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Transmitted Drug Resistance in the CFAR Network of Integrated Clinical Systems Cohort: Prevalence and Effects on Pre-Therapy CD4 and Viral Load

Art F. Y. Poon¹, Jeannette L. Aldous², W. Christopher Mathews², Mari Kitahata³, James S. Kahn⁴, Michael S. Saag⁵, Benigno Rodriguez⁶, Stephen L. Boswell⁷, Simon D. W. Frost⁸, Richard H. Haubrich²*

¹BC Centre for Excellence in HIV/AIDS, Vancouver, British Columbia, Canada, ²Department of Medicine, University of California San Diego, San Diego, California, United States of America, ³University of Washington, Seattle, Washington, United States of America, ⁴University of California San Francisco, San Francisco, California, United States of America, ⁵University of Alabama Birmingham, Birmingham, Alabama, United States of America, ⁶Case Western Reserve University, Cleveland, Ohio, United States of America, ⁷Fenway Community Health/Harvard Medical School, Boston, Massachusetts, United States of America, ⁸University of Cambridge, Cambridge, United Kingdom

Abstract

Human immunodeficiency virus type 1 (HIV-1) genomes often carry one or more mutations associated with drug resistance upon transmission into a therapy-naïve individual. We assessed the prevalence and clinical significance of transmitted drug resistance (TDR) in chronically-infected therapy-naïve patients enrolled in a multi-center cohort in North America. Pre-therapy clinical significance was quantified by plasma viral load (pVL) and CD4+ cell count (CD4) at baseline. Naïve bulk sequences of HIV-1 protease and reverse transcriptase (RT) were screened for resistance mutations as defined by the World Health Organization surveillance list. The overall prevalence of TDR was 14.2%. We used a Bayesian network to identify co-transmission of TDR mutations in clusters associated with specific drugs or drug classes. Aggregate effects of mutations by drug class were estimated by fitting linear models of pVL and CD4 on weighted sums over TDR mutations according to the Stanford HIV Database algorithm. Transmitted resistance to both classes of reverse transcriptase inhibitors was significantly associated with lower CD4, but had opposing effects on pVL. In contrast, position-specific analyses of TDR mutations revealed substantial effects on CD4 and pVL at several residue positions that were being masked in the aggregate analyses, and significant interaction effects as well. Residue positions in RT with predominant effects on CD4 or pVL (D67 and M184) were re-evaluated in causal models using an inverse probability-weighting scheme to address the problem of confounding by other mutations and demographic or risk factors. We found that causal effect estimates of mutations M184V/I (−1.7 log₁₀ pVL) and D67N/G (−2.1 √CD4 and + 0.4 log₁₀ pVL) were compensated by K103N/S and K219Q/E/N/R. As TDR becomes an increasing dilemma in this modern era of highly-active antiretroviral therapy, these results have immediate significance for the clinical management of HIV-1 infections and our understanding of the ongoing adaptation of HIV-1 to human populations.


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* E-mail: rhaubrich@ucsd.edu

Introduction

A substantial fraction (≈5%–20%) of human immunodeficiency virus type 1 (HIV-1) variants that have been transmitted and establish infections in individuals who have never been exposed to antiretroviral drugs (i.e., ARV-naïve) already carry one or more mutations that are associated with resistance to ARVs [1,2]. Resistance mutations are generally slow to revert in ARV-naïve hosts [3,4] and can persist at low frequencies in treatment-experienced hosts as well [5]. The pre-existence of resistance mutations can significantly diminish effectiveness of subsequent ARV therapy [6,7]; for example, transmitted K103N mutations are associated with increased regimen failure and poorer outcomes on non-nucleoside reverse transcriptase inhibitors (NNRTIs) [8]. On the other hand, resistance mutations can also incur a measurable cost with respect to virus replicative capacity in vitro [9–11] and competitive growth in vivo [12]. Within therapy-naïve hosts, the fitness costs of transmitted drug resistance (TDR) mutations may influence the subsequent evolution and population dynamics of HIV-1. With the exception of limiting the choice of initial ARV regimens, however, the direct clinical consequences of TDR mutations in therapy-naïve hosts remain inconclusive [13–17].

Our central hypothesis in this study is that the presence of TDR mutations in therapy-naïve hosts has a measurable effect on not only the subsequent rate of growth of the virus population within the host, but also on the rate of depletion of CD4+ T-lymphocytes...
that are targeted by HIV-1. To evaluate this hypothesis, we assess
the relationship between TDR mutations and prognostic clinical
markers – CD4+ T-cell count (CD4) and plasma HIV-1 RNA load
(pVL) – at baseline using data from the Centers for AIDS
Research (CFAR) Network of Integrated Clinical Systems
(CNICS), an observational cohort created from a data-sharing
collaboration between multiple clinical sites in North America
[18]. ‘Baseline’ refers to the measurements of clinical markers
upon HIV diagnosis and/or entry into clinical care. It does not
correspond to a consistent time point after infection and many
patients will have already progressed into the chronic phase of
infection. Nevertheless, these data can provide useful insight into
the clinical implications of TDR in therapy-naïve hosts.

