Secondary metabolism pathway polymorphisms and plasma efavirenz concentrations in HIV-infected adults with CYP2B6 slow metabolizer genotypes

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Objectives: Efavirenz is widely prescribed for HIV-1 infection, and CYP2B6 polymorphisms 516G→T and 983T→C define efavirenz slow metabolizer genotypes. To identify genetic predictors of higher plasma efavirenz concentrations beyond these two common functional alleles, we characterized associations with mid-dosing interval efavirenz concentrations in 84 HIV-infected adults, all carrying two copies of these major loss-of-function CYP2B6 alleles.

Methods: Study participants had been randomized to efavirenz-containing regimens in prospective clinical trials and had available plasma efavirenz assay data. Analyses focused on secondary metabolism pathway polymorphisms CYP2A6 -48T→G (rs28399433), UGT2B7 735A→G (rs28365062) and UGT2B7 802T→C (rs7439366). Exploratory analyses also considered 196 polymorphisms and 8 copy number variants in 41 drug metabolism/transport genes. Mid-dosing interval efavirenz concentrations at steady-state were obtained ≥8 h but <19 h post-dose. Linear regression was used to test for associations between polymorphisms and log-transformed efavirenz concentrations.

Results: Increased efavirenz concentrations were associated with CYP2A6 -48T→G in all subjects (P = 3.8×10^-4) and in Black subjects (P = 0.027) and White subjects (P = 0.0011) analysed separately; and with UGT2B7 735 G/G homozygosity in all subjects (P = 0.006) and in Black subjects (P = 0.046) and White subjects (P = 0.062) analysed separately. In a multivariable model, CYP2A6 -48T→G and UGT2B7 735 G/G homozygosity remained significant (P < 0.05 for each). No additional polymorphisms or copy number variants were significantly associated with efavirenz concentrations.

Conclusions: Among individuals with a CYP2B6 slow metabolizer genotype, CYP2A6 and possibly UGT2B7 polymorphisms contribute to even higher efavirenz concentrations.

Keywords: pharmacogenomics, pharmacogenetics, pharmacokinetics, antiretroviral therapy, non-nucleoside reverse transcriptase inhibitor

Introduction

The once-daily non-nucleoside reverse transcriptase inhibitor efavirenz is one of the most frequently prescribed antiretrovirals worldwide. It is included among recommended first-line regimens for HIV-1 infection,1 based on data from many prospective, randomized clinical trials.2–7 Efavirenz is metabolized primarily by cytochrome P450 (CYP) 2B6, with minor metabolism by CYP2A6 and CYP3A4/5,8,9 and direct N-glucuronidation by UDP-glucuronosyltransferase (UGT) 2B7.10 Three CYP2B6 polymorphisms, 516G→T (rs3745274),11–16 983T→C (rs2839949)16–19 and 15582C→T (rs4803419), have consistently been associated with increased plasma efavirenz exposure.16 The greater frequency of CYP2B6 516G→T with African ancestry than with European ancestry20 largely explains the somewhat greater mean plasma efavirenz trough concentrations.
appears only to be found with African ancestry. The per allele effect of CYP2B6
516G→T, which is frequent with European and Asian ancestry, is modest compared with 516G→T. These three polymorphisms stratify patients into 10 plasma trough concentration subgroups with medians that span an ~10-fold range. The top three strata (i.e., CYP2B6 slow metabolizer genotypes) are defined by either 516 T/T homozygosity, dual 516 G/T–983 C/T heterozygosity, or 983 C/C homozygosity. Because CYP2B6 516T, 983C and 15582T reside on mutually exclusive haplotypes, 15582T is absent in CYP2B6 slow metabolizer genotypes. These three polymorphisms explained ~35% of overall interindividual variability in efavirenz estimated Cmin.

