lag}^a	1.55 ± 0.07			
ϵ^a	1.95 ± 0.36			

^a t_{lag} , inter-individual variation of k_o and k_d (η_{ko} and η_{kd}), and intra-individual variation (ϵ) were assumed to be constant irrespective to any of regimens, in order to inflation of number of parameters to be estimated by curve-fit.

Using computer-calculated standard errors of the parameter estimates, we computed the 90% confidence intervals for the drug effect-time profiles (represented with red-colored dotted lines in Fig. 2). Almost all observed data points fell within the 90% confidence intervals and evenly distributed within the range. Thus, the visual predictive check proved good accordance between observed and predicted values.

Table 1 also allows the parameter estimates to be compared among four regimens. The E_{max} value was comparable between regimens. However, the k_o value largely differed; i.e., DTG + ABC+3TC was approximately five times higher than the EFV-based regimens. This reflects that the DTG-based regimen reaches a maximum effect much faster. Additionally, the DTG-based regimen appears to be superior in terms of sustainability. The decay of effect (k_d) for DTG + ABC+3TC was approximately three times slower than that for EFV-based regimens.

Fig. 3 shows the goodness-of-fit plot and conditional weighted residual errors (CWRES) against time plot of base model. The goodness-of-fit plot provided an adjusted coefficient of determination of 0.89, indicating a reasonable accuracy of curve fitting. The CWRES versus time plot assures that the errors symmetrically distribute centering on zero, and ranged between as small as ± 3 .

3.3. Covariate analysis

Supplementary Fig. S1 shows mutual correlation of viral load (BSL), baseline CD4 count (CD4), $\log_{10} k_o$ and $\log_{10} k_d$ in a scatter plot matrix format. $\log_{10} k_o$ showed weakly positive and negative correlations with BSL and CD4, respectively. On the other hand, $\log_{10} k_d$ showed weakly positive and negative correlations with BSL and CD4. These suggest that the drug effect tends to appear more slowly and decay faster in more severe patients. To eliminate an effect of regimen on the relationships, regimen-stratified regression analysis was conducted (Fig. 4 and Table 2). Stratification with regimens clearly indicated strong correlations between the kinetic parameters and the patient's severity indicators.

On the basis of these findings, a nonlinear mixed effect model analysis was performed by introducing BSL or CD4 to the kinetic parameters as covariates:

$$k_{o,i} = \theta_1 \times \theta_2^{COV_i - COV_{med}}$$

where $k_{o,i}$ is the covariate-adjusted mean rate constant for study arm i , θ_1 and θ_2 are parameters to be estimated, COV_i is a covariate value of study arm i , and COV_{med} is the median of the covariate. COV_i was set to COV_{med} unless specified in the literature.