First, we quantify the effects of TDR mutations at both
aggregate and position-specific levels. An aggregate approach
sums across mutations occupying different positions in HIV-1
protease and reverse transcriptase, implicitly assuming that every
mutation has a similar effect (in both direction and magnitude) on
baseline CD4 or pVL. In contrast, a position-specific analysis
recognizes the possibility that some TDR mutations will have a
disproportionately large effects while others have negligible effects.
Furthermore, it enables us to identify compensatory interactions,
such that the effect of a specific mutation on CD4 or pVL depends
on the presence or absence of other mutations; such interactions
are an important aspect of the evolution of drug resistance in HIV-
1 [11]. Second, we re-evaluate statistically significant associations
of individual TDR mutations in a causal modeling framework, i.e.,
inverse probability-of-treatment weighting [19]. A statistical
association between a treatment (a TDR mutation) and an
outcome (baseline CD4 or pVL) in an observational study may be
biased if one or more variables, such as other co-transmitted
resistance mutations, are not only correlated with the treatment
but also affect the outcome [19]. In the presence of such
confounding factors, the significant association could be wrongly
attributed to a causal effect of the treatment on the outcome.
Using statistical procedures that can adjust for confounding by
weighting observational data has become an important compo-
nent of understanding the consequences of drug resistance in HIV
[20].

Methods

Ethics statement

All patients in the CNICS database have provided informed
written consent, as reviewed and approved by the institutional
review boards of all participating sites – University of Alabama,
Birmingham (UAB); University of California, San Diego (UCSD); 
University of California, San Francisco (UCSF); University of
Washington (UW); Case Western Reserve University (CWRU); 
and Harvard University (FENWAY) – to have their clinical
information used for the purposes of research. Patients were
informed on the minimum information being collected, alterna-
tives to participation, and possible uses of the data. In addition,
CNICS has received a Certificate of Confidentiality from the
National Institutes of Health (NIH).

Data collection

The study population comprised individuals from 6 CNICS
sites: University of Alabama, Birmingham; University of Califor-
nia, San Diego; University of California, San Francisco; University
of Washington; Case Western Reserve University; and Harvard
University [18]. All patients in the CNICS database have provided
informed written consent, as reviewed and approved by the
institutional review boards of all participating sites, to have their
clinical information used for the purposes of research. HIV-1 pol
sequences in the region encoding protease and/or part of reverse
transcriptase (i.e., the first 246–400 codons of RT) were obtained at
each site by conventional Sanger sequencing directly from RT-
PCR amplification products from sample extractions of viral
RNA. The exact bulk sequencing protocol varied among sites, as
some sites used commercial laboratory services (e.g., Monogram,
Quest, Virco, LabCorp) whereas others used in-house assays based
on commercial kits. At the time of this study, 4914 codon or amino
acid sequences were available in the CNICS database but many
were obtained when patients were on-therapy. Amino acid
sequences were reconstituted from reports of residue polymor-
phisms relative to the HXB2 reference sequence. Sequences were
linked to: unique anonymized patient identifiers; CNICS site; 
sampling date; age; ARV regimens; demographic factors (self-
reported gender at baseline, race/ethnicity); HIV risk factors (men
who have sex with men, MSM; injection drug use, IDU); baseline
plasma HIV RNA titres (pVL, virus/mL plasma); and baseline
CD4 cell counts (cells/mL). A patient record was included in this
study if: (1) a sequence was sampled before therapy, and (2) CD4
and/or pVL were sampled within 120 days of the sequence sample
date. To normalize the distributions of pVL and CD4, we used
\[ log_{10} \] and cube-root transformations [21], respectively. Race and
ethnicity records were aggregated into the following groups: non-
Hispanic white, non-Hispanic black, Hispanic, and other. Non-
random associations between demographic and risk factors were
identified using log-linear models.

Sequence analysis

Sequences were aligned pairwise against the NL4-3 pol reference
sequence using an implementation of the Gotoh algorithm in
HyPhy [22,23] under default settings. Surveillance drug resistance
mutations (SDRMs) were tallied for each amino acid sequence
according to the 2009 update of the World Health Organization
list of surveillance drug resistance mutations (SDRMs) [24]. Amino
cid polymorphisms (e.g., bulk sequence mixtures) were resolved to
the resistant residue when applicable.

Statistical analysis

Resistance scores by drug class (protease inhibitors, PIs; 
nucleoside and non-nucleoside reverse transcriptase inhibitors,
NRTI/NNRTIs) were calculated according to the Stanford HIV
Drug Resistance database algorithm [25]. The Stanford scoring
system is a linear predictor of drug resistance phenotypes that
works by assigning integer weights to a sequence for encoding
resistance-associated amino acid residues at specific positions.
Weights (or ‘scores’) for a given sequence were calculated for
every drug in a given drug class. We used the highest score of any
drug in a drug class as the class-specific score. These quantitative
scores, denoted by \( S_{\text{PI}}, S_{\text{NRTI}} \) and \( S_{\text{NNRTI}} \) respectively, were used
to analyze the aggregate effects of TDR on baseline CD4 and
pVL. Aggregate or position-specific effects of TDR on baseline
CD4 or pVL were evaluated alongside demographic and risk
factors in linear models. In each case we used a bi-directional
stepwise algorithm in R (\texttt{stepAIC} [26]) to select a ‘best-fitting’ linear
model based on the Akaike information criterion (AIC), which
penalizes model likelihood by the number of parameters. We
seeded the algorithm with the full additive model (without
interaction terms) and limited model complexity to second-order
interactions. To avoid over-fitting the data from evaluating a large
number of alternative models, we averaged parameter estimates
and \( P \) values over an ensemble of models (best +5 next-best) using
Akaike weights [27].
To estimate causal effects of individual SDRMs, we used inverse probability-of-treatment weight (IPTW) estimators [19]. The conditional probability \( P(A | A) \) for a given ‘treatment’ variable \( A \) was computed by fitting a logistic model of \( A \) against the set of all potential confounding variables \( A \). To account for compensatory interactions among mutations, we combined the corresponding presence/absence variables into a single multinomial treatment as suggested to us by Miguel A. Hernán (pers. comm.). For example:

