

UCSF

UC San Francisco Previously Published Works

Title

Measuring the overall genetic component of nevirapine pharmacokinetics and the role of selected polymorphisms: towards addressing the missing heritability in pharmacogenetic phenotypes?

Permalink

<https://escholarship.org/uc/item/80711358>

Journal

Pharmacogenetics and genomics, 23(11)

ISSN

1744-6872

Authors

Micheli, Janine E
Chinn, Leslie W
Shugarts, Sarah B
[et al.](#)

Publication Date

2013-11-01

DOI

10.1097/FPC.0b013e32836533a5

Peer reviewed

Measuring the overall genetic component of nevirapine pharmacokinetics and the role of selected polymorphisms: towards addressing the missing heritability in pharmacogenetic phenotypes?

Janine E. Micheli^a, Leslie W. Chinn^a, Sarah B. Shugarts^a, Ashish Patel^a, Jeffrey N. Martin^{b,c}, David R. Bangsberg^e and Deanna L. Kroetz^{a,d}

Objective Nevirapine is an important component of highly active antiretroviral therapy used in the treatment of HIV infection. There is a considerable variation in the pharmacokinetics of nevirapine and this variation can impact the efficacy and toxicity of nevirapine. Although some of this variation can be attributed to environmental factors, the degree to which heritability influences nevirapine pharmacokinetics is unknown. This study aims to estimate how much variation in nevirapine pharmacokinetics is due to genetic factors and to investigate the contribution of selected polymorphisms to this variability.

Methods Two doses of immediate-release nevirapine were administered to European ($n=11$) and African American ($n=6$) participants recruited from the Research in Access to Care in the Homeless cohort. A repeated drug administration method was then used to determine the relative genetic contribution (r_{GC}) to variability in nevirapine AUC_{0-6h} . Nevirapine plasma levels were quantified using LC/MS/MS. Patients were also genotyped for selected polymorphisms in candidate genes that may influence nevirapine pharmacokinetics.

Results A significant r_{GC} for nevirapine AUC_{0-6h} was found in Europeans ($P=0.02$) and African Americans

($P=0.01$). A trend toward higher nevirapine AUC_{0-6h} for the *CYP2B6* 516TT (rs3745274; Q172H) genotype was observed in European Americans ($P=0.19$).

Conclusion This study demonstrates that there is a significant genetic component to variability in nevirapine pharmacokinetics. Although genetic variants such as *CYP2B6* polymorphisms attributed to some of this variation, these data suggest that there may be additional genetic factors that influence nevirapine pharmacokinetics. *Pharmacogenetics and Genomics* 23:591–596 © 2013 Wolters Kluwer Health | Lippincott Williams & Wilkins.

Pharmacogenetics and Genomics 2013, 23:591–596

Keywords: CYP2B6, human immunodeficiency virus, nevirapine, pharmacogenetics, pharmacokinetics

Departments of ^aBioengineering and Therapeutic Sciences, ^bEpidemiology, ^cMedicine, ^dThe Institute for Human Genetics, University of California, San Francisco, California and ^eRagon Institute of Massachusetts General Hospital, Massachusetts Institute of Technology and Harvard University, Massachusetts General Hospital Center for Global Health, Harvard Medical School, Boston, Massachusetts, USA

Correspondence to Deanna L. Kroetz, PhD, 1550 4th Street, Rock Hall 584E, Box 2911, San Francisco, CA 94158-2911, USA
Tel: +1 415 476 1159; fax: +1 415 514 4361; e-mail: deanna.kroetz@ucsf.edu

