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Transmission of Single and Multiple Viral Variants in Primary HIV-1 Subtype C Infection

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Abstract

To address whether sequences of viral gag and env quasispecies collected during the early post-acute period can be utilized to determine multiplicity of transmitted HIV's, recently developed approaches for analysis of viral evolution in acute HIV-1 infection [1,2] were applied. Specifically, phylogenetic reconstruction, inter- and intra-patient distribution of maximum and mean genetic distances, analysis of Poisson fitness, shape of highlighter plots, recombination analysis, and estimation of time to the most recent common ancestor (tMRCA) were utilized for resolving multiplicity of HIV-1 transmission in a set of viral quasispecies collected within 50 days post-seroconversion (p/s) in 25 HIV-infected individuals with estimated time of seroconversion. The decision on multiplicity of HIV infection was made based on the model's fit with, or failure to explain, the observed extent of viral sequence heterogeneity. The initial analysis was based on phylogeny, inter-patient distribution of maximum and mean distances, and Poisson fitness, and was able to resolve multiplicity of HIV transmission in 20 of 25 (80%) cases. Additional analysis involved distribution of individual viral distances, highlighter plots, recombination analysis, and estimation of tMRCA, and resolved 4 of the 5 remaining cases. Overall, transmission of a single viral variant was identified in 16 of 25 (64%) cases, and transmission of multiple variants was evident in 8 of 25 (32%) cases. In one case multiplicity of HIV-1 transmission could not be determined. In primary HIV-1 subtype C infection, samples collected within 50 days p/s and analyzed by a single-genome amplification/sequencing technique can provide reliable identification of transmission multiplicity in 24 of 25 (96%) cases. Observed transmission frequency of a single viral variant and multiple viral variants were within the ranges of 64% to 68%, and 32% to 36%, respectively.

Introduction

Complexity and multiplicity of HIV-1 transmission depends on multiple factors, although HIV-1 subtype [3] and mode [2,4,5] of viral transmission can be considered major determinants. A severe genetic bottleneck during heterosexual transmission of HIV-1 subtype C has been reported [3,6]. Compelling evidence for a link between multiplicity and mode of HIV-1 transmission was provided by a series of recent studies that applied the technique of single-genome amplification/sequencing (SGA) of samples collected at the very early clinical stage of HIV-1 infection, and combined this method with a model of random viral evolution as a new tool for assessment of HIV-1 transmission multiplicity [1,2,4–7]. Transmission of a single viral variant occurs in about 76–90% of cases of heterosexual transmission [2,6,7], in about 60% of cases of HIV-1-infected men who have sex with men [MSM] [3], and only in about 40% of injection drug users (IDU) who acquired HIV-1 infection [4]. Conversely, transmission of multiple viral variants gradually increases from about 20% during heterosexual transmission of HIV-1 to about 40% in MSM, and to 60% in IDU. It is likely that the mucosal barrier plays an important role in reducing multiplicity of transmitted HIV-1. Due to the absence of a mucosal barrier, IDU exhibit a higher frequency of multiple-variant transmission and a wider range of transmitted viruses than subjects infected heterosexually [4]. The important role of the mucosal barrier in viral transmission has also been demonstrated in rhesus macaque models [8,9].

Transmission of multiple viral variants is associated with faster disease progression [10–12]. Haaland et al. reported transmission of multiple viral variants in 3 of 7 individuals infected by someone other than their spouses, and significant association between transmission of multiple variants and an inflammatory genital infection [6]. Therefore, monitoring the multiplicity of new HIV-1 transmissions is important for assessing the efficiency of public health interventions including design and development of therapeutic and preventive strategies, and interventions targeting behavior change. However, the current tools for identifying multiplicity of transmitted viruses in new HIV-1 infections are suboptimal for routine monitoring.

The limited number of analyzed cases has been an inherent limitation in most primary HIV-1 infection studies due to the numerous logistical challenges in obtaining clinical samples.
during the acute and early post-acute phases of HIV-1 infection. Thus, studies addressing multiplicity of HIV-1 infection included 28 MSM from New York, Alabama, and North Carolina [5], 102 HIV-infected blood donors and healthcare patients from the USA and Trinidad [2], 69 individuals from South Africa and Malawi [7], 27 heterosexually infected individuals from Zambia and Rwanda [6], and 10 IDU in a Montreal cohort [4].

In this study we addressed whether viral sequences obtained within 50 days post-seroconversion (p/s) can be utilized for assessing the multiplicity of viral transmission in primary HIV-1 subtype C infection. The gag and env gp120 quasispecies generated by SGA from a cohort of acutely and recently HIV-1C-infected individuals in Botswana were studied. Applying recently developed techniques for analysis of viral evolution in acute HIV-1 infection [1,2], a two-step approach was explored to assess multiplicity of HIV transmission. Congruent results were obtained for 96% of analyzed samples.