Additional CYP2B6 polymorphisms suggested to affect CYP2B6 activity either have not predicted plasma efavirenz exposures or have been extremely infrequent. Polymorphisms in genes beyond CYP2B6 reported to affect interindividual variability in efavirenz pharmacokinetics include CYP2A6, UGT2B7, CYP3A5, and NR1I3 (which encodes the constitutive androstane receptor), but findings have seemed to be inconsistent, perhaps a consequence of differences in study design. Kwara et al. reported that among 94 HIV-infected Ghanaian patients, increased mid-dose interval plasma efavirenz concentrations were associated with CYP2A6 -48T→G (rs28399433, *9) or *17 carrier status and UGT2B7*1a status, in addition to CYP2B6 516G→T and 983T→C. Similarly, di Iulio et al. reported that in a predominantly Caucasian cohort of 169 HIV-infected individuals, CYP2A6 loss-of-function alleles (primarily CYP2A6 -48T→G) had an effect on efavirenz exposure, but only with concomitant CYP2B6 loss-of-function genotypes. However, in a genome-wide association study (GWAS) of efavirenz of efavirenz estimated Cmin values, which involved 856 ACTG protocol participants of various ancestries, no independent associations were found with additional polymorphisms in or beyond CYP2B6, including CYP2A6 -48T→G (P = 0.82). Similarly, a recent report by Sarfo et al. indicated that among 417 HIV-infected Ghanians, CYP2A6 -48T→G was associated with mid-dose plasma efavirenz concentrations on univariate analysis only (P = 0.002), but not after controlling for 516G→T and 983T→C (P = 0.6), suggesting that the CYP2A6 -48T→G association was not independent of CYP2B6 polymorphisms.

There were several limitations to the above GWAS. The method used to estimate efavirenz Cmin did not allow differences between some concentrations within the top concentration strata to be discriminated; subgroup analyses were not performed solely among subjects with a CYP2B6 slow metabolizer genotype; and previously implicated UGT2B7 polymorphisms were not genotyped. To assess whether higher plasma efavirenz concentrations are affected by polymorphisms in genes relevant to drug absorption, distribution, metabolism and elimination (ADME) beyond CYP2B6, the present study focused on ACTG protocol participants with a CYP2B6 slow metabolizer genotype. Plasma efavirenz concentrations in this group should be exquisitely sensitive to loss-of-function polymorphisms in minor pathways of efavirenz metabolism, as previously suggested. We only considered efavirenz concentrations from 8 to 19 h post-dose, and performed targeted genotyping of UGT2B7 polymorphisms as well as an additional 194 polymorphisms and 8 gene copy number variants in 40 ADME genes.

Materials and methods
Study participants
Most individuals in these analyses were also included in the previously reported GWAS, which involved treatment-naive individuals who were randomized to efavirenz-containing regimens in ACTG studies 384 and 5095 (including its neurologic substudy AS097s) and AS202, with DNA obtained under protocol AS128 and with available plasma efavirenz assay data. We limited the present analyses to individuals with a CYP2B6 slow metabolizer genotype (516T, 516T/983C or 983CC). Self-identified race/ethnicity categories ‘white, non-Hispanic’, ‘black, non-Hispanic’ and ‘Hispanic’ are hereafter referred to as White, Black and Hispanic, respectively. This study complied with the Helsinki Declaration, was approved by institutional review boards for each site and subjects gave written informed consent.

