

1 **Development and evaluation of an affordable real-time qualitative assay for deter-**  
2 **mining HIV-1 virological failure in plasma and dried blood spots**

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8 Running title: Qualitative HIV-1 virological failure screening assay

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24 **Abstract**

25

26 Virological failure (VF) has been identified as the earliest, most predictive determinant of  
27 HIV-1 antiretroviral treatment (ART) failure. Due to high costs and complexity of virological  
28 monitoring, VF assays are rarely performed in resource-limited settings (RLS). Rather,  
29 ART failure is determined by clinical monitoring and to a large extent immunological moni-  
30 toring. This paper describes the development and evaluation of a low-cost, dried blood  
31 spot (DBS)-compatible qualitative assay to determine VF, in accordance with current WHO  
32 guideline recommendations for therapy-switching in RLS. The described assay is an in-  
33 ternally-controlled qualitative real-time PCR targeting the conserved long terminal repeat  
34 domain of HIV-1. This assay was applied with HIV-1 subtypes A-H and further evaluated  
35 on HIV-1 clinical plasma samples from South Africa (n=191) and Tanzania (n=42). Field  
36 evaluation was performed in Uganda using local clinical plasma samples (n=176). Fur-  
37 thermore, assay performance was evaluated for DBS. The described assay is able to iden-  
38 tify VF for all major HIV-1 group-M subtypes with equal specificity, and lower detection limit  
39 of 1.00E+03 copies/ml for plasma and 5.00E+03 copies/ml for DBS. Comparative testing  
40 yielded accurate VF determination for therapy-switching in 89%-96% of samples com-  
41 pared to gold standards. The assay is robust and flexible, allowing for "open platform" ap-  
42 plications and producing comparable results to commercial assays. Assay design enables  
43 application in laboratories that can accommodate real-time PCR equipment, allowing de-  
44 centralization of testing to some extent. Compatibility with DBS extends access of sam-  
45 pling and thus access to this test to remote settings.

46

47 **Introduction**

48

49 In 2010 the HIV-1 epidemic was estimated to include 34.0 million (range 31.6-35.2 million)  
50 infected adults and children across the globe. An alarming 67.4% (n= 22.9 million) of the  
51 total global infections are people residing in Sub-Saharan Africa. As a result of antiretrovi-  
52 ral therapy (ART) scale-up initiatives, 6.65 million of infected individuals requiring treat-  
53 ment were receiving it in Sub-Saharan Africa by the end of 2010(1). However, particularly  
54 in resource-limited settings (RLS), effective treatment faces challenges, which include fail-  
55 ing supply chains resulting in drug stock-outs, drug toxicity of “older generation” 1<sup>st</sup> and  
56 2<sup>nd</sup> line drugs, failure of patient adherence, drug-drug interactions, lack of qualified  
57 healthcare staff or failing adherence support, etc. As a result HIV-1 can develop drug re-  
58 sistance to ART, leading to virological failure (VF) and subsequently ART failure. A recent  
59 report has shown that the prevalence of pre-ART HIV-1 drug resistance in 13 sites in vari-  
60 ous countries in Sub-Saharan Africa is 5.6%, ranging from 1.1% in South Africa to 12.3%  
61 in Uganda(2). Recent scientific findings have led to the consideration of “Treatment as  
62 Prevention”, which according to the most intensive “Test and Treat” scenario could ulti-  
63 mately increase the number of HIV patients qualifying for ART to 32 million(3). With rapidly  
64 increasing numbers of HIV patients on ART in RLS with weak health systems, the risk of  
65 further increase of HIV-1 drug resistance is imminent.

66

67 The success of increased access to ART in RLS has largely been due to massive donor  
68 funding and important reduction of costs of selected first-line drugs. However, reduced  
69 susceptibility to these first-line drugs and the consequent switching to second-line would at  
70 least partly undo early ART successes and result in higher expenditures and increasing  
71 numbers of patients on failing regimens with no options for effective second-line or salvage  
72 therapies(4, 5).

73 As per the definition of the WHO, VF is a repeated viral load  $\geq 5.00E+03$  RNA copies/ml in  
74 an individual taking ART for at least four to six months(6). Timely detection of VF by VL  
75 testing, which is routine in industrialized countries(7), is necessary to prevent accumula-  
76 tion of HIV drug resistance(8), or to identify poor adherence to the treatment. However, in  
77 RLS, high costs and technical complexity limit the possibility of VL monitoring and treat-  
78 ment failure is primarily determined using clinical monitoring for stage three and four AIDS-  
79 defining illnesses and, if available, immunological monitoring using CD4 counts(6). The  
80 inadequacies of CD4 for determining true treatment failure have been described on many  
81 occasions(9-12). The clinical-immunological monitoring approach results in individuals be-  
82 ing left on sub-optimal regimens for an extended period of time with the risk of accumul-  
83 ating drug resistance mutations or unnecessary switching to second-line therapy based on  
84 non-VL supported decisions(4). Both scenarios limit future treatment options and in-  
85 creased costs associated with second-line therapy(5).