### Methods

#### Ethics statement

This study was conducted according to the principles expressed in the Declaration of Helsinki. The study was approved by the Institutional Review Boards of Botswana and the Harvard School of Public Health. All patients provided written informed consent for the collection of samples and subsequent analysis.

#### Study subjects

Viral sequences analyzed in the study originated from the Primary HIV-1 Subtype C Infection Study in Botswana, the *Tshedimoso* study [13–18]. A total of 25 individuals with estimated time of seroconversion and samples collected within 50 days p/s were used in this study. In the description of study subjects the following terminology was followed: *acute* HIV infection was defined as the period from viral transmission to seroconversion; *recent* HIV infection was defined as the period from viral transmission to seroconversion;

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### Table 1. Patient characteristics, time of sampling, and number of analyzed *gag* and *env* sequences

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<th>Proviral DNA load</th>
<th>CD4 count</th>
<th>Date</th>
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<td>44</td>
<td>V</td>
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</table>

1Years at the time of sampling.
2log_{10} copies/ml.
3log_{10} copies/10^6 PBMC.
5Date of sampling (first sampling for patients with dual dates of sampling).
7Subjects A and B had viral sequences available at two time points within 50 days p/s. Both sets were included in analysis.

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until one year p/s; primary HIV infection included both the periods of acute and recent HIV infection. The time interval of 0–50 days p/s was a primary focus in this study, and was termed the early post-acute period. Subjects’ characteristics at the time of sampling, including gender, age, HIV-1 RNA load, proviral DNA load, CD4 count, timing of sample collection, and the number of analyzed gag and env sequences, are presented in Table 1. The time of seroconversion was estimated based on the laboratory results of HIV-1 RNA test, ELISA test for HIV antibodies, and Western blot test as described previously [14,15]. Eight acutely infected individuals (subjects A to H) were identified before seroconversion and the time of their seroconversion was estimated as the midpoint between the last ELISA-negative and the first ELISA-positive test, within a week in most cases. Thirty-four recently infected individuals were identified after seroconversion, and the time of their seroconversion was estimated according to Fiebig staging [19] based on incomplete Western blot. For example, subject OG’s regular ELISA test for HIV antibodies was positive indicating seroconversion, while her detuned ELISA test was negative suggesting recent HIV infection. The Western blot analysis revealed presence of the gp160-, gp120-, gp41-, p66-, p55/51-, and p24-bands, and absence of p39-, p31-, and p17-bands. Plasma HIV-1 RNA was 6.47 log_{10}/ml, and gradually declined over the next few months. Therefore, the analyzed sample of subject OG was classified as Fiebig stage V. The beginning of Fiebig stage III coincides with the time of detectable seroconversion (time 0). Given that the mean duration of Fiebig stage III is 3 days, the mean duration of Fiebig stage IV is 6 days, and the mid-point of

Figure 1. HIV-1 subtype C diversity within 50 days p/s among acutely and recently infected individuals from the Tshedimoso cohort in Botswana: gag sequences, NJ tree. Acutely infected individuals are denoted by a single letter A through H. The patient ID of recently infected individuals has two letters, OC to QT. A subscript next to the patient ID denotes time of sampling in days p/s. Asterisks denote bootstrap values ≥80. The horizontal bar represents genetic distance. doi:10.1371/journal.pone.0016714.g001
mean duration of Fiebig stage V is 35 days, the enrollment time for subject OG was assigned 44 days p/s. Details on quantification of viral load and CD4 [13,17,18], and amplification and sequencing of viral quasispecies by SGA [13,15,16] have been presented elsewhere. Analyzed sequences were tested by HYPERMUT v.2.0 [20] and hypermutated sequences that yielded a p-value of 0.05 or lower were excluded from analysis. All subjects were Botswana nationals, and all infections were HIV-1 subtype C [13,17]. All subjects were ARV-naïve at the time of sampling.

Phylogenetic analysis

The branching topology of intra-patient gag and env sequences was inferred by the Neighbor-Joining (NJ) method (Tamura-Nei model with bootstrapping) and the Maximum-Likelihood (ML) method (PhyML) as implemented by Geneious v.5.0.3 [21]. Phylogenetic trees were visualized in FigTree [22].