Received 18 April 2013 Accepted 18 July 2013

Introduction

The importance of understanding the role of genetics in variation in pharmacokinetics and pharmacodynamics has been recognized since the 1950s [1–3]. Twin studies have historically been used to determine the heritability of genetic diseases and traits; these studies have also been used to determine the heritability of pharmacodynamic and pharmacokinetic parameters [4]. Although twin studies are a useful technique to determine genetic contributions to pharmacokinetic variation, it can be impractical to use twins in pharmacogenetic studies because of the difficulty in recruitment and the need to expose them to drugs. A statistical technique that was specifically developed to address this issue is the

repeated drug administration (RDA) method, which uses repeated administrations of a drug to the same individuals to compare the within-participant and between-participant variation in pharmacokinetic parameters [5]. This comparison can be used to quantify the relative genetic contribution to variations in pharmacokinetic parameters of a drug. Although the RDA method is useful in determining whether pharmacokinetic or pharmacodynamic parameters of a drug have strong genetic components, it may vary with the route of administration, dose of drug, or patient population [5]. In addition, while one pharmacokinetic parameter for a given drug may have a strong relative genetic component, other parameters may be more highly influenced by environmental factors than by genetic factors [6]. RDA has successfully been used to characterize the genetic contribution to variability in pharmacokinetic parameters of several drugs, including erythromycin, midazolam, and metformin [7,8]. However,

Supplemental digital content is available for this article. Direct URL citations appear in the printed text and are provided in the HTML and PDF versions of this article on the journal's website (www.pharmacogeneticsandgenomics.com).

the genetic contribution to pharmacokinetic parameter variability for many drugs is still unknown.

Nevirapine is a non-nucleoside reverse transcriptase inhibitor widely used as a component of antiretroviral therapy in the treatment of HIV [9]. Nevirapine exhibits considerable variability in its pharmacokinetic properties; however, only part of this variability can be explained by environmental factors and concomitant conditions [10]. Variation in nevirapine pharmacokinetics can lead to reduced efficacy, increased viral resistance, and increased toxicities [11]. Nevirapine is metabolized to its primary metabolite 3-hydroxynevirapine by CYP2B6 [12]. The *CYP2B6* 516G > T and *CYP2B6* 983T > C variant alleles have a significant effect on nevirapine plasma levels, and the *CYP2B6* 516T allele has also been associated with increased recovery of CD4⁺ T-cell populations in pediatric patients following initiation of nevirapine-containing antiretroviral therapy [13–15]. In addition, *ABCB1* 3435C > T has been associated with protection against nevirapine-induced hepatotoxicity and increased nevirapine concentrations in cerebrospinal fluid [16,17]. Despite evidence that nevirapine pharmacokinetics are influenced by specific polymorphisms, there has not been a study conducted to quantify the relative genetic contribution to variability in nevirapine pharmacokinetics.

This study uses the RDA method to quantify the relative genetic contribution to variability in nevirapine pharmacokinetics. A significant relative genetic contribution to variation in nevirapine exposure was shown in two ethnic populations. The contribution of *CYP2B6* 516G > T and *ABCB1* 3435C > T to variability in nevirapine pharmacokinetics was also investigated.

Materials and methods

Study design and participants

Participants were recruited from the Research in Access to Care in the Homeless cohort as previously described [18]. Study participants are marginally housed HIV-positive individuals living in San Francisco. Nineteen patients were recruited to participate in a pharmacokinetic study where patients receiving 200 mg nevirapine twice daily consented to pharmacokinetic blood sampling. All patients were on therapy at least 4 months and were concomitantly receiving two nucleoside reverse transcriptase inhibitors. Patients were presumed to have reached steady state concentrations. Blood samples were drawn at 0, 1, 2, 3, and 6 h after each dose. The time between the two measured doses varied from 13 to 173 days. European American ($n = 11$) and African American ($n = 6$) patients were included in this study. Ethnicity was self-reported and verified through genotyping of 112 ancestry informative markers and analysis using the STRUCTURE program [19–21]. The study was approved by the University of California Institutional Review Board and

all participants provided written informed consent before participation.