\[
A_{\text{M184}} = \begin{cases} 
0 & \text{if } \text{M184X} = 0 \text{ and } (\text{K103X} = 0 \text{ and } \text{K219X} = 0) \\
1 & \text{if } \text{M184X} = 1 \text{ and } (\text{K103X} = 0 \text{ and } \text{K219X} = 0) \\
2 & \text{if } \text{M184X} = 1 \text{ and } (\text{K103X} = 1 \text{ or } \text{K219X} = 1) 
\end{cases}
\]

where \( X \) signifies any SDRM residue at that position. Conditional probabilities for multinomial treatments were obtained by fitting a multinomial logistic model with the \textit{multinom} function in the R package \textit{nnet}. Because weighting observations by the inverse of \( P(A | A) \) can introduce excessive variability, we used stabilized weights that normalize \( P(A | A) \) by the marginal probability \( P(A) \), which was estimated by fitting a logistic model containing only the intercept term [19]. The stabilized weights were incorporated into a linear model of baseline CD4 or pVL on treatment \( A \) using the \textit{vglm} function in the R package \textit{survey} [28], which uses an estimating equation-based approach to fitting generalized linear models with robust standard errors. Cases with missing data were omitted from these analyses.

A Bayesian network analysis to detect co-transmission of TDR mutations was carried out using a Markov chain Monte Carlo (MCMC) procedure in HyPhy [29]. A Bayesian network is a compact representation of the joint probability distribution of multiple variables (i.e., the presence/absence of TDR mutations), where ‘joint’ implies that the probability distribution of a variable may be conditional on other variables in the network [30]. In other words, a Bayesian network provides an efficient framework for exploring the statistical interactions among variables. Each variable is represented by a ‘node’ in the network, and connections between nodes (‘edges’) are drawn to indicate that one variable is conditioned on the second. The MCMC procedure obtains a random sample of Bayesian networks from the posterior probability distribution defined by the data. The Markov chain was propagated for \( 10^6 \) steps, discarding the first half as burn-in and thinning the remaining sample to 100 steps at equal intervals. Edges in the network signifying co-transmission were accepted if they were present in 90% or more of the networks in the sample.

**Results**

**Population**

The study population was comprised of 14111 individuals with a median baseline CD4 of 300 cells/mL (\( n = 14011 \)) and a median baseline pVL of 24400 copies/mL (\( n = 13953 \)). Median year of birth was 1964. The majority of the population self-reported as ‘white’ (\( n = 8694 \)), 3725 individuals self-reported as ‘black’, 207 as ‘Asian/Pacific Islander’ and 833 as ‘other’; there were 650 non-respondents. At the time of this study, the CNICS database contained 1585 sequence records that we classified as therapy-naïve. Out of these, 1575 naive sequences were linked to baseline CD4 and pVL records. 1526 naive sequences were associated with baseline CD4 records within 120 days of the sequence sampling date and were otherwise censored from subsequent analyses. Likewise, 1516 naive sequences were associated with baseline pVL within 120 days of sampling and were otherwise censored. The median baseline CD4 and pVL of patients with naïve sequences in this data set were 285 cells/mL and \( 10^4 \) copies/mL, respectively. Composition of the naïve sample with respect to race was significantly associated with gender (\( \chi^2 = 68.2, \quad df = 3, \quad P = 1.03 \times 10^{-14} \); e.g., the sample included a disproportionately greater number of naïve sequences from white males (odds ratio, \( OR = 3.1 \)) and black females (\( OR = 3.0 \)). Sample composition by race was also significantly associated with MSM (\( \chi^2 = 138.8, \quad df = 3, \quad P = 7.05 \times 10^{-30} \)), largely because of a greater number of white MSMs than expected by marginal frequencies (\( OR = 2.85 \)).

