

Limited clinical benefit of minority K103N and Y181C-variant detection in addition to routine genotypic resistance testing in antiretroviral therapy-naïve patients

Karin J. Metzner^{a,*}, Alexandra U. Scherrer^{a,*}, Viktor Von Wyl^{a,*},
Jürg Böni^b, Sabine Yerly^c, Thomas Klimkait^d, Vincent Aubert^e,
Hansjakob Furrer^f, Hans H. Hirsch^g, Pietro L Vernazza^h,
Matthias Cavassiniⁱ, Alexandra Calmy^j, Enos Bernasconi^k,
Rainer Weber^a, and Huldrych F. Günthard^a and the Swiss HIV Cohort
Study

Objective: The presence of minority nonnucleoside reverse transcriptase inhibitor (NNRTI)-resistant HIV-1 variants prior to antiretroviral therapy (ART) has been linked to virologic failure in treatment-naïve patients.

Design: We performed a large retrospective study to determine the number of treatment failures that could have been prevented by implementing minority drug-resistant HIV-1 variant analyses in ART-naïve patients in whom no NNRTI resistance mutations were detected by routine resistance testing.

Methods: Of 1608 patients in the Swiss HIV Cohort Study, who have initiated first-line ART with two nucleoside reverse transcriptase inhibitors (NRTIs) and one NNRTI before July 2008, 519 patients were eligible by means of HIV-1 subtype, viral load and sample availability. Key NNRTI drug resistance mutations K103N and Y181C were measured by allele-specific PCR in 208 of 519 randomly chosen patients.

Results: Minority K103N and Y181C drug resistance mutations were detected in five out of 190 (2.6%) and 10 out of 201 (5%) patients, respectively. Focusing on 183 patients for whom virologic success or failure could be examined, virologic failure occurred in seven out of 183 (3.8%) patients; minority K103N and/or Y181C variants were present prior to ART initiation in only two of those patients. The NNRTI-containing, first-line ART was effective in 10 patients with preexisting minority NNRTI-resistant HIV-1 variant.

Conclusion: As revealed in settings of case-control studies, minority NNRTI-resistant HIV-1 variants can have an impact on ART. However, the sole implementation of minority NNRTI-resistant HIV-1 variant analysis in addition to genotypic resistance

^aDivision of Infectious Diseases and Hospital Epidemiology, University Hospital Zurich, ^bInstitute of Medical Virology, Swiss National Center for Retroviruses, University of Zurich, Zurich, ^cLaboratory of Virology and AIDS Center, University Hospital Geneva, Geneva, ^dDepartment of Biomedicine, Haus Petersplatz, University of Basel, Basel, ^eDivision of Immunology, University Hospital Lausanne, Lausanne, ^fDepartment of Infectious Diseases, Bern University Hospital and University of Bern, Bern, ^gDivision of Infectious Diseases and Hospital Epidemiology, University Hospital Basel, University of Basel, Basel, ^hDivision of Infectious Diseases, Cantonal Hospital St. Gallen, ⁱInfectious Diseases Service, University Hospital Lausanne, Lausanne, ^jDivision of Infectious Diseases, Geneva University Hospitals, Geneva, and ^kDivision of Infectious Diseases, Regional Hospital Lugano, Lugano, Switzerland.

Correspondence to Karin J. Metzner, MD, University of Zurich, University Hospital Zurich, Department of Medicine, Division of Infectious Diseases and Hospital Epidemiology, Rämistrasse 100, CH-8091 Zurich, Switzerland.

Tel: +41 (0)44 255 3029; fax: +41 (0)44 255-3291; e-mail: Karin.Metzner@usz.ch

* Karin J. Metzner, Alexandra U. Scherrer and Viktor Von Wyl contributed equally to this work.

Received: 19 May 2014; revised: 30 June 2014; accepted: 2 July 2014.

DOI:10.1097/QAD.0000000000000397

testing (GRT) cannot be recommended in routine clinical settings. Additional associated risk factors need to be discovered.

© 2014 Wolters Kluwer Health | Lippincott Williams & Wilkins

AIDS 2014, **28**:000–000

Keywords: antiretroviral therapy, antiretroviral therapy naive patients, drug resistance testing, minority drug-resistant HIV-1 variants, virological failure

Introduction

The HIV type 1 (HIV-1) establishes a chronic infection that is incurable to date. Combination antiretroviral therapy (ART) substantially decreases the morbidity and mortality in HIV-1 infected patients [1]. To achieve this outcome, the majority of patients have to be treated lifelong. This goes along with the risk of virologic failure and development of drug resistance that limits further treatment options [2,3]. Furthermore, as drug-resistant viruses can be transmitted, it is recommended to test for the presence of drug resistance mutations before initiating ART in treatment-naïve patients [4].

Routine genotypic resistance testing based on population sequencing (GRT) misses minority drug-resistant HIV-1 variants representing less than 20–25% of the virus population [5–7]. The application of more sensitive technologies to detect and quantify minority drug-resistant HIV-1 variants has revealed that these low abundant viruses can cause virologic failure especially in the context of ART regimens with a low genetic barrier to resistance, for instance, nonnucleoside reverse transcriptase inhibitor (NNRTI)-containing regimens [8–11]. A pooled analysis of 10 studies and almost 1000 patients has shown that preexisting minority NNRTI-resistant HIV-1 variants are associated with virologic failure [9]. A recent European multicohort case–control study [11] of 368 individuals using centralized ultra-sensitive 454 sequencing showed a significantly increased risk of virologic failure to first-line NNRTI-based ART when minority drug-resistant HIV-1 variants preexisted. These studies were designed as case–control or cohort studies focusing on patients experiencing virologic failure [9].