Nevirapine quantification

Plasma was prepared from blood samples by centrifugation and stored at -80°C until analysis. Nevirapine was extracted using Oasis HLB SPE columns (Waters Corp., Milford, Massachusetts, USA) and plasma concentrations were quantified by LC/MS/MS analysis as described by Mistri *et al.* [22]. Briefly, each 0.5 ml plasma aliquot was heated for 1.5 h at 56°C to inactivate HIV-1 virus and then spiked with 25 μl of 20 $\mu\text{mol/l}$ metaxolone (Toronto Research Chemicals, Toronto, Ontario, Canada) in methanol, which served as an internal standard. SPE columns were equilibrated with 1 ml methanol followed by 1 ml distilled water. Samples were then loaded on the column and washed with 1 ml of 2 mmol/l ammonium acetate followed by 1 ml of water. Samples were eluted in 1 ml mobile phase (80:20 acetonitrile:water, 0.1% acetic acid) and a 5 μl aliquot was injected onto a 5 μm Hypersil BDS C18 column, $50 \times 4.6 \mu\text{m}$ (Thermo Fisher Scientific, Waltham, Massachusetts, USA). The flow rate into the API4000 mass spectrometer (AbSciex, Framingham, Massachusetts, USA) was 0.2 ml/min and nevirapine retention time was 1.7 min. The parent ion (m/z 267.2 amu) and product ion (m/z 226.2 amu) were monitored at Q1 and Q3, respectively. Nevirapine standard curves were linear from 50 to 5000 ng/ml ($r^2 > 0.9$). Assay accuracy was between 100.3 and 112.9% relative SD. Assay precision ranged from 8.2 to 18.5% coefficient of variation.

Genotyping

Genomic DNA was extracted from whole blood samples. Genotyping of polymorphisms of interest (*CYP2B6* 516G > T and *ABCB1* 3435C > T) was accomplished using the ABI Prism 7900HT Sequence Detection System (Applied Biosystems, Foster City, California, USA). TaqMan assays were used to genotype *CYP2B6* 516G > T (rs3745274, Assay ID: C__7817765_60) and *ABCB1* 3435C > T (rs1045642, Assay ID: C__7586657_20). Genotypes were called using the ABI Sequence Detection System software (version 2.1; Applied Biosystems).

Calculation of pharmacokinetic parameters

Because of the long half-life of nevirapine (45 h), only $\text{AUC}_{0-6\text{h}}$ was calculated [23]. $\text{AUC}_{0-6\text{h}}$ was calculated for each dose administration using the trapezoidal rule.

Calculation of the relative genetic component

The genetic contribution to the variability in nevirapine $\text{AUC}_{0-6\text{h}}$ was assessed with a modified analysis of variance (ANOVA) formula for estimating the relative genetic component or r_{GC} and 95% confidence intervals (CIs) proposed by Kalow *et al.* [24]:

$$r_{\text{GC}} = (\text{SD}_b^2 - \text{SD}_w^2) / \text{SD}_b^2,$$

which can be rearranged as:

$$r_{GC} = 1 - (1/F),$$

where $F = SD_b^2 / SD_w^2$.

Upper and lower CIs can be calculated as follows:

$$\text{Lower 95\% CI} = F_{\text{observed}} / F_{0.025, b.d.f., w.d.f.},$$

$$\text{Upper 95\% CI} = F_{\text{observed}} \times F_{0.025, b.d.f., w.d.f.},$$

where r_{GC} represents the estimated relative genetic component, SD_b^2 is the between-participant variation, SD_w^2 is the within-participant variation, $b.d.f.$ is the between-participant degrees of freedom, $w.d.f.$ is the within-participant degrees of freedom, and $F_{0.025}$ is the tabulated F statistic at the 2.5% significance level at the appropriate degrees of freedom. Because of well-characterized differences in allele frequency and linkage disequilibrium patterns, European Americans ($n = 11$) and African Americans ($n = 6$) were analyzed separately in this study.

Statistical methods

Statistical significance for genetic contribution to AUC_{0-6h} variability was calculated using an F -test, $\alpha = 0.05$, to determine whether the interindividual and intraindividual variation was significantly different. One-way ANOVA, $\alpha = 0.05$, was used to determine significance for the effect of genetic polymorphisms on AUC_{0-6h} values. All other calculations of P -values were obtained using two-sided t tests or one-way ANOVA as appropriate [25]. Calculations were performed using R and Microsoft Excel [26]. All figures were produced in Prism Version 5.01 (GraphPad Software Inc., San Diego, California, USA).

