Cellular HIV-1 DNA Levels in Drug Sensitive Strains Are Equivalent to Those in Drug Resistant Strains in Newly-Diagnosed Patients in Europe

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Abstract

Background: HIV-1 genotypic drug resistance is an important threat to the success of antiretroviral therapy and transmitted resistance has reached 9% prevalence in Europe. Studies have demonstrated that HIV-1 DNA load in peripheral blood mononuclear cells (PBMC) have a predictive value for disease progression, independently of CD4 counts and plasma viral load.

Methodology/Principal Findings: Molecular-beacon-based real-time PCR was used to measure HIV-1 second template switch (STS) DNA in PBMC in newly-diagnosed HIV-1 patients across Europe. These patients were representative for the HIV-1 epidemic in the participating countries and were carrying either drug-resistant or sensitive viral strains. The assay design was improved from a previous version to specifically detect M-group HIV-1 and human CCR5 alleles. The findings resulted in a high similarity between the two.

Conclusions/Significance: An improved molecular-beacon-based real-time PCR assay is reported for the measurement of HIV-1 DNA in PBMC and has investigated the association between cellular HIV-1 DNA levels and transmitted resistance to antiretroviral therapy in newly-diagnosed patients from across Europe. The findings show no correlation between these two parameters, suggesting that transmitted resistance does not impact disease progression in HIV-1 infected individuals. The CCR5 co-receptor tropism predominance implies that both resistant and non-resistant strains behave similarly in early infection. Furthermore, a correlation found between RNA- and DNA-derived sequences in the pol region suggests that genotypic drug-resistance testing could be carried out on either template.

Introduction

The development of antiretroviral therapy to fight HIV-1 infection has led to a significant decrease in mortality and morbidity among infected populations. Nevertheless, the emergence of viral species resistant to drugs presents a major problem in the desired response to therapy. In the past decade, studies have been focusing on the transmission of such species in different parts of the world and it has been estimated that transmitted drug resistance occurs in about 9% of all newly diagnosed HIV-1...
patients across Europe, USA and Canada [1,2,3,4,5,6]. Also, transmitted resistance cases are frequently found to be clustered [7,8]. This is probably explained by transmitted cases introduced before HAART became available, continuing to be transmitted today.

Integrated HIV-1 DNA in host genomic DNA acts as a latent reservoir and ensures viral persistence in spite of prolonged antiretroviral therapy [9,10,11,12,13,14,15]. This persistent cellular reservoir can reactivate itself and replenish viral infection, presenting itself as one of the current challenges for the control of HIV-1 infection progression [16,17,18]. Cellular HIV-1 DNA load is a marker associated with the viral reservoir and with the spread of the virus. Studies in patients with primary HIV-1 infection and advanced HIV-1 disease have demonstrated that early levels of HIV-1 DNA load in peripheral blood mononuclear cells (PBMC) and in CD4+ T-cells have a predictive value for long-term virological outcome and for disease progression, independently of CD4 counts and plasma viral RNA load [19,20,21,22,23,24,25,26,27,28,29,30,31,32]. Many in-house protocols have been developed for the quantification of cellular HIV-1 DNA in its different forms, including end-point and real-time PCR assays [33]. However, there is still no universal or standardised way to monitor and report HIV-1 DNA quantities.

Here we present an improved method of quantification of cellular HIV-1 DNA levels. We measure the concentration of HIV-1 DNA forms which have undergone the second template switch (STS DNA) in PBMC. This detects a pool of HIV-1 forms isolated PBMC using the QIAmp DNA Blood Mini kit (Qiagen, DE, USA). This reservoir can be measured in blood samples [34]. Genomic DNA was extracted from the quality and function of PBMC from HIV seropositive infected individuals as the presence of at least one of the following mutations in

Sample and data collection

Included in this study were samples from 253 newly-diagnosed HIV-1 seropositive individuals from ten countries-members of the EuropeHIVResistance network: Belgium, Croatia, Cyprus, Denmark, Greece, Israel, Italy, Luxembourg, Slovenia and Spain. Sample data were obtained from the database of the E. C.-funded project EuropeHIVResistance [1], which studies the epidemiology of drug resistance among patients newly diagnosed with HIV-1 across Europe [6]. Patients were representative for the risk group and geographical distribution of the national HIV epidemic and were included within six months after diagnosis.