Current antiretroviral regimens are very efficient and the number of virologic failures due to drug resistance is low in ART-naïve patients. However, to minimize this risk of virologic failure of first-line ART even further, it is currently discussed to implement more sensitive genotypic resistance testing in routine clinical settings to detect systematically preexisting minority drug-resistant HIV-1 variants. To answer this, we have designed a study composed of a representative group of patients from the nation-wide, observational Swiss HIV Cohort Study (SHCS). Patients selected for inclusion were ART-naïve,

started with a NNRTI-containing ART and in whom no NNRTI or NRTI resistance mutation was detected by routine GRT prior to ART. Minority drug-resistant HIV-1 variants were measured and analysed in the context of virologic success or failure.

Materials and methods

Study participants and study design

The SHCS is an observational, nation-wide cohort, including at least 45% of the cumulative number of HIV-1 infected individuals declared to the Swiss health authorities [12]. The inclusion criteria for this substudy were as follows: chronic infection with HIV-1 subtype B or 01_AE, start of first-line ART with NNRTI and two NRTIs before 1 July 2008, no NNRTI or NRTI resistance mutations prior to ART detected by population sequencing, baseline viral load above 1000 HIV-1 RNA copies/ml plasma and available plasma sample within 6 months before initiation of first-line ART.

Random selection was performed within strata of HIV-1 subtype and time periods (4-year intervals of estimated year of HIV-1 infection between 1980 and 2008; time band sampling). The number of samples per stratum was selected proportionally to the fraction observed in all eligible patients. The infection date was estimated according to the method developed by P. Taffè and M. May [13]. The SHCS has been approved by ethical committees from all participating institutions and written informed consent has been obtained from all individuals [12].

Twenty-four months follow-up data were used to differentiate two groups of patients: those who experienced virologic failure and those who were successfully treated. Virologic failure was defined as virologic rebound with two consecutive viral loads more than 200 HIV-1 RNA copies/ml plasma after having achieved a viral load less than 50 copies/ml after initiation of first-line ART or one viral load of more than 200 HIV-1 RNA copies/ml plasma after 6–24 months of continuous treatment, followed by a modification of treatment or as virologic nonresponse, that is failing to achieve a decrease in viral load less than 200 HIV-1 RNA copies/ml plasma within 16 weeks of continuous treatment.

Viral load, resistance testing and allele-specific real-time PCR

Plasma HIV-1 viral load was quantified and genotypic resistance testing by population sequencing was performed as described [14]. Drug resistance mutations were defined as recommended by the International Antiviral Society-USA (IAS-USA) Drug Resistance Mutations Group and the surveillance drug resistance mutations list [2,15]. Minority K103N, Y181C and M184V drug-resistant HIV-1 variants were quantified by allele-specific real-time PCRs (AS-PCRs) as previously described in detail [10,14,16–18]. Each AS-PCR has a dynamic range of six logs and a detection limit of 10 HIV-1 DNA copies per reaction. The discriminatory abilities are as follows: 0.01% for the K103N, 0.2% for the Y181C and M184V mutations. Mutational load was calculated by multiplying the percentage of a given minority drug-resistant HIV-1 variant with the viral load.

Data and statistical analyses

Clinical data from the SHCS were used as well as HIV-1 *pol* sequences from the SHCS drug resistance database, which are stored in SmartGene's Integrated Database Network System (IDNS version 3.6.6) [19]. Statistical analyses were performed with Stata 12 SE software (StataCorp). All *P* values were two-sided, and the level of significance was set at 0.05.

Results

Baseline characteristics

The SHCS comprised 15 857 participants on 30 June 2010. One thousand six hundred and eight participants were chronically HIV-1 infected, ART-naïve and started first-line ART containing one NNRTI and two NRTIs before 1 July 2008 (Fig. 1). Another inclusion criterion was the infection with HIV-1 subtype B or 01_AE, which was necessary, because the AS-PCR primer design is only optimal for those two subtypes. For other HIV-1 subtypes, individual confirmation of the homology of primer binding sites would have been necessary that could potentially have jeopardized the random selection of patients. As shown in Fig. 1, 519 patients were deemed eligible for this study, of whom 221 individuals were randomly selected for minority drug-resistant HIV-1 variant testing. Finally, data from 208 patients were included in the analysis. Thirteen exclusions were due to sample unavailability, previously not reported NNRTI or NRTI resistance in the majority of viruses, or unsuccessful RT-PCR (Fig. 1).