**Prevalence of transmitted SDRMs**

Overall, 225 out of 1585 naïve sequences (14.2%) contained one or more SDRMs. Of these 225 sequences, 66 (4.2%) contained at least one PI-associated SDRM, 130 (8.2%) contained at least one NRTI-associated SDRM, and 131 (8.3%) contained at least one NNRTI-associated SDRM. In addition, 17 (1.1%) sequences contained SDRMs in all three drug classes, which is substantially greater than the number expected by chance (<0.5 sequences) if the joint transmission of mutations was independent of drug class. A decline from pre-2003 levels in the fraction of naïve sequences with at least 1 SDRM was mirrored by a similar decline in the mean number of SDRMs per naïve sequence (Figure 1). However, we observed an increase in the most recent sample year (2008) in the upper 95% quartile of the distribution in the number of SDRMs. Neither measure of prevalence was significantly associated with demographic or risk factors in generalized linear models (\( \chi^2 > 0.05 \)). Counts of SDRMs by residue position are provided in Table 1. A Bayesian network analysis detected significant co-transmission of SDRMs in four groups (Figure 2). The largest group generally corresponded to NRTI resistance-associated

![Figure 1. Prevalence of transmitted surveillance drug resistance mutations (SDRMs) over time.](https://example.com/figure1.png)

**Figure 1. Prevalence of transmitted surveillance drug resistance mutations (SDRMs) over time.** Sampling years 1998–2002 were grouped into a single level (‘pre-2003’) to adjust for small sample sizes (\( n = 3,518, \) and 56, respectively). Sample sizes for the bins are displayed below the x-axis. Dashes (−) indicate the fraction of naïve sequences in a given sampling period that contain at least one SDRM (right y-axis). The trend in mean number of SDRMs per naïve sequence (left y-axis) over time is displayed as a solid line annotated with the actual values. The 95% quantile of each time point is depicted by a lighter line bounding a shaded region to illustrate the trend in the distributions (all medians were zero).

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mutations (with the exception of K103, I54 and V82) and contained well-characterized mutational pathways, e.g., D67/T69/K70/K219 and T215/M41/L210. Two smaller groups (M46/I84/I85 and D30/N88) comprised mutations associated with PI resistance, the latter group being associated with resistance to nelfinavir in particular. The remaining group (K101/G190) comprised mutations associated with resistance to NNRTIs. In sum, co-transmitted SDRMs tended to confer resistance to the same drug or drug class.

### Aggregate SDRM predictors of baseline CD4 and HIV RNA

The summated Stanford scores for NRTI and NNRTI ($S_{NRTI}$, $S_{NNRTI}$) and race/ethnicity were significantly ($\alpha = 0.05$) associated with baseline CD4 (Table 2). For every 10 units of $S_{NRTI}$ and $S_{NNRTI}$, the model predicted a decline in $\sqrt[3]{CD4}$ by about 0.07 and 0.04 units, respectively. For example, if a hypothetical patient whose CD4 count matched the study median (285 cells/mL) became infected by an HIV-1 variant carrying SDRMs such that $S_{NRTI} \sim 100$ and $S_{NNRTI} \sim 100$, we would predict a baseline CD4 count of $(\sqrt[3]{285} - 0.069 \times 10 - 0.044 \times 10^2) \approx 162$ cells/mL. The joint effect of transmitted RTI resistance on CD4 is illustrated in Figure 3. Only about 5.8% of the variance in $\sqrt[3]{CD4}$ was explained by this model. Similarly, $S_{NRTI}$, $S_{NNRTI}$, gender and race/ethnicity were significantly associated with baseline pVL (Table 2). For every 10 units in $S_{NNRTI}$, pVL was predicted to decline by about 0.03 log10 units; in contrast, pVL was predicted to increase by about 0.02 log10 units for every 10 units in $S_{NNRTI}$ (Figure 4). Only 2% of the variance in $\log_{10}$ pVL was explained by this model. $S_{PI}$ was not significantly associated with either CD4 or pVL at baseline.

### Position-specific SDRM predictors of baseline CD4 and HIV RNA

Although aggregate SDRM-based statistics such as Stanford scores are convenient and easy to interpret as proximate measures of drug class-specific resistance, they may mask the effects of individual mutations on clinical outcome. Consequently, we assessed the effects of position-specific SDRMs in linear models of baseline CD4 and pVL. To minimize the number of predictor variables and avoid over-fitting of the data, we limited our analysis to positions with a minimum SDRM frequency of 1% in naive sequences (see Table 1). These positions were: M46, I54, and L90 in protease, and M41, D67, M184, L210, T215, K219, K103, Y181, and G190 in reverse transcriptase. The presence or absence of SDRMs at each position was represented by a binary variable (herein denoted by appending an ‘X’ to the amino acid positional notation, e.g., M46X = {0,1}).

D67X and K219X were each associated with significantly lower baseline CD4 ($P<0.04$; Table 3); both sets of SDRMs are thymidine analog mutations (TAMs) conferring resistance to NRTIs. For example, the model would predict a hypothetical decline from 400 cells/mL to 146 and 235 cells/mL with the introduction of SDRMs at positions D67 and K219, respectively.

In addition, there was a significant interaction effect between D67X and K219X associated with a compensatory increase by

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**Table 1. Number and percentage prevalence of putatively transmitted surveillance drug resistance mutations (SDRMs) by residue position in antiretroviral (ARV)-naive sequences.**