PBMC isolation and genomic DNA extraction

PBMC were isolated from blood samples by one of two methods. Samples from 120 individuals were isolated from blood collected in BD Vacutainer® CPT™ (BD, Franklin Lakes, NJ, USA) tubes according to manufacturer’s instructions. Samples from 71 individuals were extracted from blood collected in EDTA tubes by Ficoll density gradient centrifugation (Lymphoprep; Nycemed, Oslo, Norway). CPT™ and Ficoll density gradient separation have been found to perform equivalently in maintaining the quality and function of PBMC from HIV seropositive blood samples [34]. Genomic DNA was extracted from the isolated PBMC using the QiAmp DNA Blood Mini kit (Qiagen, Valencia, CA, USA) and eluted with 100 µl AE buffer following the manufacturer’s instructions. DNA quality and quantity was evaluated for all samples by UV spectrophotometry using NanoDrop ND-1000 (NanoDrop Technologies, Wilmington, DE, USA).

Genomic DNA extraction from whole blood

DNA from samples from 62 individuals was extracted from whole blood collected in EDTA tubes. For 15 samples, DNA was isolated from 0.5 ml whole blood using the QiAmp DNA Blood Mini kit (Qiagen) and eluted in 100 µl AE buffer. For 47 samples, DNA was isolated from 0.3 ml whole blood using the High Pure PCR Template Preparation kit (Roche Molecular Diagnostics, Manheim, Germany), and eluted in 50 µl dH2O. Due to the production of irregular signals from the real-time PCR, the latter samples were cleaned using the cleaning and elution steps of the QiAmp DNA Blood Mini kit (Qiagen), and eluted in 100 µl AE buffer.

HIV-1 subtyping and determination of drug-resistance

Samples were amplified and sequenced in the pol region as described previously [35]. Subtype was determined by uploading the sequences individually into the REGA HIV-1 & 2 Automated Subtyping Tool v2.0 [36]. This was confirmed with phylogenetic analysis by constructing a Neighbour-Joining tree [37] using the Kimura-2-parameter distance estimation approach [38] with MEGA v4 [39]. The reliability of clustering was evaluated using bootstrap analysis with 1,000 replicates [40], where bootstrap values above 70 were considered significant for subtype assignment. Standard reference sequences used in the REGA HIV subtyping tool [36] were downloaded from the website (http://www.bioafrica.net/rega-genotype/html/subtypinghiv.html).

Drug resistance in the samples was determined by examination of the PR/RT sequence of each for mutations known to confer resistance to protease and reverse transcriptase inhibitors. This was done by manually examining the sequences and verified automatically using the Stanford drug-resistance algorithm [41,42], as described previously [35]. TDRM have been defined as the presence of at least one of the following mutations in
Comparison of RNA- and DNA-associated pol sequences

HIV-1 pol nucleotide sequences covering the PR/RT region derived from plasma viral RNA and cellular DNA were compared to determine any correlation between the two. The sequences were examined in the positions known to confer resistance to antiretroviral drugs, in order to establish whether the genotypic drug resistance testing on the two types of sequences resulted in different data.