These 208 patients were representative of all 519 eligible patients, thus representing chronically HIV-1 subtype B or 01_AE infected patients in Switzerland receiving first-line, NNRTI-containing ART. No significant

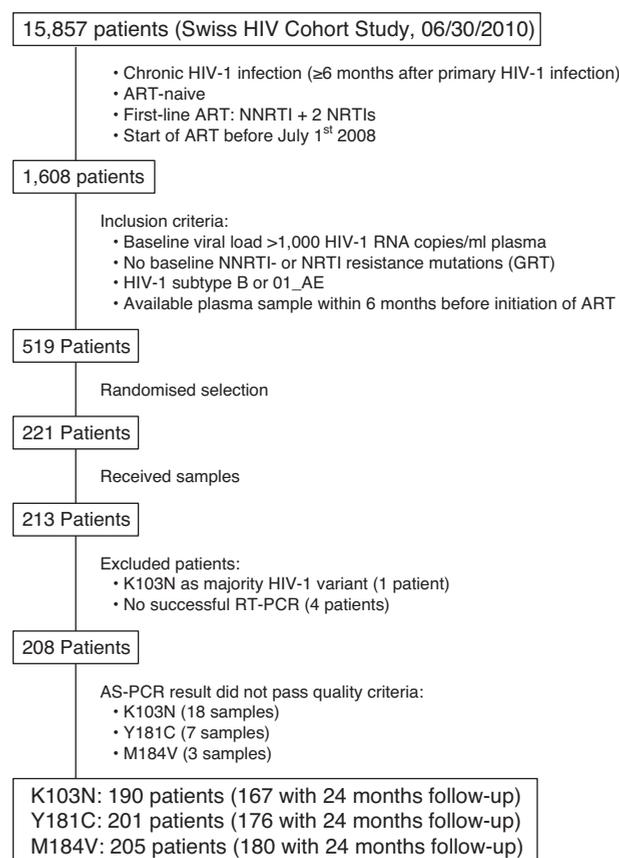


Fig. 1. Scheme of study design.

differences were observed in terms of age, sex, ethnicity, route of transmission, estimated year of HIV-1 infection, CD4⁺ cell count and viral load at baseline, and first-line ART regimens (Table 1). It has to be noted that certain clinical parameters differed significantly between the 519 eligible patients and the remaining 1089 of all 1608 patients who started first-line treatment with an NNRTI-containing regimen. Due to the exclusion of almost all HIV-1 non-B subtypes, these groups differed in terms of sex distribution, transmission routes, ethnicity and, naturally, HIV-1 subtype distribution (data not shown). Patients who matched our inclusion criteria were predominantly white MSM and were infected with HIV-1 subtype B. Both groups did not differ in terms of the rate of virologic failure, viral load prior to initiation of ART and first-line NNRTI.

Low prevalence of preexisting minority nonnucleoside reverse transcriptase inhibitor resistant HIV-1 variants in antiretroviral therapy naive patients in routine clinical settings and missing association with virologic failure

Minority NNRTI-resistant HIV-1 variants were present prior to first-line NNRTI-containing ART in 14 of 208 patients (6.7%). The K103N mutation was detected in five out of 190 (2.6%) patients at frequencies of 0.08–7.46% (3 x <1%, 2 x >2%) and the Y181C mutation in 10 out of 201 (5%) patients at frequencies of

0.5–2.7% (7 x <1%, 2 x 1–2%, 1 x >2%). Calculating the mutational load, that is the total amount of HIV-1 RNA copies/ml plasma carrying a drug resistance mutation, the results were as follows: K103N: 104–20 579 (3 x <1000, 2 x >2000) and Y181C: 215–6489 (9 x <1000, 1 x >2000) mutant HIV-1 RNA copies/ml plasma. The M184V mutation was verified in one of 205 (0.5%) patients representing 0.9% of the virus population, that is 91 mutant HIV-1 RNA copies/ml plasma. Virus replication was successfully suppressed in this patient.

For 183 of the 208 randomly chosen patients, virologic success or failure could be examined, because 24 or more months of follow-up was available. Twenty-five patients were not eligible for this analysis due to the following reasons: two patients died, two were lost to follow-up, 13 patients switched to another regimen due to side effects, four patients decided to switch or stop treatment, and in four patients the reason for discontinuation of treatment was unknown; virological failure was not reported, and two patients harboured the Y181C mutation as minority variant.

Of those 183 patients, 176 patients (96.2%) were virologically suppressed until month 24 while receiving their first-line, NNRTI-containing regimen. Seven patients (3.8%) experienced virologic failure as defined in the Materials and Methods section (Table 1). Two of

Table 1. Baseline characteristics of randomized/tested patients and remaining patients of a total of 519 eligible patients in the investigation of usefulness of implementing more sensitive drug resistance assays in routine clinical settings.