Genotyping
Genotypes for CYP2B6 516G→T, 983T→C and CYP2A6 -48T→G were available from a custom-designed MassARRAY® iPLEX gold assay (Sequenom Inc.), as previously described and confirmed by genotyping with the iPLEX ADME PGx panel (Sequenom Inc.). Genotypes of five UGT2B7 polymorphisms, including 735A→G (rs28365062), 801A→T (rs7438284), 802T→C (rs7439366), 870+115G→A (rs7441750) and 870+148G→A (rs7441774) were determined using genomic PCR amplification and direct sequencing as described previously, with minor modifications using Platinum® PCR SuperMix, High Fidelity (Life Technologies Inc.). The PCR reactions were denatured initially at 94°C for 2 min, then 35 cycles of 94°C for 30 s, 55°C for 30 s and 68°C for 1 min, followed by 68°C for 5 min. Four of the five UGT2B7 polymorphisms (rs7438284, rs7439366, rs7441750, rs7441774) were in complete linkage disequilibrium in our subjects, so analyses only included 735A→G (rs28365062) and 802T→C (rs7439366). These polymorphisms were chosen for analysis since they discriminate the three most common UGT2B7 alleles identified to date, including UGT2B7*1a (reference), UGT2B7*1c (735A→G) and UGT2B7*2 (802T→C). Furthermore, 802T→C is non-synonymous, causing a histidine to tyrosine transition at codon 268, while 735A→G was associated with altered clearance and glucuronidation of zidovudine, a specific substrate. Two NR1I3 polymorphisms previously associated with efavirenz plasma concentrations, rs2307424 and rs3003596, were genotyped by TaqMan™ assay with ABI PRISM 7900 HT Sequence Detection System (Applied Biosystems Inc., Foster City, CA). From iPLEX ADME PGx, we only included data from specimens with >95% genotyping efficiency and polymorphisms with >95% genotyping efficiency. Laboratory personnel with no knowledge of the clinical data performed the genotyping. Within each race/ethnicity group, each iPLEX ADME PGx polymorphism was in Hardy–Weinberg equilibrium after Bonferroni correction for multiple comparisons. All assays were run in duplicate.

Plasma efavirenz concentrations
Plasma efavirenz concentrations were assayed by HPLC at treatment weeks 1, 4, 12 and 24, as described elsewhere. Sampling times were not pre-specified, and time of prior dose was self-report. We only included mid-dose interval efavirenz concentrations obtained ≥8 h but <19 h post-dose. Efavirenz is typically taken at bedtime to minimize CNS side effects, and mid-dose concentrations are more convenient for therapeutic drug monitoring than AUC. At steady-state, efavirenz mid-dose concentrations (~12 h post-dose) very strongly correlate with AUC values. We also only included subjects with at least two efavirenz determinations within this window, and with relatively consistent values. For subjects with only two such determinations, subjects with a difference between log10 efavirenz concentrations ≥0.3 µg/mL were excluded. For subjects with more than two determinations, subjects with a standard
deviation of $\log_{10}$ efavirenz concentrations $\geq 0.2$ $\mu$g/mL were excluded. These standard deviation cut-offs, chosen based on visual inspection of frequency distribution plots, only excluded a few outlier subjects with extreme inter-assay variability.

**Statistical analysis**

For each subject, the mean of $\log_{10}$-transformed efavirenz concentrations was used in analyses. Linear regression was used to test for association between polymorphisms and efavirenz concentrations. Primary analyses used additive genetic models. Exploratory post hoc analyses also considered recessive models. For CYP2A6 -48T $\rightarrow$ G, UGT2B7 735A $\rightarrow$ G, 802T $\rightarrow$ C and composite CYP2B6 516/983 genotype, nominal two-way $P$ values $<0.05$ were considered significant. For other polymorphisms, $P$ values were Bonferroni corrected for multiple comparisons. Statistical analyses were performed with PLINK software v1.07 \cite{Purcell2007} and with STATA software v13.0 \cite{STATA2013}.

**Results**

**Study subjects**

These analyses included 84 subjects, of which 73 (86.9%) were male, 44 (52.4%) Black, 24 (28.6%) White and 16 (19.1%) Hispanic. Mean age ($\pm$ SD) was 38.3 $\pm$ 9.2 years. The mean of $\log_{10}$ plasma efavirenz concentrations (of each subject’s mean value) was 0.79 $\log_{10}$ 0.19 $\log_{10}$ $\mu$g/mL. On a linear scale, median was 5.8 $\mu$g/mL, minimum 2.4 $\mu$g/mL, IQR 4.3–8.5 $\mu$g/mL and maximum 17.4 $\mu$g/mL. Mean time post-dose was 12.8 $\pm$ 2.0 h (based on within-subject means).