Determination of co-receptor tropism by HIV-1 V3-loop amplification and sequencing

All samples were amplified by PCR in the V3-loop region with a nested PCR using extracted genomic DNA from the PBMC samples. The primary PCR was performed using 3 μl DNA in a 50 μl reaction using Platinum® PCR SuperMix (Invitrogen, Carlsbad, CA, USA) with 20 pmol each of the outer forward (5’-ATGGGATCAAGCCGATGGAAGC-3’) and reverse (5’-AGTGGCTTCTGCTGCCAAGAAC-3’), primers. The cycling conditions were one cycle at 94°C for 2 min, 40 cycles at 94°C for 20 s, 55°C for 30 s, 72°C for 30 s, and a final step at 72°C for 7 min. A nested PCR was performed using 3 μl of the primary PCR product with 20 pmol each of the inner forward (5’-CCAATTCCCATACAT-3’) and reverse (5’-TTAC-3’) primers. The cycling conditions were as follows: 1 cycle for 2 min at 95°C followed by 50 cycles each consisting of the data collection step for 30 s and a second step for 10 s, starting at 80°C with an auto-incrementation of −1°C per half-minute cycle until 31°C were reached. The reaction consisted of a 25 μl mixture containing 1X Platinum® Quantitative PCR Supermix-UDG (Invitrogen, Carlsbad, CA), 5.7 pmol of the beacon probe with or without 100 pmol of a perfectly complementary single-stranded oligonucleotide target. Changes in fluorescence were measured at 490 nm and the data collected at each temperature interval were plotted to form these thermal denaturation profiles and determine the optimal annealing temperature for the real-time PCR reaction.

Table 1. Molecular beacons and primers used in the real-time PCR assay.

<table>
<thead>
<tr>
<th>Name</th>
<th>Oligonucleotide Sequence (5’-3’)</th>
<th>Position</th>
<th>Reference</th>
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<tbody>
<tr>
<td>HIV-1</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>MB684</td>
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<td></td>
<td>FAM-CCGCTGCAAGCCGAGTCGCACATGCAGACACGAGGC-Dabcyl</td>
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<td>Forward primer</td>
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<td>CCR5</td>
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<tr>
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<td>TET-TGGCCCTATGACAAGACGCGCAGCGGAGGGC-Dabcyl</td>
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<td>GCCTGTTTGGCGCTCTCCAGGA</td>
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<tr>
<td>LK47.new</td>
<td>Reverse primer</td>
<td></td>
<td>CAGACCCCTCTGCTCTCTGCTCA</td>
</tr>
</tbody>
</table>

*FAM, fluorescein; TET, Tetrachloro-6-carboxylfluorescein; Dabcyl, 4-(4′-dimethylaminophenylazo)benzoic acid; underlined sequences indicate the complementary sequences forming the molecular beacon hairpin structures.

**Positions correspond to the GenBank sequences K03455 and U83326.1 for HIV-1 and CCR5, respectively. For molecular beacons, the nucleotide positions correspond to the target recognition sequences (non-underlined sequences). doi:10.1371/journal.pone.0010976.t001
Figure 1. Schematic diagram of the HIV-1 assay design. Schematic diagram of the HIV-1 genome (A) and the region targeted in this study (B). Below (C), a sequence alignment of the HXB2 strain and consensus sequences of the most widely distributed subtypes in the M group from nucleotide position 600 to 800 according to the numbering of strain HXB2, constructed from sequences available on the Los Alamos HIV sequence database (labelled as CONS). For each of the subtypes H, CRF03_AB and CRF08_BC only one sequence was available in this region and a consensus could not be made (labelled as STRAIN). No sequences were available for subtypes J and K in this region. The sequences and names of the primers and molecular beacon used in this study are seen in bold above the alignment. Directly below the beacon and reverse primer sequence is the complementary sequence corresponding to the viral positive strand. Above the beacon sequence is a schematic representation of the beacon in its closed conformation (hairpin loop). The beacon probe is labelled with a fluorophore (FAM) on the 5’ end (seen as a green circle) and a DABCYL quencher on the 3’ end (seen as a dark grey circle). The primer and molecular beacon sequences and their exact targets in the alignments are highlighted in grey. Dots in the sequences represent unseen regions of the alignment and dashes represent gaps in the sequences produced by the alignment.