Results

Ethnicity does not play a role in nevirapine AUC_{0-6h} variability

As there are well-characterized differences in the genetic structure and linkage disequilibrium patterns in various ethnic populations, a statistical analysis to examine any overall differences in nevirapine AUC_{0-6h} between African and European Americans was conducted. A total of 17 participants were included in this study, 11 European Americans and six African Americans (Table 1). Median ages and concomitant medications were similar in the two ethnic groups, whereas the African American group had a higher proportion of women than the European American group.

Analysis of nevirapine plasma concentrations indicated very little intraparticipant variability in concentrations during the 6 h after drug administration, consistent with the long terminal half-life of this drug (Figs 1 and 2, Supplemental digital content, Fig. 1, <http://links.lww.com/FPC/A639>). In contrast, there is considerable variation in nevirapine concentrations between individuals; three individuals in the African American and two in the European American groups never reach plasma concen-

Table 1 Patient demographics and relative genetic contribution (r_{GC}) to nevirapine AUC_{0-6h}

	European Americans	African Americans
Sample size (n)	11	6
Sex [n (%)]		
Male	4 (36)	1 (17)
Female	7 (64)	5 (83)
Age (years)		
Median	45	49
Range	29–57	33–74
Nevirapine AUC_{0-6h} (mg/l h) ^a		
SD_w^2	2.39	5.34
SD_b^2	24.9	54.7
Estimated relative genetic component		
r_{GC}^b (95% CI)	0.904 (0.64–0.97)	0.902 (0.42–0.98)
F	10.4	10.2
P	0.02	0.01

AUC, area under the curve; CI, confidence interval.

^a SD_w^2 is within-individual variation and SD_b^2 is within-participant variation.

^bEstimated relative genetic component.

trations above the minimum effective concentration for nevirapine of 3000 $\mu\text{g/l}$ [27]. Average AUC_{0-6h} did not differ between the two visits, although there was significant interpatient variability in these values (Table 1). For example, the mean AUC_{0-6h} was 22.5 mg nevirapine/l h (SEM = 3.81 mg nevirapine/l h) and 18.3 mg nevirapine/l h (SEM = 2.69 mg nevirapine/l h) for European and African Americans, respectively. There was no significant difference in AUC_{0-6h} between the two populations (t -test, $P = 0.45$).

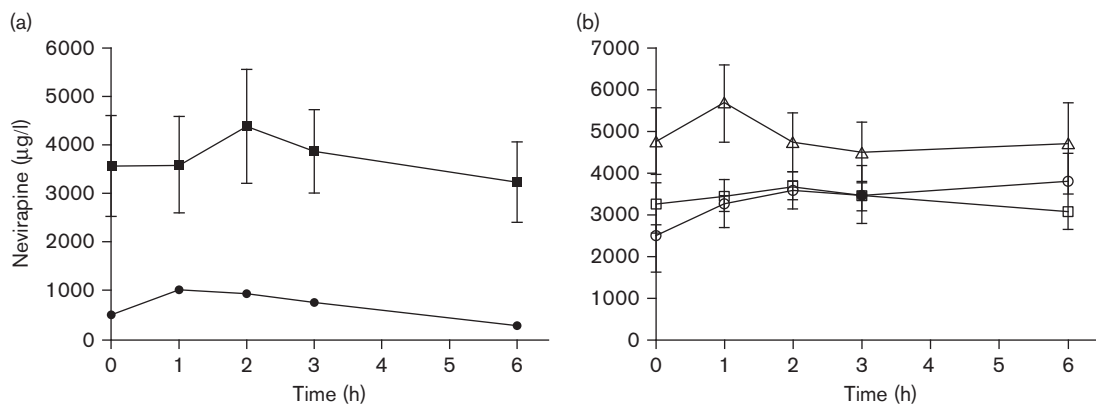
Age and sex do not play a role in the variability of nevirapine AUC_{0-6h}

To ensure that further analyses were not confounded by demographic factors, the effect of age and sex on nevirapine AUC_{0-6h} was examined by linear regression and t tests, respectively. Age had no effect on nevirapine AUC_{0-6h} with an r^2 of 0.04. Men tended to have slightly lower AUC_{0-6h} (16.2 mg nevirapine/l h, SEM = 37.0 mg nevirapine/l h) than women (23.0 mg nevirapine/l h, SEM = 24.2 mg nevirapine/l h), however this difference was not statistically significant ($P = 0.14$).