Analysis of viral distances

Viral pairwise ML-corrected distances were analyzed using DIVEIN [23]. The Kimura-2-parameters (K2P)-corrected and Hamming distances were analyzed in MEGA v4 [24]. The MRCA and pairwise ML-corrected distances to MRCA were estimated in DIVEIN [23]. The MRCA, a hypothetical viral sequence that represents the most recent viral variant from which a subject’s viral quasispecies are descended, was reconstructed in DIVEIN [23] by the joint maximum likelihood procedure [25]. The majority consensus sequence, another hypothetical viral sequence that indicates the most abundant nucleotide in the

Figure 2. HIV-1 subtype C diversity within 50 days p/s among acutely and recently infected individuals from the Tshedimoso cohort in Botswana: gag sequences, ML tree. Acutely infected individuals are denoted by a single letter A through H. The patient ID of recently infected individuals has two letters, OC to QT. A subscript next to the patient ID denotes time of sampling in days p/s. The horizontal bar represents genetic distance.

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multiple sequence alignment at each position, was built in BioEdit [26]. The pairwise K2P-corrected and Hamming distances to the consensus sequence were quantified in MEGA v4 [24].

**Poisson fitness**

Poisson fitness analysis was performed using the online tool at Los Alamos National Laboratory at http://www.hiv.lanl.gov/content/sequence/POISSON_FITTER/poisson_fitter.html [27]. The tool analyzes frequency of Hamming distances by computing the best fitting Poisson distribution through ML and evaluating results of the Goodness of Fit test (GOF).

**Highlighter plots**

Highlighter plots were generated by Highlighter at www.hiv.lanl.gov, a visualization tool of aligned nucleotide sequences that highlights nucleotide polymorphisms and marks APOBEC signatures.

**Recombination analysis**

Recombination analysis was performed using package RDP3, a computer program for statistical identification and characterization of recombination events in DNA sequences [28]. RDP3 utilizes a range of non-parametric recombination detection methods.

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**Figure 3. HIV-1 subtype C diversity within 50 days p/s among acutely and recently infected individuals from the Tshedimoso cohort in Botswana: env sequences, NJ tree.** Acutely infected individuals are denoted by a single letter A through H. The patient ID of recently infected individuals has two letters, OC to QT. A subscript next to the patient ID denotes time of sampling in days p/s. Asterisks denote bootstrap values ≥80. The horizontal bar represents genetic distance.

doi:10.1371/journal.pone.0016714.g003
methods including BOOTSCAN, MAXCHI, CHIMAERA, 3SEQ, GENECONV, SISCAN, PHYLPRO and VISRD [29–34]. RDP3 treats every sequence within the analyzed alignment as a potential recombinant, and systematically screens sequence triplets and/or quartets to identify sequences that contain a recombinant and two sequences that could serve as parents, and performs a statistical evaluation of recombination signal [28]. Such an approach eliminates the need for reference sequences, which makes analysis of viral quasispecies from epidemiologically unlinked patients more practical.

Estimation of tMRCA
Analysis was performed using Bayesian inference with a Markov Chain Monte Carlo (MCMC) method implemented in BEAST v.1.5.4 [35]. Longitudinal viral quasispecies dated according to the day of sampling from a subset of six acutely infected individuals were utilized to identify the rate of viral evolution within HIV-1 subtype C gag and env. For acutely infected individuals, the MRCA of viral quasispecies sampled at a given time was constrained to a uniform calibration prior bounded between the time of sample collection in relation to the estimated time of seroconversion (lower bound) and the same value plus 30 days as an average time period between the time of infection and seroconversion. The rate of evolution over the entire tree was estimated as the meanRate parameter for each case of acute HIV-1 infection. The geometric mean evolutionary rate in HIV-1C gag was estimated at $1.23 \times 10^{-5}$ (95% CI $8.07 \times 10^{-6} - 1.64 \times 10^{-5}$) substitutions per site per day. The geometric mean evolutionary rate in HIV-1C env gp120 was estimated at $3.71 \times 10^{-5}$ (95% CI $1.97 \times 10^{-5} - 5.45 \times 10^{-5}$) substitutions per site per day. The estimated rate of gag and env gp120 evolution.

![Figure 4](https://doi.org/10.1371/journal.pone.0016714.g004)

**Figure 4.** HIV-1 subtype C diversity within 50 days p/s among acutely and recently infected individuals from the Tshedimoso cohort in Botswana: env sequences, ML tree. Acutely infected individuals are denoted by a single letter A through H. The patient ID of recently infected individuals has two letters, OC to QT. A subscript next to the patient ID denotes time of sampling in days p/s. The horizontal bar represents genetic distance.