Clinical parameter		Randomized/tested patients (n = 208)	Not tested patients (n = 311)	P
Age, median (IQR), years		39 (32–45)	39 (34–45)	0.159
Sex, No. (%)	Male	170 (81.7)	263 (84.6)	0.395
	Female	38 (18.3)	48 (15.4)	
Ethnicity, No. (%)	White	188 (90.4)	279 (89.7)	0.802
	Nonwhite	20 (9.6)	32 (10.3)	
Route of transmission, No. (%)	MSM	114 (54.8)	178 (57.2)	0.841
	Het	67 (32.2)	93 (29.9)	
	IDU	27 (13.0)	40 (12.9)	
HIV-1 subtype, No. (%)	B	198 (95.2)	292 (93.9)	0.527
	01_AE	10 (4.8)	19 (6.1)	
Estimated year of HIV-1 infection, median (IQR), years	1999 (1995–2001)	1998 (1995–2001)	0.582	
CD4 ⁺ cell count median (IQR), cells/ μ l blood	218.5 (159.5–292)	216 (150–308)	1	
HIV-1 viral load, median (IQR), log ₁₀ HIV-1 RNA copies/ml plasma	4.9 (4.5–5.3)	4.9 (4.4–5.2)	0.276	
start of first-line ART, median (IQR), years	2005 (2003–2007)	2005 (2002–2006)	0.086	
NNRTI, No. (%)	EFV	180 (86.5)	275 (88.4)	0.522
	NVP	28 (13.5)	36 (11.6)	
NRTI, No. (%)	AZT and 3TC	73 (35.1)	135 (43.4)	0.295
	TDF and FTC	61 (29.3)	86 (27.6)	
	TDF and 3TC	31 (14.9)	44 (14.2)	
	ABC and 3TC	21 (10.1)	21 (6.8)	
	Others	22 (10.6)	25 (8.0)	
Virologic outcome of first-line ART, No. (%)	n = 183	n = 471		
	Virologic success	176 (96.2)	269 (93.4)	0.199
	Virologic failure	7 (3.8)	19 (6.6)	

ABC, abacavir; AZT, zidovudine; 3TC, lamivudine; EFV, efavirenz; FTC, emtricitabine; Het, heterosexual; HIV-1, human immunodeficiency virus type 1; IDU, intravenous drug use; IQR, interquartile range; MSM, men who have sex with men; NNRTI, nonnucleoside reverse transcriptase inhibitor; NRTI, nucleoside reverse transcriptase inhibitor; NVP, nevirapine; TDF, tenofovir.

them harboured minority NNRTI-resistant HIV-1 variants prior to first-line ART (Fig. 2). In patient 8, who failed with the exclusive selection of the M184I mutation, 0.6% of the virus population carried the Y181C mutation prior to ART. Patient 13, who harboured both NNRTI mutations in high mutational loads prior to ART, failed rapidly within the first

4 months, accompanied by the selection of K103N and Y181C mutations (Fig. 2). For this patient, a likely association existed between preexisting minority NNRTI-resistant HIV-1 variants and virologic failure. However, the virologic failures in the other five patients cannot be explained by the preexistence of minority K103N or Y181C HIV-1 variants. In contrast, another