There is a significant genetic contribution to variation in nevirapine AUC_{0-6h}

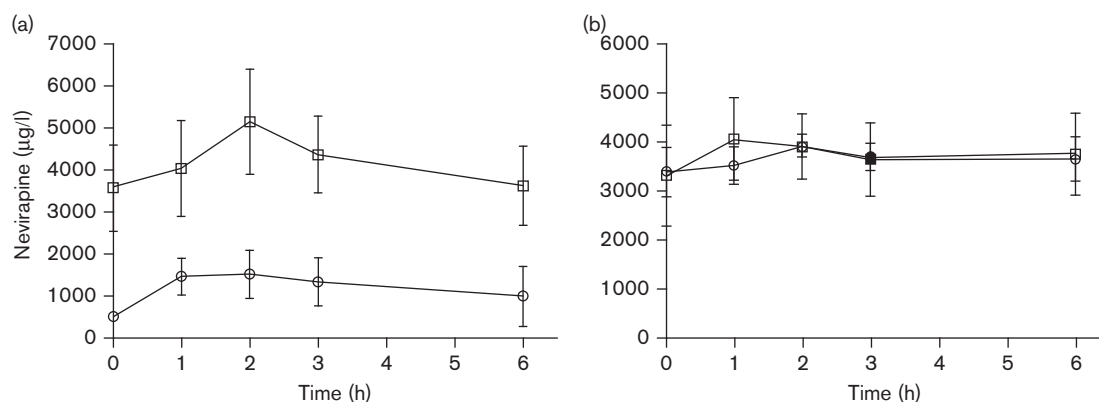
The relative genetic contribution to nevirapine pharmacokinetics was calculated using the RDA method as described previously [5,7]. The between-participant (SD_b^2) variation in AUC_{0-6h} was about 10-fold greater than the within-participant variation (SD_w^2) in both ethnic groups (Table 1). The r_{GC} calculated for the European Americans and African Americans was 0.904 (95% CIs 0.64–0.97) and 0.902 (95% CIs 0.42–0.98), respectively. F tests indicate that there is a significant genetic contribution to the variability in AUC_{0-6h} in both Europeans ($P = 0.02$) and African Americans ($P = 0.01$).

Fig. 1



Nevirapine plasma concentrations following a 200 mg dose to (a) African Americans and (b) European Americans. The concentrations (mean±SEM) are stratified by *CYP2B6* 516G>T genotype: circles: GG, squares: GT, and triangles: TT.

Fig. 2



Nevirapine plasma concentrations following a 200 mg dose to (a) African Americans and (b) European Americans. The concentrations (mean±SEM) are stratified by *ABCB1* 3435C>T genotype: circles: CC and squares: CT.

CYP2B6 516G>T may influence nevirapine AUC_{0-6h}

Considering the evidence for a significant genetic contribution to the variability in nevirapine exposure, polymorphisms in candidate genes implicated in the metabolism and transport of nevirapine were tested for association with nevirapine pharmacokinetics. In African Americans, there is a trend for increased plasma nevirapine levels in individuals carrying the *CYP2B6* 516G>T allele or the *ABCB1* 3435C>T allele (Figs 1a and 2a); however, the sample sizes are too small for formal statistical analysis (Table 2). A similar trend was observed for the *CYP2B6* 516G>T allele in European Americans, but these differences did not reach statistical significance (Fig. 1b and Table 2). There was no indication of an association between the *ABCB1* 3435C>T polymorphism and nevirapine pharmacokinetics in European Americans (Fig. 2b and Table 2).