doi:10.1371/journal.pone.0016714.g004
Figure 5. Distribution of HIV-1 subtype C gag and env maximum distances. y-axis denotes count of subjects per bin. x-axis denotes maximum distances. Single and double letters above the bins correspond to patients IDs. A: gag sequences, ML-corrected pairwise distances; B: gag sequences, K2P-corrected pairwise distances; C: gag sequences, Hamming distances; D: env sequences, ML-corrected pairwise distances; E: env sequences, K2P-corrected pairwise distances; F: env sequences, Hamming distances; G: gag sequences, ML-corrected distances to MRCA; H: gag sequences, K2P-corrected distances to MRCA; I: gag sequences, Hamming distances to MRCA; J: env sequences, ML-corrected pairwise distances; K: env sequences, K2P-corrected pairwise distances; L: env sequences, Hamming distances.
sequences, K2P-corrected distances to consensus sequence; I: gag sequences, Hamming distances to consensus sequence; J: env sequences, ML-corrected distances to MRCA; K: env sequences, K2P-corrected distances to consensus sequence; L: env sequences, Hamming distances to consensus sequence.

doi:10.1371/journal.pone.0016714.g005

was applied to determine tMRCA for five “undetermined” cases in the study, and the tMRCA was estimated as the treeModel:-rootHeight parameter. The gag and env gp120 sequence data were analyzed using the evolutionary model selected by the Akaike information criterion in jModeltest 0.1.1 [36] and a relaxed molecular clock (uncorrelated lognormal) under the Yule model. The value of the effective sampling size (ESS) was controlled to be above 200, and the length of the MCMC chain was at least 20,000,000.

The decision on multiplicity of HIV infection

The decision on multiplicity of HIV infection was made based on the model’s fit with or failure to explain the observed extent of viral sequence heterogeneity. The model’s fit was associated with transmission of a single viral variant, while the model’s failure was interpreted as either transmission of multiple viral variants, or the result of rapid immune selection driving the observed level of viral diversification [1,37–39].

Results

Heterogeneity of HIV-1 subtype C gag and env sequences

Using samples collected within 50 days p/s, gag quasispecies were generated for 25 and env for 24 HIV-infected individuals with estimated time of seroconversion (Fiebig stage less than VI). Patient demographic and laboratory data, time of sampling, and number of analyzed gag and env sequences at the time of sampling are presented in Table 1. The phylogeny of gag and env sequences was inferred by the NJ and ML methods. The overall length of branches was shorter for gag sequences (Fig. 1 – gag NJ tree, and Fig. 2 – gag ML tree) as presented on the same scale with env sequences (Fig. 3 – env NJ tree, and Fig. 4 – env ML tree), which is consistent with lower diversity of HIV-1 gag as compared with HIV-1 env.

Branching topology of gag sequences

The differences among gag sequences were less discernible as compared to env sequences. Three subjects in the NJ tree (Fig. 1; subjects D, OG, and OW) and three subjects in the ML tree (Fig. 2; subjects OG, OW, and PP) demonstrated extended length of branches suggesting transmission of multiple viral variants, and highlighting the necessity of using alternative methods for inferring phylogenetic trees. Subjects A, D (ML tree), E, F, OJ, PK, PP (NJ tree), and QP (NJ and ML trees) demonstrated moderate diversity of gag sequences. Fifteen of 25 subjects demonstrated short (13 subjects) or zero (subjects OU and QS) branch length of gag quasispecies collected within 50 days p/s. Thus, branching length and topology of gag sequences was consistent with transmission of multiple viral variants in 20% cases (subjects D, OG, OW, PK, and PP), undetermined multiplicity of transmission in 20% cases (subjects A, E, F, OJ, and QP), and transmission of a single viral variant in 60% cases.

Branching topology of env sequences

Branching topology and length of env sequences in both NJ (Fig. 3) and ML (Fig. 4) suggested transmission of multiple viral variants in 5 cases (subjects A, OG, OW, PK, and PP). Moderate length of branches was evident in four additional cases, subjects D, OJ, PO, and QP. The remaining 15 subjects revealed short branches indicating little intra-patient env diversity and apparent transmission of a single virus upon HIV infection. The topology and branching length of env quasispecies inferred by the NJ and ML methods suggested that 5 of 24 (20.8%) subjects were infected with multiple viral variants, and 15 (62.5%) subjects were infected with a single viral variant. The remaining 4 cases (16.7%) showed intermediate branching length suggesting that multiplicity of viral transmission in these cases is uncertain and requires additional analysis.

Maximum and mean distances

The distribution of maximum and mean pairwise distances for gag and env sequences was studied to address whether applied evolutionary model[s] or specifics of viral distances can help to segregate HIV infections with transmission of single and multiple viral variants. Three types of maximum and mean pairwise distances, ML-corrected, K2P-corrected, and Hamming distances, as well as maximum and mean ML-corrected distances to MRCA sequence and K2P-corrected and Hamming distances to the consensus sequence, were analyzed.