86

87 The current paper addresses the challenge of determination of VF in RLS by taking sever-  
88 al premises into consideration that reflect the actual public health situation in these set-  
89 tings. First of all, the standpoint was taken that determination of an exact VL is not re-  
90 quired to determine ART failure and therefore a less complex, and thus less expensive,  
91 assay that classifies a sample as either above or below a treatment success threshold  
92 would suffice. Secondly, in order to implement the WHO recommendations of task shifting  
93 and decentralization of ART to remote settings, the consequence would be that complex  
94 procedures, including drawing blood, isolation and storage of plasma, cold chain ship-  
95 ments to qualified labs for VL testing, should be avoided. Rather, VF should be detectable  
96 on dried blood spots (DBS), a sampling alternative that is inexpensive, easy to collect and  
97 transport, and has proven application for VL testing(13, 14). Thirdly, given the fact that for  
98 accurate detection of VF a nucleic acid amplification step remains necessary and taking

99 into consideration the realities of contamination risks in remote labs, it was decided to con-  
100 centrate on a real-time PCR approach. This allows for VF determination in a closed sys-  
101 tem and with equipment that is continuously evolving, regularly reducing in price, and be-  
102 ing adapted to local circumstances through battery and solar energy applications. Finally, it  
103 was considered essential that the protocol for VF testing should be generic, “open plat-  
104 form”, applicable on a wide array of real-time PCR instruments in various African settings,  
105 and freely available in the public domain.

106

107 With the above assumptions in mind, the Affordable Resistance Test for Africa (ARTA)  
108 consortium was established, consisting of a unique combination of academia, industry and  
109 non-government organizations both in Africa and Europe. Here we report on the results of  
110 ARTA research to develop a real-time PCR assay that can be used as a screening tool to  
111 determine VF in RLS. This “virological failure assay” (VFA) can be readily applied in basic  
112 laboratories, using either plasma or DBS as the sample input. The VFA is applicable for  
113 all major HIV-1 group-M subtypes, and is specifically designed to identify VF as defined by  
114 the WHO as a VL of  $\geq 5.00E+03$  copies/ml(6).

115

## 116 **Materials and Methods**

117

### 118 **Samples**

#### 119 *HIV-1 Subtype Reference panel*

120 A panel of virus isolates consisting of HIV-1 subtypes A through H (Table 1) was obtained  
121 from BBI (BBI Biotech Research Laboratories Inc., Gaithersburg, USA) for assay optimiza-  
122 tion and evaluation at the University Medical Centre in Utrecht (UMCU), The Netherlands.  
123 Serial dilutions were prepared from these stocks using HIV-1 negative human plasma.  
124 These dilutions were also used to spike HIV-1 negative whole blood for DBS preparation.

125

126 *Clinical samples*

127 Clinical plasma samples from HIV-1 infected individuals from several African sites were  
128 included for further evaluation at the UMCU, the Netherlands. Samples were selected to  
129 include several subtypes with a variety of VL in accepted ranges for subsequent analysis.  
130 Samples from South Africa (n=191) were plasma samples sent for routine VL testing, per-  
131 formed on the COBAS®AmpliPrep/COBAS®TaqMan®System v2 (Roche, Penzberg,  
132 Germany), and represented HIV-1 subtype-C with a VL range of 1.30E+03-3.00E+06 (me-  
133 dian 5.50E+04) copies/ml. Samples from Tanzania (n=42) were part of an ongoing preven-  
134 tion-of-mother-to-child-transmission (PMTCT) study(15), where VL was determined using  
135 the COBAS® AmpliCor HIV-1 Monitor test v1.5 (Roche). Samples included subtypes A  
136 (n=23), C (n=10), and D (n=6), and three samples with undetermined subtype, with a VL  
137 range of 6.65E+02-3.07E+05 (median 2.67E+04) copies/ml.

138

139 In addition, as part of a technology transfer program, the described assay was applied in  
140 three Joint Clinical Research Centre (JCRC) laboratory sites in Uganda, where retrospec-  
141 tive plasma samples collected from HIV-1 positive individuals as part of the PASER pro-  
142 gram were included(16). These samples represented baseline and follow-up clinical sam-  
143 ples at yearly intervals after therapy initiation. For these samples, routine VL had been per-  
144 formed in Uganda using the COBAS®AmpliPrep/COBAS®TaqMan®System v2(Roche). A  
145 total of 176 plasma samples were included comprising of subtypes A (n=89), D (n=64),  
146 and 23 with an unknown subtype, with a VL range of 1.00E+02-1.00E+06 (median  
147 1.00E+04) copies/ml. Twenty-five confirmed HIV-1 negative plasma samples were in-  
148 cluded for assay specificity control.