Discussion

Although there have been many candidate gene studies on nevirapine pharmacokinetics, this is the first study to determine the overall relative genetic influence on nevirapine pharmacokinetics. A significant relative genetic contribution to the variability in nevirapine pharmacokinetics was demonstrated in European and African Americans. This supports previous findings that have implicated polymorphisms in drug metabolism and transport genes in nevirapine pharmacokinetic variability and toxicity [14–16]. A trend consistent with previous studies of elevated plasma concentrations in participants homozygous for the *CYP2B6* 516G>T allele was also observed [13,15].

Variability in nevirapine pharmacokinetics and toxicity has been observed since its approval for the treatment of

Table 2 The effect of ethnicity and genotype on nevirapine exposure

Ethnicity	n	Nevirapine AUC _{0-6h} (mg/lh) ^a	P
African American	6	18.3±3.81	0.45
European American	12	22.5±2.69	
<i>CYP2B6</i> 516G>T			
African Americans			
GG	1	4.23	ND
GT	5	21.2±5.63	
TT	0	-	
European Americans			
GG	4	20.5±3.16	0.19
GT	5	20.3±2.82	
TT	3	28.8±3.64	
<i>ABCB1</i> 3435C>T			
African Americans			
CC	2	7.31±7.97	0.17
CT	4	23.8±12.8	
European Americans			
CC	6	22.0±3.03	0.96
CT	5	22.2±3.32	

AUC, area under the curve; ND, not determined.

^aMean±SEM.

HIV. Many candidate gene studies have confirmed that a portion of pharmacokinetic variability is because of polymorphisms in *CYP2B6* [14,28,29]. However, the variation in pharmacokinetics due to genetic versus environmental factors has never been examined. The current study demonstrates that there is a significant genetic component to nevirapine pharmacokinetics in African and European Americans. Although the population examined here is small, one advantage of the RDA method is the ability to use small populations to estimate relative genetic components of drugs [6]. In our European population, we have a reasonable number of participants to estimate a 95% lower confidence limit of ~0.65 for an r_{GC} of 0.9 [6]. This suggests that interindividual variation in nevirapine drug levels could be reduced through knowledge of a patient's genetic background. The importance of this is reflected in the observation that several patients did not reach the minimum effective concentration of nevirapine, which could lead to decreased efficacy against HIV and increased viral resistance to nevirapine. The RDA method has been successfully used to identify drugs whose renal clearance has a strong genetic component and could also be used to identify antiretroviral drugs that are good candidates for pharmacogenomics research [8].

To further investigate the influence of genetics on nevirapine pharmacokinetics, two candidate polymorphisms were selected for study. A trend was observed toward elevated AUC_{0-6h} of nevirapine in both European and African Americans homozygous for the *CYP2B6* 516G>T polymorphism. This polymorphism has been associated with a slight decrease in hepatic protein expression and function, therefore increases in AUC_{0-6h} are expected [30]. Although the results in European Americans did not reach statistical significance, the analysis was limited by a small sample size and may have been confounded by unidentified

environmental factors. The trend observed is consistent with other published work, which supports the need for a larger study population [14,15,31]. No association of *ABCB1* 3435C>T with nevirapine exposure was observed in our study. The effect of this polymorphism on nevirapine pharmacokinetics remains controversial, with many studies not showing an effect on nevirapine plasma pharmacokinetics [13-15,29,32]. AUC_{0-6h} may not be the most appropriate pharmacokinetic parameter to observe the effects of these polymorphisms; however, because of the long half-life of nevirapine, it was not possible to calculate other pharmacokinetic parameters such as half-life or oral clearance.

The current study demonstrates that there is a significant relative genetic component to nevirapine pharmacokinetics. Although *CYP2B6* polymorphisms have been attributed to some of this variation [14,15,31], this study suggests that there may be additional genetic factors that influence nevirapine pharmacokinetics. These data support additional research to discover novel genetic factors influencing nevirapine variability. Further, the RDA method could also be used to study endpoints of antiretroviral drugs other than pharmacokinetic parameters, including pharmacodynamic and metabolomic endpoints [33]. Additional knowledge of genetic factors that affect nevirapine pharmacokinetics may help increase the efficacy of nevirapine in the treatment of HIV and lead to less viral resistance.