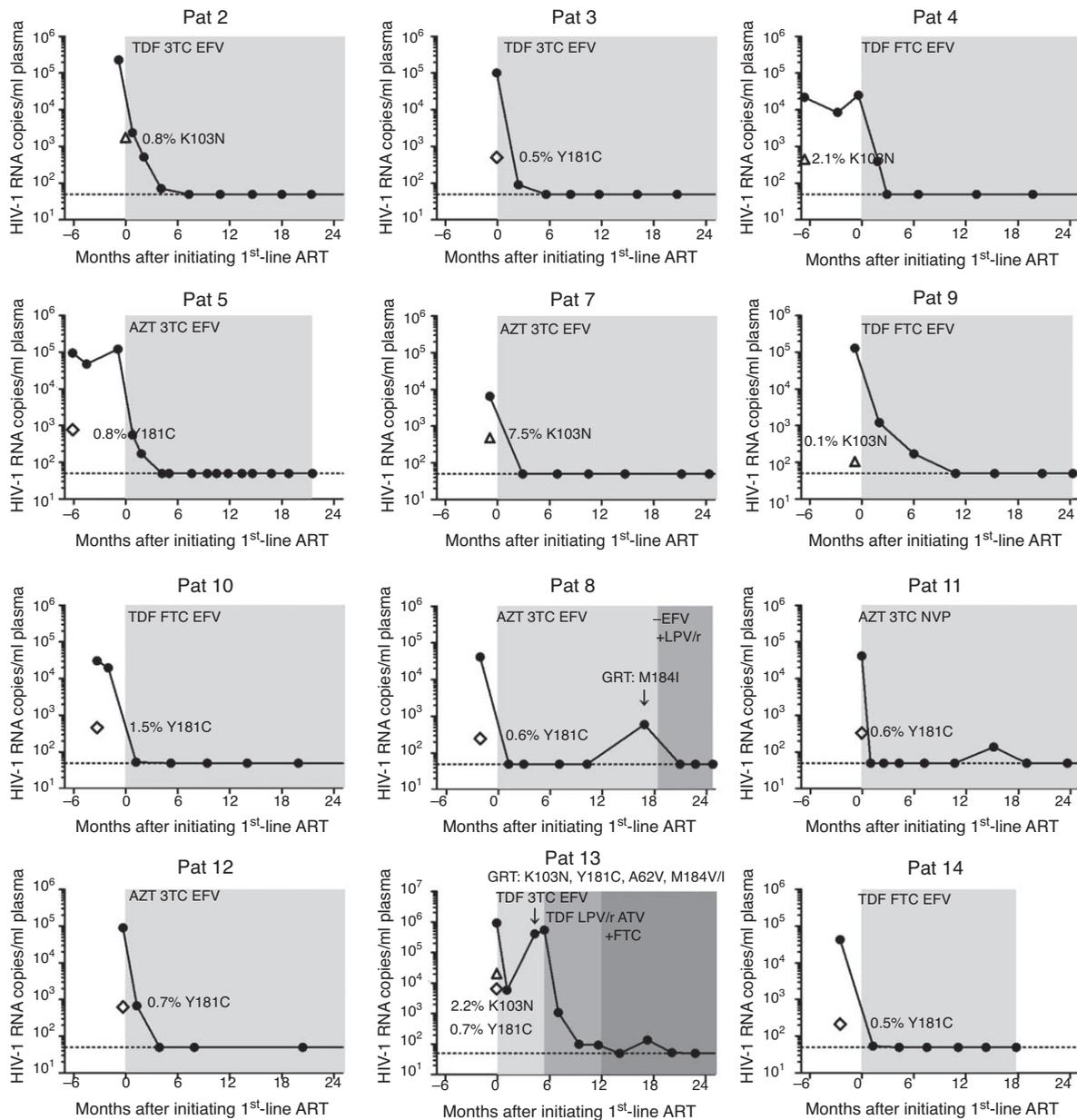


Fig. 2. Preexisting minority nonnucleoside reverse transcriptase inhibitor resistant HIV-1 variants and virologic outcome of first-line, nonnucleoside reverse transcriptase inhibitor containing antiretroviral therapy. Plasma viral load was measured using Cobas AmpliPrep/Cobas TaqMan HIV-1 Test, versions 1 and 2.0 (black circles). The limit of detection was fixed to 50 HIV-1 RNA copies/ml plasma and is shown in dashed lines. Minority K103N (green circles) and Y181C (blue circles) HIV-1 variants were quantified by AS-PCR; percentages are given and were used to calculate the absolute amounts of these variants based on the viral load. Periods of ART are depicted in grey shaded areas. /r, ritonavir-boosted; 3TC, lamivudine; ART, antiretroviral therapy; ATV, atazanavir; AZT, zidovudine; EFV, efavirenz; FTC, emtricitabine; GRT, genotypic resistance testing; LPV, lopinavir; NVP, nevirapine; TDF, tenofovir.

10 patients harboured minority NNRTI-resistant HIV-1 variants prior to first-line ART without experiencing virologic failure.

As the number of well defined virologic failures was low (seven patients of whom just two harboured preexisting minority NNRTI-resistant HIV-1 variants), we measured minority NNRTI-resistant HIV-1 variants in additional 10 patients from the 19 not tested patients experiencing virologic failure (Table 1). The K103N mutation was not detected in any of those patients. The Y181C mutation was detected in one of 10 patients prior to ART at a frequency of 0.5%, that is 725 Y181C RNA copies/ml plasma. This patient showed the following drug resistance mutations during virologic failure: K65R, K103N, Y181C and M184V. In total, three of 13 patients carrying minority NNRTI-resistant HIV-1 variants prior to first-line ART experienced virological failure, that is this results in a positive predictive value for any of these minority NNRTI resistance mutations of 23% meaning that first-line, NNRTI-containing ART would be wrongfully withheld from a large proportion of patients. Vice versa, in a total of 17 patients experiencing virological failure, only three harboured minority NNRTI-resistant variants prior to ART.

Discussion

We performed an investigation to test the hypothesis that additional implementation of more sensitive assays for the detection of minority drug-resistant HIV-1 variants in routine clinical settings would prevent those few virologic failures in treatment-naïve patients who are initiating ART with a NNRTI-containing regimen, although the routine genotypic resistance test based on population sequencing does not detect any NNRTI resistance mutation. The SHCS reported low virologic failure rates in patients receiving an NNRTI-containing, first-line regimen: 45 out of 805 (6%) patients starting ART between 1999 and 2005 [19]. Our most recent analysis, including all patients between 1999 and 2006–2008, showed no change in the rate of virologic failure (84/1309; 6.4%). And our inclusion criteria, such as HIV-1 subtype B or 01_AE, did not change this either (26/471; 5.5%). Minority NNRTI-resistant HIV-1 variants were measured by AS-PCR in 208 randomly chosen patients to determine whether more sensitive genotypic resistance testing would have prevented those virologic failures. Similar to the low rate of virologic failure, the prevalence of preexisting minority NNRTI-resistant HIV-1 variants was low. Yet, the observed overlap was minimal, meaning that only two out of seven patients with virologic failure harboured preexisting minority NNRTI-resistant HIV-1 variants, whereas only two out of 12 patients with preexisting minority NNRTI-resistant HIV-1 variants experienced virologic

failure. Minority M184V variants were irrelevant in our cohort.

These results are contradictory to a pooled analysis of 10 studies [9] and a recent European multicohort case–control study, both showing an increased risk of virologic failure to first-line NNRTI-based ART when minority drug-resistant HIV-1 variants were detected prior to ART [11]. However, when separately examining each of these studies included in the pooled analysis [9], it shows that all four case–control studies resulted in a significant association between virologic failure and preexisting minority drug-resistant HIV-1 variants in ART-naïve individuals [10,20–22], but four of the included six cohort studies did not reveal this association [23–26]. In terms of the other two cohort studies, an association was found when the mutational load was more than 2000 K103N copies/ml plasma [27] or when all preexisting NNRTI-resistance mutations were included in the analysis independent of their frequency [28]. In the meantime, three other cohort studies have been published and none of them show an association between virologic failure and preexisting minority drug-resistant HIV-1 variants in ART-naïve individuals [29–31]. This failure in detecting an association could be due to the small number of individuals included in most of the cohort studies ($n < 100$ in each study), but in the most recently published study, more than 200 individuals were included [29].