149

150 To investigate the application of the assay with DBS samples, DBS were prepared from

151 EDTA collected whole blood for participants of the PASER program(16). The same blood  
152 sample was then centrifuged and the plasma was removed for analysis. These samples  
153 are subsequently referred to as paired plasma and DBS samples. A total of 82 paired  
154 samples were tested in Uganda, with a VL range of 4.40E+01-7.18E+06 (median  
155 2.61E+03) copies/ml. DBS samples were stored at -70°C for 270-515 (median 485) days  
156 (n=31), -20°C for 45-112 (median 82) days (n=21), or room temperature for 2-192 (median  
157 126) days (n=30).

158

#### 159 *Internal Control*

160 An internal control (IC) was added to each clinical sample at a fixed amount of ten percent  
161 of the elution volume at the start of nucleic acid isolation. The IC comprised of the non-  
162 human RNA virus Encephalomyocarditis virus (EMC) and was prepared at the UMCU, the  
163 Netherlands, in batches of single-use aliquots and stored at -80°C until use.

164

#### 165 **VFA**

##### 166 *Nucleic Acid Isolation, Plasma*

167 At the UMCU, the Netherlands, viral nucleic acid (NA) isolation was performed using  
168 NucliSENS magnetic extraction reagents in combination with the MINIMAG (BioMérieux,  
169 Boxtel, The Netherlands). For each sample, an input of 100µl plasma was used, or two  
170 DBS of 50µl each, and 2.5µl IC. Positive and negative controls were included in each run.  
171 Upon completion of the isolation procedure, purified nucleic acids were eluted in 25µl elu-  
172 tion buffer.

173

174 In Uganda, NA isolation was performed using the QIAamp RNA kit (Qiagen GmbH, Ger-  
175 many), as per manufactures instructions. Input was 100µl of plasma, or two 50 µl DBS,  
176 and 5µl IC. Isolated NA was eluted in 50µl elution buffer.

177

178 Upon completion of both isolation procedures, the eluates were used immediately for re-  
179 verse transcription (RT), and remaining nucleic acids stored at -20°C.

180

#### 181 *Nucleic Acid Isolation, DBS*

182 At both sites, a pre-incubation step for DBS was performed. DBS samples were excised  
183 by hand using scissors, which were decontaminated between samples with 70% ethanol.  
184 For the Nuclisens method, DBS were placed in the provided 2ml lysis buffer (BioMérieux)  
185 in a 9ml tube. For the QIAamp RNA method (Qiagen GmbH), DBS were placed in 700ul of  
186 the provided Buffer AVL lysis buffer that was aliquoted in 2ml Eppendorf tubes for use. For  
187 both methods, samples were incubated at room temperature with gentle rotation for 30  
188 minutes, after which filters were removed and NA isolated as per the plasma samples.

189

#### 190 *Reverse Transcription*

191 Purified NA, containing both HIV-1 RNA and IC RNA, was reverse transcribed using the  
192 TaqMan® Real-time PCR system Random Hexamers RT kit (Life Technologies, Foster  
193 City, CA) according to manufacturer's instructions. An input of 10µl NA isolate was used in a  
194 final reaction volume of 25µl. Reactions were carried out according to the following condi-  
195 tions: 25°C for 10 minutes, 48°C for 30 minutes and 95°C for 5 minutes. Generated cDNA  
196 was used immediately for real-time PCR or stored at 4°C.

197

#### 198 *Real-time PCR*

199 HIV-1 and IC cDNA fragments were amplified in multiplex format. A 25µl real-time PCR  
200 reaction contained 12.5µl universal TaqMan® Master Mix (Life Technologies), 10µl cDNA,  
201 300nM primer *EMC-forward*, 900nM primer *EMC-reverse*, 100nM probe *EMC-VIC*, 300nM  
202 forward primer *LTR S4*, a mixture of 600nM HIV-LTR reverse primers *3'UNI-KS-6* and

203 3'UNI-KS-6-AG, and 100nM MGB probe *HIV-LTR-FAM* (Table 2). The assay was per-  
204 formed at the UMCU, the Netherlands, using an Applied Biosystem 7500 Real-Time PCR  
205 System (Life Technologies), and in Uganda using a MiniOpticon™ Real-Time PCR Detec-  
206 tion System (BioRad, Hercules, CA). Both systems included a temperature profile allowing  
207 for dUTP/UNG decontamination, namely 50°C for 2 minutes; 95°C for 10 minutes; 45 cy-  
208 cles of 95°C for 15 seconds and 60°C for 1 minute. In order to enable run-to-run compari-  
209 son, a fixed threshold was established for both systems (data not shown).