<table>
<thead>
<tr>
<th>Class</th>
<th>position</th>
<th>count</th>
<th>% prevalence</th>
<th>Class</th>
<th>position</th>
<th>count</th>
<th>% prevalence</th>
</tr>
</thead>
<tbody>
<tr>
<td>PI</td>
<td>L23</td>
<td>1</td>
<td>0.06</td>
<td>NRTI (cont’d)</td>
<td>K70</td>
<td>9</td>
<td>0.57</td>
</tr>
<tr>
<td></td>
<td>L24</td>
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<td>0.06</td>
<td></td>
<td>L74</td>
<td>11</td>
<td>0.69</td>
</tr>
<tr>
<td></td>
<td>D30</td>
<td>15</td>
<td>0.95</td>
<td></td>
<td>V75</td>
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<td>0.13</td>
</tr>
<tr>
<td></td>
<td>V32</td>
<td>2</td>
<td>0.13</td>
<td></td>
<td>F77</td>
<td>1</td>
<td>0.06</td>
</tr>
<tr>
<td></td>
<td>M46</td>
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<td></td>
<td>Y115</td>
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</tr>
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<td>0.13</td>
<td></td>
<td>F116</td>
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<tr>
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<td>Y181</td>
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<td>Y188</td>
<td>10</td>
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<td>49</td>
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<td></td>
<td>G190</td>
<td>24</td>
<td>1.51</td>
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<td>K65</td>
<td>3</td>
<td>0.19</td>
<td></td>
<td>P225</td>
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<td>0.06</td>
</tr>
<tr>
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<td></td>
<td>M230</td>
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<td>0.57</td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>

$PI =$ protease inhibitor; $NRTI =$ nucleoside reverse transcriptase inhibitor; $NNRTI =$ non-nucleoside reverse transcriptase inhibitor.

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about +2.5 units √CD4 (P = 0.006; Figure 5). This model accounted for 6.8% of the variance in √CD4.

M184X was significantly associated with an approximately tenfold lower pVL at baseline (P = 1.3 × 10⁻²; Table 3). M46X and L210X were also significantly associated with lower baseline pVL (P < 0.01) and D67X was associated with greater pVL (P = 0.009). We also observed several significant mutational interaction terms in the model. For instance, interactions between M184X and either K103X or K219X were associated with a compensatory increase in pVL (P = 0.018 and P = 0.023, respectively; Figure 5). Similarly, a decline in pVL associated with M46X was compensated by T215X (P = 0.033). An interaction term between D67 and K219, which was encountered in the preceding model on CD4, was also statistically significant in this model of pVL.

Table 2. Coefficient estimates from Akaike Information Criterion (AIC)-selected linear models of baseline √CD4 and plasma HIV RNA on Stanford scores by drug class and demographic and risk factors.

<table>
<thead>
<tr>
<th></th>
<th>√CD4</th>
<th>log₁₀ plasma HIV RNA</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Estimate (95% CI)</td>
<td>P value</td>
</tr>
<tr>
<td>S_NRTI</td>
<td>−6.9 (−12.2, −1.1) × 10⁻¹</td>
<td>0.02</td>
</tr>
<tr>
<td>S_NNRTI</td>
<td>−4.4 (−8.4, −0.5) × 10⁻³</td>
<td>0.035</td>
</tr>
<tr>
<td>Male</td>
<td>NS</td>
<td>0.19 (0.06, 0.32)</td>
</tr>
<tr>
<td>Race/ethnicity</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Black</td>
<td>−0.35 (−0.61, 0.09)</td>
<td>0.008</td>
</tr>
<tr>
<td>Hispanic</td>
<td>−0.57 (−0.86, −0.28)</td>
<td>1.1 × 10⁻⁴</td>
</tr>
</tbody>
</table>

All estimates were averaged over an ensemble of linear models using Akaike weights. Only statistically significant (α = 0.05) terms after weighting are reported. Linear effects of factors were estimated relative to the model intercept, i.e., a hypothetical female white individual. NS = not significant.

doi:10.1371/journal.pone.0021189.t002

Figure 2. Bayesian network depicting conditional dependencies among surveillance drug resistance mutations (SDRMs) in ARV-naïve sequences. Each labeled node corresponds to a position in protease (rectangular) or RT (rounded). Nodes without dependencies (L23, L24, V32, I47, I50, F53, G73, L76, K65, V75, F77, Y115, F116, L100, V106, V179, Y181, and Y188) were omitted from the graph for clarity. Connections between nodes (edges) are labeled with the log₁₀ odds ratio of the 2 × 2 contingency table for the presence/absence of SDRMs at the respective sites, e.g., an SDRM at position PR-D30 is estimated to be 10⁻¹ ≈ 3000 times more likely to be present in an ARV-naïve sequence that contains an SDRM at position PR-N88. Line widths for edges are also drawn in proportion to the log₁₀ odds ratios. Inf = infinity, i.e., unable to estimate because of zero count(s) in the contingency table.

doi:10.1371/journal.pone.0021189.g002

Figure 3. CD4 cell count (raw) plotted against the sum of Stanford scores for nucleoside and non-nucleoside reverse transcriptase inhibitors (S_NRTI and S_NNRTI, respectively). The upper limit of CD4 (2073 cells/mL) was truncated to 1000 cells/mL (omitting 19 outliers) to emphasize the overall trend. Because the predicted baseline CD4 tended to decline with both S_NRTI and S_NNRTI we combined the scores into a single ordinal variable to facilitate interpretation. The linear model prediction is displayed as a solid line (generated by fitting a smoothing spline to the predicted values with smoothing parameter 2 = 0.9), with 95% confidence intervals displayed as dashed lines.