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Assay design for quantification of human CCR5 alleles

To quantify the number of cells in the input DNA, a molecular-beacon-based real-time PCR assay was used for the detection of CCR5 alleles. The design was based on a previously published protocol [20] and is an improved version for the quantification of a region of the human CCR5 gene adjacent to the A32 deletion, which exists at two copies per cell (L. G. Kostrikis, unpublished data), allowing the quantification of genomic equivalents in a given sample. The PCR primers and the target recognition sequence of the molecular beacon are listed in Table 1. A thermal denaturation curve was constructed as described above, with 6.5 pmol of the CCR5-specific molecular beacon.

CCR5 and HIV-1 standards and standard curves

Cloned plasmids containing within them the targeted HIV-1 DNA and CCR5 amplicons of the real-time PCR assays were used as external quantification standards in the experiments. The amplicons were cloned into plasmids (TOPO TA Cloning™ Kit, pCR-4-TOPO vector, Invitrogen, Carlsbad, CA, USA) following PCR with the primers shown in Table 1. Five clones of each were selected and sequenced on the ABI 3130 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA) using the vector primers available from the cloning kit (Invitrogen) as sequencing primers, to ensure correct insertion of the amplicons into the plasmids. Concentrations were measured by UV absorbance using a NanoDrop 1000 spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA) and the copy number per unit volume was calculated. Tenfold serial dilutions of the purified plasmids of known molar concentrations were used as templates to generate standard curves in the selective amplification assays. Standard curves were made by plotting the threshold cycle of known CCR5 and HIV-1 copies per reaction. The slope and correlation coefficient of each standard curve were calculated based on the median threshold cycle \(C_t\) values measured for replicates of each dilution point ranging from \(10^6\) to \(10^1\) DNA templates. The PCR efficiency, \(E\), corresponding to the experimentally derived dynamic range was computed as \(10^{(-1/s)} - 1\)×100, where \(s\) is the slope of the standard curve generated.

For the real-time PCR reaction, each 25 µl reaction mixture contained 5 µl of extracted genomic DNA, 20 pmol each of forward and reverse primer, 1X Platinum® qPCR Supermix-UDG (Invitrogen, Carlsbad, CA, USA). For the CCR5 reaction, 6.5 pmol of beacon LK155 were used and in the HIV-1 reaction, 5.7 pmol of beacon MB694. The cycling conditions were the same for the two reactions and are as follows: one cycle of denaturation (95°C for 10 min), followed by 50 cycles of amplification (denaturation at 95°C for 15 s, annealing and data collection at 55°C for 30 s, and polymerization at 72°C for 30 s), performed on the 7900HT Real-Time PCR System (Applied Biosystems, Foster City, CA, USA). During the data-collection stage of each cycle, fluorescence emission was recorded at 490 nm.

Quantification of cellular HIV-1 STS DNA in newly-diagnosed, drug-naive samples

Two uniplex molecular beacon-based real-time assays were carried out in triplicate for absolute quantification of CCR5 copies and HIV-1 STS DNA copies in clinical samples, as described above for the standards. In each experiment, standard curves for HIV-1 and human CCR5 templates were also run in triplicate by using six serial dilutions, ranging from \(10^6\) to \(10^3\) copies, along with no-template negative controls. Each experiment was assessed by the quality of its standard curves, i.e., slope, \(R^2\)-value and y-intercept. CCR5 and HIV-1 copies in each sample were quantified by use of the obtained threshold values from the samples and the corresponding standard curve, constructed from multiple measurements of standards. In each sample, the number of cells was quantified as one cell per two CCR5 copies, and the HIV-1 STS DNA levels were calculated per \(10^6\) PBMC. The cellular viral load of a sample is, therefore, the number of HIV-1 copies per million cells.

For samples whose DNA was extracted from whole blood, HIV-1 STS DNA was quantified per ml blood and CCR5 measurements were not made, as whole blood contains many cell types, and not only PBMC. Hence, HIV-1 STS DNA load in samples obtained from whole blood are not comparable to samples extracted from PBMC.