210

#### 211 *Assay Controls*

212 Positive and negative controls were included in each run. Appropriate performance of the  
213 run was judged based on the results of these controls. The positive control consisted of a  
214 plasma sample spiked with a fixed concentration of 2.50E+04 copies/ml HIV-1, the Ct val-  
215 ue acceptance range of which was determined for each real-time system. For this evalua-  
216 tion the positive control range was set at Ct 29-32. The IC was used to monitor for inhibi-  
217 tion of each individual sample. As with the positive control, the Ct value acceptance range  
218 of the IC was determined for each real-time system. For this evaluation the positive control  
219 range was set at Ct 30-33. Three negative controls were included, an isolation negative  
220 that consisted of HIV-1 negative human plasma and IC, and negative RT and PCR con-  
221 trols which consisted of nuclease-free water and no IC. The result obtained for a sample  
222 was considered valid when the positive and IC controls were within their predetermined  
223 ranges, and the negative controls were below detection.

224 **Data Analysis**

225

226 *Assay Range*

227 A five-fold serial dilution series of viral RNA for plasma and DBS for all panel subtypes  
228 (Table 1) was used to assess dynamic range, level of detection (LOD), and inter- and in-  
229 tra-assay reproducibility. For the ABI7500 (Life Technologies) the serial dilution series  
230 ranged from 5.00E+06-3.20E+02 copies/ml, and for the MiniOpticon (BioRad) from  
231 1.00E+06-1.6E+03 copies/ml. Linearity was determined and reported as a  $R^2$  value and  
232 slope gradient. Positive control and IC Ct values were averaged to determine assay preci-  
233 sion and reproducibility. Multiple measurements of 5.00E+03 copies/ml dilutions were per-  
234 formed and averaged to establish the VF Ct cut-off range. Theoretically, a one Ct differ-  
235 ence reflects a two-fold change in target NA in the amplification reaction. The slope of gra-  
236 dient determined using the dilution series gave the number of Cts difference to result in a  
237 one Log change in VL, which were used to interpret an equivalent  $\text{Log}_{10}$  copies/ml value to  
238 assess precision and reproducibility.

239

240 For clinical samples, a Chi-squared test was performed in order to determine the propor-  
241 tion of virological failures detected using the 5.00E+03 copies/ml cut-off range according to  
242 the determined Ct value. A positive result was regarded as a Ct value equal to or lower  
243 than the Ct value range designated for 5.00E+03 copies/ml, and a negative result as a Ct  
244 value greater than that Ct value range. Ct values that were within the 5.00E+03 copies/ml  
245 Ct range were considered positive, with a suggestion to repeat in a follow-up. Samples  
246 that were positive or negative in the VFA, but not in the corresponding commercial VL as-  
247 say were classified as false positive or false negative, respectively. Sensitivity was calcu-  
248 lated as “true positive/(true positive +false negative)”; specificity was calculated as “true  
249 negative/ (true negative + false positive)”.

250

251 **Results**

252

253 *Assay Design*

254 An alignment of LTR sequences obtained from the Los Alamos database was created representing all HIV-1 reference subtypes (n=37) and Circulating Recombinant Forms (CRF's; n=18). A 145 nucleotide fragment of the HIV-1 5'LTR R/U5 region was subsequently used for real-time PCR assay design using ABI primer express 2.0 software (Life Technologies, CA, USA). Mixed nucleotides were introduced at positions of inter-subtype heterogeneity. The most efficient combinations of designed VFA primers-probes and a previously published 5'LTR-based VL primer(17) (Table 2) were optimized and extensively tested in several independent runs with all isolated samples of the subtype panel.

262

263 *Analytical sensitivity*

264 All HIV-1 subtypes in the panel could be detected with equal efficiency. The assay demonstrated good overall linearity across subtypes, determined by plotting mean Ct values for all subtypes tested. The ABI7500 (Life Technologies) and the MiniOpticon (BioRad) had co-efficients of determination ( $R^2$ ) of 0.996 and 0.975, respectively (Figure 1). The level of detection (LOD) for both plasma and DBS samples was defined by the lowest concentration where no negative VFA result for any subtype was observed in replicates. Results from the serial dilutions determined LOD for plasma to be 1.00E+03 copies/ml, mean Ct 36.18 and SD 1.19 (data not shown), and for DBS samples to be 5.00E+03 copies/ml mean Ct 36.65 and SD 1.12 (data not shown).