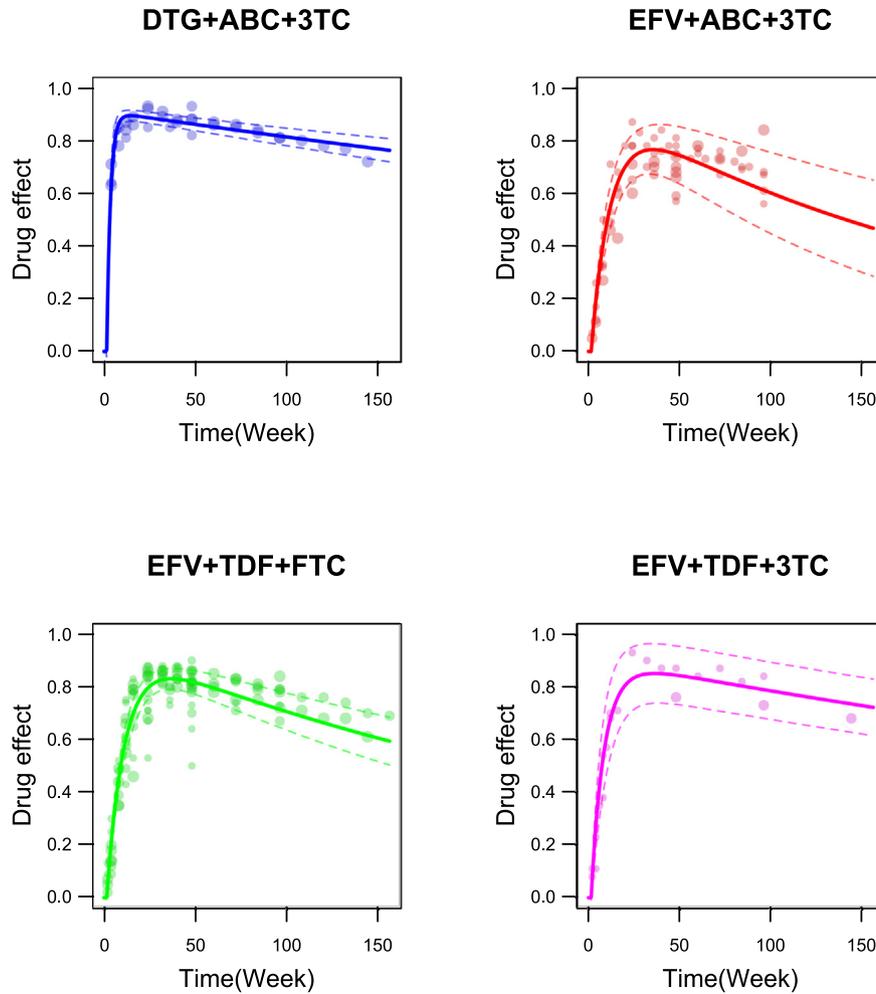


Fig. 2. Time courses of observed and simulated drug effect for each regimen. The drug effect was defined as proportion of participants with viral load of <50 copies/mL in plasma. Symbols represent observed data, of which the size is proportional to the number of patients in the studies. Each solid line represents the median, and the corresponding dashed lines represent the 5th and 95th percentiles estimated by exploiting 1000 times Monte Carlo simulations. Parameters used for the simulation are summarized in [Table 1](#).

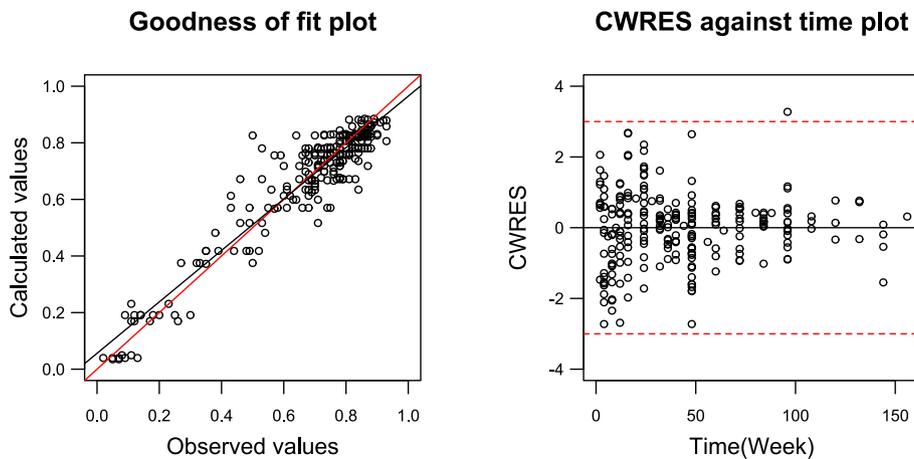


Fig. 3. Goodness of fit and CWRES plots associated with the base population model. Black and red lines represent regression and 1:1 correspondence lines, respectively.

Summarizes the results of covariate screening. Introduction of either *BSL* or *CD4* to k_0 provided significant decrease in the objective function value (OFV), where *CD4* was more effective. The covariate model comprising both *BSL* and *CD4* was not significantly different from that of *CD4* alone. [Table 3](#) summarizes the parameter

estimates for the *CD4* model. As discussed with the base model, a larger θ_1 for the DTG-based regimen reflects its faster-acting drug effect. The θ_2 was greater than unity, suggesting that appearance of drug effect be slower in severe patients having smaller baseline *CD4* count.