The best segregation of HIV-1C infections was observed for maximum env pairwise distances including ML-corrected, K2P-corrected, and Hamming pairwise distances (Figs. 5D, 5E, and 5F). Consistent with the branching topology, the distribution of maximum env pairwise distances suggested transmission of multiple viral variants in five subjects, A, OG, OW, PP, and PK. The segregation of HIV-1C infections based on distribution of maximum gag pairwise distances was less discernible: only two subjects, OG and OW, showed separation from the remaining cases (Figs. 5A, 5B, and 5C). Two subjects, PK and PP, were on the right edge of the histogram tail but without separation from the main group of gag sequences. The continuous histograms with poor separation between cases, such as maximum ML-corrected distances to MRCA in Figs. 5G (gag) and 5J (env), produced the largest number of discrepant assignments. For example, ML-corrected distances to MRCA in gag generated assignments that were not congruent with other distance measurements in 7 of 25 cases of maximum distances and in 15 of 25 mean distances (see Cumulative Preliminary Summary discussion and Summary Table below). Similarly, little to no segregation was found for the maximum K2P-corrected (Figs. 5H – gag and 5K – env) and Hamming (Figs. 5I – gag and 5L – env) distances to the consensus sequence.

The distribution of mean distances resembled the profiles of maximum distances. Interestingly, 7 out of 12 measurements (Figs. 6D, 6E, 6F, 6H, 6I, 6K, and 6L) segregated 4 samples, OG, OW, PP, and PK, out of five selected by the maximum env pairwise distances as cases with transmission of multiple viral variants. In addition, three of these 4 samples, OG, OW, and PK, were also separated from the main pool of samples by three mean gag pairwise distances (Figs. 6A, 6B, and 6C).

The decision thresholds (Table 2) were estimated based on the scale and distribution of maximum and mean distances, i.e., based on data presented in Figures 5 and 6. The decision thresholds differ between analyzed HIV-1 genes: env-related thresholds were 3 to 4 times higher than gag-related thresholds. The thresholds for maximum distances were 2 to 4 times higher than for mean distances. The thresholds for pairwise distances were higher than for distances to consensus sequence. The distribution specifics of ML-corrected distances to MRCA resulted in similar thresholds.
Figure 6. Distribution of HIV-1 subtype C gag and env mean distances. y-axis denotes count of subjects per bin. x-axis denotes mean distances. Single and double letters above the bins correspond to patient IDs: A: gag sequences, ML-corrected pairwise distances; B: gag sequences, K2P-corrected pairwise distances; C: gag sequences, Hamming distances; D: env sequences, ML-corrected pairwise distances; E: env sequences, K2P-corrected pairwise distances; F: env sequences, Hamming distances; G: gag sequences, ML-corrected distances to MRCA; H: gag sequences, K2P-corrected distances to MRCA; I: gag sequences, Hamming distances to consensus; J: env sequences, ML-corrected distances to MRCA; K: env sequences, K2P-corrected distances to consensus; L: env sequences, Hamming distances to consensus.
with ML-corrected pairwise distances. It is likely that this congruency between analyses of maximum and mean distances in segregation of viral sequences solidifies the evidence for the multiplicity of HIV transmission.

Poisson fitness

The Hamming distance frequencies were analyzed by computing the best fitting Poisson distribution and evaluating results of the GOF. P-values of less than 0.05 indicate divergence from Poisson distribution and can be interpreted as transmission of multiple viral variants. The results of this analysis should be taken cautiously due to two limitations: the small number of sequences and the few relatively late (close to 50 days p/s) time points of sampling. Nevertheless it seemed important to compare results of the phylogenetic inference and viral diversity analyses with the new tool, Poisson-Fitter, which was developed for identification of transmissions caused by a single viral variant.

Four cases identified as transmission of multiple viral variants by both phylogenetic reconstruction and analysis of genetic distances (subjects OG, OW, PK, and PP) were also classified as multiple HIV infections in the Poisson-Fitter by GOF p-value of less than 0.05 for both gag and env sequences. Cases of HIV-1C infection considered “undetermined” by phylogeny and distance analyses (4 in gag analysis and 5 in env analysis) were also rejected as transmissions of single viral variant by the Poisson-Fitter method. However, the Poisson-Fitter rejected a few additional cases that were identified as transmissions of a single viral variant by phylogenetic and distance analyses: 3 in gag (subjects E, F, and QI) and 3 in env (subjects C, OU, and QI).