Statistical analysis

Viral loads were log-transformed. The cellular viral load was compared between patients infected with or without a drug resistant virus using the Mann-Whitney test. Categorical variables were compared using chi-square test. To determine whether a differential cellular viral load was observed between subtypes a Kruskal-Wallis test was performed. The 95% confidence interval of the prevalence of transmitted resistance was calculated using the Wilson score interval. The association between the plasma viral load and the cellular viral load was determined using Pearson’s correlation coefficient.

Results

Description of the population

Available were 191 PBMC samples from HIV-1 infected individuals from eight country-members of the EuropeHIVResistance network. A total of 30 samples were excluded from the analysis due to failure of PCR in the pol region (n = 10), or a polymorphic nature of the sequence (n = 12), and drug-resistance could therefore not be determined. Table 2 lists the baseline characteristics of the 161 study subjects that were included in the analysis. The median age of the participants was 34 (interquartile range IQR 29–42) and they were predominately male (72.0%), a fact also reflected by a large proportion of MSM (50.3%). The median \(log_{10}\) plasma RNA load in the samples was 4.43 copies per ml (IQR 3.87–5.14) and the median \(CD^+\) T-cell count was 425 per ml (IQR 255.3–578.5).

HIV-1 subtyping, drug-resistance and co-receptor tropism

HIV-1 subtype was determined using the pol sequences obtained above using REGA [36] and by phylogenetic analysis. The results are listed in Table 2 and the phylogenetic tree is seen in Figure 2. The most frequently observed subtype was B (64.0%), followed by A (14.3%) and C (8.7%). Interestingly, cases of complex recombinants (C/H/K, CRF2/B) were also present in the dataset. Sequences of all samples were examined for known resistance mutations to available protease and reverse transcriptase inhibitors. Transmitted resistance in the form of major drug resistant mutations was observed in 11.7% (95% confidence interval 7.6 to 17.6%) of the samples.

All samples were sequenced in the V3-loop and tropism was determined by the geno2pheno and WebPSSM automated bioinformatics tools. The majority of samples were CCR5-tropic (147 samples, 91.3%), and the rest were CXCR4-tropic (5 samples, 3.1%) or a mixture of CCR5 and CXCR4 (7 samples, 4.3%). Two samples (1.2%) could not be determined due to the polymorphic nature of the V3-loop sequence. None of the five CXCR4-tropic samples displayed genotypic drug-resistance, but
three of the mixed-tropism samples did. The rest of the drug-resistant samples were purely CCR5-tropic.

Comparison of RNA- and DNA-associated pol sequences

Known positions conferring resistance to antiretroviral therapy from HIV-1 pol nucleotide sequences covering the PR/RT region derived from plasma viral RNA and cellular DNA were compared for each sample, to determine any correlation between the two. The comparison showed that there is a high similarity between the two types of sequences.

Characteristics of the real-time PCR assay for quantification of HIV-1 STS DNA in PBMC

Thermal denaturation profiles of both molecular beacons were constructed as described in Materials and Methods and are seen in Figure 3. The optimum concentrations of the molecular beacons were determined, as was the optimum temperature for annealing and data collection in the PCR reactions (55°C). The HIV-1 STS DNA and CCR5 assays’ specificity was established by accurate detection of 10 DNA copies with a 6-log10 linear dynamic range. The slopes of the standard curves (Figure 3) were -3.3 cycles/log10 DNA templates for both assays, corresponding to PCR efficiencies of >99%. The capability of the STS DNA assay to detect HIV-1 strains within the M group was evaluated by using DNA extracted from primary PBMC samples isolated from patients infected with HIV-1 strains from genetic subtypes A, B, C, D, F1 and G and recombinant strains A/G, C/H/K, CRF01_AE, CRF02_AG and CRF02/B. The specificity of the STS DNA assay against human genomic DNA were examined using DNA extracted from individuals not infected with HIV-1; the results were negative, with no detection after 50 PCR cycles (data not shown).