By measuring only the K103N, Y181C and M184V mutations, we might have missed other important and maybe more predictive drug resistance mutations. However, almost all analyses on the impact of preexisting minority drug-resistant HIV-1 variants on NNRTI-containing regimens are based on AS-PCR focusing exactly on these three mutations, which are key drug resistance mutations [9]. It might be possible to close this gap by applying next-generation technologies, but this technology has currently a lower sensitivity than AS-PCR [32,33]. Noteworthy, expanding the spectrum of measured drug resistance mutations would not change the observation that most of the patients harbouring preexisting minority NNRTI-resistant HIV-1 variants were successfully treated with an NNRTI-containing regimen. Thus, for those patients, NNRTIs would have been wrongfully withheld.

The mutational load, that is the absolute number of viruses harbouring drug resistance mutations within the viral population, might be more predictive for virologic failure than the percentage of minority drug-resistant variants. It has been shown that a preexisting mutational load of more than 2000 K103N HIV-1 RNA copies/ml plasma, quantified by AS-PCR specific for this mutation, is highly predictive of virologic failure in patients starting with a first-line, NNRTI-containing regimen [27]. Patient 13 harboured more than 20 000 K103N and more than 6000 Y181C HIV-1 RNA copies/ml plasma prior to ART,

whereas the mutational load was less than 2000 copies/ml in all other patients. Also, in a recent pooled analysis of almost 1000 patients, an increase of the mutational load was associated with an increased risk of virologic failure, but the risk increased already significantly at low mutational loads of 10–99 copies/ml plasma [9].

We studied the impact of preexisting minority NNRTI-resistant HIV-1 variants on the outcome of NNRTI-containing, first-line ART in a retrospective manner. Undoubtedly, a prospective study would be the ultimate concept to proof or to deny the relevance of those minority NNRTI-resistant HIV-1 variants on the outcome of first-line regimens, particularly for treatments with a low genetic barrier to resistance. But due to the low rate of virologic failure, the low prevalence of preexisting minority NNRTI-resistant HIV-1 variants in ART-naïve patients and a variety of other factors such as the numerous possibilities of ART regimens, a huge number of patients would need to be included in such a study.

Cost effectiveness was not explicitly analysed in our study. Our data show that applying a more sensitive drug resistance assay in 100 patients would have prevented one virologic failure. However, in the case of preexisting minority NNRTI-resistant HIV-1 variants, potentially prevented failures have to be balanced against the costs of NNRTI-sparing regimens, which often are more costly and less often available as single tablet regimens. As virologic failure did not occur in most of the patients with preexisting minority NNRTI-resistant HIV-1 variants, this suggests that standard pretreatment screening for minority variants will not be the most cost-effective option.

In summary, our study shows that preexisting K103N, Y181C or M184V variants only have a very low positive predictive value for ART-naïve patients in routine clinical settings wherein the rate of virologic failure is very low as it is the case for the SHCS [34]. Hence, the number of possibly preventable virologic failures in patients harbouring minority NNRTI-resistant HIV-1 variants was small. Noteworthy, most virologic failures occurred without evidence for preexisting minority NNRTI-resistant HIV-1 variants, and in contrast, most of the patients harbouring minority NNRTI resistant variants did not experience virologic failure. Although preexisting minority NNRTI-resistant HIV-1 variants may have an impact on ART as revealed in settings of case-control studies, the sole implementation of minority NNRTI-resistant HIV-1 variant analysis in addition to GRT cannot be recommended in routine clinical settings. Additional associated cofactors need to be discovered.

Acknowledgements

We are grateful to our patients for their commitment. We are very thankful to Christine Leemann for her

outstanding technical support. We are thankful to Nottania K. Campbell for her help in editing this manuscript.

The members of the SHCS are V. Aubert, J. Barth, M. Battegay, E. Bernasconi, J. Böni, H.C. Bucher, C. Burton-Jeangros, A. Calmy, M. Cavassini, M. Egger, L. Elzi, J. Fehr, J. Fellay, P. Francioli, H. Furrer (Chairman of the Clinical and Laboratory Committee), C.A. Fux, M. Gorgievski, H. Günthard (President of the SHCS), D. Haerry (deputy of 'Positive Council'), B. Hasse, H.H. Hirsch, B. Hirschel, I. Hösl, C. Kahlert, L. Kaiser, O. Keiser, C. Kind, T. Klimkait, H. Kovari, B. Ledergerber, G. Martinetti, B. Martinez de Tejada, K. Metzner, N. Müller, D. Nadal, G. Pantaleo, A. Rauch (Chairman of the Scientific Board), S. Regenass, M. Rickenbach (Head of Data Center), C. Rudin (Chairman of the Mother & Child Substudy), P. Schmid, D. Schultze, F. Schöni-Affolter, J. Schüpbach, R. Speck, P. Taffé, P. Tarr, A. Telenti, A. Trkola, P. Vernazza, R. Weber, S. Yerly.