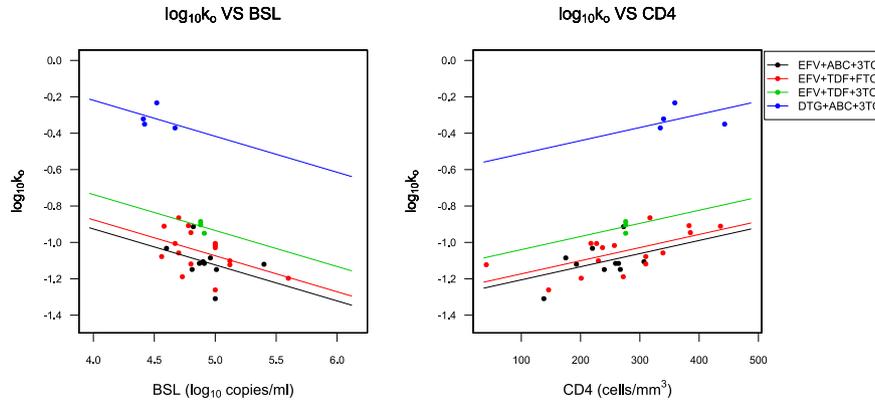


Fig. 4. Plots of regimen-stratified regression analysis for the onset rate constant ($\log_{10} k_o$). $\log_{10} k_o$ was estimated by Bayesian post hoc analysis.

Table 2
Regimen-stratified regression analysis for the onset rate constant ($\log_{10} k_o$).

Regimen	BSL		CD4	
	Equation	Adjusted R ²	Equation	Adjusted R ²
DTG + ABC+3TC	$\log_{10} k_o = -0.198 \times BSL + 0.572$	0.884	$\log_{10} k_o = 7.21 \times 10^{-4} \times CD4 - 0.585$	0.901
EFV + ABC+3TC	$\log_{10} k_o = -0.198 \times BSL - 0.135$		$\log_{10} k_o = 7.21 \times 10^{-4} \times CD4 - 1.28$	
EFV + TDF + FTC	$\log_{10} k_o = -0.198 \times BSL - 0.0845$		$\log_{10} k_o = 7.21 \times 10^{-4} \times CD4 - 1.24$	
EFV + TDF+3TC	$\log_{10} k_o = -0.198 \times BSL - 0.0544$		$\log_{10} k_o = 7.21 \times 10^{-4} \times CD4 - 1.11$	

Table 3
Parameter estimates for each regimen based on a final population model.

Parameters	Parameter estimates			
	DTG + ABC+3TC	EFV + ABC+3TC	EFV + TDF + FTC	EFV + TDF+3TC
E_{max}	0.833 ± 0.014	0.909 ± 0.054	0.959 ± 0.017	0.909 ± 0.073
θ_1	0.416 ± 0.079	0.0779 ± 0.0076	0.0861 ± 0.0064	0.122 ± 0.017
θ_2^a	11.9 ± 6.3			
$\eta_{k_o}^a$	0.0387 ± 0.0155			
$k_d (\times 10^{-3})$	0.845 ± 0.358	3.93 ± 1.43	2.75 ± 0.48	1.70 ± 0.24
$\eta_{k_d}^a$	0.153 ± 0.076			
t_{lag}^a	1.55 ± 0.07			
ϵ	1.96 ± 0.36			

^a θ_2 of k_o , t_{lag} , inter-individual variation of k_o and k_d (η_{k_o} and η_{k_d}), and intra-individual variation (ϵ) were assumed to be constant irrespective to any of regimens, in order to inflation of number of parameters to be estimated by curve-fit.

4. Discussion

This is the first MBMA that modeled and quantitatively compared the time course of drug effect from DTG-based and EFV-based regimens in HIV-infected patients. MBMA presents two major advantages over conventional meta-analyses; that is, it allows to deal with the longitudinal kinetics and to enlarge available data sources. Quantitative characterization of the kinetics of onset and decay of drug effect provides additional information on drug products or regimens. Richer data enable us to gain a more reliable and accurate account of their comparative efficacy.

Simple consecutive first-order reaction kinetics were adopted to describe the time course of drug effect from each regimen. Since the drug effect was defined with the proportion of participants with viral load less than of <50 copies/mL in plasma, E_{max} should not exceed unity. Indeed, EFV + TDF + FTC has the highest E_{max} (0.950). However, the regimen did not necessarily provide the highest drug effect. The highest peak of observed drug effect was with DTG + ABC+3TC with a E_{max} of 0.900, which was due to higher k_o and lower k_d . Comparative superiority among the regimens must be evaluated comprehensively with all the three parameters. It

should also be noted that the decay rate constant k_d does not simply reflect weakening of the effect (e.g., viral drug resistance) but also tapering and premature discontinuation of participants in clinical trials.