**Genetic associations with mid-dose efavirenz concentrations**

All 84 subjects had a CYP2B6 slow metabolizer genotype, including 71 (84.5%) homozygous for CYP2B6 516TT, 12 (14.3%) heterozygous for CYP2B6 516GT with 983TC and 1 (1.2%) homozygous for CYP2B6 983CC. There was a trend toward association between increasing CYP2B6 983C allele copy number and higher efavirenz concentrations in all subjects ($P=0.12$). To address possible confounding by genetic substructure, we analysed each race/ethnicity group separately. This relationship was also apparent in Black subjects analysed separately. The one Hispanic subject with a 983C allele self-identified as ‘Black, Hispanic’. No White subject had a 983C allele (Figure 1).

Among all subjects, CYP2A6 -48T $\rightarrow$ G was significantly associated with increased efavirenz concentrations by univariate analysis ($P=3.8 \times 10^{-4}$). This association was also apparent in Black subjects ($P=0.027$) and White subjects ($P=0.0011$) analysed separately, but not in Hispanic subjects ($P=0.70$), perhaps due to small sample size (Figure 2). Of note, the only subject with apparent homozygosity for CYP2A6 -48 G/G was also heterozygous for deletion of the CYP2A6 gene, and so this subject had only one CYP2A6 -48G allele (see later regarding iPLEX ADME PGx genotypes). Among all subjects, UGT2B7 735A $\rightarrow$ G was not associated with increased efavirenz concentrations by univariate analysis ($P=0.32$) or in Black, White and Hispanic subjects analysed separately ($P>0.1$ for each). However, among all subjects, using a recessive genetic model, UGT2B7 735 G/G homozygosity was associated with higher efavirenz concentrations than the combined A/A and A/G genotypes ($P=0.0063$), although only three

![Figure 1](image-url)
subjects were homozygous for G/G. This association appeared to be consistent in Black subjects (P=0.046) and White subjects (P=0.062) analysed separately (Figure 3). There was no significant association between either UGT2B7 802T→C, NR1I3 rs2307424 or NR1I3 rs3003596 and efavirenz concentrations by univariate analysis in all subjects, or in Black, White or Hispanic subjects analysed separately (P>0.3 for each analysis; Figures S1 to S3, available as Supplementary data at JAC Online).

Multivariable models were used to test for independent associations. Among all 84 subjects, in additive genetic models that controlled for CYP2B6 slow metabolizer subgroup (516TT, 516T/983C and 983CC), efavirenz concentrations remained significantly associated with CYP2A6 -48T→G (P=0.0010) but not with UGT2B7 735A→G (P=0.29), UGT2B7 802T→C (P=0.89), NR1I3 rs2307424 (P=0.49) or rs3003596 (P=0.43); in a recessive genetic model, UGT2B7 735 G/G homozygosity was associated with efavirenz concentrations (P=0.0085). In a multivariable model that controlled for both CYP2B6 slow metabolizer subgroup and CYP2A6 -48T→G genotype, CYP2A6 -48T→G (P=0.0036) and UGT2B7 735A→G (P=0.025, recessive model), but not CYP2B6 516/983C subgroup (P=0.33), were significantly associated with efavirenz concentrations.

In separate univariate linear regression models, CYP2A6 -48T→G explained 15% of interindividual variance in log_{10} plasma efavirenz concentrations, UGT2B7 735 (G/G homozygosity) explained 9%, CYP2B6 983T→C explained 3% and time post-dose explained 2%. A multivariable model that included CYP2A6 -48T→G and UGT2B7 735 (G/G homozygosity) explained 21% of interindividual variance in log_{10} plasma efavirenz concentrations.

Inclusion of CYP2B6 983T→C only increased this to 22%, and time post-dose only to 24%. The final model, which included CYP2A6 -48T→G, UGT2B7 735 G/G homozygosity and CYP2B6 983T→C, is shown in Table 1.