Acknowledgements

This work was funded by NIH grants GM61390 and MH54907. Janine Micheli was supported by NIH T32 GM007175.

Conflicts of interest

There are no conflicts of interest.

References

- Motulsky AG. Drug reactions, enzymes and biochemical genetics. *JAMA* 1957; **165**:835-837.
- Carson PE, Flanagan CL, Ickes CE, Alving AS. Enzymatic deficiency in primaquine-sensitive erythrocytes. *Science* 1956; **124**:484-485.
- Kalow W. Genetic factors in relation to drugs. *Annu Rev Pharmacol* 1964; **5**:9-26.
- Wesell ES. Pharmacogenetic perspectives gained from twin and family studies. *Pharmacol Ther* 1989; **41**:535-552.
- Kalow W, Endrenyi L, Tang B. Repeat administration of drugs as a means to assess the genetic component in pharmacological variability. *Pharmacology* 1999; **58**:281-284.
- Ozdemir V, Kalow W, Tothfalusi L, Bertilsson L, Endrenyi L, Graham JE. Multigenic control of drug response and regulatory decision-making in pharmacogenomics: the need for an upper-bound estimate of genetic contributions. *Curr Pharmacogenomics* 2005; **3**:53-71.
- Ozdemir V, Kalow W, Tang BK, Paterson AD, Walker SE, Endrenyi L, et al. Evaluation of the genetic component of variability in CYP3A4 activity: a repeated drug administration method. *Pharmacogenetics* 2000; **10**:373-388.
- Leabman MK, Giacomini KM. Estimating the contribution of genes and environment to variation in renal drug clearance. *Pharmacogenetics* 2003; **13**:581-584.
- Department of Health and Human Services. *Guidelines for the use of antiretroviral agents in HIV-infected adults and adolescents*. Washington, DC: Department of Health and Human Services; 2009. pp. 1-161.