A comparison of phylogenetic inference, analysis of viral diversity, and the Poisson-Fitter analysis revealed overall good congruence between these methods for identification of HIV-1 transmission multiplicity. All cases that were identified as transmission of multiple viral variants or “undetermined” (implying that transmission of multiple viral variants cannot be excluded) were correctly rejected by the Poisson-Fitter through the GOF test. However, the Poisson-Fitter seemed to over-reject transmission of a single viral variant in some cases. This was observed for both gag (n = 10) and env (n = 16) sequences in subject QI, who was sampled during Fiebig stage IV at day 20 p/s. A few other cases that were identified as transmission of single viral variants by the phylogenetic and viral diversity analyses were rejected by the Poisson-Fitter either in gag (subjects E and F) or in env (subjects C and OU) analyses. This observation suggests that consistency of the Poisson-Fitter results for gag and env analysis produce reliable results of identification of multiplicity of HIV transmission, while discrepant gag and env results indicate a high level of uncertainty and warrant further analysis by alternative methods.

Cumulative preliminary summary

The cumulative summary of results obtained by phylogeny, distance analysis, and the Poisson-Fitter is presented in Figure 7. The results are coded by “0” for transmission of single viral variant, “1” for transmission of undetermined number of viral variants (with additional blue coloring), and “2” for transmission of multiple viral variants (with additional light red coloring). The distribution of cumulative scores produced clear segregation of HIV-1C infections into groups that were associated with the multiplicity of viral transmission as “single,” “undetermined” and “multiple” (Fig. 8). The shape of cumulative score histograms provided better separation of single and multiple HIV-1C infection than any single method of analysis, highlighting the importance of multiple analyses in determining multiplicity of HIV-1 transmission.

The combined analysis of phylogeny, maximum and mean distances, and Poisson fitness suggested that transmission of multiple HIV-1C variants occurred in 4 (20% of resolved, or 16% of analyzed) cases, while transmission of a single viral variant occurred in 16 (80% of resolved, or 64% of analyzed) cases. Therefore, a conclusive decision on the multiplicity of HIV-1 transmission based on sampling within 50 days p/s was obtained for 80% of the analyzed cases. The multiplicity of HIV-1 transmission in the remaining five cases (20%), subjects A, D, QJ, PO and QP, was inconclusive and warranted further analyses.

Detailed analysis of initially “undetermined” cases

Initial analysis based on the phylogenetic inference, analysis of viral diversity, and Poisson fitness analysis produced “undetermined” results for five subjects, A, D, QJ, PO, and QP. To resolve

### Table 2. Decision thresholds for transmission of single and multiple HIV-1 variants

<table>
<thead>
<tr>
<th>Analysis</th>
<th>Maximum distances</th>
<th>Mean distances</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>gag</td>
<td>env</td>
</tr>
<tr>
<td></td>
<td>Multi</td>
<td>Single</td>
</tr>
<tr>
<td>ML pairwise</td>
<td>&gt;1.25%</td>
<td>&lt;0.5%</td>
</tr>
<tr>
<td>K2P pairwise</td>
<td>&gt;1.25%</td>
<td>&lt;0.5%</td>
</tr>
<tr>
<td>Hamming pairwise</td>
<td>&gt;15</td>
<td>&lt;8</td>
</tr>
<tr>
<td>ML to MRCA</td>
<td>&gt;1.2%</td>
<td>&lt;1%</td>
</tr>
<tr>
<td>K2P to consensus</td>
<td>&gt;1%</td>
<td>&lt;0.5%</td>
</tr>
<tr>
<td>Hamming to consensus</td>
<td>&gt;10</td>
<td>&lt;5</td>
</tr>
</tbody>
</table>

Note: The following decision strategy was applied for each analysis of subject’s maximum and mean distances within gag and env: A sample with value exceeding the “Multi” threshold was associated with transmission of multiple HIV-1 variants. A sample with value smaller than the “Single” threshold was associated with transmission of a single HIV-1 variant. A sample with value exceeding the “Single” threshold but less than the “Multi” threshold was considered undetermined in relation to multiplicity of HIV-1 transmission.

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the multiplicity of HIV-1 infection in these cases, the following methods were applied: distribution of individual gag and env distances, shape analysis of highlighter plots, recombination analysis, and estimation of time to MRCA.

Distribution of individual HIV-1C gag and env distances. For individual sets of gag and env sequences in subjects A, D, OJ, PO, and QP, the distribution of pairwise ML-corrected, K2P-corrected, Hamming distances, ML-corrected distances to MRCA, K2P-corrected distances to consensus sequence, and Hamming distances to consensus sequence. The last column “Multiplicity of infection” represents summary of initial analysis per subject indicating transmission of “Single” or “Multiple” viral variants in successfully resolved cases. The uncertain and non-congruent results are interpreted as “Undetermined” cases, and are subjects for detailed analysis by additional methods.

doi:10.1371/journal.pone.0016714.g007

[Table and diagram as in the original text]
viral variants in subjects A, D, OJ, and QP. Taking into account only conclusive shapes, the combined results of the PO. Taking into account only conclusive shapes, the combined results of the multiplicity of HIV-1C transmission. The results of detailed analyses suggested that four subjects—A, D, OJ, and QP—were infected with multiple viral variants, while multiplicity of HIV-1 transmission in one subject, PO, remained inconclusive.