Associations with additional polymorphisms were explored based on iPLEX ADME PGx genotypes, which were available for 68 subjects (21 White, 39 Black and 8 Hispanic) representing 194 loci in 40 genes (of which 103 were polymorphic and 74 had minor allele frequencies >5%). This platform also assayed for copy number variants of CYP2A6, CYP2B6, CYP2D6, GSTM1, GSTT1, GSTT2B, SULT1A1 and UGT2B17. Information regarding iPLEX ADME PGx genes, polymorphisms and minor allele frequencies are shown in Table S1 (available as Supplementary data at JAC Online). In univariate analyses with correction for multiple comparisons, only CYP2A6 -48T→G in the iPLEX ADME PGx panel was significantly associated with plasma efavirenz concentrations (P=5.8×10^{-6}). This association was also apparent in Whites (P=0.0063) and Blacks (P=0.024) analysed separately. Considering nominal significance (without correcting for multiple comparisons), six polymorphisms in CYP2C9, CYP2C19, CYP3A5, GSTM1 and SULT1A1 had P values between 0.02 and 0.05, but associations were not consistent in White and Black subjects analysed separately. These included the CYP3A5 loss-of-function polymorphism rs776746 (CYP3A5*3), which had nominal significance for association in all subjects (P=0.048) but not in White subjects (P=0.54) or Black subjects (P=0.80) analysed separately. In a multivariable analysis that controlled for CYP2A6 -48T→G, the lowest nominal P value was in GSTM1 (P=0.040). None was significant after correcting for multiple comparisons.
Association analysis results for iPLEX ADME PGx genotypes and gene copy number variants are shown in Tables S2 to S6 (available as Supplementary data at JAC Online). Frequencies of gene copy number variants are shown in Table S7.

For three subjects heterozygous for a CYP2A6 gene deletion (one with a CYP2A6-48G allele, as noted above), there was no significant association with plasma efavirenz concentrations. (This gene deletion is also known as CYP2A6*4).38 The two individuals with a single CYP2A6-48T allele gene copy did not have particularly high plasma efavirenz concentrations (4.4 µg/mL and 9.3 µg/mL). Similarly, two subjects heterozygous for CYP2A6 rs28399454 A/G (also known as CYP2A6*17)39 did not have particularly high plasma efavirenz concentrations (4.0 µg/mL and 5.3 µg/mL). A Q–Q plot of observed versus expected –log10P values showed that only the CYP2A6-48T→G P value was substantially less than expected by chance (Figure 4).

Sensitivity analyses assessed the effect of censoring single plasma efavirenz concentration values from selected analyses. With removal of the one subject with a single CYP2A6-48G allele, the univariate association with CYP2A6-48T→G remained significant (P=9.4×10⁻⁴). With removal of the one subject with the highest efavirenz value (heterozygous for CYP2A6-48 G/T, homozygous for UGT2B7 735 G/G), the association with CYP2A6-48T→G again remained significant (P=0.0014), but the association with UGT2B7 735A→G did not (recessive model, P=0.11).

Discussion

Efavirenz is one of the most frequently prescribed antiretrovirals worldwide. The present study shows that, among individuals with already increased efavirenz concentrations due to a CYP2B6
In vivo study subjects. We conclude that CYP3A5 either does not contribute to compensatory increase in CYP3A4 activity (or of some other enzyme) in these subjects offsets the decreased CYP3A5 activity.

In summary, knowledge of CYP2A6 -48T→G genotype improves stratification of plasma efavirenz concentrations in individuals with a CYP2B6 slow metabolizer genotype. Stratification may also be improved by UGT2B7 genotype, although this slow metabolizer genotype, CYP2A6 -48T→G is associated with even greater increases in plasma efavirenz concentrations. This polymorphism, which defines the CYP2A6*9 haplotype, disrupts the TATA box and is associated with reduced CYP2A6 expression.40,41 This association was seen in all subjects and in Black subjects and White subjects analysed separately. In multivariable analyses, the association with CYP2A6 -48T→G was independent of CYP2B6 slow metabolizer genotype subgroup (i.e. 516TT, 516T/983C and 983CC). The validity of this association is further supported by the Q–Q plot, which clearly shows that CYP2A6 -48T→G stands out among the many ADME polymorphisms genotyped. A possible association between UTG2B7 735A→G and higher plasma efavirenz concentrations was only seen with 735 G/G homozygosity, which was independent of both CYP2A6 -48T→G and CYP2B6 slow metabolizer genotype subgroup in multivariable analyses. However, loss of UTG2B7 735A→G significance in a sensitivity analysis that censored a single subject shows the tenuousness of this association. In addition, increasing number of CYP2B6 983C alleles tended toward association with higher plasma efavirenz concentrations, consistent with previous reports.16