doi:10.1371/journal.pone.0021189.g003
plasma viral load (pVL) as a function of Stanford scores for associated with higher pVL, while associated with a unweighted univariate linear model, M184X was significantly i.e. multinomial outcome their compensatory interactions with M184X. Consequently, the model exposed a greater deleterious effect of M184X on \( \log_{10} pVL \) to 18.72 with a mean of 1.016. Adding stabilized weights to the conditional probability of carrying M184X ranged from 0.02 to 25% [1]. On the other hand, the transmission of a specific mutation is a relatively infrequent event whose prevalence requires very large samples (over 1000 individuals) to estimate. This requirement has generally been achieved by integrating study populations from similar geographic regions, such as the Combined Analysis of Resistance Transmission over Time of Chronically and Acute Infected HIV Patients (CATCH) study encompassing 27 countries in Europe [31], the Swiss HIV Cohort Study [32], the UK Collaborative HIV cohort study [14], and the Centers for AIDS Research (CFAR) Network of Integrated Clinical Systems (CNICS) cohort reported in this study. Here we briefly compare and contrast the prevalence of drug class-specific and site-specific TDR across these integrated cohorts. First, NRTI-associated SDRMs generally tend to be more prevalent than SDRMs associated with PIs or NNRTIs. Our sample deviates slightly from this trend in that the prevalence of naive sequences with \( \geq 1 \) NNRTI-associated SDRM is similar to sequences with \( \geq 1 \) NRTI-associated SDRM, largely due to an atypically high frequency of transmitted mutations at RT-K103 (5.2%) in our sample. Second, SDRMs that are slow to revert in the absence of selection (e.g., M41L, K103N, and T215X in RT and L90M in protease), implying a negligible cost to fitness [1], tend to have relatively high prevalence in therapy-naive sequences.

The foremost and best -documented clinical implication of TDR is that it impedes the virological response to subsequent drug therapy [6–8]. In contrast, the clinical implications of TDR in the absence of drug therapy are subtle and less well understood. These effects have been difficult to elucidate because the transmission of SDRMs remains an infrequent event at the scale of individual mutations. Investigators have attempted to overcome the limitations of insufficient sample sizes by evaluating the effects of aggregate statistics of TDR, such as an ‘all-or-none’ statistic that groups sequences carrying one or more SDRMs [14,16,17]. While this approach is convenient and easy to interpret, it is subject to confounding because different drug classes or mutations can have opposite effects on prognostic clinical markers. Our use of a large data set from a multi-center cohort enabled us to overcome some limitations of sample size, and to break down the effects of TDR on baseline CD4 and pVL by drug class or amino acid position. For example, we found that \( S_{NNRTI} \) had opposing associations with pVL; because these quantities are correlated, their effects on pVL would have been confounded in an ‘all-or-none’ analysis. Similarly, we have observed several compensatory interactions among mutations that would otherwise mask the actual effects of individual mutations on CD4 or pVL (e.g., D67N/G and K219Q/E).

Because this study population was comprised of seroprevalent rather than seroincident individuals , each baseline measurement of CD4 and pVL was sampled at a point in time following an unknown date of transmission. Consequently, there is no guarantee that these baseline measurements were taken at a consistent stage of infection. In other words, the CD4 count or pVL at baseline is the result of dynamics over an unknown period of time, starting from an unknown value upon infection. These missing data would be required to calculate rates of change, which would be easier to generalize to specific cases in clinical practice where these quantities (time since infection and prognostic markers at infection) may be known. This is a common problem of observational cohort studies and may explain why a substantial
Table 3. Coefficient estimates from AIC-selected linear models of baseline $\sqrt{CD4}$ and log$_{10}$ plasma HIV RNA on position-specific SDRMs and demographic and risk factors.