This study has been financed in the framework of the SHCS (SHCS), supported by the Swiss National Science Foundation (SNF) (grant 33CS30_134277) and by the SHCS research foundation. Further support was provided by SNF grants 324700-120793 (to H.F.G. and K.J.M.), 320000-116035 and 324730-130865 (to H.F.G.), the SHCS [project 605] (to H.F.G. and K.J.M.), the University of Zurich's Clinical Research Priority Programme (CRPP) 'Viral infectious diseases: Zurich Primary HIV Infection Study' (to H.F.G.), the European Community's Seventh Framework Programme [grant number FP7/2007–2013], under the Collaborative HIV and Anti-HIV Drug Resistance Network (CHAIN) [grant number 223131] (to H.F.G.); the Yvonne-Jacob Foundation (to H.F.G.), an unrestricted research grant from the Vontobel Stiftung (to H.F.G. and K.J.M.) and one from Gilead (to H.F.G.).

Conflicts of interest

None declared.

References

1. Ray M, Logan R, Sterne JA, Hernandez-Diaz S, Robins JM, Sabin C, et al. **The effect of combined antiretroviral therapy on the overall mortality of HIV-infected individuals.** *AIDS* 2010; **24**:123–137.
2. Hirsch MS, Gunthard HF, Schapiro JM, Brun-Vezinet F, Clotet B, Hammer SM, et al. **Antiretroviral drug resistance testing in adult HIV-1 infection: 2008 recommendations of an International AIDS Society-USA panel.** *Clin Infect Dis* 2008; **47**:266–285.
3. Vandamme AM, Camacho RJ, Ceccherini-Silberstein F, de Luca A, Palmisano L, Paraskevis D, et al. **European recommendations for the clinical use of HIV drug resistance testing: 2011 update.** *AIDS Rev* 2011; **13**:77–108.
4. Thompson MA, Aberg JA, Hoy JF, Telenti A, Benson C, Cahn P, et al. **Antiretroviral treatment of adult HIV infection: 2012 recommendations of the International Antiviral Society-USA panel.** *JAMA* 2012; **308**:387–402.