The present analyses only included individuals with a CYP2B6 slow metabolizer genotype, because only in the setting of markedly reduced CYP2B6 activity are minor metabolism pathway effects most apparent, as previously suggested.24 Although UTG2B7 can directly N-glucuronidate efavirenz in vitro,16 our finding that an association with UTG2B7 735A→G was only seen with G/G homozygosity suggests that the effect (if any) of this polymorphism is weak. This is consistent with data from a study of 10 HIV-negative healthy volunteers (eight Caucasians and two African Americans), which suggested that the contribution of UTG2B7 to efavirenz metabolism in vivo is minimal.62 However, there were likely no CYP2B6 slow metabolizer genotypes in the latter study (although genotyping was not done), and the contribution of UTG2B7 might be more substantial in such individuals.

We found no additional ADME polymorphisms in or beyond CYP2B6, CYP2A6 and UTG2B7 associated with plasma efavirenz concentrations. This includes CYP3A5*3 (rs776746), which markedly reduces CYP3A5 expression and was very frequent in our study subjects. We conclude that CYP3A5 either does not contribute substantially to efavirenz metabolism in vivo or that a compensatory increase in CYP3AA4 activity (or of some other enzyme) in these subjects offsets the decreased CYP3A5 activity.

In summary, knowledge of CYP2A6 -48T→G genotype improves stratification of plasma efavirenz concentrations in individuals with a CYP2B6 slow metabolizer genotype. Stratification may also be improved by UTG2B7 genotype, although this

![Figure 4. Q–Q plot of observed versus expected −log₁₀ P values for iPLEX ADME PGx panel polymorphisms. Each marker represents a different polymorphism. The arrowhead identifies CYP2A6 -48T→G (rs28399433).](image-url)
association was less robust. These findings support the importance of minor metabolism pathways of efavirenz metabolism in CYP2B6 slow metabolizers, and suggest that individuals with CYP2A6 -48T→G, and possibly UGT2B7 735 G/G, are at increased risk for considerably higher plasma efavirenz exposure.

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Supplementary data
Tables S1 to S7 and Figures S1 to S3 are available as supplementary data at JAC Online (http://jac.oxfordjournals.org/).

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References
2. van Leth F, Phanuphak P, Ruxrungtham K et al. Comparison of first-line antiretroviral therapy with regimens including nevirapine, efavirenz, or both drugs, plus stavudine and lamivudine: a randomised open-label trial, the 2NN Study. Lancet 2004; 363: 1253–63.


36 Purcell S, Neale B, Todd-Brown K et al. PLINK: a tool set for whole-genome association and population-based linkage analyses. Am J Hum Genet 2007; 81: 559–75.

37 StataCorp. Stata Statistical Software: Release 13. College Station, TX: StataCorp LP, 2013.

38 Nunoya K, Yokoi T, Kimura K et al. A new deleted allele in the human cytochrome P450 2A6 (CYP2A6) gene found in individuals showing poor metabolic capacity to coumarin and (+)-cis-3,5-dimethyl-2-(3-pyridyl) thiazolidin-4-one hydrochloride (SM-12502). Pharmacogenetics 1998; 8: 239–49.


50 Puls R, Group TES. A daily dose of 400 mg efavirenz (EFV) is non-inferior to the standard 600 mg dose: week 48 data from the ENCORE1 study, a randomised, double-blind, placebo controlled, non-inferiority trial. In: Abstracts of the Seventh IAS Conference on HIV Pathogenesis, Treatment and Prevention, Kuala Lumpur, Malaysia, 2013. Abstract WELBB01.