<table>
<thead>
<tr>
<th></th>
<th>Estimate (95% CI)</th>
<th>$P$ value</th>
<th></th>
<th>Estimate (95% CI)</th>
<th>$P$ value</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\sqrt{CD4}$</td>
<td></td>
<td></td>
<td>$log_{10}$ plasma HIV RNA</td>
<td></td>
<td></td>
</tr>
<tr>
<td>M41X</td>
<td>1.0 (0.05, 1.95)</td>
<td>0.04</td>
<td>NS</td>
<td>-0.98 (-1.6, -0.35)</td>
<td>0.003</td>
</tr>
<tr>
<td>M46X</td>
<td>NS</td>
<td></td>
<td>NS</td>
<td>0.96 (0.25, 1.7)</td>
<td>0.009</td>
</tr>
<tr>
<td>D67X</td>
<td>-2.1 (-3.9, -0.4)</td>
<td>0.026</td>
<td>NS</td>
<td>-1.06 (-1.44, -0.67)</td>
<td>1.3 x 10^{-7}</td>
</tr>
<tr>
<td>M184X</td>
<td>NS</td>
<td></td>
<td>NS</td>
<td>-0.6 (-1.0, -0.17)</td>
<td>0.007</td>
</tr>
<tr>
<td>L210X</td>
<td>NS</td>
<td></td>
<td>NS</td>
<td></td>
<td></td>
</tr>
<tr>
<td>K219X</td>
<td>-1.2 (-2.4, -0.08)</td>
<td>0.037</td>
<td>NS</td>
<td></td>
<td></td>
</tr>
<tr>
<td>D67X:X219X</td>
<td>2.5 (0.14, 4.8)</td>
<td>0.006</td>
<td>NS</td>
<td>-0.59 (-1.6, 0.4)</td>
<td>0.047</td>
</tr>
<tr>
<td>K219X:G190X</td>
<td>-3.0 (-5.6, -0.4)</td>
<td>0.014</td>
<td>NS</td>
<td></td>
<td></td>
</tr>
<tr>
<td>L90X:M41X</td>
<td>-1.7 (-4.4, 0.1)</td>
<td>0.007</td>
<td>NS</td>
<td></td>
<td></td>
</tr>
<tr>
<td>IS4X:L210X</td>
<td>2.0 (-0.59, 4.7)</td>
<td>0.04</td>
<td>NS</td>
<td></td>
<td></td>
</tr>
<tr>
<td>M46X:T215X</td>
<td>NS</td>
<td></td>
<td>NS</td>
<td>1.7 (0.88, 2.5)</td>
<td>0.033</td>
</tr>
<tr>
<td>M184X:K103X</td>
<td>NS</td>
<td></td>
<td>NS</td>
<td>0.58 (-0.14, 1.3)</td>
<td>0.018</td>
</tr>
<tr>
<td>M184X:X219X</td>
<td>NS</td>
<td></td>
<td>NS</td>
<td>0.87 (-0.07, 1.8)</td>
<td>0.23</td>
</tr>
<tr>
<td>K219X:Y181X</td>
<td>NS</td>
<td></td>
<td>NS</td>
<td>1.43 (0.34, 2.5)</td>
<td>0.013</td>
</tr>
<tr>
<td>Male</td>
<td>-0.58 (-0.9, -0.24)</td>
<td>7.5 x 10^{-5}</td>
<td>NS</td>
<td>-20.0 (-38.4, 0.1)</td>
<td>10^{-5}</td>
</tr>
<tr>
<td>Sample date</td>
<td>23.3 (7.4, 38.9) $\times 10^{-5}$</td>
<td>0.004</td>
<td></td>
<td>-20.0 (-38.4, 0.1) $\times 10^{-5}$</td>
<td>0.04</td>
</tr>
<tr>
<td>Race/ethnicity</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Black</td>
<td>-0.35 (-0.61, -0.10)</td>
<td>0.007</td>
<td>-0.16 (-0.26, -0.05)</td>
<td>0.003</td>
<td></td>
</tr>
<tr>
<td>Hispanic</td>
<td>-0.57 (-0.83, -0.29)</td>
<td>8.3 x 10^{-5}</td>
<td>NS</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Other</td>
<td>-0.53 (-0.98, -0.08)</td>
<td>0.02</td>
<td>NS</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

SDRMs are annotated by HXB2 reference residue and position (gene-specific numbering), followed by an ‘X’ to indicate a non-reference residue. Positions 46, 54, and 90 are in protease and all others are in reverse transcriptase. All estimates were averaged over an ensemble of linear models using Akaike weights. Only terms that were statistically significant ($|z| = 0.05$) are reported here. NS = not significant.

doi:10.1371/journal.pone.0021189.t003

Figure 5. Box-and-whisker plots illustrating (A) the effects of SDRMs at positions D67 and K219 on CD4 cell count and (B) the effects of SDRMs at positions M184 and K103 on plasma viral load (pVL). ‘Wildtype’ denotes sequences lacking SDRMs at both positions, irrespective of whether any other SDRMs were present at other positions in protease or RT. Solid lines indicate the group median and open circles denote outliers that fall outside the region defined by 1.5 times the interquartile range. Plot (A) was rescaled with respect to untransformed CD4 counts to emphasize differences among groups, trimming 4 outliers from the ‘wildtype’ group (1602, 1626, 1838, and 2073 cells/mL) from the plot region. Sample sizes per group are annotated on each plot.

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fraction (~90%) of variation in baseline CD4 or pVL remained unaccounted for in the linear models. Furthermore, because the baseline samples were taken either upon entry into care or prior to initiating ARV therapy (ART), they may constitute a biased sample of the patient population with respect to CD4 and pVL. Recent guidelines, for example, indicate that patients should be initiated on ART when their CD4 cell count falls below a threshold of 500 cells per mL regardless of HIV RNA [33]. However, treatment guidelines have evolved over time [34] and using a large sample size covering a decade of clinical practice can ameliorate some of these biases. As guidelines have pushed initiation of therapy to earlier time points, it could be argued that less fit virus, with lower HIV RNA and higher CD4, would not merit clinical significance since virtually every patient should start therapy soon after identification; in other words, an association of TDR with lower viral load would not result in a longer delay between detection of HIV and the need to start therapy. However, viral fitness and replication level may be very significant in the prevalence of resistance mutations in the circulating virus population, the pool of virus in a community that could potentially be transmitted. As the pool of patients with suppressed virus increases due to ARV treatment, the relative rates of transmitted resistance may paradoxically increase due to a diminishing pool of untreated wildtype virus and a greater prevalence of resistance in the circulating virus population (~10%–20% of patients who are failing therapy [1]). In this scenario, viral fitness and its effect on HIV RNA could determine which viruses are transmitted. Mutations such as M184V may be transmitted less often due to the reduced overall viral load in those subjects, whereas mutations such as K103N may increase in prevalence. The overall rates of transmitted resistance would be a complex interplay between many host and viral factors.