273

274 *Assay precision and reproducibility*

275 To determine precision, the assay was performed using positive controls (n=12) with a VL

276 of 2.50E+04 copies/ml (4.40 log<sub>10</sub> copies/ml) by two different operators in 12 individual  
277 runs. Results were highly reproducible for both the HIV-1 positive controls, mean VL of  
278 4.17 log<sub>10</sub> copies/ml with SD of 0.10 log<sub>10</sub> copies/ml, and the corresponding IC values,  
279 mean VL of 4.14 log<sub>10</sub> copies/ml with SD of 0.17 log<sub>10</sub> copies/ml. Intra-assay precision was  
280 further assessed in quadruplicate, from isolation to result, for each isolate of the subtype  
281 panel, with a VL of 5.00E+03 copies/ml (3.70 log<sub>10</sub> copies/ml). The mean, SD, and %CV of  
282 the VL were 3.98 log<sub>10</sub> copies/ml, 0.24 log<sub>10</sub> copies/ml, and 8.0% for plasma, and 3.50  
283 log<sub>10</sub> copies/ml, 0.33 log<sub>10</sub> copies/ml, and 13.2% for DBS.

284

285 Inter-assay reproducibility was determined at two of the JCRC laboratory sites in Uganda.  
286 The assay was performed on 10 high VL plasma samples, VL 1.25E+05 - 2.0E+06 cop-  
287 ies/ml, by 4 different users on different days. The results were highly reproducible with a  
288 mean SD of 0.13 log<sub>10</sub> copies/ml (range 0.04-0.19). For all high VL sample runs (n=40 re-  
289 actions), the IC results were highly comparable, with a mean SD of 0.11 log<sub>10</sub> copies/ml  
290 (range 0.03-0.23).

291

#### 292 *Accuracy*

293 Three sample sets are shown in Table 3 depicting the qualitative comparison of the VFA  
294 and relative commercial assays using plasma samples. A total of 91.6% (175/191) of the  
295 South African samples were accurately classified, as compared to the commercial assay.  
296 Two samples were invalid in the assay, ten (5.2%) were over-estimated (false positive)  
297 and six samples (3.1%) were under-estimated (false negative) by the assay (Table 2). The  
298 sensitivity and specificity was 96.2% and 79.2% respectively. A total of 92.9% (39/42) of  
299 the samples from Tanzania were accurately classified compared to the commercial assay.  
300 A further three samples (7.1%) were over-estimated and no under-estimation was ob-  
301 served, with sensitivity and specificity of 100.0% and 76.9%, respectively.

302

303 Results from all the JCRC laboratory sites, Uganda, showed a 96.0% (169/176) compara-  
304 ble classification of the VFA performed as compared to the commercial assay (Table 3).  
305 Seven samples (4.0%) were over-estimated and no under-estimation was observed, with a  
306 specificity of 100.0% and a sensitivity of 92.2%. In addition, 100.0% of the HIV-1 negative  
307 plasma samples (n=25) were undetectable in the VFA.

308

### 309 *Plasma versus DBS*

310 Assay linearity and within-run precision was determined for both plasma and DBS samples  
311 for subtype A of the subtype panel by plotting mean Ct values for the serial dilutions using  
312 the ABI 7500 at the UMCU, The Netherlands. The slope and R<sup>2</sup> of standard curves derived  
313 from plasma and DBS were highly comparable, -4.067, -4.224, and 0.951, 0.971, respec-  
314 tively. On average, results for plasma were 0.32 log<sub>10</sub> copies/ml lower as compared to  
315 DBS of the same dilution, while the mean SD for plasma was 0.18 versus 0.19 log<sub>10</sub> cop-  
316 ies/ml for DBS (excluding 2.0E+02 dilution) (Figure 2).

317

318 The performance of the VFA on DBS samples was determined at the JCRC laboratory  
319 sites in Uganda. Results were compared with plasma VL results of the same sample that  
320 were previously measured with the commercial assay and the VFA. Figure 3 shows a  
321 comparison of VFA results for paired plasma and DBS (n=31) samples given in Log cop-  
322 ies/ml, determined using a standard curve, compared to plasma VL results generated us-  
323 ing TaqMan®System v2 (Roche). Above 3.00 log<sub>10</sub> copies/ml it is clear to see comparable  
324 qualitative classifications between sample types and assays. In Table 3 there is a sum-  
325 mary of qualitative results from all paired plasma and DBS samples. A total of 89.0%  
326 (73/82) of the samples compared with the TaqMan were accurately classified. Four sam-  
327 ples (4.9%) were overestimated and five samples (6.10%) were under-estimated, with

328 sensitivity and specificity of 92.5% and 83.3% respectively. The DBS VFA results com-  
329 pared to the plasma VFA results showed a 91.5% (75/82) comparability in classification,  
330 with seven (8.5%) being incorrectly classified, and respective sensitivity and specificity of  
331 90.7% and 100.0%. Five of the seven false negative samples were the same samples that  
332 were false negative compared to the TaqMan plasma results, four of which had been  
333 stored at room temperature for 40, 70, 184, and 192 days. The remaining three had been  
334 stored at -70°C for 330, 455, and 486 days.