HIV-1C RNA load

We tested whether HIV-1 RNA load differs between subjects infected with single and multiple viral variants. Although subjects with transmission of multiple viral variants seemed to have higher HIV-1 RNA load at the time of sampling (median 5.75 log_{10} copies/ml; IQR 3.58–6.31) than subjects with single transmitted virus (median 4.89 log_{10} copies/ml; IQR 2.60–5.58), the difference did not reach statistical significance (p = 0.11; Mann-Whitney Rank Sum test).

Summary of results

Transmission of a single viral variant was identified in 16 of 25 (64%; 95% CI 45% to 83%) analyzed cases. Transmission of multiple viral variants was confirmed in 8 of 25 (32%; 95% CI 14% to 50%) cases. For one subject, PO, we were unable to determine the multiplicity of transmission. Based on self-reports collected at enrollment, all HIV-1 transmissions in this study occurred heterosexually. Therefore, based on analysis of samples collected within 50 days p/s we estimate that the frequency of heterosexual transmission of a single viral variant in HIV-1 subtype C infection ranges from 64% to 68%, and that transmission of multiple viral variants ranges from 32% to 36% of HIV-1C infections.

Discussion

The study demonstrated the utility of viral quasispecies analysis obtained within 50 days p/s for identifying multiplicity of HIV-1 subtype C infection. The suggested two-step approach was able to resolve 24 of 25 (96%) cases. The first step of the analysis was fast and straightforward, and was based on a combination of phylogenetic reconstruction, distribution of viral distances, and analysis of Poisson fit. Application of the first-step analysis resulted in successful assignment of multiplicity of HIV-1C infection in 20 of 25 (80%) cases as two extremes representing clear separation of single viral variant transmission from transmission of multiple viral variants. However “undetermined” results were produced in 5 (20%) cases due to inconsistency among the applied methods. The second step of the analysis attempted to resolve cases with “undetermined” initial results based on more detailed analysis that included intra-patient distribution of viral genetic distances, shape
Figure 9. Distribution of individual HIV-1 subtype C gag and env distances for 5 “undetermined” cases. Patient IDs are shown on the left and on the right. All gag distances are shown on the left with light blue background. All env distances are shown on the right with light yellow background. Each gene/patient block includes 6 histograms with ML-corrected pairwise distances, K2P-corrected pairwise distances, Hamming distances, ML-corrected distances to MRCA, K2P-corrected distances to consensus sequence, and Hamming distances to consensus sequence. y-axis denotes count. x-axis denotes distances. Pairwise distances are shown in orange, and distances to MRCA and consensus sequences are shown in gray.

doi:10.1371/journal.pone.0016714.g009
Figure 10. Highlighter plots and results of recombination analysis for 5 “undetermined” cases. Patient IDs are shown on the left and on the right. All gag data are shown on the left with light blue background. All env data are shown on the right with light yellow background. Highlighter plots were generated by the sequence visualization tool Highlighter. The recombination analysis was performed by RDP3. The order of analyzed sequences in the Highlighter plot corresponds to the order of sequences presented in the output from RDP3. The recombination events were identified in gag sequences 04 and 11 in subject QP, in env sequences 006_05 and 022_05 in subject A, sequence 10 in subject OJ, and in sequence 05 in subject QP.

doi:10.1371/journal.pone.0016714.g010
analysis of highlighter plots, recombination analysis, and estimation of tMRCA. Four of 5 initially "undetermined" cases were resolved in the second-step analysis.

The study highlights the complexity of early post-seroconversion evolution in HIV-1 subtype C infection among subjects. The study suggests that multiplicity of HIV transmission in the majority of HIV infections can be resolved by a combination of relatively simple analytical methods. However, a smaller fraction of about 20% of cases might require more sophisticated analyses. There was an evident discrepancy between some of the analyses in estimating multiplicity of HIV infection. The underlying possible reasons might include, but are not limited to, different sensitivity of evolutionary models used for distance correction, uncertainty in reconstruction of MRCA, and accelerated viral evolution within key epitopes in response to immune pressure from the host that can affect reconstruction of MRCA and subsequent estimation of tMRCA. These results indicate the imprecise nature of current methods and warrant further studies to better understand why different conclusions may be reached via different analyses. The observed complementary nature of applied multiple methods in identifying multiplicity of HIV transmission suggests the necessity of further development of alternative methodologies and bioinformatic techniques to improve the reliability of diagnostic and monitoring of the number of transmitted viral variants on a population level in the HIV/AIDS epidemic.