Some of these issues might be resolved by the analysis of longitudinal data that are available for this study population [18]. However, this approach would create even more problems than it could potentially address. First, we would have to accommodate the effects of antiretroviral therapy that generally follows soon after HIV genotyping at baseline. This is not a trivial task, not only because it introduces a potentially large number of variables to the analysis (one for every drug, or a minimum of three for the predominant drug classes), but also because variation in adherence and confounding due to variation in prescribed regimens across clinical sites would severely complicate the interpretation of results. Second, we would have to accommodate large amounts of missing data due to differential follow-up among patients as well as a sparsity of HIV sequence data relative to CD4 and pVL measurements. In other words, HIV genotyping is performed much less frequently. Third, it is more difficult to adjust for confounding in longitudinal than cross-sectional data sets by inverse probability weighting. Previous studies have successfully employed a marginal structural modelling approach in similar but simplified contexts [20,33]. Marginal structural models are essentially a time-dependent generalization of the inverse probability weighting approach used here [19]. However, they are difficult to apply in highly-structured contexts (where pVL, CD4, drug regimen and HIV genotype all influence one another over time) and large numbers of missing data. In sum, the analysis of longitudinal data is a substantially different question outside the scope of this study on the effect of TDR on pre-therapy pVL and CD4 and must be left to future work.

Of all position-specific effects of SDRMs on baseline prognostic markers inferred from these data, one of the largest and most statistically significant was M184V/I. The effects of these substitutions on the kinetics and fidelity of HIV-1 reverse transcriptase and replication capacity in vitro are well-characterized [36–38]. Previous studies have also documented compensatory/epistatic interactions of other mutations acting on M184V/I, including K219Q [11] and N364I [39]. Furthermore, Paredes and colleagues have recently observed that in vivo fitness is reduced in viruses carrying the M184V mutation in the absence of lamivudine [12]. Even so, the effect of M184V/I on viral fitness in vivo is confounded by the effects of other SDRMs and demographic/risk factors that should be handled using a causal modeling approach [19]. Taking such an approach, we have found that uncompensated M184V/I mutations are causally associated with a 50-fold reduction (10−1.7) in baseline pVL in therapy-naive patients.

### Table 4. Unadjusted and stabilized weight-adjusted linear models of multinomial exposure variables A_{M184} (M184X and (K103X or K219X)) and A_{D67} (D67X and K219X) on log_{10} plasma HIV RNA and \sqrt{CD4}, respectively.

<table>
<thead>
<tr>
<th>Level</th>
<th>Unadjusted model</th>
<th>Adjusted model</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Estimate (95% C.I.)</td>
<td>P</td>
</tr>
<tr>
<td>\log_{10} plasma HIV RNA ~ A_{M184}</td>
<td>4.63 (4.58,4.67)</td>
<td>0.016</td>
</tr>
<tr>
<td>A_{M184} = 0</td>
<td>-1.10 (-1.57, -0.63)</td>
<td>4.4 × 10^{-6}</td>
</tr>
<tr>
<td>A_{M184} = 1</td>
<td>-0.236 (-0.568,0.096)</td>
<td>0.16</td>
</tr>
<tr>
<td>\sqrt{CD4} ~ A_{D67}</td>
<td>6.22 (6.12,6.33)</td>
<td>0.016</td>
</tr>
<tr>
<td>A_{D67} = 0</td>
<td>-1.77 (-2.8, -0.74)</td>
<td>7.97 × 10^{-4}</td>
</tr>
<tr>
<td>A_{D67} = 1</td>
<td>-0.768 (-1.93,0.40)</td>
<td>0.196</td>
</tr>
<tr>
<td>A_{D67} = 2</td>
<td>-0.21 (-0.64,0.22)</td>
<td>0.34</td>
</tr>
</tbody>
</table>

The model intercepts are taken to be \( a = 0 \) by default, i.e., none of the designated mutations are present; these estimates are unchanged in the adjusted model and are not repeated for clarity of presentation. Significant (\( p < 0.05 \)) effect estimates are bolded.

doi:10.1371/journal.pone.0021189.t004
Previous studies have reported no greater than a 3-fold (0.5 – 5) reduction in pVL due to M184V/I [39,40,41], while M184H itself has been estimated to reduce fitness by 23% relative to M184V [42]. This discrepancy may be due to failing to account for interactions with other mutations such as the compensatory interactions with K103 and K210, or confounding by other genetic and non-genetic factors affecting pVL. On the other hand, experimental studies of M184V/I-containing recombinant HIV-1 are potentially not subject to these confounding factors, and M184V has been reported to reduce fitness by as much as 16-fold in vitro [11]. However, it is difficult to estimate the fitness effect of a mutation in vivo from in vitro measures of its effect on replication efficiency as there are other components of RT functionality that can be affected [43].

In contrast, the clinical consequences of D67N/G and K219Q/E are not as well known. The effects of D67N/G and K219Q/E on CD4 levels in our study were mirrored by significant effects on pVL; however, it is difficult to estimate the fitness effect of a mutation in vivo from in vitro measures of its effect on replication efficiency as there are other components of RT functionality that can be affected [43].


References

Clinical Effects of Transmitted Resistance in HIV