Cellular HIV-1 STS load in newly-diagnosed drug-naïve samples

The DNA samples extracted from whole blood produced very low proportion of detectable HIV-1 DNA levels (data not shown), due to the fact that whole blood contains many cell types, and were not used in the analysis. The values of cellular HIV-1 STS DNA loads in 191 samples extracted from PBMC of newly-diagnosed individuals from eight European countries were measured using molecular beacon-based real-time PCR assays quantifying HIV-1 STS DNA and human CCR5 copies per sample. The cellular HIV-1 STS DNA load was calculated as HIV-1 STS DNA copies per million cells and the median log10 value measured was 3.32 (IQR 2.92–3.75 log10 copies/10^6 PBMC) (Figure 4A). These values were investigated according to the various known parameters of the samples.

The relationship between the cellular HIV-1 DNA loads measured in this study and other clinical parameters and characteristics of the samples at the time of sampling were also investigated. The results show that the cellular HIV-1 STS levels have a weak correlation with the corresponding plasma RNA load.
levels (Pearson correlation coefficient $R^2 = 0.20; P = 0.001$) and a very weak correlation with CD4$^+$ T-cell counts (Pearson correlation coefficient $R^2 = 0.04; P = 0.013$) (Figure 4B and C), confirming previously acquired data [20]. For statistical reasons, the analysis regarding subtypes was limited to the three most frequently observed subtypes, A, B and C. The median cellular HIV-1 DNA load was different in the three groups (2.91, 3.26 and 3.56 log$_{10}$ copies/10$^6$ PBMC respectively), but this difference did not reach statistical significance ($P = 0.40$).

Figure 5 shows the comparison of the cellular HIV-1 DNA loads for patients infected with drug-resistant or non-resistant strains of the virus. The results indicate a trend towards a higher cellular HIV-1 DNA load in patients with transmitted drug-resistant strains of the virus (3.64 log$_{10}$ copies/10$^6$ PBMC, IQR 2.63–4.25) than in patients infected with wild-type strains (3.27 log$_{10}$ copies/10$^6$ PBMC, IQR 2.90–3.73). This difference did, however, not reach statistical significance ($P = 0.14$). The possibility of higher cellular viral loads being explained by more recent infections in the resistance group was investigated but the proportions of recent infections in patients with or without evidence of transmitted resistant strains was (3/22) 13.6% and (10/66) 15.2% respectively ($P = 1.00$), meaning this was not the case.

**Discussion**

In this study the association between cellular HIV-1 DNA load and transmitted drug resistance was examined for the first time, using an improved molecular beacon-based real-time PCR assay for quantification of HIV-1 STS DNA and human CCR5 alleles. The median cellular HIV-1 STS DNA load calculated in this study is 3.32 log$_{10}$ copies per 10$^6$ PBMC. The results of this study
indicate no statistically significant difference in cellular HIV-1 DNA load in patients with transmitted drug-resistant strains of the virus compared to that of patients infected with wild-type strains. The cellular viral DNA levels found here are higher than those quantified with the previous version of the assay [20] (P<0.001) due to the improvement of the specificity of the CCR5 components. This study includes a significant number of patients from Israel and countries distributed throughout Europe. The criteria of inclusion, the well-defined datasets and the consistent sampling method are encouraging parameters supporting the strength of this report. The results found are comparable to those found in previous studies of cellular HIV-1 DNA quantification in treatment-naive patients where levels of 2.85–3.2 log₁₀ copies/10⁶ PBMC were reported [19,21,29,50,51]. The findings of this study also indicate a weak association between the cellular HIV-1 DNA counts and viral RNA levels or CD4⁺ T-cell counts, in agreement with previous findings [20,50,52]. The three main subtypes also appeared not to have an impact on cellular viral DNA load.