A combined use of viral quasispecies representing different genes (i.e., env and gag) was important for analysis of multiplicity of HIV transmission. Thus, a congruence between HIV-1C env gp120 V1-C5 and gag quasispecies supported the conclusion regarding multiplicity of HIV transmission. In contrast, discrepancy between viral genes might indicate the presence of early selection (immune) pressure within one but not another viral gene, and would argue for transmission of a single viral variant, as in the cases of subjects A and D. The gp120 V1-C5 sequences generally showed better segregation between transmission of single and multiple viral variants than HIV-1C gag quasispecies, apparently due to a higher viral diversity within env as compared with gag. For viral quasispecies obtained within 50 days p/s, the distribution of maximum pairwise ML-corrected distances was useful for separation of HIV-1C infections with transmission of single and multiple viral variants.

Knowledge of the multiplicity of HIV-1 transmission is a critical component of successful public health management of the HIV/AIDS epidemic, and advancement of HIV-1 transmission prevention. The multiplicity of HIV-1 transmission is strongly associated with the mode of viral transmission. Other factors, such as risk behavior, plasma HIV-1 RNA levels, and co-infections, can also affect both multiplicity of viral transmission and disease progression. Studies on estimating and monitoring of multiplicity of HIV-1 transmission are likely to reveal complex dynamics in the HIV/AIDS epidemic. Better understanding of underlying causes

### Table 3. Recombination analysis, p-values (absence of p-value indicates no recombination event identified by the specified method)

<table>
<thead>
<tr>
<th>Subject (sequence)</th>
<th>HIV-1 gene</th>
<th>Method</th>
<th>RDP</th>
<th>GENECONV</th>
<th>BootScan</th>
<th>MaxChi</th>
<th>Chiemaera</th>
<th>SIScan</th>
<th>PhylPro</th>
<th>LARD</th>
<th>3Seq</th>
</tr>
</thead>
<tbody>
<tr>
<td>A(006_05) env</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>0.013</td>
<td>-</td>
<td>3.3x10^-3</td>
<td>-</td>
<td>7.1x10^-2</td>
<td>0.03</td>
<td></td>
</tr>
<tr>
<td>A(022_05) env</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>4.2x10^-4</td>
<td>-</td>
<td>4.1x10^-4</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>OJ (10) env</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>1.4x10^-3</td>
<td>-</td>
<td>1.4x10^-3</td>
<td>0.041</td>
<td></td>
</tr>
<tr>
<td>QP (04) gag</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>6.8x10^-4</td>
<td>0.042</td>
<td></td>
</tr>
<tr>
<td>QP (11) gag</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>6.8x10^-4</td>
<td>0.042</td>
<td></td>
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<tr>
<td>QP (05) env</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>0.038</td>
<td>3.5x10^-3</td>
<td>1.7x10^-8</td>
<td>-</td>
<td>0.02</td>
<td>6.8x10^-3</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

doi:10.1371/journal.pone.0016714.t003

### Table 4. Estimated tMRCA, days.

<table>
<thead>
<tr>
<th>Subject</th>
<th>Estimated time p/s(^1) by Fiebig stage</th>
<th>Estimated tMRCA</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(\text{gag}) geo mean (95% lower and upper HPD)(^2)</td>
<td>(\text{env}) geo mean (95% lower and upper HPD)(^2)</td>
</tr>
<tr>
<td></td>
<td>ESS(^3)</td>
<td>ESS(^3)</td>
</tr>
<tr>
<td>A</td>
<td>6</td>
<td>193 (27; 753)</td>
</tr>
<tr>
<td>D</td>
<td>6</td>
<td>194 (55; 528)</td>
</tr>
<tr>
<td>OJ</td>
<td>44</td>
<td>174 (23; 1,039)</td>
</tr>
<tr>
<td>PO</td>
<td>6</td>
<td>41 (2; 178)</td>
</tr>
<tr>
<td>QP</td>
<td>48</td>
<td>351 (63; 1,520)</td>
</tr>
</tbody>
</table>

\(^1\)Days post-seroconversion.

\(^2\)HPD is the highest posterior density interval, which represents the most compact interval on the selected parameter that contains 95% of the posterior probability. It is a Bayesian analog to a confidence interval.

\(^3\)ESS: Effective Sample Size – should be higher than 100, and characterizes the posterior distribution.

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leading to transmission of multiple viral variants could improve public health strategies aimed at containing and containing the spread of HIV. The extent of transmission of multiple viral variants in local epidemics should be taken into account in the design and testing of HIV vaccine candidates.

In summary, the study suggests a two-step strategy for identification of multiplicity of HIV infection based on sequences of viral quasispecies obtained within 50 days p/s. This approach enables the resolution of transmission of single or multiple viral variants in nearly all analyzed samples.

References