5. Gunthard HF, Wong JK, Ignacio CC, Havlir DV, Richman DD. **Comparative performance of high-density oligonucleotide sequencing and dideoxynucleotide sequencing of HIV type 1 pol from clinical samples.** *AIDS Res Hum Retroviruses* 1998; **14**:869–876.
6. Schuurman R, Demeter L, Reichelderfer P, Tijnagel J, de Groot T, Boucher C. **Worldwide evaluation of DNA sequencing approaches for identification of drug resistance mutations in the human immunodeficiency virus type 1 reverse transcriptase.** *J Clin Microbiol* 1999; **37**:2291–2296.
7. Halvas EK, Aldrovandi GM, Balfe P, Beck IA, Boltz VF, Coffin JM, et al. **Blinded, multicenter comparison of methods to detect a drug-resistant mutant of human immunodeficiency virus type 1 at low frequency.** *J Clin Microbiol* 2006; **44**:2612–2614.
8. Bansal V, Metzner KJ, Niederost B, Leemann C, Boni J, Gunthard HF, et al. **Minority K65R variants and early failure of antiretroviral therapy in HIV-1-infected eritrean immigrant.** *Emerg Infect Dis* 2011; **17**:1966–1968.
9. Li JZ, Paredes R, Ribaudo HJ, Svarovskaia ES, Metzner KJ, Kozal MJ, et al. **Low-frequency HIV-1 drug resistance mutations and risk of NNRTI-based antiretroviral treatment failure: a systematic review and pooled analysis.** *JAMA* 2011; **305**:1327–1335.
10. Metzner KJ, Giulieri SG, Knoepfel SA, Rauch P, Burgisser P, Yerly S, et al. **Minority quasiespecies of drug-resistant HIV-1 that lead to early therapy failure in treatment-naïve and -adherent patients.** *Clin Infect Dis* 2009; **48**:239–247.
11. Cozzi-Lepri A, Noguera-Julian M, Di Giallonardo F, Schuurman R, Däumer M, Aitken S, et al. **Low-frequency drug-resistant HIV-1 confers an increased risk of virological failure to first-line NNRTI-based ART: a multicohort European case-control study using centralized ultrasensitive 454 sequencing [abstract 41].** *Antiviral Ther* 2013; **18**:33.
12. Schoeni-Affolter F, Ledergerber B, Rickenbach M, Rudin C, Gunthard HF, Telenti A, et al. **Cohort profile: the Swiss HIV Cohort study.** *Int J Epidemiol* 2010; **39**:1179–1189.
13. Taffe P, May M. **A joint back calculation model for the imputation of the date of HIV infection in a prevalent cohort.** *Stat Med* 2008; **27**:4835–4853.
14. Metzner KJ, Scherrer AU, Preiswerk B, Joos B, von Wyl V, Leemann C, et al. **Origin of minority drug-resistant HIV-1 variants in primary HIV-1 infection.** *J Infect Dis* 2013; **208**:1102–1112.
15. Bennett DE, Camacho RJ, Otelea D, Kuritzkes DR, Fleury H, Kiuchi M, et al. **Drug resistance mutations for surveillance of transmitted HIV-1 drug-resistance: 2009 update.** *PLoS One* 2009; **4**:e4724.
16. Metzner KJ, Bonhoeffer S, Fischer M, Karanickolas R, Allers K, Joos B, et al. **Emergence of minor populations of human immunodeficiency virus type 1 carrying the M184V and L90M mutations in subjects undergoing structured treatment interruptions.** *J Infect Dis* 2003; **188**:1433–1443.
17. Metzner KJ, Rauch P, Walter H, Boesecke C, Zollner B, Jessen H, et al. **Detection of minor populations of drug-resistant HIV-1 in acute seroconverters.** *AIDS* 2005; **19**:1819–1825.
18. Metzner KJ, Rauch P, von Wyl V, Leemann C, Grube C, Kuster H, et al. **Efficient suppression of minority drug-resistant HIV type 1 (HIV-1) variants present at primary HIV-1 infection by ritonavir-boosted protease inhibitor-containing antiretroviral therapy.** *J Infect Dis* 2010; **201**:1063–1071.
19. von Wyl V, Yerly S, Boni J, Burgisser P, Klimkait T, Battegay M, et al. **Emergence of HIV-1 drug resistance in previously untreated patients initiating combination antiretroviral treatment: a comparison of different regimen types.** *Arch Intern Med* 2007; **167**:1782–1790.
20. Geretti AM, Fox ZV, Booth CL, Smith CJ, Phillips AN, Johnson M, et al. **Low-frequency K103N strengthens the impact of transmitted drug resistance on virologic responses to first-line efavirenz or nevirapine-based highly active antiretroviral therapy.** *J Acquir Immune Defic Syndr* 2009; **52**:569–573.
21. Johnson JA, Li JF, Wei X, Lipscomb J, Irlbeck D, Craig C, et al. **Minority HIV-1 drug resistance mutations are present in antiretroviral treatment-naïve populations and associate with reduced treatment efficacy.** *PLoS Med* 2008; **5**:e158.
22. Paredes R, Lalama CM, Ribaudo HJ, Schackman BR, Shikuma C, Giguél F, et al. **Preexisting minority drug-resistant HIV-1 variants, adherence, and risk of antiretroviral treatment failure.** *J Infect Dis* 2010; **201**:662–671.
23. Balduin M, Oette M, Daumer MP, Hoffmann D, Pfister HJ, Kaiser R. **Prevalence of minor variants of HIV strains at reverse transcriptase position 103 in therapy-naïve patients and their impact on the virological failure.** *J Clin Virol* 2009; **45**:34–38.
24. Jakobsen MR, Tolstrup M, Sogaard OS, Jorgensen LB, Gorry PR, Laursen A, et al. **Transmission of HIV-1 drug-resistant variants: prevalence and effect on treatment outcome.** *Clin Infect Dis* 2010; **50**:566–573.
25. Metzner KJ, Rauch P, Braun P, Knechten H, Ehret R, Korn K, et al. **Prevalence of key resistance mutations K65R, K103N, and M184V as minority HIV-1 variants in chronically HIV-1 infected, treatment-naïve patients.** *J Clin Virol* 2011; **50**:156–161.
26. Peuchant O, Thiebaut R, Capdepon S, Lavignolle-Aurillac V, Neau D, Morlat P, et al. **Transmission of HIV-1 minority-resistant variants and response to first-line antiretroviral therapy.** *AIDS* 2008; **22**:1417–1423.
27. Goodman DD, Zhou Y, Margot NA, McColl DJ, Zhong L, Borroto-Esoda K, et al. **Low level of the K103N HIV-1 above a threshold is associated with virological failure in treatment-naïve individuals undergoing efavirenz-containing therapy.** *AIDS* 2011; **25**:325–333.
28. Simen BB, Simons JF, Hullsiek KH, Novak RM, Macarthur RD, Baxter JD, et al. **Low-abundance drug-resistant viral variants in chronically HIV-infected, antiretroviral treatment-naïve patients significantly impact treatment outcomes.** *J Infect Dis* 2009; **199**:693–701.
29. Boltz VF, Bao Y, Lockman S, Halvas EK, Kearney MF, McIntyre JA, et al. **Low-frequency nevirapine (NVP)-resistant HIV-1 variants are not associated with failure of antiretroviral therapy in women without prior exposure to single-dose NVP.** *J Infect Dis* 2014; **209**:703–710.
30. Messiaen P, Verhofstede C, Vandenbroucke I, Dinakis S, Van Eygen V, Thys K, et al. **Ultra-deep sequencing of HIV-1 reverse transcriptase before start of an NNRTI-based regimen in treatment-naïve patients.** *Virology* 2012; **426**:7–11.
31. Stekler JD, Ellis GM, Carlsson J, Eilers B, Holte S, Maenza J, et al. **Prevalence and impact of minority variant drug resistance mutations in primary HIV-1 infection.** *PLoS One* 2011; **6**:e28952.
32. Di Giallonardo F, Zagordi O, Dupont Y, Leemann C, Joos B, Kunzli-Gontarczyk M, et al. **Next-generation sequencing of HIV-1 RNA genomes: determination of error rates and minimizing artificial recombination.** *PLoS One* 2013; **8**:e74249.
33. Gilles A, Meglec E, Pech N, Ferreira S, Malausa T, Martin JF. **Accuracy and quality assessment of 454 GS-FLX Titanium pyrosequencing.** *BMC Genomics* 2011; **12**:245.
34. Gupta RK, Hill A, Sawyer AW, Cozzi-Lepri A, von Wyl V, Yerly S, et al. **Virological monitoring and resistance to first-line highly active antiretroviral therapy in adults infected with HIV-1 treated under WHO guidelines: a systematic review and meta-analysis.** *Lancet Infect Dis* 2009; **9**:409–417.