Among the 3 EFV-based regimens, EFV + ABC+3TC showed the most inferior performance (the lowest E_{max} , lowest k_o and highest k_d). WHO recommends TDF + FTC or TDF+3TC as NRTI combinations of EFV-based regimens, because these two combinations have offered the opportunity to harmonize regimens across different populations. TDF + FTC and TDF+3TC have been preferred for people co-infected with HIV and HBV, in addition to being effective for people co-infected with tuberculosis and pregnant women [49]. In addition, several clinical trials have indicated that EFV + ABC+3TC are more likely to cause adverse events than EFV + TDF + FTC [19,22]. A higher k_d value of EFV + ABC+3TC might be due to the adverse event-associated discontinuation of participants in clinical trials. Thus, the result of the present analysis supports that EFV + TDF + FTC or EFV + TDF+3TC might be superior to EFV + ABC+3TC.

DTG + ABC+3TC yielded a much greater k_o than EFV-based regimens, resulting in faster-acting drug effect. Despite their

different mechanisms, both DTG and EFV inhibit the proliferation of HIV. The present result that DTG is more effective than EFV was consistent with the viral dynamics study [50] and experimental data in cell culture [51]. Another notable feature of the DTG-based regimen was that DTG + ABC+3TC provided an approximately three times lower k_d than EFV-based regimens. As mentioned above, the k_d could be affected by premature discontinuation of participants in clinical trials. Indeed, Patel et al. [11] revealed in their meta-analysis that patients receiving the DTG-based regimen are less likely to suffer from adverse events than those receiving the EFV-based regimen. The low k_d for DTG + ABC+3TC would be attributed to the lower incidence of adverse event-associated discontinuation than the EFV-based regimen. DTG has been known to have high genetic barrier and minimal cross-resistance [52,53]. In contrast, EFV is characterized by a low barrier to the development of resistance [53,54]. Walmsley et al. [18] has shown that no patients developed resistance mutation in DTG group whereas six patients developed NNRTI-resistance mutations in EFV group, indicating that DTG was less likely to cause virological failure. Difference in resistance profile of each drug might also be due to difference in k_d between DTG + ABC+3TC and EFV-based regimens.

The covariate model analysis revealed a positive relationship between baseline CD4 count and k_o regardless of the regimens. This means that the appearance of drug effect would be slower in patients with a smaller baseline CD4 count, as has been demonstrated in the meta-analysis of Skowron et al. [55]. However, it should be remembered that the therapeutic outcome of the regimens in clinical trials, *i.e.*, the proportion of participants with a minimal viral load, has been evaluated as a summary level. Lambert et al. [56] indicated that meta-analysis using summary-level data might be effective in estimating drug effects but not in investigating relationships between patient characteristics and drug effects. They suggested that individual-level data are generally required to discover any such relationships. The positive relationship between the speed of appearance of anti-HIV effect and baseline CD4 count still remains to be confirmed.

Limitations of this study include difference in demographic characteristics of HIV-infected patients between clinical trials and real world. According to UNAIDS data [1], approximately half of the HIV-infected adults are women, and more than 70% of HIV-infected patients are African. However, clinical trials have been conducted mostly with male Caucasians. It has been reported that gender difference in HIV disease progression exists, where females have lower risks of AIDS dementia complex, tuberculosis, Kaposi's sarcoma, lymphomas, and death without AIDS [57]. A major metabolizing enzyme of EFV is CYP2B6, which are polymorphic in different ethnicities [58]. Naidoo et al. [59] described that ethnic differences and the associated prevalence of CYP2B6 polymorphisms result in significant differences in the pharmacokinetics/pharmacodynamics of EFV, warranting dosage reduction in carriers of specific CYP2B6 polymorphisms. Such gender and ethnic difference might affect the result of meta-analyses. Future data on DTG-based regimens promises to gain more reliable analysis results.

In conclusion, the DTG-based regimen provided faster and more sustainable drug effect than the EFV-based regimen. MBMA would be a powerful tool for investigating the kinetics of drug effect, which can be applied by compiling pieces of data from different sources.

Conflicts of interest

The authors have no potential conflicts of interest to declare.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.jiac.2019.03.015>.

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