335

### 336 **Discussion**

337

338 We have developed and evaluated a qualitative assay to screen for VF during ART with  
339 particular emphasis on application in RLS. The described VFA can assess ART adherence  
340 and inform therapy switching, earlier and with predicted better specificity than clinical and  
341 immunological monitoring. Informed therapy switching can prevent unnecessary treatment-  
342 switching(4) to more expensive and less accessible second-line therapies. Moreover, early  
343 detection of VF using the VFA can prevent extended exposure to a failing regimen and  
344 possible accumulation of drug resistance mutations that may confer cross-resistance to  
345 other drugs or drug classes(8). Using the VFA for early detection of treatment failure could  
346 also prevent HIV-1 transmission(18). VL monitoring to determine treatment failure is rec-  
347 ommended, including in RLS such as sub-Saharan Africa(19), and should preferably be  
348 performed according to the WHO guidelines(6), which suggest targeted use to confirm  
349 suspected clinical or immunological failure to prevent unnecessary therapy switching, or  
350 earlier use, within four to six months after ART initiation, to assess adherence and introduce  
351 adherence counseling if necessary. The presented assay meets these WHO requirements,  
352 and is suitable for use in decentralized settings with less trained medical personnel, com-  
353 patible with task shifting of ART implementation.

354

355 The assay was designed as “open platform”: all primer sequences and protocols are open-  
356 ly accessible and the assay can use various equipment and reagents that can be ordered  
357 from multiple manufacturers. This open access and open platform approach increase the  
358 affordability and scalability of molecular diagnostics in Africa. Reagent costs for the assay  
359 are country dependent, with a per sample cost, based on a run of ten samples including  
360 controls, of 22.00 USD calculated for UMCU, The Netherlands, and 27.00 USD for JCRC,  
361 Uganda. The Southern African Treatment Resistance Network (SATuRN) and ARTA are  
362 key supporters of this open movement. SATuRN has negotiated discounted reagents and  
363 technical support with Life Technologies in order to decrease the cost and increase access  
364 of HIV genotypic drug resistance testing in Africa (<http://www.bioafrica.net/saturn/>). The  
365 described VF screening assay has the potential to use the same approach. In addition,  
366 SATuRN and ARTA have been providing extensive training on the usage of molecular di-  
367 agnostics for treatment monitoring with over 1,500 physicians, nurses and health care  
368 workers trained in Africa. These organization training platforms can be used to expand  
369 and support the usage of this VF screening assay in Africa.

370

371 It is possible to use the VFA in a central laboratory with higher-throughput systems such  
372 as the Applied Biosystem 7500 Real-Time PCR System (Life Technologies), but the VFA  
373 has also shown remarkable ease-of-use in smaller, district laboratories with the  
374 MiniOpticon™ Real-Time PCR Detection System (BioRad), as we have shown in Uganda.  
375 This is important, as decentralizing VL testing enables faster turnaround times in result  
376 reporting to clinicians and their patients, and consequently more efficient treatment moni-  
377 toring. In addition, a compact real-time thermocycler requires minimal maintenance due to  
378 the use of LED instead of Xenon-lamps and lasers, has no filter wheels, and is easily  
379 transportable. However, it has to be emphasized that the assay still requires a laboratory

380 equipped for some molecular diagnostic techniques and staff with medium to high-level  
381 training.

382 The VFA is designed to control for all steps in the laboratory procedure, ensuring quality  
383 and reliability of results. The performance of the assay has demonstrated good correlation  
384 to other available VL screening assays within this evaluation, as well as between the two  
385 instruments and three Ugandan field sites tested. The evaluation of the VFA for plasma  
386 and DBS samples determined the lower limit of detection to be  $1.00E+03$  and  $5.00E+03$   
387 copies/ml, respectively. Although not being designed for quantitative application, assay  
388 linearity was shown to be adequate, with comparable equations for plasma and DBS. The  
389 assay demonstrated good intra- and inter-assay precision, with highly reproducible results  
390 at the  $5.00E+03$  copies/ml cut-off for plasma and DBS. The accuracy of the described as-  
391 say to determine VF showed good correlation with VL results previously determined using  
392 commercial VL assays.

393

394 The next step to improving access to VL monitoring and reducing associated costs in RLS  
395 is routine application with DBS sampling. The use of DBS with commercial and in-house  
396 VL assays has already been shown to have some success(20, 21). Preliminary data using  
397 spiked whole blood has shown that the current VFA performs well with DBS, however with  
398 reduced sensitivity compared to plasma, which has been previously described(20, 22).  
399 Possible reasons for this decreased sensitivity could be due to RNA degradation during  
400 storage, or loss of sample due to incomplete elution from the filter paper as part of the nu-  
401 cleic acid isolation process. Accuracy of VF determination by commercial assays can also  
402 be affected by the DBS method of collection, specifically when blood is either collected  
403 directly from finger- or heel-prick, or spotted with a dropper instead of a pipette from  
404 EDTA-blood. Unless blood is spotted in exact volumes, it is not possible to determine pre-

405 cise VL using commercial assays. A prospective clinical validation into these collection  
406 methods would be needed to investigate their effect on VF determination using the de-  
407 scribed assay.