Positions known to confer resistance to antiretroviral drugs in plasma RNA- and cellular DNA-derived nucleotide sequences covering the PR/RT region were compared for each patient in order to assess the level of similarity between them. Significantly, a high similarity was found between the two, suggesting that genotypic drug-resistance testing could be carried out on either starting material.

The co-receptor tropism of all samples was determined from the cellular DNA and it was found that 91% of the samples were CCR5-tropic, as expected for early infections, 3% were CXCR4-tropic and 4% were a mixture of the two types. Hence, it appears that the existence of transmitted drug resistance mutations does not affect the co-receptor tropism of the virus. This data suggests that resistant and susceptible viral species behave similarly in early infection.
A limitation to the study is the possibility of the occurrence of reversion of viral strains to wild-type in those samples considered non-resistant, as this may play a role on cellular viral DNA load as minority species in the viral population. Nonetheless, reversion only appears to occur to a limited extent [53]. Another factor that may influence such findings is the fact that known mutations that confer resistance to antiretroviral drugs are heterogeneous and may have differential impact of resistance. The study of different TDRM individually, however, is not possible with the datasets currently available. Also, mutations associated with reduced viral fitness, and therefore lower viral loads, are not found frequently in transmitted resistant strains due to the fact that the level of plasma viral load is a key factor in the transmission of the virus [54]. Another point is the possibility of the inclusion of patients who are in the acute phase of infection at the time of sampling, who may account for values on the high end of the range of HIV cellular DNA levels obtained in this study.

The results show for the first time that there is no association between cellular viral DNA levels and the existence of transmitted drug resistant mutations in newly-diagnosed patients. Cellular HIV-1 DNA load has been shown to be associated with disease progression [19,20,21,23,24,26,29,30,32] and transmitted drug resistance does not currently have an impact on the time of treatment initiation. From this data, it is implied that transmitted drug resistance is not associated with disease progression.

Overall, this report presents an improved methodology of cellular HIV-1 DNA quantification with molecular beacon-based real-time PCR. The patients included in the study were newly-diagnosed individuals from Israel and all over Europe. The data show a similar co-receptor tropism for resistant and non-resistant viral species, implying that both behave in a similar manner in early infection. Significantly, a high correlation was found between RNA- and DNA-associated PR/RT sequencing indicating that genotypic drug resistance testing could be carried out on either type of sample. It was found that no correlation exists between cellular HIV-1 DNA levels and transmitted drug resistance, indicating that the latter may not be associated with disease progression and should continue not having an impact on the time to initiate treatment in patients.
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Author Contributions

Conceived and designed the experiments: LGK. Performed the experiments: VLD IK CB BC ZG LBJ SZL IL CN DP MP FR LR JCS AMV KVL JV LGK. Analyzed the data: VLD DAMCvdV IK CB BC ZG LBJ SZL IL CN DP MP FR LR JCS AMV KVL JV LGK. Contributed reagents/materials/analysis tools: CB BC ZG LBJ SZL IL CN DP MP FR LR JCS AMV KVL JV LGK. Wrote the paper: VLD DAMCvdV LGK. Helped with coordination of the project and assisted in setting up the real-time assay: VLD. Statistical analysis and interpretation of results: DAMCvdV. Data collection and manuscript preparation: IK. Organisation of sampling, sample preparation, and data collection: CB BC ZG LBJ SZL IL CN DP MP FR LR JCS AMV KVL. Organisation of data collection and contribution: JV. Devised original hypothesis: LGK. Coordinated the study: LGK.

References


52. Carr JM, Cheneau KM, Cooon C, Davis A, Shaw D, et al. (2007) Development of methods for coordinate measurement of total cell-associated and integrated human immunodeficiency virus type 1 (HIV-1) DNA forms in routine clinical samples: levels are not associated with clinical parameters, but low levels of integrated HIV-1 DNA may be prognostic for continued successful therapy. J Clin Microbiol 45: 1281–1287.