- 10 Gandhi M, Benet LZ, Bacchetti P, Kalinowski A, Anastos K, Wolfe AR, *et al.* Nonnucleoside reverse transcriptase inhibitor pharmacokinetics in a large unselected cohort of HIV-infected women. *J Acquir Immune Defic Syndr* 2009; **50**:482–491.
- 11 Cooper CL, Van Heeswijk RPG. Once-daily nevirapine dosing: a pharmacokinetics, efficacy and safety review. *HIV Med* 2007; **8**:1–7.
- 12 Riska P, Lamson M, Macgregor T, Sabo J, Hattox S, Pav J, *et al.* Disposition and biotransformation of the antiretroviral drug nevirapine in humans abstract. *Pharmacology* 1999; **27**:895–901.
- 13 Mahungu T, Smith C, Turner F, Egan D, Youle M, Johnson M, *et al.* Cytochrome P450 2B6 516G→T is associated with plasma concentrations of nevirapine at both 200 mg twice daily and 400 mg once daily in an ethnically diverse population. *HIV Med* 2009; **10**:310–317.
- 14 Penzak SR, Kabuye G, Mugenyi P, Mbamanya F, Natarajan V, Alfaro RM, *et al.* Cytochrome P450 2B6 (CYP2B6) G516T influences nevirapine plasma concentrations in HIV-infected patients in Uganda. *HIV Med* 2007; **8**:86–91.
- 15 Haas DW, Gebretsadik T, Mayo G, Menon UN, Acosta EP, Shintani A, *et al.* Associations between CYP2B6 polymorphisms and pharmacokinetics after a single dose of nevirapine or efavirenz in African Americans. *J Infect Dis* 2009; **199**:872–880.
- 16 Ciccacci C, Borgiani P, Ceffa S, Sirianni E, Marazzi MC, Altan AM, *et al.* Nevirapine-induced hepatotoxicity and pharmacogenetics: a retrospective study in a population from Mozambique. *Pharmacogenomics* 2007; **11**: 23–31.
- 17 Varatharajan L, Thomas SA. The transport of anti-HIV drugs across blood-CNS interfaces: summary of current knowledge and recommendations for further research. *Antiviral Res* 2009; **82**:A99–109.
- 18 Moss AR, Hahn JA, Perry S, Charlebois ED, Guzman D, Clark RA, *et al.* Adherence to highly active antiretroviral therapy in the homeless population in San Francisco: a prospective study. *Clin Infect Dis* 2004; **39**: 1190–1198.
- 19 Tsai H-J, Choudhry S, Naqvi M, Rodriguez-Cintron W, Burchard EG, Ziv E. Comparison of three methods to estimate genetic ancestry and control for stratification in genetic association studies among admixed populations. *Hum Genet* 2005; **118**:424–433.
- 20 Pritchard JK, Stephens M, Donnelly P. Inference of population structure using multilocus genotype data. *Genetics* 2000; **155**:945–959.
- 21 Falush D, Stephens M, Pritchard JK. Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. *Genetics* 2003; **164**:1567–1587.
- 22 Mistri HN, Jangid AG, Pudage A, Gomes N, Sanyal M, Shrivastav P. High throughput LC-MS/MS method for simultaneous quantification of lamivudine, stavudine and nevirapine in human plasma. *J Chromatogr B Analyt Technol Biomed Life Sci* 2007; **853**:320–332.
- 23 Viramune ® (nevirapine) Tablets [package insert]. Ridgefield, CT: Boehringer Ingelheim Pharmaceuticals, Inc.; 2005.
- 24 Kalow W, Tang BK, Endrenyi L. Hypothesis: comparisons of inter- and intra-individual variations can substitute for twin studies in drug research. *Pharmacogenetics* 1998; **8**:283–289.
- 25 Venables WN, Ripley BD. *Modern applied statistics with S-plus*. New York, NY: Springer-Verlag; 1994.
- 26 R Core Team. *R: a language and environment for statistical computing*. Vienna, Austria: R Foundation for Statistical Computing; 2012.
- 27 De Vries-sluijs TEMS, Dieleman JP, Arts D, Huitema ADR, Beijnen JH, Schutten M, *et al.* Concentrations predict virological failure in an unselected HIV-1-infected population. *Clin Pharmacokinet* 2003; **42**:599–605.
- 28 Ramachandran G, Ramesh K, Hemanth Kumar AK, Jagan I, Vasantha M, Padmapriyadarsini C, *et al.* Association of high T allele frequency of CYP2B6 G516T polymorphism among ethnic South Indian HIV-infected patients with elevated plasma efavirenz and nevirapine. *J Antimicrob Chemother* 2009; **63**:841–843.
- 29 Saitoh A, Sarles E, Capparelli E, Aweeka F, Kovacs A, Burchett SK, *et al.* CYP2B6 genetic variants are associated with nevirapine pharmacokinetics and clinical response in HIV-1-infected children. *AIDS* 2007; **21**: 2191–2199.
- 30 Lang T, Klein K, Fischer J, Nüssler AK, Neuhaus P, Hofmann U, *et al.* Extensive genetic polymorphism in the human CYP2B6 gene with impact on expression and function in human liver. *Pharmacogenetics* 2001; **11**:399–415.
- 31 Heil SG, van der Ende ME, Schenk PW, van der Heiden I, Lindemans J, Burger D, *et al.* Associations between ABCB1, CYP2A6, CYP2B6, CYP2D6, and CYP3A5 alleles in relation to efavirenz and nevirapine pharmacokinetics in HIV-infected individuals. *Ther Drug Monit* 2012; **34**:153–159.
- 32 Chen J, Sun J, Ma Q, Yao Y, Wang Z, Zhang L, *et al.* CYP2B6 polymorphism and nonnucleoside reverse transcriptase inhibitor plasma concentrations in Chinese HIV-infected patients. *Ther Drug Monit* 2010; **32**:573–578.
- 33 Ghannoum MA, Mukherjee PK, Jurevic RJ, Retuerto M, Brown RE, Sikaroodi M, *et al.* Metabolomics reveals differential levels of oral metabolites in HIV-infected patients: toward novel diagnostic targets. *OMICS* 2013; **17**:5–15.