408

409 In summary, we have developed a robust and affordable test for VF determination, open  
410 platform and compatible with finger- or heel-prick DBS collection also in pediatric applica-  
411 tions and particularly suitable for application in RLS, such as sub-Saharan Africa. The  
412 unique aspect of the described assay is its multiplex design enabling detection of an inter-  
413 nal control in each sample, ensuring accurate and reliable results from isolation to amplifi-  
414 cation. The VFA could contribute to improved quality of ART and prevention of the devel-  
415 opment of HIV drug resistance. Further explorations are needed to assess the perfor-  
416 mance of this test in clinical patient management in African settings. A study along these  
417 lines has been performed in Uganda(23).

418

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434

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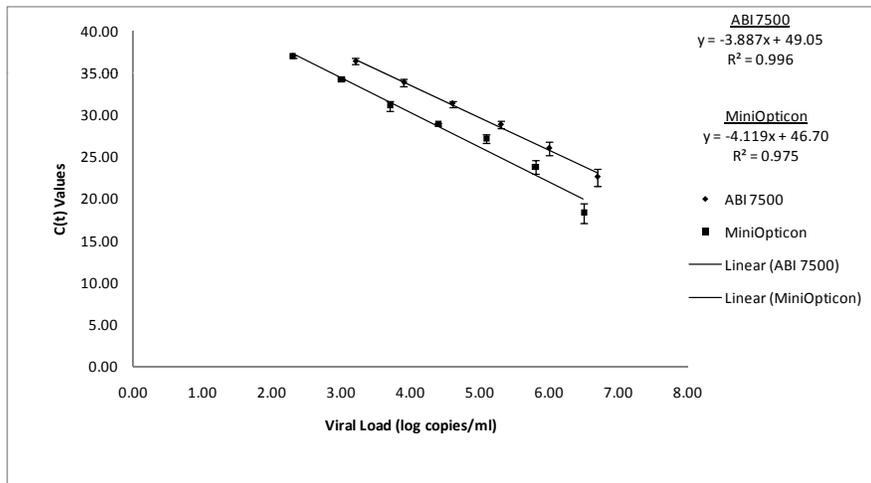
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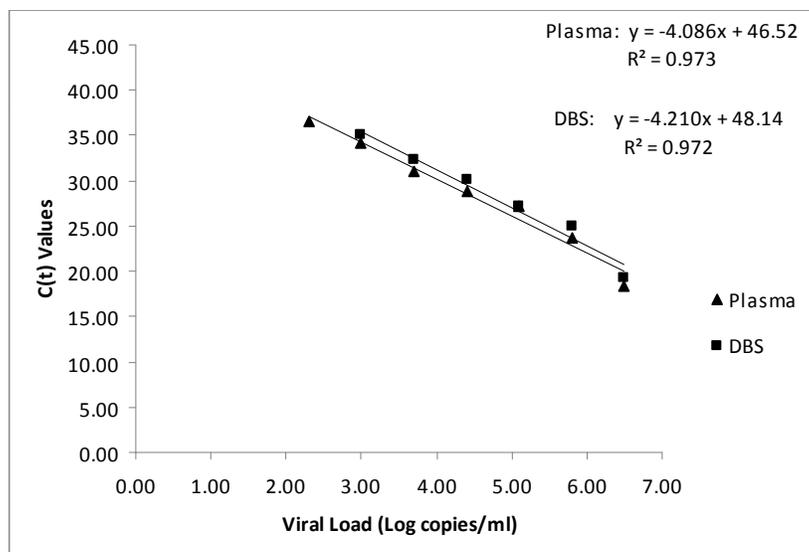
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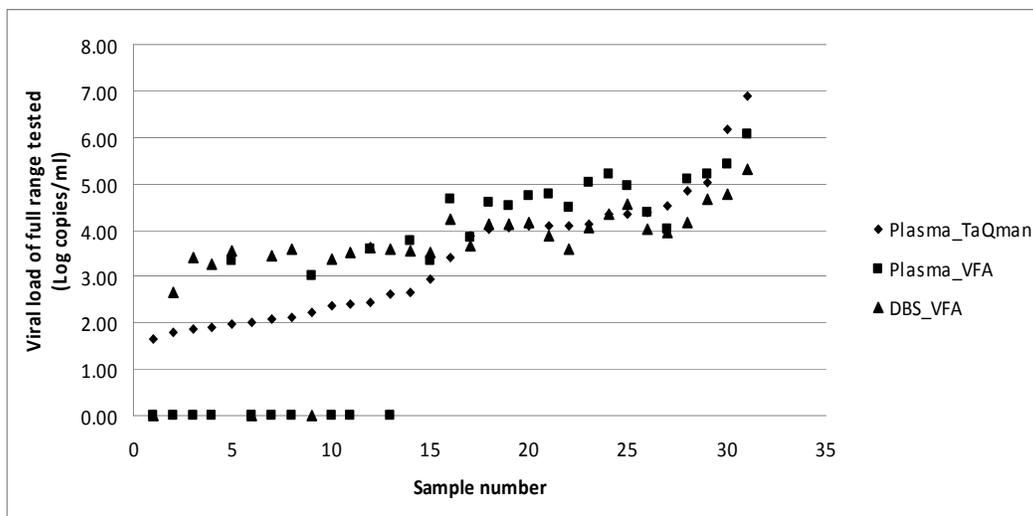
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**Figure 1.** Linearity of VFA in two different instruments, ABI7500 and MiniOpticon.



**Figure 2.** Standard curve of HIV-1 subtype A plasma and DBS samples determined using the ABI 7500.



**Figure 3.** Comparison of viral loads obtained for plasma on the TaqMan®System v2 (Roche); and for plasma and DBS for the same samples using the described VFA method.

**Table 1.** HIV-1 isolates used from the BBI subtype reference panel

<b>Subtype</b>	<b>Strain</b>	<b>Country of Origin</b>	<b>Accession Number</b>
A	UG275	Uganda	AB485632
B	BK132	Thailand	AY173951
C	ZB18	Zambia	AB485641
D	SE365	Senegal	AB485648
CRF01_AE	CM240	Thailand	AF067154
F	BZ126	Brazil	AY173957
G	BCFDIOUM	Zaire	AB485661
H	BCPKITA	Zaire	AB485665

**Table 2.** Primer and probe sequences for the HIV-1 Virological Failure screening Assay (VFA).

<b>Primer/Probe</b>	<b>Sequence</b>	<b>Function</b>	<b>Target</b>
<i>EMC-forward</i>	5'-TGACCACGCCACCGC-3'	Forward primer	EMC
<i>EMC-reverse</i>	5'-TAAAGATTTCCCTTGCCCCG-3'	Reverse primer	EMC
<i>EMC-VIC</i>	5'-TGTGAGCCAGTCGTGATTGTGCTCC-3'	Probe	EMC
<i>HIV-LTR S4</i>	5'-AAGCCTCAATAAAGCTTGCCTTGA-3'	Forward primer	HXB2 nt520-543
<i>3'UNI-KS-6</i>	5'-GAGGGATCTCTAGTTACCAGAGTCACA-3'	Reverse primer	HXB2 nt574-600
<i>3'UNI-KS-6-AG</i>	5'-GAGGGATCTCTAGTTACCAGAGTCCTA-3'		
<i>HIV-LTR-FAM</i>	5'-TAGTGTGTGCCCGTCTG-3'	MGB probe	HXB2 nt554-570

EMC: Encephalomyocarditis virus (internal control); LTR: long terminal repeat region of HIV-1; HXB2: HIV-1 reference sequence.

**Table 3.** Qualitative comparison and method agreement summary of clinical plasma and DBS samples for the VFA.

Standard Compared	Sample Standard	Sample VFA	n	True Pos	True Neg	Correctly Classified	False Pos	False Neg	Incorrectly Classified	Sensitivity	Specificity
Taqman*	Plasma	Plasma	191	153	38	175 (91.6%)	10	6	16 (8.4%)	96.2%	79.2%
Amplicor*	Plasma	Plasma	42	32	10	39 (92.9%)	3	0	3 (7.1%)	100.0%	76.9%
Taqman**	Plasma	Plasma	176	93	83	169 (96.0%)	7	0	7 (4.0%)	100.0%	92.2%
Taqman**	Plasma	DBS	82	62	20	73 (89.0%)	4	5	9 (11.0%)	92.5%	83.3%
VFA**	Plasma	DBS	82	68	14	75 (91.5%)	0	7	7 (8.5%)	90.7%	100.0%

Taqman: COBAS®TaqMan®System v2 (Roche); Amplicor: COBAS® Amplicor HIV-1 Monitor test v1.5 (Roche); VFA: Virological Failure assay; DBS: Dried blood spot sample; \*: test performed at UMCU, The Netherlands; \*\*: test performed at JCRC, Uganda; n: number of samples tested; True Positive (Pos): Number of samples identified by Standard compared as being  $\geq 5.00E+03$  copies/ml; True Negative (Neg): Number of samples identified by Standard Compared as being  $< 5.00E+03$  copies/ml; False Positive (Pos): Number of samples identified by VFA as being  $\geq 5.00E+03$  copies/ml, and as being negative by Standard Compared; False Negative (Neg): Number of samples identified by VFA as being  $< 5.00E+03$  copies/ml, and as being positive by Standard Compared.